**NetMHCII 2.0 Server - prediction results**

**Technical University of Denmark**

---

```
# Input is in FSA format
        NetMHCII version 2.0.

Strong binder threshold  50.00. Weak binder threshold 500.00.

------------------------------------------------------------------------------------------------
      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
------------------------------------------------------------------------------------------------
   DRB1_0101  140  PANIMISATNAVKVM  IMISATNAV        0.8537          4.9         SB      2.00     Sequence
   DRB1_0101  139  KPANIMISATNAVKV  NIMISATNA        0.8534          4.9         SB      2.00     Sequence
   DRB1_0101  328  VGRWVAVVAVLAVLT  WVAVVAVLA        0.8434          5.4         SB      4.00     Sequence
   DRB1_0101  327  SVGRWVAVVAVLAVL  WVAVVAVLA        0.8403          5.6         SB      4.00     Sequence
   DRB1_0101  141  ANIMISATNAVKVMD  IMISATNAV        0.8398          5.7         SB      4.00     Sequence
   DRB1_0101  326  GSVGRWVAVVAVLAV  WVAVVAVLA        0.8390          5.7         SB      4.00     Sequence
   DRB1_0101  142  NIMISATNAVKVMDF  ISATNAVKV        0.8369          5.8         SB      4.00     Sequence
   DRB1_0101   29  DLRLHRDVAVKVLRA  LHRDVAVKV        0.8319          6.2         SB      4.00     Sequence
   DRB1_0101  325  IGSVGRWVAVVAVLA  WVAVVAVLA        0.8284          6.4         SB      4.00     Sequence
   DRB1_0101   30  LRLHRDVAVKVLRAD  LHRDVAVKV        0.8266          6.5         SB      4.00     Sequence
   DRB1_0101   33  HRDVAVKVLRADLAR  VKVLRADLA        0.8264          6.5         SB      4.00     Sequence
   DRB1_0101   34  RDVAVKVLRADLARD  VKVLRADLA        0.8230          6.8         SB      4.00     Sequence
   DRB1_0101   35  DVAVKVLRADLARDP  VKVLRADLA        0.8225          6.8         SB      4.00     Sequence
   DRB1_0101   20  GMSEVHLARDLRLHR  VHLARDLRL        0.8208          6.9         SB      8.00     Sequence
   DRB1_0101   21  MSEVHLARDLRLHRD  VHLARDLRL        0.8208          7.0         SB      8.00     Sequence
   DRB1_0101  259  ENRYQTAAEMRADLV  YQTAAEMRA        0.8170          7.2         SB      8.00     Sequence
   DRB1_0101  329  GRWVAVVAVLAVLTV  WVAVVAVLA        0.8164          7.3         SB      8.00     Sequence
   DRB1_0101  138  VKPANIMISATNAVK  NIMISATNA        0.8147          7.4         SB      8.00     Sequence
   DRB1_0101   88  YIVMEYVDGVTLRDI  MEYVDGVTL        0.8130          7.6         SB      8.00     Sequence
   DRB1_0101  482  VVIIIVGSGPATKDI  IIVGSGPAT        0.8114          7.7         SB      8.00     Sequence
   DRB1_0101   36  VAVKVLRADLARDPS  VKVLRADLA        0.8105          7.8         SB      8.00     Sequence
   DRB1_0101  290  AERTSLLSSAAGNLS  TSLLSSAAG        0.8055          8.2         SB      8.00     Sequence
   DRB1_0101   52  YLRFRREAQNAAALN  FRREAQNAA        0.7995          8.7         SB      8.00     Sequence
   DRB1_0101   32  LHRDVAVKVLRADLA  VKVLRADLA        0.7995          8.8         SB      8.00     Sequence
   DRB1_0101  480  TNVVIIIVGSGPATK  IIVGSGPAT        0.7983          8.9         SB      8.00     Sequence
   DRB1_0101  143  IMISATNAVKVMDFG  ISATNAVKV        0.7982          8.9         SB      8.00     Sequence
   DRB1_0101   28  RDLRLHRDVAVKVLR  LHRDVAVKV        0.7975          8.9         SB      8.00     Sequence
   DRB1_0101  260  NRYQTAAEMRADLVR  YQTAAEMRA        0.7968          9.0         SB      8.00     Sequence
   DRB1_0101   27  ARDLRLHRDVAVKVL  LRLHRDVAV        0.7960          9.1         SB      8.00     Sequence
   DRB1_0101  330  RWVAVVAVLAVLTVV  WVAVVAVLA        0.7929          9.4         SB      8.00     Sequence
   DRB1_0101  372  AIATLQNRGFKIRTL  TLQNRGFKI        0.7917          9.5         SB      8.00     Sequence
   DRB1_0101  481  NVVIIIVGSGPATKD  IIVGSGPAT        0.7868         10.0         SB      8.00     Sequence
   DRB1_0101  291  ERTSLLSSAAGNLSG  LLSSAAGNL        0.7865         10.1         SB      8.00     Sequence
   DRB1_0101   31  RLHRDVAVKVLRADL  LHRDVAVKV        0.7864         10.1         SB      8.00     Sequence
   DRB1_0101  151  VKVMDFGIARAIADS  MDFGIARAI        0.7854         10.2         SB      8.00     Sequence
   DRB1_0101   86  LPYIVMEYVDGVTLR  MEYVDGVTL        0.7803         10.8         SB      8.00     Sequence
   DRB1_0101  293  TSLLSSAAGNLSGPR  LSSAAGNLS        0.7782         11.0         SB     16.00     Sequence
   DRB1_0101  292  RTSLLSSAAGNLSGP  LLSSAAGNL        0.7764         11.2         SB     16.00     Sequence
   DRB1_0101  289  DAERTSLLSSAAGNL  TSLLSSAAG        0.7734         11.6         SB     16.00     Sequence
   DRB1_0101  152  KVMDFGIARAIADSG  MDFGIARAI        0.7733         11.6         SB     16.00     Sequence
   DRB1_0101  137  DVKPANIMISATNAV  NIMISATNA        0.7730         11.7         SB     16.00     Sequence
   DRB1_0101  331  WVAVVAVLAVLTVVV  WVAVVAVLA        0.7692         12.1         SB     16.00     Sequence
   DRB1_0101   22  SEVHLARDLRLHRDV  VHLARDLRL        0.7690         12.2         SB     16.00     Sequence
   DRB1_0101  153  VMDFGIARAIADSGN  FGIARAIAD        0.7690         12.2         SB     16.00     Sequence
   DRB1_0101   53  LRFRREAQNAAALNH  FRREAQNAA        0.7680         12.3         SB     16.00     Sequence
```

```
DRB1_0101   14  EILGFGGMSEVHLAR  FGGMSEVHL         0.7670          12.4          SB    16.00     Sequence
DRB1_0101  261  RYQTAAEMRADLVRV  YQTAAEMRA         0.7653          12.7          SB    16.00     Sequence
DRB1_0101   15  ILGFGGMSEVHLARD  FGGMSEVHL         0.7644          12.8          SB    16.00     Sequence
DRB1_0101  483  VIIIVGSGPATKDIP  IIVGSGPAT         0.7633          12.9          SB    16.00     Sequence
DRB1_0101   19  GGMSEVHLARDLRLH  VHLARDLRL         0.7628          13.0          SB    16.00     Sequence
DRB1_0101   89  IVMEYVDGVTLRDIV  MEYVDGVTL         0.7616          13.2          SB    16.00     Sequence
DRB1_0101  150  AVKVMDFGIARAIAD  MDFGIARAI         0.7592          13.5          SB    16.00     Sequence
DRB1_0101   37  AVKVLRADLARDPSF  VKVLRADLA         0.7580          13.7          SB    16.00     Sequence
DRB1_0101   51  FYLRFRREAQNAAAL  FRREAQNAA         0.7562          14.0          SB    16.00     Sequence
DRB1_0101   87  PYIVMEYVDGVTLRD  MEYVDGVTL         0.7550          14.2          SB    16.00     Sequence
DRB1_0101  373  IATLQNRGFKIRTLQ  TLQNRGFKI         0.7528          14.5          SB    16.00     Sequence
DRB1_0101  149  NAVKVMDFGIARAIA  MDFGIARAI         0.7511          14.8          SB    16.00     Sequence
DRB1_0101   85  PLPYIVMEYVDGVTL  YIVMEYVDG         0.7502          14.9          SB    16.00     Sequence
DRB1_0101  258  PENRYQTAAEMRADL  YQTAAEMRA         0.7485          15.2          SB    16.00     Sequence
DRB1_0101  371  DAIATLQNRGFKIRT  TLQNRGFKI         0.7440          16.0          SB    16.00     Sequence
DRB1_0101  448  FGRFKQANSPSTPEL  FKQANSPST         0.7437          16.0          SB    16.00     Sequence
DRB1_0101  203  CVLYEVLTGEPPFTG  YEVLTGEPP         0.7436          16.0          SB    16.00     Sequence
DRB1_0101  479  ITNVVIIIVGSGPAT  VIIIVGSGP         0.7404          16.6          SB    16.00     Sequence
DRB1_0101  557  GNQFVMPDLSGMFWV  FVMPDLSGM         0.7397          16.7          SB    16.00     Sequence
DRB1_0101  370  ADAIATLQNRGFKIR  IATLQNRGF         0.7384          17.0          SB    16.00     Sequence
DRB1_0101  262  YQTAAEMRADLVRVH  AAEMRADLV         0.7323          18.1          SB    16.00     Sequence
DRB1_0101   13  GEILGFGGMSEVHLA  FGGMSEVHL         0.7303          18.5          SB    16.00     Sequence
DRB1_0101  294  SLLSSAAGNLSGPRT  LSSAAGNLS         0.7231          20.0          SB    16.00     Sequence
DRB1_0101  502  QTVDVAQKNLNVYGF  DVAQKNLNV         0.7229          20.1          SB    16.00     Sequence
DRB1_0101  212  EPPFTGDSPVSVAYQ  FTGDSPVSV         0.7226          20.1          SB    16.00     Sequence
DRB1_0101  148  TNAVKVMDFGIARAI  MDFGIARAI         0.7209          20.5          SB    16.00     Sequence
DRB1_0101   16  LGFGGMSEVHLARDL  FGGMSEVHL         0.7189          20.9          SB    16.00     Sequence
DRB1_0101   18  FGGMSEVHLARDLRL  VHLARDLRL         0.7180          21.1          SB    16.00     Sequence
DRB1_0101  154  MDFGIARAIADSGNS  FGIARAIAD         0.7138          22.1          SB    16.00     Sequence
DRB1_0101  144  MISATNAVKVMDFGI  ISATNAVKV         0.7133          22.2          SB    16.00     Sequence
DRB1_0101  340  VLTVVVTIAINTFGG  VVVTIAINT         0.7119          22.6          SB    16.00     Sequence
DRB1_0101  599  HNRVVYQNPPAGTGV  VVYQNPPAG         0.7112          22.8          SB    16.00     Sequence
DRB1_0101   54  RFRREAQNAAALNHP  FRREAQNAA         0.7072          23.8          SB    32.00     Sequence
DRB1_0101  332  VAVVAVLAVLTVVVT  VVAVLAVLT         0.7040          24.6          SB    32.00     Sequence
DRB1_0101   23  EVHLARDLRLHRDVA  VHLARDLRL         0.7033          24.8          SB    32.00     Sequence
DRB1_0101  558  NQFVMPDLSGMFWVD  FVMPDLSGM         0.7027          24.9          SB    32.00     Sequence
DRB1_0101  437  AEAVKKLTAAGFGRF  VKKLTAAGF         0.7021          25.1          SB    32.00     Sequence
DRB1_0101  202  GCVLYEVLTGEPPFT  YEVLTGEPP         0.7008          25.5          SB    32.00     Sequence
DRB1_0101  567  GMFWVDAEPRLRALG  WVDAEPRLR         0.7005          25.5          SB    32.00     Sequence
DRB1_0101  473  ANQTSAITNVVIIIV  TSAITNVVI         0.7002          25.6          SB    32.00     Sequence
DRB1_0101   38  VKVLRADLARDPSFY  VKVLRADLA         0.6992          25.9          SB    32.00     Sequence
DRB1_0101  204  VLYEVLTGEPPFTGD  YEVLTGEPP         0.6992          25.9          SB    32.00     Sequence
DRB1_0101   12  LGEILGFGGMSEVHL  FGGMSEVHL         0.6987          26.0          SB    32.00     Sequence
DRB1_0101   90  VMEYVDGVTLRDIVH  MEYVDGVTL         0.6970          26.5          SB    32.00     Sequence
DRB1_0101  374  ATLQNRGFKIRTLQK  TLQNRGFKI         0.6950          27.1          SB    32.00     Sequence
DRB1_0101  484  IIIVGSGPATKDIPD  IIVGSGPAT         0.6948          27.2          SB    32.00     Sequence
DRB1_0101  556  KGNQFVMPDLSGMFW  FVMPDLSGM         0.6940          27.4          SB    32.00     Sequence
DRB1_0101   26  LARDLRLHRDVAVKV  LRLHRDVAV         0.6938          27.5          SB    32.00     Sequence
DRB1_0101  566  SGMFWVDAEPRLRAL  WVDAEPRLR         0.6934          27.6          SB    32.00     Sequence
DRB1_0101  213  PPFTGDSPVSVAYQH  FTGDSPVSV         0.6929          27.7          SB    32.00     Sequence
DRB1_0101  600  NRVVYQNPPAGTGVN  VYQNPPAGT         0.6926          27.8          SB    32.00     Sequence
DRB1_0101  136  RDVKPANIMISATNA  NIMISATNA         0.6924          27.9          SB    32.00     Sequence
DRB1_0101  339  AVLTVVVTIAINTFG  VVVTIAINT         0.6882          29.2          SB    32.00     Sequence
DRB1_0101  166  GNSVTQTAAVIGTAQ  VTQTAAVIG         0.6862          29.8          SB    32.00     Sequence
DRB1_0101  341  LTVVVTIAINTFGGI  VVVTIAINT         0.6783          32.5          SB    32.00     Sequence
DRB1_0101   58  EAQNAAALNHPAIVA  NAAALNHPA         0.6752          33.6          SB    32.00     Sequence
DRB1_0101  288  TDAERTSLLSSAAGN  TSLLSSAAG         0.6707          35.3          SB    32.00     Sequence
DRB1_0101  361  VPDVRGQSSADAIAT  VRGQSSADA         0.6703          35.4          SB    32.00     Sequence
DRB1_0101  333  AVVAVLAVLTVVVTI  VVAVLAVLT         0.6684          36.2          SB    32.00     Sequence
DRB1_0101  449  GRFKQANSPSTPELV  FKQANSPST         0.6683          36.2          SB    32.00     Sequence
DRB1_0101  338  LAVLTVVVTIAINTF  VVVTIAINT         0.6680          36.3          SB    32.00     Sequence
DRB1_0101  285  KVLTDAERTSLLSSA  TDAERTSLL         0.6673          36.6          SB    32.00     Sequence
DRB1_0101  555  SKGNQFVMPDLSGMF  FVMPDLSGM         0.6668          36.8          SB    32.00     Sequence
DRB1_0101   50  SFYLRFRREAQNAAA  FRREAQNAA         0.6663          37.0          SB    32.00     Sequence
DRB1_0101  211  GEPPFTGDSPVSVAY  FTGDSPVSV         0.6650          37.5          SB    32.00     Sequence
DRB1_0101  165  SGNSVTQTAAVIGTA  SVTQTAAVI         0.6621          38.7          SB    32.00     Sequence
```

```
DRB1_0101  568  MFWVDAEPRLRALGW  WVDAEPRLR        0.6605         39.4         SB    32.00       Sequence
DRB1_0101  503  TVDVAQKNLNVYGFT  DVAQKNLNV        0.6600         39.6         SB    32.00       Sequence
DRB1_0101   84  GPLPYIVMEYVDGVT  YIVMEYVDG        0.6590         40.0         SB    32.00       Sequence
DRB1_0101  214  PFTGDSPVSVAYQHV  FTGDSPVSV        0.6588         40.1         SB    32.00       Sequence
DRB1_0101  559  QFVMPDLSGMFWVDA  FVMPDLSGM        0.6575         40.7         SB    32.00       Sequence
DRB1_0101  369  SADAIATLQNRGFKI  IATLQNRGF        0.6564         41.2         SB    32.00       Sequence
DRB1_0101  295  LLSSAAGNLSGPRTD  LSSAAGNLS        0.6552         41.7         SB    32.00       Sequence
DRB1_0101   24  VHLARDLRLHRDVAV  VHLARDLRL        0.6542         42.2         SB    32.00       Sequence
DRB1_0101   59  AQNAAALNHPAIVAV  NAAALNHPA        0.6538         42.3         SB    32.00       Sequence
DRB1_0101  432  STLTYAEAVKKLTAA  TYAEAVKKL        0.6533         42.6         SB    32.00       Sequence
DRB1_0101  472  PANQTSAITNVVIII  TSAITNVVI        0.6528         42.8         SB    32.00       Sequence
DRB1_0101  601  RVVYQNPPAGTGVNR  VYQNPPAGT        0.6516         43.4         SB    32.00       Sequence
DRB1_0101  565  LSGMFWVDAEPRLRA  MFWVDAEPR        0.6490         44.6         SB    32.00       Sequence
DRB1_0101   17  GFGGMSEVHLARDLR  FGGMSEVHL        0.6480         45.1         SB    32.00       Sequence
DRB1_0101  431  VSTLTYAEAVKKLTA  TYAEAVKKL        0.6461         46.0         SB    32.00       Sequence
DRB1_0101  438  EAVKKLTAAGFGRFK  VKKLTAAGF        0.6443         46.9         SB    32.00       Sequence
DRB1_0101  474  NQTSAITNVVIIIVG  TSAITNVVI        0.6440         47.1         SB    32.00       Sequence
DRB1_0101  501  GQTVDVAQKNLNVYG  DVAQKNLNV        0.6434         47.4         SB    32.00       Sequence
DRB1_0101  205  LYEVLTGEPPFTGDS  YEVLTGEPP        0.6422         48.0         SB    32.00       Sequence
DRB1_0101  257  NPENRYQTAAEMRAD  YQTAAEMRA        0.6420         48.1         SB    32.00       Sequence
DRB1_0101  256  KNPENRYQTAAEMRA  YQTAAEMRA        0.6420         48.1         SB    32.00       Sequence
DRB1_0101  436  YAEAVKKLTAAGFGR  VKKLTAAGF        0.6419         48.1         SB    32.00       Sequence
DRB1_0101  342  TVVVTIAINTFGGIT  VTIAINTFG        0.6389         49.8         SB    32.00       Sequence
DRB1_0101  334  VVAVLAVLTVVVTIA  VVAVLAVLT        0.6360         51.4         WB    32.00       Sequence
DRB1_0101  478  AITNVVIIIVGSGPA  VIIIVGSGP        0.6324         53.4         WB    32.00       Sequence
DRB1_0101  574  EPRLRALGWTGMLDK  LRALGWTGM        0.6288         55.5         WB    32.00       Sequence
DRB1_0101  375  TLQNRGFKIRTLQKP  TLQNRGFKI        0.6280         56.0         WB    32.00       Sequence
DRB1_0101  145  ISATNAVKVMDFGIA  ISATNAVKV        0.6264         56.9         WB    32.00       Sequence
DRB1_0101   55  FRREAQNAAALNHPA  FRREAQNAA        0.6264         57.0         WB    32.00       Sequence
DRB1_0101  201  LGCVLYEVLTGEPPF  YEVLTGEPP        0.6259         57.2         WB    32.00       Sequence
DRB1_0101  447  GFGRFKQANSPSTPE  FKQANSPST        0.6258         57.3         WB    32.00       Sequence
DRB1_0101   49  PSFYLRFRREAQNAA  FRREAQNAA        0.6236         58.7         WB    32.00       Sequence
DRB1_0101  337  VLAVLTVVVTIAINT  LTVVVTIAI        0.6208         60.5         WB    32.00       Sequence
DRB1_0101   42  RADLARDPSFYLRFR  LARDPSFYL        0.6192         61.5         WB    32.00       Sequence
DRB1_0101  215  FTGDSPVSVAYQHVR  FTGDSPVSV        0.6186         62.0         WB    32.00       Sequence
DRB1_0101  579  ALGWTGMLDKGADVD  WTGMLDKGA        0.6163         63.6         WB    32.00       Sequence
DRB1_0101  450  RFKQANSPSTPELVG  FKQANSPST        0.6162         63.6         WB    32.00       Sequence
DRB1_0101  578  RALGWTGMLDKGADV  WTGMLDKGA        0.6153         64.2         WB    32.00       Sequence
DRB1_0101  167  NSVTQTAAVIGTAQY  VTQTAAVIG        0.6135         65.5         WB    32.00       Sequence
DRB1_0101   60  QNAAALNHPAIVAVY  NAAALNHPA        0.6130         65.9         WB    32.00       Sequence
DRB1_0101  169  VTQTAAVIGTAQYLS  TAAVIGTAQ        0.6107         67.5         WB    32.00       Sequence
DRB1_0101   91  MEYVDGVTLRDIVHT  MEYVDGVTL        0.6099         68.1         WB    32.00       Sequence
DRB1_0101  335  VAVLAVLTVVVTIAI  VLAVLTVVV        0.6093         68.5         WB    32.00       Sequence
DRB1_0101  512  NVYGFTKFSQASVDS  FTKFSQASV        0.6083         69.2         WB    32.00       Sequence
DRB1_0101  287  LTDAERTSLLSSAAG  TSLLSSAAG        0.6080         69.5         WB    32.00       Sequence
DRB1_0101  513  VYGFTKFSQASVDSP  FTKFSQASV        0.6079         69.5         WB    32.00       Sequence
DRB1_0101  263  QTAAEMRADLVRVHN  AAEMRADLV        0.6077         69.8         WB    32.00       Sequence
DRB1_0101  284  PKVLTDAERTSLLSS  TDAERTSLL        0.6044         72.2         WB    32.00       Sequence
DRB1_0101  164  DSGNSVTQTAAVIGT  SVTQTAAVI        0.6021         74.1         WB    32.00       Sequence
DRB1_0101  282  EAPKVLTDAERTSLL  KVLTDAERT        0.6010         75.0         WB    50.00       Sequence
DRB1_0101  343  VVVTIAINTFGGITR  TIAINTFGG        0.6000         75.8         WB    50.00       Sequence
DRB1_0101  194  ARSDVYSLGCVLYEV  DVYSLGCVL        0.5999         75.8         WB    50.00       Sequence
DRB1_0101  155  DFGIARAIADSGNSV  FGIARAIAD        0.5998         76.0         WB    50.00       Sequence
DRB1_0101  439  AVKKLTAAGFGRFKQ  VKKLTAAGF        0.5990         76.6         WB    50.00       Sequence
DRB1_0101  336  AVLAVLTVVVTIAIN  LTVVVTIAI        0.5990         76.6         WB    50.00       Sequence
DRB1_0101  433  TLTYAEAVKKLTAAG  TYAEAVKKL        0.5985         77.0         WB    50.00       Sequence
DRB1_0101  572  DAEPRLRALGWTGML  LRALGWTGM        0.5978         77.6         WB    50.00       Sequence
DRB1_0101  286  VLTDAERTSLLSSAA  TDAERTSLL        0.5969         78.4         WB    50.00       Sequence
DRB1_0101  573  AEPRLRALGWTGMLD  LRALGWTGM        0.5956         79.4         WB    50.00       Sequence
DRB1_0101  560  FVMPDLSGMFWVDAE  FVMPDLSGM        0.5938         81.1         WB    50.00       Sequence
DRB1_0101   83  AGPLPYIVMEYVDGV  YIVMEYVDG        0.5931         81.6         WB    50.00       Sequence
DRB1_0101  283  APKVLTDAERTSLLS  KVLTDAERT        0.5924         82.3         WB    50.00       Sequence
DRB1_0101   99  LRDIVHTEGPMTPKR  IVHTEGPMT        0.5921         82.6         WB    50.00       Sequence
DRB1_0101  362  PDVRGQSSADAIATL  VRGQSSADA        0.5920         82.6         WB    50.00       Sequence
DRB1_0101  485  IIVGSGPATKDIPDV  IIVGSGPAT        0.5917         82.9         WB    50.00       Sequence
DRB1_0101  321  RDRSIGSVGRWVAVV  SIGSVGRWV        0.5910         83.5         WB    50.00       Sequence
```

```
DRB1_0101  445  AAGFGRFKQANSPST  FKQANSPST       0.5904        84.0        WB    50.00     Sequence
DRB1_0101  446  AGFGRFKQANSPSTP  FKQANSPST       0.5895        84.9        WB    50.00     Sequence
DRB1_0101  598  QHNRVVYQNPPAGTG  VVYQNPPAG       0.5895        84.9        WB    50.00     Sequence
DRB1_0101  576  RLRALGWTGMLDKGA  LRALGWTGM       0.5864        87.8        WB    50.00     Sequence
DRB1_0101  240  EGLSADLDAVVLKAL  SADLDAVVL       0.5862        88.0        WB    50.00     Sequence
DRB1_0101  500  AGQTVDVAQKNLNVY  DVAQKNLNV       0.5856        88.6        WB    50.00     Sequence
DRB1_0101  171  QTAAVIGTAQYLSPE  AVIGTAQYL       0.5853        88.8        WB    50.00     Sequence
DRB1_0101   57  REAQNAAALNHPAIV  NAAALNHPA       0.5852        88.9        WB    50.00     Sequence
DRB1_0101  324  SIGSVGRWVAVVAVL  GRWVAVVAV       0.5841        90.0        WB    50.00     Sequence
DRB1_0101  475  QTSAITNVVIIIVGS  TSAITNVVI       0.5838        90.3        WB    50.00     Sequence
DRB1_0101  504  VDVAQKNLNVYGFTK  DVAQKNLNV       0.5830        91.1        WB    50.00     Sequence
DRB1_0101  429  PDVSTLTYAEAVKKL  STLTYAEAV       0.5829        91.2        WB    50.00     Sequence
DRB1_0101  430  DVSTLTYAEAVKKLT  STLTYAEAV       0.5822        91.8        WB    50.00     Sequence
DRB1_0101  435  TYAEAVKKLTAAGFG  VKKLTAAGF       0.5814        92.7        WB    50.00     Sequence
DRB1_0101  546  VDSVIELQVSKGNQF  VIELQVSKG       0.5807        93.4        WB    50.00     Sequence
DRB1_0101  364  VRGQSSADAIATLQN  VRGQSSADA       0.5794        94.7        WB    50.00     Sequence
DRB1_0101  510  NLNVYGFTKFSQASV  YGFTKFSQA       0.5794        94.7        WB    50.00     Sequence
DRB1_0101  360  QVPDVRGQSSADAIA  VRGQSSADA       0.5791        95.0        WB    50.00     Sequence
DRB1_0101    5  HLSDRYELGEILGFG  DRYELGEIL       0.5788        95.4        WB    50.00     Sequence
DRB1_0101  168  SVTQTAAVIGTAQYL  TAAVIGTAQ       0.5782        95.9        WB    50.00     Sequence
DRB1_0101  511  LNVYGFTKFSQASVD  YGFTKFSQA       0.5782        96.0        WB    50.00     Sequence
DRB1_0101  170  TQTAAVIGTAQYLSP  AVIGTAQYL       0.5777        96.5        WB    50.00     Sequence
DRB1_0101  100  RDIVHTEGPMTPKRA  VHTEGPMTP       0.5775        96.7        WB    50.00     Sequence
DRB1_0101  195  RSDVYSLGCVLYEVL  DVYSLGCVL       0.5757        98.6        WB    50.00     Sequence
DRB1_0101  323  RSIGSVGRWVAVVAV  SIGSVGRWV       0.5742       100.2        WB    50.00     Sequence
DRB1_0101  471  PPANQTSAITNVVII  TSAITNVVI       0.5737       100.7        WB    50.00     Sequence
DRB1_0101  434  LTYAEAVKKLTAAGF  TYAEAVKKL       0.5728       101.7        WB    50.00     Sequence
DRB1_0101  575  PRLRALGWTGMLDKG  LRALGWTGM       0.5704       104.4        WB    50.00     Sequence
DRB1_0101  156  FGIARAIADSGNSVT  FGIARAIAD       0.5700       104.8        WB    50.00     Sequence
DRB1_0101  363  DVRGQSSADAIATLQ  VRGQSSADA       0.5683       106.8        WB    50.00     Sequence
DRB1_0101   61  NAAALNHPAIVAVYD  NAAALNHPA       0.5663       109.2        WB    50.00     Sequence
DRB1_0101  569  FWVDAEPRLRALGWT  WVDAEPRLR       0.5653       110.3        WB    50.00     Sequence
DRB1_0101  322  DRSIGSVGRWVAVVA  SIGSVGRWV       0.5645       111.3        WB    50.00     Sequence
DRB1_0101  320  DRDRSIGSVGRWVAV  SIGSVGRWV       0.5636       112.3        WB    50.00     Sequence
DRB1_0101  564  DLSGMFWVDAEPRLR  MFWVDAEPR       0.5625       113.7        WB    50.00     Sequence
DRB1_0101  477  SAITNVVIIIVGSGP  ITNVVIIIV       0.5604       116.4        WB    50.00     Sequence
DRB1_0101   62  AAALNHPAIVAVYDT  LNHPAIVAV       0.5601       116.7        WB    50.00     Sequence
DRB1_0101  210  TGEPPFTGDSPVSVA  FTGDSPVSV       0.5592       117.8        WB    50.00     Sequence
DRB1_0101  241  GLSADLDAVVLKALA  SADLDAVVL       0.5581       119.3        WB    50.00     Sequence
DRB1_0101  200  SLGCVLYEVLTGEPP  YEVLTGEPP       0.5569       120.8        WB    50.00     Sequence
DRB1_0101  554  VSKGNQFVMPDLSGM  FVMPDLSGM       0.5568       120.9        WB    50.00     Sequence
DRB1_0101  547  DSVIELQVSKGNQFV  IELQVSKGN       0.5549       123.4        WB    50.00     Sequence
DRB1_0101  113  RAIEVIADACQALNF  EVIADACQA       0.5545       124.0        WB    50.00     Sequence
DRB1_0101   25  HLARDLRLHRDVAVK  LRLHRDVAV       0.5508       129.0        WB    50.00     Sequence
DRB1_0101  206  YEVLTGEPPFTGDSP  YEVLTGEPP       0.5486       132.1        WB    50.00     Sequence
DRB1_0101  602  VVYQNPPAGTGVNRD  VYQNPPAGT       0.5485       132.2        WB    50.00     Sequence
DRB1_0101  163  ADSGNSVTQTAAVIG  SVTQTAAVI       0.5481       132.9        WB    50.00     Sequence
DRB1_0101  580  LGWTGMLDKGADVDA  WTGMLDKGA       0.5450       137.5        WB    50.00     Sequence
DRB1_0101  440  VKKLTAAGFGRFKQA  VKKLTAAGF       0.5441       138.7        WB    50.00     Sequence
DRB1_0101  124  ALNFSHQNGIIHRDV  FSHQNGIIH       0.5425       141.2        WB    50.00     Sequence
DRB1_0101  243  SADLDAVVLKALAKN  LDAVVLKAL       0.5416       142.6        WB    50.00     Sequence
DRB1_0101  264  TAAEMRADLVRVHNG  AAEMRADLV       0.5405       144.3        WB    50.00     Sequence
DRB1_0101  193  DARSDVYSLGCVLYE  DVYSLGCVL       0.5402       144.7        WB    50.00     Sequence
DRB1_0101  548  SVIELQVSKGNQFVM  IELQVSKGN       0.5401       144.9        WB    50.00     Sequence
DRB1_0101  247  DAVVLKALAKNPENR  VLKALAKNP       0.5401       145.0        WB    50.00     Sequence
DRB1_0101  242  LSADLDAVVLKALAK  LDAVVLKAL       0.5397       145.5        WB    50.00     Sequence
DRB1_0101  476  TSAITNVVIIIVGSG  TSAITNVVI       0.5379       148.4        WB    50.00     Sequence
DRB1_0101  462  LVGKVIGTNPPANQT  KVIGTNPPA       0.5357       151.9        WB    50.00     Sequence
DRB1_0101  319  TDRDRSIGSVGRWVA  SIGSVGRWV       0.5356       152.2        WB    50.00     Sequence
DRB1_0101  296  LSSAAGNLSGPRTDP  LSSAAGNLS       0.5355       152.3        WB    50.00     Sequence
DRB1_0101  172  TAAVIGTAQYLSPEQ  AVIGTAQYL       0.5336       155.4        WB    50.00     Sequence
DRB1_0101   48  DPSFYLRFRREAQNA  YLRFRREAQ       0.5335       155.6        WB    50.00     Sequence
DRB1_0101  245  DLDAVVLKALAKNPE  AVVLKALAK       0.5335       155.6        WB    50.00     Sequence
DRB1_0101  451  FKQANSPSTPELVGK  FKQANSPST       0.5335       155.7        WB    50.00     Sequence
DRB1_0101  577  LRALGWTGMLDKGAD  WTGMLDKGA       0.5326       157.2        WB    50.00     Sequence
DRB1_0101  196  SDVYSLGCVLYEVLT  VYSLGCVLY       0.5326       157.2        WB    50.00     Sequence
```

```
DRB1_0101  132  GIIHRDVKPANIMIS  HRDVKPANI         0.5325         157.3          WB    50.00      Sequence
DRB1_0101   11  ELGEILGFGGMSEVH  ILGFGGMSE         0.5311         159.8          WB    50.00      Sequence
DRB1_0101    4  SHLSDRYELGEILGF  DRYELGEIL         0.5306         160.6          WB    50.00      Sequence
DRB1_0101  246  LDAVVLKALAKNPEN  AVVLKALAK         0.5291         163.3          WB    50.00      Sequence
DRB1_0101  105  TEGPMTPKRAIEVIA  MTPKRAIEV         0.5289         163.6          WB    50.00      Sequence
DRB1_0101  244  ADLDAVVLKALAKNP  LDAVVLKAL         0.5287         163.9          WB    50.00      Sequence
DRB1_0101  597  SQHNRVVYQNPPAGT  VVYQNPPAG         0.5278         165.6          WB    50.00      Sequence
DRB1_0101  248  AVVLKALAKNPENRY  VLKALAKNP         0.5251         170.4          WB    50.00      Sequence
DRB1_0101  106  EGPMTPKRAIEVIAD  MTPKRAIEV         0.5251         170.5          WB    50.00      Sequence
DRB1_0101   43  ADLARDPSFYLRFRR  LARDPSFYL         0.5235         173.5          WB    50.00      Sequence
DRB1_0101  134  IHRDVKPANIMISAT  DVKPANIMI         0.5231         174.1          WB    50.00      Sequence
DRB1_0101  514  YGFTKFSQASVDSPR  FTKFSQASV         0.5230         174.4          WB    50.00      Sequence
DRB1_0101  239  HEGLSADLDAVVLKA  SADLDAVVL         0.5227         174.8          WB    50.00      Sequence
DRB1_0101  368  SSADAIATLQNRGFK  IATLQNRGF         0.5210         178.2          WB    50.00      Sequence
DRB1_0101   41  LRADLARDPSFYLRF  LARDPSFYL         0.5207         178.8          WB    50.00      Sequence
DRB1_0101    6  LSDRYELGEILGFGG  DRYELGEIL         0.5184         183.3          WB    50.00      Sequence
DRB1_0101  133  IIHRDVKPANIMISA  HRDVKPANI         0.5173         185.4          WB    50.00      Sequence
DRB1_0101  192  VDARSDVYSLGCVLY  DVYSLGCVL         0.5171         185.8          WB    50.00      Sequence
DRB1_0101  505  DVAQKNLNVYGFTKF  DVAQKNLNV         0.5145         191.1          WB    50.00      Sequence
DRB1_0101  197  DVYSLGCVLYEVLTG  SLGCVLYEV         0.5144         191.3          WB    50.00      Sequence
DRB1_0101   82  PAGPLPYIVMEYVDG  YIVMEYVDG         0.5133         193.7          WB    50.00      Sequence
DRB1_0101  344  VVTIAINTFGGITRD  TIAINTFGG         0.5129         194.4          WB    50.00      Sequence
DRB1_0101    9  RYELGEILGFGGMSE  LGEILGFGG         0.5120         196.3          WB    50.00      Sequence
DRB1_0101  428  IPDVSTLTYAEAVKK  VSTLTYAEA         0.5081         204.8          WB    50.00      Sequence
DRB1_0101  463  VGKVIGTNPPANQTS  VIGTNPPAN         0.5071         207.1          WB    50.00      Sequence
DRB1_0101  162  IADSGNSVTQTAAVI  SVTQTAAVI         0.5058         209.9          WB    50.00      Sequence
DRB1_0101  147  ATNAVKVMDFGIARA  VKVMDFGIA         0.5043         213.4          WB    50.00      Sequence
DRB1_0101  198  VYSLGCVLYEVLTGE  LGCVLYEVL         0.5023         218.1          WB    50.00      Sequence
DRB1_0101   63  AALNHPAIVAVYDTG  LNHPAIVAV         0.5001         223.5          WB    50.00      Sequence
DRB1_0101  112  KRAIEVIADACQALN  IEVIADACQ         0.4994         225.0          WB    50.00      Sequence
DRB1_0101  122  CQALNFSHQNGIIHR  LNFSHQNGI         0.4987         226.7          WB    50.00      Sequence
DRB1_0101  135  HRDVKPANIMISATN  VKPANIMIS         0.4972         230.5          WB    50.00      Sequence
DRB1_0101  470  NPPANQTSAITNVVI  TSAITNVVI         0.4962         233.0          WB    50.00      Sequence
DRB1_0101   98  TLRDIVHTEGPMTPK  IVHTEGPMT         0.4935         240.0          WB    50.00      Sequence
DRB1_0101    7  SDRYELGEILGFGGM  YELGEILGF         0.4918         244.5          WB    50.00      Sequence
DRB1_0101    8  DRYELGEILGFGGMS  LGEILGFGG         0.4917         244.5          WB    50.00      Sequence
DRB1_0101  114  AIEVIADACQALNFS  VIADACQAL         0.4917         244.7          WB    50.00      Sequence
DRB1_0101  199  YSLGCVLYEVLTGEP  LGCVLYEVL         0.4910         246.5          WB    50.00      Sequence
DRB1_0101  346  TIAINTFGGITRDVQ  INTFGGITR         0.4903         248.3          WB    50.00      Sequence
DRB1_0101   10  YELGEILGFGGMSEV  ILGFGGMSE         0.4877         255.5          WB    50.00      Sequence
DRB1_0101   80  ETPAGPLPYIVMEYV  AGPLPYIVM         0.4876         255.8          WB    50.00      Sequence
DRB1_0101  173  AAVIGTAQYLSPEQA  AVIGTAQYL         0.4875         256.1          WB    50.00      Sequence
DRB1_0101   79  AETPAGPLPYIVMEY  PAGPLPYIV         0.4862         259.6          WB    50.00      Sequence
DRB1_0101   47  RDPSFYLRFRREAQN  SFYLRFRRE         0.4861         259.9          WB    50.00      Sequence
DRB1_0101  131  NGIIHRDVKPANIMI  HRDVKPANI         0.4843         265.1          WB    50.00      Sequence
DRB1_0101  125  LNFSHQNGIIHRDVK  FSHQNGIIH         0.4838         266.5          WB    50.00      Sequence
DRB1_0101  107  GPMTPKRAIEVIADA  MTPKRAIEV         0.4836         267.1          WB    50.00      Sequence
DRB1_0101   56  RREAQNAAALNHPAI  NAAALNHPA         0.4825         270.2          WB    50.00      Sequence
DRB1_0101  238  RHEGLSADLDAVVLK  SADLDAVVL         0.4788         281.3          WB    50.00      Sequence
DRB1_0101  563  PDLSGMFWVDAEPRL  MFWVDAEPR         0.4785         282.0          WB    50.00      Sequence
DRB1_0101  359  VQVPDVRGQSSADAI  VRGQSSADA         0.4784         282.3          WB    50.00      Sequence
DRB1_0101  499  VAGQTVDVAQKNLNV  DVAQKNLNV         0.4783         282.7          WB    50.00      Sequence
DRB1_0101  376  LQNRGFKIRTLQKPD  NRGFKIRTL         0.4783         282.8          WB    50.00      Sequence
DRB1_0101   81  TPAGPLPYIVMEYVD  AGPLPYIVM         0.4776         284.9          WB    50.00      Sequence
DRB1_0101  549  VIELQVSKGNQFVMP  LQVSKGNQF         0.4776         284.9          WB    50.00      Sequence
DRB1_0101  571  VDAEPRLRALGWTGM  LRALGWTGM         0.4774         285.6          WB    50.00      Sequence
DRB1_0101  545  PVDSVIELQVSKGNQ  VIELQVSKG         0.4770         286.9          WB    50.00      Sequence
DRB1_0101  101  DIVHTEGPMTPKRAI  VHTEGPMTP         0.4769         287.0          WB    50.00      Sequence
DRB1_0101  103  VHTEGPMTPKRAIEV  EGPMTPKRA         0.4768         287.4          WB    50.00      Sequence
DRB1_0101   44  DLARDPSFYLRFRRE  LARDPSFYL         0.4756         291.1          WB    50.00      Sequence
DRB1_0101  509  KNLNVYGFTKFSQAS  YGFTKFSQA         0.4737         297.2          WB    50.00      Sequence
DRB1_0101  345  VTIAINTFGGITRDV  TIAINTFGG         0.4709         306.4          WB    50.00      Sequence
DRB1_0101   45  LARDPSFYLRFRREA  LARDPSFYL         0.4693         311.9          WB    50.00      Sequence
DRB1_0101  265  AAEMRADLVRVHNGE  AAEMRADLV         0.4687         313.8          WB    50.00      Sequence
DRB1_0101  347  IAINTFGGITRDVQV  TFGGITRDV         0.4684         314.7          WB    50.00      Sequence
DRB1_0101  318  DTDRDRSIGSVGRWV  SIGSVGRWV         0.4682         315.6          WB    50.00      Sequence
```

```
DRB1_0101  427  EIPDVSTLTYAEAVK  VSTLTYAEA         0.4675         317.7          WB     50.00      Sequence
DRB1_0101  104  HTEGPMTPKRAIEVI  MTPKRAIEV         0.4650         326.4          WB     50.00      Sequence
DRB1_0101  158  IARAIADSGNSVTQT  AIADSGNSV         0.4646         327.8          WB     50.00      Sequence
DRB1_0101  209  LTGEPPFTGDSPVSV  FTGDSPVSV         0.4646         328.1          WB     50.00      Sequence
DRB1_0101  516  FTKFSQASVDSPRPA  FSQASVDSP         0.4644         328.8          WB     50.00      Sequence
DRB1_0101  236  SARHEGLSADLDAVV  HEGLSADLD         0.4636         331.4          WB     50.00      Sequence
DRB1_0101  123  QALNFSHQNGIIHRD  FSHQNGIIH         0.4633         332.5          WB     50.00      Sequence
DRB1_0101  603  VYQNPPAGTGVNRDG  VYQNPPAGT         0.4625         335.6          WB     50.00      Sequence
DRB1_0101  378  NRGFKIRTLQKPDST  NRGFKIRTL         0.4619         337.6          WB     50.00      Sequence
DRB1_0101  237  ARHEGLSADLDAVVL  HEGLSADLD         0.4615         339.3          WB     50.00      Sequence
DRB1_0101  102  IVHTEGPMTPKRAIE  VHTEGPMTP         0.4586         349.8          WB     50.00      Sequence
DRB1_0101  367  QSSADAIATLQNRGF  IATLQNRGF         0.4558         360.7          WB     50.00      Sequence
DRB1_0101  452  KQANSPSTPELVGKV  NSPSTPELV         0.4555         361.9          WB     50.00      Sequence
DRB1_0101  174  AVIGTAQYLSPEQAR  AVIGTAQYL         0.4547         365.0          WB     50.00      Sequence
DRB1_0101  348  AINTFGGITRDVQVP  TFGGITRDV         0.4519         376.2          WB     50.00      Sequence
DRB1_0101  377  QNRGFKIRTLQKPDS  NRGFKIRTL         0.4504         382.3          WB     50.00      Sequence
DRB1_0101  130  QNGIIHRDVKPANIM  IIHRDVKPA         0.4504         382.4          WB     50.00      Sequence
DRB1_0101  515  GFTKFSQASVDSPRP  FTKFSQASV         0.4503         382.9          WB     50.00      Sequence
DRB1_0101  111  PKRAIEVIADACQAL  IEVIADACQ         0.4500         384.3          WB     50.00      Sequence
DRB1_0101  570  WVDAEPRLRALGWTG  WVDAEPRLR         0.4498         385.0          WB     50.00      Sequence
DRB1_0101   39  KVLRADLARDPSFYL  LRADLARDP         0.4484         390.6          WB     50.00      Sequence
DRB1_0101   46  ARDPSFYLRFRREAQ  SFYLRFRRE         0.4478         393.5          WB     50.00      Sequence
DRB1_0101    3  PSHLSDRYELGEILG  DRYELGEIL         0.4476         394.2          WB     50.00      Sequence
DRB1_0101  146  SATNAVKVMDFGIAR  VKVMDFGIA         0.4468         397.4          WB     50.00      Sequence
DRB1_0101   64  ALNHPAIVAVYDTGE  LNHPAIVAV         0.4462         400.2          WB     50.00      Sequence
DRB1_0101  175  VIGTAQYLSPEQARG  AQYLSPEQA         0.4456         402.7          WB     50.00      Sequence
DRB1_0101  108  PMTPKRAIEVIADAC  MTPKRAIEV         0.4453         404.1          WB     50.00      Sequence
DRB1_0101  281  PEAPKVLTDAERTSL  KVLTDAERT         0.4451         405.0          WB     50.00      Sequence
DRB1_0101  461  ELVGKVIGTNPPANQ  KVIGTNPPA         0.4446         407.1          WB     50.00      Sequence
DRB1_0101  191  SVDARSDVYSLGCVL  DVYSLGCVL         0.4441         409.6          WB     50.00      Sequence
DRB1_0101   92  EYVDGVTLRDIVHTE  YVDGVTLRD         0.4439         410.2          WB     50.00      Sequence
DRB1_0101  464  GKVIGTNPPANQTSA  VIGTNPPAN         0.4435         412.1          WB     50.00      Sequence
DRB1_0101  508  QKNLNVYGFTKFSQA  YGFTKFSQA         0.4433         413.0          WB     50.00      Sequence
DRB1_0101  581  GWTGMLDKGADVDAG  WTGMLDKGA         0.4431         413.9          WB     50.00      Sequence
DRB1_0101   78  EAETPAGPLPYIVME  PAGPLPYIV         0.4424         417.0          WB     50.00      Sequence
DRB1_0101  610  GTGVNRDGIITLRFG  RDGIITLRF         0.4410         423.4          WB     50.00      Sequence
DRB1_0101  398  VIGTDPAANTSVSAG  TDPAANTSV         0.4393         431.3          WB     50.00      Sequence
DRB1_0101  543  TVPVDSVIELQVSKG  VDSVIELQV         0.4392         431.7          WB     50.00      Sequence
DRB1_0101  395  PDHVIGTDPAANTSV  VIGTDPAAN         0.4392         431.7          WB     50.00      Sequence
DRB1_0101  611  TGVNRDGIITLRFGQ  RDGIITLRF         0.4378         438.1          WB     50.00      Sequence
DRB1_0101  544  VPVDSVIELQVSKGN  VIELQVSKG         0.4370         442.1          WB     50.00      Sequence
DRB1_0101  397  HVIGTDPAANTSVSA  VIGTDPAAN         0.4369         442.4          WB     50.00      Sequence
DRB1_0101  176  IGTAQYLSPEQARGD  AQYLSPEQA         0.4364         445.0          WB     50.00      Sequence
DRB1_0101  441  KKLTAAGFGRFKQAN  KLTAAGFGR         0.4345         454.3          WB     50.00      Sequence
DRB1_0101  121  ACQALNFSHQNGIIH  ALNFSHQNG         0.4341         456.1          WB     50.00      Sequence
DRB1_0101  506  VAQKNLNVYGFTKFS  QKNLNVYGF         0.4326         463.7          WB     50.00      Sequence
DRB1_0101  115  IEVIADACQALNFSH  EVIADACQA         0.4322         465.6          WB     50.00      Sequence
DRB1_0101  109  MTPKRAIEVIADACQ  MTPKRAIEV         0.4306         474.0          WB     50.00      Sequence
DRB1_0101  396  DHVIGTDPAANTSVS  VIGTDPAAN         0.4302         475.6          WB     50.00      Sequence
DRB1_0101  249  VVLKALAKNPENRYQ  VLKALAKNP         0.4302         475.9          WB     50.00      Sequence
DRB1_0101  609  AGTGVNRDGIITLRF  RDGIITLRF         0.4291         481.6          WB     50.00      Sequence
DRB1_0101   77  GEAETPAGPLPYIVM  PAGPLPYIV         0.4272         491.5          WB     50.00      Sequence
DRB1_0101    2  TPSHLSDRYELGEIL  DRYELGEIL         0.4264         495.7          WB     50.00      Sequence
DRB1_0101   40  VLRADLARDPSFYLR  LARDPSFYL         0.4238         509.8                 50.00      Sequence
DRB1_0101   97  VTLRDIVHTEGPMTP  IVHTEGPMT         0.4204         528.9                 50.00      Sequence
DRB1_0101  126  NFSHQNGIIHRDVKP  FSHQNGIIH         0.4201         530.6                 50.00      Sequence
DRB1_0101  562  MPDLSGMFWVDAEPR  MFWVDAEPR         0.4158         555.9                 50.00      Sequence
DRB1_0101   96  GVTLRDIVHTEGPMT  IVHTEGPMT         0.4151         560.4                 50.00      Sequence
DRB1_0101  426  REIPDVSTLTYAEAV  VSTLTYAEA         0.4148         561.8                 50.00      Sequence
DRB1_0101  157  GIARAIADSGNSVTQ  AIADSGNSV         0.4148         562.1                 50.00      Sequence
DRB1_0101   93  YVDGVTLRDIVHTEG  YVDGVTLRD         0.4139         567.5                 50.00      Sequence
DRB1_0101  379  RGFKIRTLQKPDSTI  IRTLQKPDS         0.4134         570.5                 50.00      Sequence
DRB1_0101  507  AQKNLNVYGFTKFSQ  QKNLNVYGF         0.4124         576.6                 50.00      Sequence
DRB1_0101  530  AGEVTGTNPPAGTTV  VTGTNPPAG         0.4080         605.2                 50.00      Sequence
DRB1_0101  272  LVRVHNGEPPEAPKV  VHNGEPPEA         0.4074         608.8                 50.00      Sequence
DRB1_0101  235  PSARHEGLSADLDAV  HEGLSADLD         0.4060         618.0                 50.00      Sequence
```

```
DRB1_0101  561  VMPDLSGMFWVDAEP  DLSGMFWVD        0.4043        629.4                50.00     Sequence
DRB1_0101  365  RGQSSADAIATLQNR  QSSADAIAT        0.4038        633.4                50.00     Sequence
DRB1_0101  380  GFKIRTLQKPDSTIP  IRTLQKPDS        0.4025        641.8                50.00     Sequence
DRB1_0101  442  KLTAAGFGRFKQANS  KLTAAGFGR        0.4009        653.2                50.00     Sequence
DRB1_0101  127  FSHQNGIIHRDVKPA  FSHQNGIIH        0.4003        657.5                50.00     Sequence
DRB1_0101  178  TAQYLSPEQARGDSV  YLSPEQARG        0.4003        657.8                50.00     Sequence
DRB1_0101  216  TGDSPVSVAYQHVRE  PVSVAYQHV        0.3986        669.9                50.00     Sequence
DRB1_0101  596  GSQHNRVVYQNPPAG  VVYQNPPAG        0.3970        681.3                50.00     Sequence
DRB1_0101   65  LNHPAIVAVYDTGEA  NHPAIVAVY        0.3969        682.2                50.00     Sequence
DRB1_0101  542  TTVPVDSVIELQVSK  VDSVIELQV        0.3966        684.5                50.00     Sequence
DRB1_0101  349  INTFGGITRDVQVPD  TFGGITRDV        0.3959        689.4                50.00     Sequence
DRB1_0101  582  WTGMLDKGADVDAGG  WTGMLDKGA        0.3958        690.4                50.00     Sequence
DRB1_0101  589  GADVDAGGSQHNRVV  VDAGGSQHN        0.3943        701.8                50.00     Sequence
DRB1_0101  387  QKPDSTIPPDHVIGT  DSTIPPDHV        0.3939        704.8                50.00     Sequence
DRB1_0101  255  AKNPENRYQTAAEMR  NRYQTAAEM        0.3939        704.9                50.00     Sequence
DRB1_0101  159  ARAIADSGNSVTQTA  AIADSGNSV        0.3936        707.4                50.00     Sequence
DRB1_0101  465  KVIGTNPPANQTSAI  VIGTNPPAN        0.3917        721.8                50.00     Sequence
DRB1_0101  217  GDSPVSVAYQHVRED  PVSVAYQHV        0.3908        728.9                50.00     Sequence
DRB1_0101  495  DIPDVAGQTVDVAQK  DVAGQTVDV        0.3849        776.8                50.00     Sequence
DRB1_0101  406  NTSVSAGDEITVNVS  VSAGDEITV        0.3801        818.7                50.00     Sequence
DRB1_0101  460  PELVGKVIGTNPPAN  KVIGTNPPA        0.3794        824.0                50.00     Sequence
DRB1_0101  455  NSPSTPELVGKVIGT  STPELVGKV        0.3793        825.7                50.00     Sequence
DRB1_0101  552  LQVSKGNQFVMPDLS  SKGNQFVMP        0.3777        839.6                50.00     Sequence
DRB1_0101  553  QVSKGNQFVMPDLSG  NQFVMPDLS        0.3772        844.1                50.00     Sequence
DRB1_0101  116  EVIADACQALNFSHQ  EVIADACQA        0.3760        855.8                50.00     Sequence
DRB1_0101  110  TPKRAIEVIADACQA  IEVIADACQ        0.3748        866.9                50.00     Sequence
DRB1_0101  550  IELQVSKGNQFVMPD  LQVSKGNQF        0.3737        876.7                50.00     Sequence
DRB1_0101  517  TKFSQASVDSPRPAG  FSQASVDSP        0.3733        880.9                50.00     Sequence
DRB1_0101  366  GQSSADAIATLQNRG  SADAIATLQ        0.3715        898.4                50.00     Sequence
DRB1_0101  358  DVQVPDVRGQSSADA  VRGQSSADA        0.3711        902.1                50.00     Sequence
DRB1_0101  219  SPVSVAYQHVREDPI  PVSVAYQHV        0.3698        915.0                50.00     Sequence
DRB1_0101  453  QANSPSTPELVGKVI  NSPSTPELV        0.3697        915.3                50.00     Sequence
DRB1_0101   71  VAVYDTGEAETPAGP  YDTGEAETP        0.3670        943.2                50.00     Sequence
DRB1_0101  120  DACQALNFSHQNGII  ALNFSHQNG        0.3666        946.6                50.00     Sequence
DRB1_0101  541  GTTVPVDSVIELQVS  VDSVIELQV        0.3651        962.0                50.00     Sequence
DRB1_0101  496  IPDVAGQTVDVAQKN  DVAGQTVDV        0.3651        962.8                50.00     Sequence
DRB1_0101  129  HQNGIIHRDVKPANI  IIHRDVKPA        0.3650        963.5                50.00     Sequence
DRB1_0101  456  SPSTPELVGKVIGTN  STPELVGKV        0.3650        963.6                50.00     Sequence
DRB1_0101  297  SSAAGNLSGPRTDPL  AGNLSGPRT        0.3645        968.5                50.00     Sequence
DRB1_0101   70  IVAVYDTGEAETPAG  YDTGEAETP        0.3633        981.0                50.00     Sequence
DRB1_0101    1  TTPSHLSDRYELGEI  SHLSDRYEL        0.3623        992.4                50.00     Sequence
DRB1_0101  540  AGTTVPVDSVIELQV  TVPVDSVIE        0.3609       1007.0                50.00     Sequence
DRB1_0101  250  VLKALAKNPENRYQT  VLKALAKNP        0.3584       1034.5                50.00     Sequence
DRB1_0101  394  PPDHVIGTDPAANTS  VIGTDPAAN        0.3583       1035.9                50.00     Sequence
DRB1_0101  399  IGTDPAANTSVSAGD  TDPAANTSV        0.3556       1066.1                50.00     Sequence
DRB1_0101  218  DSPVSVAYQHVREDP  PVSVAYQHV        0.3553       1069.7                50.00     Sequence
DRB1_0101  590  ADVDAGGSQHNRVVY  VDAGGSQHN        0.3551       1072.3                50.00     Sequence
DRB1_0101  119  ADACQALNFSHQNGI  CQALNFSHQ        0.3551       1072.5                50.00     Sequence
DRB1_0101  177  GTAQYLSPEQARGDS  AQYLSPEQA        0.3546       1078.6                50.00     Sequence
DRB1_0101  266  AEMRADLVRVHNGEP  EMRADLVRV        0.3542       1082.4                50.00     Sequence
DRB1_0101  179  AQYLSPEQARGDSVD  LSPEQARGD        0.3526       1101.4                50.00     Sequence
DRB1_0101  222  SVAYQHVREDPIPPS  YQHVREDPI        0.3468       1172.8                50.00     Sequence
DRB1_0101  220  PVSVAYQHVREDPIP  YQHVREDPI        0.3457       1187.2                50.00     Sequence
DRB1_0101  493  TKDIPDVAGQTVDVA  IPDVAGQTV        0.3445       1202.7                50.00     Sequence
DRB1_0101  551  ELQVSKGNQFVMPDL  VSKGNQFVM        0.3443       1205.8                50.00     Sequence
DRB1_0101  355  ITRDVQVPDVRGQSS  DVQVPDVRG        0.3434       1216.5                50.00     Sequence
DRB1_0101  273  VRVHNGEPPEAPKVL  VHNGEPPEA        0.3426       1228.3                50.00     Sequence
DRB1_0101  381  FKIRTLQKPDSTIPP  IRTLQKPDS        0.3423       1231.9                50.00     Sequence
DRB1_0101  529  PAGEVTGTNPPAGTT  EVTGTNPPA        0.3418       1238.3                50.00     Sequence
DRB1_0101   76  TGEAETPAGPLPYIV  PAGPLPYIV        0.3406       1254.2                50.00     Sequence
DRB1_0101  531  GEVTGTNPPAGTTVP  VTGTNPPAG        0.3394       1271.6                50.00     Sequence
DRB1_0101  454  ANSPSTPELVGKVIG  NSPSTPELV        0.3379       1292.0                50.00     Sequence
DRB1_0101  466  VIGTNPPANQTSAIT  TNPPANQTS        0.3361       1317.1                50.00     Sequence
DRB1_0101  592  VDAGGSQHNRVVYQN  GGSQHNRVV        0.3354       1327.7                50.00     Sequence
DRB1_0101  267  EMRADLVRVHNGEPP  EMRADLVRV        0.3333       1357.4                50.00     Sequence
DRB1_0101  444  TAAGFGRFKQANSPS  FGRFKQANS        0.3330       1362.1                50.00     Sequence
```

```
DRB1_0101  271  DLVRVHNGEPPEAPK  VHNGEPPEA         0.3324       1371.6                  50.00     Sequence
DRB1_0101  393  IPPDHVIGTDPAANT  DHVIGTDPA         0.3322       1374.6                  50.00     Sequence
DRB1_0101  160  RAIADSGNSVTQTAA  AIADSGNSV         0.3318       1380.2                  50.00     Sequence
DRB1_0101  117  VIADACQALNFSHQN  VIADACQAL         0.3314       1385.5                  50.00     Sequence
DRB1_0101  591  DVDAGGSQHNRVVYQ  VDAGGSQHN         0.3302       1403.5                  50.00     Sequence
DRB1_0101  425  QREIPDVSTLTYAEA  VSTLTYAEA         0.3301       1405.5                  50.00     Sequence
DRB1_0101  350  NTFGGITRDVQVPDV  TFGGITRDV         0.3293       1417.6                  50.00     Sequence
DRB1_0101  457  PSTPELVGKVIGTNP  STPELVGKV         0.3293       1417.7                  50.00     Sequence
DRB1_0101  443  LTAAGFGRFKQANSP  FGRFKQANS         0.3288       1424.8                  50.00     Sequence
DRB1_0101  494  KDIPDVAGQTVDVAQ  DVAGQTVDV         0.3273       1449.1                  50.00     Sequence
DRB1_0101  608  PAGTGVNRDGIITLR  GVNRDGIIT         0.3259       1471.3                  50.00     Sequence
DRB1_0101  518  KFSQASVDSPRPAGE  FSQASVDSP         0.3249       1487.4                  50.00     Sequence
DRB1_0101  234  PPSARHEGLSADLDA  HEGLSADLD         0.3247       1490.2                  50.00     Sequence
DRB1_0101  407  TSVSAGDEITVNVST  VSAGDEITV         0.3240       1501.8                  50.00     Sequence
DRB1_0101   69  AIVAVYDTGEAETPA  YDTGEAETP         0.3212       1546.9                  50.00     Sequence
DRB1_0101  459  TPELVGKVIGTNPPA  KVIGTNPPA         0.3211       1548.6                  50.00     Sequence
DRB1_0101  405  ANTSVSAGDEITVNV  VSAGDEITV         0.3204       1560.3                  50.00     Sequence
DRB1_0101  388  KPDSTIPPDHVIGTD  DSTIPPDHV         0.3199       1569.4                  50.00     Sequence
DRB1_0101  351  TFGGITRDVQVPDVR  TFGGITRDV         0.3184       1595.5                  50.00     Sequence
DRB1_0101   66  NHPAIVAVYDTGEAE  NHPAIVAVY         0.3180       1603.0                  50.00     Sequence
DRB1_0101  458  STPELVGKVIGTNPP  STPELVGKV         0.3171       1617.8                  50.00     Sequence
DRB1_0101  386  LQKPDSTIPPDHVIG  DSTIPPDHV         0.3169       1620.9                  50.00     Sequence
DRB1_0101  223  VAYQHVREDPIPPSA  YQHVREDPI         0.3146       1661.7                  50.00     Sequence
DRB1_0101  469  TNPPANQTSAITNVV  PANQTSAIT         0.3140       1673.3                  50.00     Sequence
DRB1_0101  128  SHQNGIIHRDVKPAN  QNGIIHRDV         0.3125       1700.2                  50.00     Sequence
DRB1_0101  224  AYQHVREDPIPPSAR  YQHVREDPI         0.3123       1703.4                  50.00     Sequence
DRB1_0101  221  VSVAYQHVREDPIPP  YQHVREDPI         0.3117       1715.7                  50.00     Sequence
DRB1_0101  207  EVLTGEPPFTGDSPV  LTGEPPFTG         0.3115       1718.2                  50.00     Sequence
DRB1_0101   72  AVYDTGEAETPAGPL  YDTGEAETP         0.3112       1724.6                  50.00     Sequence
DRB1_0101  519  FSQASVDSPRPAGEV  ASVDSPRPA         0.3088       1769.7                  50.00     Sequence
DRB1_0101  269  RADLVRVHNGEPPEA  VHNGEPPEA         0.3086       1773.7                  50.00     Sequence
DRB1_0101  280  PPEAPKVLTDAERTS  KVLTDAERT         0.3075       1794.4                  50.00     Sequence
DRB1_0101  532  EVTGTNPPAGTTVPV  VTGTNPPAG         0.3068       1808.1                  50.00     Sequence
DRB1_0101  181  YLSPEQARGDSVDAR  PEQARGDSV         0.3066       1811.6                  50.00     Sequence
DRB1_0101  354  GITRDVQVPDVRGQS  DVQVPDVRG         0.3063       1818.7                  50.00     Sequence
DRB1_0101  180  QYLSPEQARGDSVDA  LSPEQARGD         0.3060       1824.5                  50.00     Sequence
DRB1_0101  412  GDEITVNVSTGPEQR  ITVNVSTGP         0.3045       1853.4                  50.00     Sequence
DRB1_0101  588  KGADVDAGGSQHNRV  VDAGGSQHN         0.3024       1896.4                  50.00     Sequence
DRB1_0101  298  SAAGNLSGPRTDPLP  AGNLSGPRT         0.3024       1897.6                  50.00     Sequence
DRB1_0101   94  VDGVTLRDIVHTEGP  VDGVTLRDI         0.3016       1912.9                  50.00     Sequence
DRB1_0101  270  ADLVRVHNGEPPEAP  VHNGEPPEA         0.3015       1916.0                  50.00     Sequence
DRB1_0101  353  GGITRDVQVPDVRGQ  TRDVQVPDV         0.3005       1937.0                  50.00     Sequence
DRB1_0101  254  LAKNPENRYQTAAEM  NRYQTAAEM         0.2997       1953.8                  50.00     Sequence
DRB1_0101  400  GTDPAANTSVSAGDE  TDPAANTSV         0.2987       1974.1                  50.00     Sequence
DRB1_0101  356  TRDVQVPDVRGQSSA  DVQVPDVRG         0.2979       1992.0                  50.00     Sequence
DRB1_0101  538  PPAGTTVPVDSVIEL  GTTVPVDSV         0.2965       2022.0                  50.00     Sequence
DRB1_0101  583  TGMLDKGADVDAGGS  LDKGADVDA         0.2959       2034.1                  50.00     Sequence
DRB1_0101  268  MRADLVRVHNGEPPE  VRVHNGEPP         0.2953       2047.7                  50.00     Sequence
DRB1_0101  392  TIPPDHVIGTDPAAN  DHVIGTDPA         0.2948       2058.9                  50.00     Sequence
DRB1_0101  251  LKALAKNPENRYQTA  LAKNPENRY         0.2926       2109.5                  50.00     Sequence
DRB1_0101  492  ATKDIPDVAGQTVDV  IPDVAGQTV         0.2914       2136.5                  50.00     Sequence
DRB1_0101  539  PAGTTVPVDSVIELQ  GTTVPVDSV         0.2910       2144.7                  50.00     Sequence
DRB1_0101  497  PDVAGQTVDVAQKNL  DVAGQTVDV         0.2903       2161.5                  50.00     Sequence
DRB1_0101  274  RVHNGEPPEAPKVLT  VHNGEPPEA         0.2903       2162.5                  50.00     Sequence
DRB1_0101    0  MTTPSHLSDRYELGE  SHLSDRYEL         0.2901       2167.7                  50.00     Sequence
DRB1_0101  161  AIADSGNSVTQTAAV  AIADSGNSV         0.2878       2220.1                  50.00     Sequence
DRB1_0101  352  FGGITRDVQVPDVRG  DVQVPDVRG         0.2871       2238.0                  50.00     Sequence
DRB1_0101  424  EQREIPDVSTLTYAE  EIPDVSTLT         0.2868       2245.8                  50.00     Sequence
DRB1_0101  233  IPPSARHEGLSADLD  HEGLSADLD         0.2864       2255.0                  50.00     Sequence
DRB1_0101  533  VTGTNPPAGTTVPVD  TNPPAGTTV         0.2863       2258.4                  50.00     Sequence
DRB1_0101  118  IADACQALNFSHQNG  CQALNFSHQ         0.2861       2262.6                  50.00     Sequence
DRB1_0101  423  PEQREIPDVSTLTYA  REIPDVSTL         0.2838       2318.7                  50.00     Sequence
DRB1_0101  190  DSVDARSDVYSLGCV  DARSDVYSL         0.2837       2323.3                  50.00     Sequence
DRB1_0101  414  EITVNVSTGPEQREI  ITVNVSTGP         0.2822       2359.9                  50.00     Sequence
DRB1_0101  225  YQHVREDPIPPSARH  YQHVREDPI         0.2821       2363.0                  50.00     Sequence
DRB1_0101  528  RPAGEVTGTNPPAGT  EVTGTNPPA         0.2818       2370.3                  50.00     Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0101 | 467 | IGTNPPANQTSAITN | TNPPANQTS | 0.2803 | 2409.5 | 50.00 | Sequence |
| DRB1_0101 | 408 | SVSAGDEITVNVSTG | VSAGDEITV | 0.2794 | 2432.4 | 50.00 | Sequence |
| DRB1_0101 | 413 | DEITVNVSTGPEQRE | ITVNVSTGP | 0.2793 | 2434.7 | 50.00 | Sequence |
| DRB1_0101 | 68 | PAIVAVYDTGEAETP | YDTGEAETP | 0.2788 | 2449.5 | 50.00 | Sequence |
| DRB1_0101 | 385 | TLQKPDSTIPPDHVI | DSTIPPDHV | 0.2779 | 2471.5 | 50.00 | Sequence |
| DRB1_0101 | 182 | LSPEQARGDSVDARS | PEQARGDSV | 0.2776 | 2481.0 | 50.00 | Sequence |
| DRB1_0101 | 317 | DDTDRDRSIGSVGRW | TDRDRSIGS | 0.2768 | 2501.7 | 50.00 | Sequence |
| DRB1_0101 | 316 | LDDTDRDRSIGSVGR | TDRDRSIGS | 0.2745 | 2564.7 | 50.00 | Sequence |
| DRB1_0101 | 382 | KIRTLQKPDSTIPPD | IRTLQKPDS | 0.2742 | 2573.0 | 50.00 | Sequence |
| DRB1_0101 | 584 | GMLDKGADVDAGGSQ | LDKGADVDA | 0.2741 | 2576.0 | 50.00 | Sequence |
| DRB1_0101 | 67 | HPAIVAVYDTGEAET | IVAVYDTGE | 0.2738 | 2584.3 | 50.00 | Sequence |
| DRB1_0101 | 409 | VSAGDEITVNVSTGP | ITVNVSTGP | 0.2736 | 2590.5 | 50.00 | Sequence |
| DRB1_0101 | 411 | AGDEITVNVSTGPEQ | ITVNVSTGP | 0.2735 | 2593.9 | 50.00 | Sequence |
| DRB1_0101 | 404 | AANTSVSAGDEITVN | VSAGDEITV | 0.2719 | 2637.4 | 50.00 | Sequence |
| DRB1_0101 | 498 | DVAGQTVDVAQKNLN | DVAGQTVDV | 0.2693 | 2714.3 | 50.00 | Sequence |
| DRB1_0101 | 73 | VYDTGEAETPAGPLP | YDTGEAETP | 0.2680 | 2751.0 | 50.00 | Sequence |
| DRB1_0101 | 593 | DAGGSQHNRVVYQNP | GGSQHNRVV | 0.2678 | 2759.0 | 50.00 | Sequence |
| DRB1_0101 | 594 | AGGSQHNRVVYQNPP | GGSQHNRVV | 0.2675 | 2766.1 | 50.00 | Sequence |
| DRB1_0101 | 401 | TDPAANTSVSAGDEI | TDPAANTSV | 0.2675 | 2768.2 | 50.00 | Sequence |
| DRB1_0101 | 410 | SAGDEITVNVSTGPE | ITVNVSTGP | 0.2659 | 2815.0 | 50.00 | Sequence |
| DRB1_0101 | 468 | GTNPPANQTSAITNV | TNPPANQTS | 0.2653 | 2832.7 | 50.00 | Sequence |
| DRB1_0101 | 357 | RDVQVPDVRGQSSAD | DVQVPDVRG | 0.2652 | 2835.7 | 50.00 | Sequence |
| DRB1_0101 | 403 | PAANTSVSAGDEITV | VSAGDEITV | 0.2650 | 2842.9 | 50.00 | Sequence |
| DRB1_0101 | 208 | VLTGEPPFTGDSPVS | LTGEPPFTG | 0.2645 | 2857.8 | 50.00 | Sequence |
| DRB1_0101 | 300 | AGNLSGPRTDPLPRQ | LSGPRTDPL | 0.2636 | 2886.0 | 50.00 | Sequence |
| DRB1_0101 | 95 | DGVTLRDIVHTEGPM | LRDIVHTEG | 0.2635 | 2890.4 | 50.00 | Sequence |
| DRB1_0101 | 299 | AAGNLSGPRTDPLPR | AGNLSGPRT | 0.2626 | 2917.3 | 50.00 | Sequence |
| DRB1_0101 | 422 | GPEQREIPDVSTLTY | QREIPDVST | 0.2608 | 2974.8 | 50.00 | Sequence |
| DRB1_0101 | 520 | SQASVDSPRPAGEVT | ASVDSPRPA | 0.2603 | 2989.5 | 50.00 | Sequence |
| DRB1_0101 | 252 | KALAKNPENRYQTAA | LAKNPENRY | 0.2601 | 2997.8 | 50.00 | Sequence |
| DRB1_0101 | 536 | TNPPAGTTVPVDSVI | PAGTTVPVD | 0.2598 | 3007.8 | 50.00 | Sequence |
| DRB1_0101 | 415 | ITVNVSTGPEQREIP | ITVNVSTGP | 0.2591 | 3030.5 | 50.00 | Sequence |
| DRB1_0101 | 585 | MLDKGADVDAGGSQH | LDKGADVDA | 0.2572 | 3091.6 | 50.00 | Sequence |
| DRB1_0101 | 587 | DKGADVDAGGSQHNR | VDAGGSQHN | 0.2567 | 3108.4 | 50.00 | Sequence |
| DRB1_0101 | 537 | NPPAGTTVPVDSVIE | PAGTTVPVD | 0.2557 | 3143.9 | 50.00 | Sequence |
| DRB1_0101 | 391 | STIPPDHVIGTDPAA | DHVIGTDPA | 0.2555 | 3149.2 | 50.00 | Sequence |
| DRB1_0101 | 586 | LDKGADVDAGGSQHN | VDAGGSQHN | 0.2547 | 3178.7 | 50.00 | Sequence |
| DRB1_0101 | 183 | SPEQARGDSVDARSD | QARGDSVDA | 0.2543 | 3193.3 | 50.00 | Sequence |
| DRB1_0101 | 490 | GPATKDIPDVAGQTV | TKDIPDVAG | 0.2537 | 3213.3 | 50.00 | Sequence |
| DRB1_0101 | 189 | GDSVDARSDVYSLGC | VDARSDVYS | 0.2514 | 3295.1 | 50.00 | Sequence |
| DRB1_0101 | 595 | GGSQHNRVVYQNPPA | GGSQHNRVV | 0.2510 | 3307.4 | 50.00 | Sequence |
| DRB1_0101 | 315 | DLDDTDRDRSIGSVG | TDRDRSIGS | 0.2503 | 3331.2 | 50.00 | Sequence |
| DRB1_0101 | 390 | DSTIPPDHVIGTDPA | DHVIGTDPA | 0.2502 | 3337.8 | 50.00 | Sequence |
| DRB1_0101 | 186 | QARGDSVDARSDVYS | QARGDSVDA | 0.2495 | 3361.9 | 50.00 | Sequence |
| DRB1_0101 | 275 | VHNGEPPEAPKVLTD | VHNGEPPEA | 0.2482 | 3409.4 | 50.00 | Sequence |
| DRB1_0101 | 383 | IRTLQKPDSTIPPDH | TLQKPDSTI | 0.2477 | 3428.4 | 50.00 | Sequence |
| DRB1_0101 | 521 | QASVDSPRPAGEVTG | ASVDSPRPA | 0.2475 | 3435.0 | 50.00 | Sequence |
| DRB1_0101 | 384 | RTLQKPDSTIPPDHV | DSTIPPDHV | 0.2471 | 3450.1 | 50.00 | Sequence |
| DRB1_0101 | 188 | RGDSVDARSDVYSLG | VDARSDVYS | 0.2470 | 3455.7 | 50.00 | Sequence |
| DRB1_0101 | 314 | QDLDDTDRDRSIGSV | TDRDRSIGS | 0.2442 | 3560.3 | 50.00 | Sequence |
| DRB1_0101 | 279 | EPPEAPKVLTDAERT | KVLTDAERT | 0.2441 | 3565.3 | 50.00 | Sequence |
| DRB1_0101 | 232 | PIPPSARHEGLSADL | SARHEGLSA | 0.2423 | 3633.5 | 50.00 | Sequence |
| DRB1_0101 | 74 | YDTGEAETPAGPLPY | YDTGEAETP | 0.2422 | 3639.0 | 50.00 | Sequence |
| DRB1_0101 | 389 | PDSTIPPDHVIGTDP | DSTIPPDHV | 0.2416 | 3663.3 | 50.00 | Sequence |
| DRB1_0101 | 534 | TGTNPPAGTTVPVDS | TNPPAGTTV | 0.2398 | 3732.0 | 50.00 | Sequence |
| DRB1_0101 | 604 | YQNPPAGTGVNRDGI | YQNPPAGTG | 0.2394 | 3750.7 | 50.00 | Sequence |
| DRB1_0101 | 491 | PATKDIPDVAGQTVD | TKDIPDVAG | 0.2378 | 3814.9 | 50.00 | Sequence |
| DRB1_0101 | 184 | PEQARGDSVDARSDV | QARGDSVDA | 0.2374 | 3833.2 | 50.00 | Sequence |
| DRB1_0101 | 313 | RQDLDDTDRDRSIGS | TDRDRSIGS | 0.2358 | 3900.9 | 50.00 | Sequence |
| DRB1_0101 | 527 | PRPAGEVTGTNPPAG | EVTGTNPPA | 0.2355 | 3913.5 | 50.00 | Sequence |
| DRB1_0101 | 607 | PPAGTGVNRDGIITL | GVNRDGIIT | 0.2342 | 3967.4 | 50.00 | Sequence |
| DRB1_0101 | 522 | ASVDSPRPAGEVTGT | ASVDSPRPA | 0.2338 | 3983.1 | 50.00 | Sequence |
| DRB1_0101 | 253 | ALAKNPENRYQTAAE | LAKNPENRY | 0.2321 | 4057.3 | 50.00 | Sequence |
| DRB1_0101 | 402 | DPAANTSVSAGDEIT | PAANTSVSA | 0.2314 | 4090.7 | 50.00 | Sequence |
| DRB1_0101 | 421 | TGPEQREIPDVSTLT | QREIPDVST | 0.2312 | 4099.1 | 50.00 | Sequence |
| DRB1_0101 | 227 | HVREDPIPPSARHEG | EDPIPPSAR | 0.2296 | 4171.1 | 50.00 | Sequence |

```
   DRB1_0101  187  ARGDSVDARSDVYSL  VDARSDVYS        0.2288       4204.8                  50.00     Sequence
   DRB1_0101  185  EQARGDSVDARSDVY  QARGDSVDA        0.2286       4214.4                  50.00     Sequence
   DRB1_0101  226  QHVREDPIPPSARHE  VREDPIPPS        0.2259       4337.8                  50.00     Sequence
   DRB1_0101  535  GTNPPAGTTVPVDSV  TNPPAGTTV        0.2247       4395.7                  50.00     Sequence
   DRB1_0101  231  DPIPPSARHEGLSAD  SARHEGLSA        0.2134       4967.7                  50.00     Sequence
   DRB1_0101  230  EDPIPPSARHEGLSA  SARHEGLSA        0.2115       5072.4                  50.00     Sequence
   DRB1_0101   75  DTGEAETPAGPLPYI  AETPAGPLP        0.2080       5269.2                  50.00     Sequence
   DRB1_0101  420  STGPEQREIPDVSTL  QREIPDVST        0.2067       5341.1                  50.00     Sequence
   DRB1_0101  301  GNLSGPRTDPLPRQD  LSGPRTDPL        0.2041       5495.1                  50.00     Sequence
   DRB1_0101  305  GPRTDPLPRQDLDDT  TDPLPRQDL        0.2020       5621.7                  50.00     Sequence
   DRB1_0101  302  NLSGPRTDPLPRQDL  LSGPRTDPL        0.2017       5641.0                  50.00     Sequence
   DRB1_0101  416  TVNVSTGPEQREIPD  VNVSTGPEQ        0.1986       5830.5                  50.00     Sequence
   DRB1_0101  489  SGPATKDIPDVAGQT  TKDIPDVAG        0.1981       5862.5                  50.00     Sequence
   DRB1_0101  228  VREDPIPPSARHEGL  EDPIPPSAR        0.1959       6001.7                  50.00     Sequence
   DRB1_0101  526  SPRPAGEVTGTNPPA  EVTGTNPPA        0.1917       6285.2                  50.00     Sequence
   DRB1_0101  419  VSTGPEQREIPDVST  QREIPDVST        0.1911       6321.2                  50.00     Sequence
   DRB1_0101  312  PRQDLDDTDRDRSIG  DDTDRDRSI        0.1901       6393.0                  50.00     Sequence
   DRB1_0101  486  IVGSGPATKDIPDVA  VGSGPATKD        0.1878       6554.8                  50.00     Sequence
   DRB1_0101  303  LSGPRTDPLPRQDLD  LSGPRTDPL        0.1871       6604.0                  50.00     Sequence
   DRB1_0101  487  VGSGPATKDIPDVAG  TKDIPDVAG        0.1850       6758.5                  50.00     Sequence
   DRB1_0101  311  LPRQDLDDTDRDRSI  DDTDRDRSI        0.1839       6835.8                  50.00     Sequence
   DRB1_0101  606  NPPAGTGVNRDGIIT  AGTGVNRDG        0.1834       6870.1                  50.00     Sequence
   DRB1_0101  488  GSGPATKDIPDVAGQ  TKDIPDVAG        0.1828       6915.0                  50.00     Sequence
   DRB1_0101  523  SVDSPRPAGEVTGTN  VDSPRPAGE        0.1803       7104.7                  50.00     Sequence
   DRB1_0101  306  PRTDPLPRQDLDDTD  TDPLPRQDL        0.1800       7133.5                  50.00     Sequence
   DRB1_0101  276  HNGEPPEAPKVLTDA  GEPPEAPKV        0.1767       7387.7                  50.00     Sequence
   DRB1_0101  307  RTDPLPRQDLDDTDR  TDPLPRQDL        0.1764       7415.2                  50.00     Sequence
   DRB1_0101  417  VNVSTGPEQREIPDV  VNVSTGPEQ        0.1705       7904.6                  50.00     Sequence
   DRB1_0101  229  REDPIPPSARHEGLS  PIPPSARHE        0.1699       7951.1                  50.00     Sequence
   DRB1_0101  304  SGPRTDPLPRQDLDD  TDPLPRQDL        0.1658       8315.3                  50.00     Sequence
   DRB1_0101  605  QNPPAGTGVNRDGII  TGVNRDGII        0.1657       8325.1                  50.00     Sequence
   DRB1_0101  524  VDSPRPAGEVTGTNP  VDSPRPAGE        0.1608       8781.8                  50.00     Sequence
   DRB1_0101  308  TDPLPRQDLDDTDRD  TDPLPRQDL        0.1604       8817.4                  50.00     Sequence
   DRB1_0101  418  NVSTGPEQREIPDVS  EQREIPDVS        0.1572       9121.6                  50.00     Sequence
   DRB1_0101  310  PLPRQDLDDTDRDRS  RQDLDDTDR        0.1487      10001.8                  50.00     Sequence
   DRB1_0101  525  DSPRPAGEVTGTNPP  GEVTGTNPP        0.1484      10038.7                  50.00     Sequence
   DRB1_0101  277  NGEPPEAPKVLTDAE  GEPPEAPKV        0.1477      10111.7                  50.00     Sequence
   DRB1_0101  309  DPLPRQDLDDTDRDR  RQDLDDTDR        0.1459      10308.9                  50.00     Sequence
   DRB1_0101  278  GEPPEAPKVLTDAER  GEPPEAPKV        0.1425      10694.4                  50.00     Sequence
-----------------------------------------------------------------------------------------------

Allele: DRB1_0101. Number of high binders 134. Number of weak binders 228. Number of peptides 612

-----------------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------------
      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
-----------------------------------------------------------------------------------------------
   DRB1_0301   23  EVHLARDLRLHRDVA  EVHLARDLR        0.7734         11.6          SB     0.20     Sequence
   DRB1_0301   22  SEVHLARDLRLHRDV  EVHLARDLR        0.7646         12.8          SB     0.20     Sequence
   DRB1_0301   26  LARDLRLHRDVAVKV  DLRLHRDVA        0.7461         15.6          SB     0.30     Sequence
   DRB1_0301   21  MSEVHLARDLRLHRD  EVHLARDLR        0.7395         16.8          SB     0.40     Sequence
   DRB1_0301   27  ARDLRLHRDVAVKVL  DLRLHRDVA        0.7325         18.1          SB     0.40     Sequence
   DRB1_0301   28  RDLRLHRDVAVKVLR  DLRLHRDVA        0.7137         22.1          SB     0.80     Sequence
   DRB1_0301   20  GMSEVHLARDLRLHR  EVHLARDLR        0.7069         23.8          SB     0.80     Sequence
   DRB1_0301   25  HLARDLRLHRDVAVK  LARDLRLHR        0.7029         24.9          SB     0.80     Sequence
   DRB1_0301   29  DLRLHRDVAVKVLRA  DLRLHRDVA        0.6899         28.7          SB     0.80     Sequence
   DRB1_0301   24  VHLARDLRLHRDVAV  LARDLRLHR        0.6840         30.6          SB     0.80     Sequence
   DRB1_0301  283  APKVLTDAERTSLLS  VLTDAERTS        0.6791         32.2          SB     1.00     Sequence
   DRB1_0301  284  PKVLTDAERTSLLSS  VLTDAERTS        0.6598         39.7          SB     2.00     Sequence
   DRB1_0301   38  VKVLRADLARDPSFY  VKVLRADLA        0.6473         45.4          SB     2.00     Sequence
   DRB1_0301  282  EAPKVLTDAERTSLL  VLTDAERTS        0.6473         45.4          SB     2.00     Sequence
   DRB1_0301   37  AVKVLRADLARDPSF  VKVLRADLA        0.6441         47.0          SB     2.00     Sequence
   DRB1_0301  566  SGMFWVDAEPRLRAL  MFWVDAEPR        0.6327         53.2          WB     2.00     Sequence
   DRB1_0301   36  VAVKVLRADLARDPS  VKVLRADLA        0.6192         61.5          WB     2.00     Sequence
   DRB1_0301  285  KVLTDAERTSLLSSA  KVLTDAERT        0.6130         65.8          WB     4.00     Sequence
   DRB1_0301  567  GMFWVDAEPRLRALG  MFWVDAEPR        0.6088         68.9          WB     4.00     Sequence
```

```
DRB1_0301  565  LSGMFWVDAEPRLRA  MFWVDAEPR         0.6055          71.4           WB     4.00      Sequence
DRB1_0301  568  MFWVDAEPRLRALGW  MFWVDAEPR         0.5998          76.0           WB     4.00      Sequence
DRB1_0301   35  DVAVKVLRADLARDP  VKVLRADLA         0.5920          82.6           WB     4.00      Sequence
DRB1_0301  281  PEAPKVLTDAERTSL  VLTDAERTS         0.5907          83.8           WB     4.00      Sequence
DRB1_0301  151  VKVMDFGIARAIADS  VMDFGIARA         0.5887          85.7           WB     4.00      Sequence
DRB1_0301   30  LRLHRDVAVKVLRAD  RLHRDVAVK         0.5787          95.4           WB     4.00      Sequence
DRB1_0301   19  GGMSEVHLARDLRLH  EVHLARDLR         0.5731         101.4           WB     4.00      Sequence
DRB1_0301  114  AIEVIADACQALNFS  VIADACQAL         0.5721         102.5           WB     4.00      Sequence
DRB1_0301   34  RDVAVKVLRADLARD  VKVLRADLA         0.5709         103.8           WB     4.00      Sequence
DRB1_0301  150  AVKVMDFGIARAIAD  VMDFGIARA         0.5680         107.1           WB     4.00      Sequence
DRB1_0301  152  KVMDFGIARAIADSG  VMDFGIARA         0.5541         124.6           WB     4.00      Sequence
DRB1_0301  131  NGIIHRDVKPANIMI  NGIIHRDVK         0.5527         126.4           WB     4.00      Sequence
DRB1_0301  143  IMISATNAVKVMDFG  MISATNAVK         0.5508         129.1           WB     8.00      Sequence
DRB1_0301  558  NQFVMPDLSGMFWVD  NQFVMPDLS         0.5502         129.9           WB     8.00      Sequence
DRB1_0301  241  GLSADLDAVVLKALA  LSADLDAVV         0.5469         134.7           WB     8.00      Sequence
DRB1_0301  564  DLSGMFWVDAEPRLR  MFWVDAEPR         0.5442         138.6           WB     8.00      Sequence
DRB1_0301  113  RAIEVIADACQALNF  VIADACQAL         0.5424         141.3           WB     8.00      Sequence
DRB1_0301  239  HEGLSADLDAVVLKA  LSADLDAVV         0.5421         141.9           WB     8.00      Sequence
DRB1_0301  142  NIMISATNAVKVMDF  MISATNAVK         0.5395         145.9           WB     8.00      Sequence
DRB1_0301  557  GNQFVMPDLSGMFWV  NQFVMPDLS         0.5351         152.9           WB     8.00      Sequence
DRB1_0301  130  QNGIIHRDVKPANIM  NGIIHRDVK         0.5337         155.3           WB     8.00      Sequence
DRB1_0301  240  EGLSADLDAVVLKAL  LSADLDAVV         0.5298         161.9           WB     8.00      Sequence
DRB1_0301  149  NAVKVMDFGIARAIA  KVMDFGIAR         0.5261         168.6           WB     8.00      Sequence
DRB1_0301  395  PDHVIGTDPAANTSV  DHVIGTDPA         0.5241         172.2           WB     8.00      Sequence
DRB1_0301  396  DHVIGTDPAANTSVS  DHVIGTDPA         0.5234         173.7           WB     8.00      Sequence
DRB1_0301   86  LPYIVMEYVDGVTLR  LPYIVMEYV         0.5100         200.7           WB     8.00      Sequence
DRB1_0301   31  RLHRDVAVKVLRADL  RLHRDVAVK         0.5073         206.6           WB     8.00      Sequence
DRB1_0301  556  KGNQFVMPDLSGMFW  NQFVMPDLS         0.5058         209.9           WB     8.00      Sequence
DRB1_0301   33  HRDVAVKVLRADLAR  VKVLRADLA         0.5056         210.4           WB     8.00      Sequence
DRB1_0301  115  IEVIADACQALNFSH  VIADACQAL         0.5023         218.1           WB     8.00      Sequence
DRB1_0301   39  KVLRADLARDPSFYL  RADLARDPS         0.5007         221.9           WB     8.00      Sequence
DRB1_0301  238  RHEGLSADLDAVVLK  LSADLDAVV         0.4976         229.6           WB     8.00      Sequence
DRB1_0301  394  PPDHVIGTDPAANTS  DHVIGTDPA         0.4974         230.1           WB     8.00      Sequence
DRB1_0301  280  PPEAPKVLTDAERTS  VLTDAERTS         0.4974         230.1           WB     8.00      Sequence
DRB1_0301  129  HQNGIIHRDVKPANI  NGIIHRDVK         0.4941         238.3           WB     8.00      Sequence
DRB1_0301  112  KRAIEVIADACQALN  VIADACQAL         0.4926         242.3           WB     8.00      Sequence
DRB1_0301  242  LSADLDAVVLKALAK  LSADLDAVV         0.4881         254.4           WB     8.00      Sequence
DRB1_0301   49  PSFYLRFRREAQNAA  SFYLRFRRE         0.4879         254.9           WB     8.00      Sequence
DRB1_0301   48  DPSFYLRFRREAQNA  FYLRFRREA         0.4853         262.2           WB     8.00      Sequence
DRB1_0301  148  TNAVKVMDFGIARAI  KVMDFGIAR         0.4821         271.5           WB     8.00      Sequence
DRB1_0301   85  PLPYIVMEYVDGVTL  LPYIVMEYV         0.4786         282.0           WB    16.00      Sequence
DRB1_0301  141  ANIMISATNAVKVMD  MISATNAVK         0.4777         284.6           WB    16.00      Sequence
DRB1_0301   50  SFYLRFRREAQNAAA  SFYLRFRRE         0.4768         287.5           WB    16.00      Sequence
DRB1_0301  431  VSTLTYAEAVKKLTA  VSTLTYAEA         0.4728         300.2           WB    16.00      Sequence
DRB1_0301   42  RADLARDPSFYLRFR  RADLARDPS         0.4727         300.3           WB    16.00      Sequence
DRB1_0301  153  VMDFGIARAIADSGN  VMDFGIARA         0.4709         306.3           WB    16.00      Sequence
DRB1_0301   40  VLRADLARDPSFYLR  RADLARDPS         0.4701         308.9           WB    16.00      Sequence
DRB1_0301   41  LRADLARDPSFYLRF  RADLARDPS         0.4701         309.0           WB    16.00      Sequence
DRB1_0301  144  MISATNAVKVMDFGI  ISATNAVKV         0.4684         314.8           WB    16.00      Sequence
DRB1_0301  563  PDLSGMFWVDAEPRL  MFWVDAEPR         0.4677         317.3           WB    16.00      Sequence
DRB1_0301  265  AAEMRADLVRVHNGE  AAEMRADLV         0.4675         317.9           WB    16.00      Sequence
DRB1_0301   18  FGGMSEVHLARDLRL  EVHLARDLR         0.4672         318.9           WB    16.00      Sequence
DRB1_0301   47  RDPSFYLRFRREAQN  FYLRFRREA         0.4667         320.7           WB    16.00      Sequence
DRB1_0301   32  LHRDVAVKVLRADLA  LHRDVAVKV         0.4629         334.0           WB    16.00      Sequence
DRB1_0301  555  SKGNQFVMPDLSGMF  NQFVMPDLS         0.4621         337.1           WB    16.00      Sequence
DRB1_0301  352  FGGITRDVQVPDVRG  FGGITRDVQ         0.4613         340.0           WB    16.00      Sequence
DRB1_0301  212  EPPFTGDSPVSVAYQ  EPPFTGDSP         0.4611         340.5           WB    16.00      Sequence
DRB1_0301  128  SHQNGIIHRDVKPAN  NGIIHRDVK         0.4597         345.8           WB    16.00      Sequence
DRB1_0301  393  IPPDHVIGTDPAANT  DHVIGTDPA         0.4582         351.4           WB    16.00      Sequence
DRB1_0301  430  DVSTLTYAEAVKKLT  VSTLTYAEA         0.4559         360.2           WB    16.00      Sequence
DRB1_0301  483  VIIIVGSGPATKDIP  IIIVGSGPA         0.4518         376.5           WB    16.00      Sequence
DRB1_0301  111  PKRAIEVIADACQAL  VIADACQAL         0.4411         422.9           WB    16.00      Sequence
DRB1_0301   89  IVMEYVDGVTLRDIV  EYVDGVTLR         0.4405         425.6           WB    16.00      Sequence
DRB1_0301  351  TFGGITRDVQVPDVR  FGGITRDVQ         0.4401         427.4           WB    16.00      Sequence
DRB1_0301  264  TAAEMRADLVRVHNG  AAEMRADLV         0.4351         451.1           WB    16.00      Sequence
DRB1_0301  211  GEPPFTGDSPVSVAY  EPPFTGDSP         0.4329         462.3           WB    16.00      Sequence
```

```
DRB1_0301   84  GPLPYIVMEYVDGVT  LPYIVMEYV         0.4296         478.9          WB    16.00      Sequence
DRB1_0301   46  ARDPSFYLRFRREAQ  FYLRFRREA         0.4241         508.4                16.00      Sequence
DRB1_0301  237  ARHEGLSADLDAVVL  LSADLDAVV         0.4239         509.7                16.00      Sequence
DRB1_0301  140  PANIMISATNAVKVM  MISATNAVK         0.4202         530.1                16.00      Sequence
DRB1_0301  132  GIIHRDVKPANIMIS  IIHRDVKPA         0.4200         531.3                16.00      Sequence
DRB1_0301   91  MEYVDGVTLRDIVHT  EYVDGVTLR         0.4193         535.2                16.00      Sequence
DRB1_0301  145  ISATNAVKVMDFGIA  ISATNAVKV         0.4193         535.5                16.00      Sequence
DRB1_0301   90  VMEYVDGVTLRDIVH  EYVDGVTLR         0.4174         546.5                16.00      Sequence
DRB1_0301  428  IPDVSTLTYAEAVKK  IPDVSTLTY         0.4150         560.7                16.00      Sequence
DRB1_0301  397  HVIGTDPAANTSVSA  VIGTDPAAN         0.4147         563.0                16.00      Sequence
DRB1_0301  429  PDVSTLTYAEAVKKL  VSTLTYAEA         0.4141         566.7                16.00      Sequence
DRB1_0301  482  VVIIIVGSGPATKDI  IIIVGSGPA         0.4122         578.0                16.00      Sequence
DRB1_0301  147  ATNAVKVMDFGIARA  KVMDFGIAR         0.4121         578.7                16.00      Sequence
DRB1_0301  116  EVIADACQALNFSHQ  VIADACQAL         0.4095         595.2                16.00      Sequence
DRB1_0301  484  IIIVGSGPATKDIPD  IIIVGSGPA         0.4090         598.6                16.00      Sequence
DRB1_0301  263  QTAAEMRADLVRVHN  AAEMRADLV         0.4052         623.5                16.00      Sequence
DRB1_0301  349  INTFGGITRDVQVPD  FGGITRDVQ         0.4040         631.6                16.00      Sequence
DRB1_0301  610  GTGVNRDGIITLRFG  GTGVNRDGI         0.4038         633.5                16.00      Sequence
DRB1_0301  117  VIADACQALNFSHQN  VIADACQAL         0.4011         651.8                16.00      Sequence
DRB1_0301   88  YIVMEYVDGVTLRDI  IVMEYVDGV         0.3988         668.4                16.00      Sequence
DRB1_0301  350  NTFGGITRDVQVPDV  FGGITRDVQ         0.3947         698.3                32.00      Sequence
DRB1_0301   83  AGPLPYIVMEYVDGV  LPYIVMEYV         0.3913         725.2                32.00      Sequence
DRB1_0301  210  TGEPPFTGDSPVSVA  EPPFTGDSP         0.3858         769.0                32.00      Sequence
DRB1_0301  392  TIPPDHVIGTDPAAN  DHVIGTDPA         0.3845         780.1                32.00      Sequence
DRB1_0301  546  VDSVIELQVSKGNQF  VIELQVSKG         0.3837         786.9                32.00      Sequence
DRB1_0301  213  PPFTGDSPVSVAYQH  PPFTGDSPV         0.3834         789.7                32.00      Sequence
DRB1_0301  262  YQTAAEMRADLVRVH  AAEMRADLV         0.3834         789.8                32.00      Sequence
DRB1_0301   95  DGVTLRDIVHTEGPM  DGVTLRDIV         0.3825         797.3                32.00      Sequence
DRB1_0301   92  EYVDGVTLRDIVHTE  EYVDGVTLR         0.3807         813.2                32.00      Sequence
DRB1_0301  547  DSVIELQVSKGNQFV  VIELQVSKG         0.3772         844.7                32.00      Sequence
DRB1_0301  609  AGTGVNRDGIITLRF  GTGVNRDGI         0.3770         846.4                32.00      Sequence
DRB1_0301   94  VDGVTLRDIVHTEGP  DGVTLRDIV         0.3765         851.2                32.00      Sequence
DRB1_0301  133  IIHRDVKPANIMISA  IIHRDVKPA         0.3735         878.7                32.00      Sequence
DRB1_0301   45  LARDPSFYLRFRREA  SFYLRFRRE         0.3732         881.3                32.00      Sequence
DRB1_0301  548  SVIELQVSKGNQFVM  VIELQVSKG         0.3725         888.2                32.00      Sequence
DRB1_0301  191  SVDARSDVYSLGCVL  SVDARSDVY         0.3716         897.0                32.00      Sequence
DRB1_0301  311  LPRQDLDDTDRDRSI  QDLDDTDRD         0.3704         908.5                32.00      Sequence
DRB1_0301  569  FWVDAEPRLRALGWT  FWVDAEPRL         0.3701         911.7                32.00      Sequence
DRB1_0301  122  CQALNFSHQNGIIHR  CQALNFSHQ         0.3697         915.3                32.00      Sequence
DRB1_0301  549  VIELQVSKGNQFVMP  VIELQVSKG         0.3691         921.3                32.00      Sequence
DRB1_0301  205  LYEVLTGEPPFTGDS  LYEVLTGEP         0.3690         922.9                32.00      Sequence
DRB1_0301  353  GGITRDVQVPDVRGQ  GGITRDVQV         0.3688         924.4                32.00      Sequence
DRB1_0301  432  STLTYAEAVKKLTAA  STLTYAEAV         0.3688         924.8                32.00      Sequence
DRB1_0301   87  PYIVMEYVDGVTLRD  IVMEYVDGV         0.3672         941.0                32.00      Sequence
DRB1_0301  286  VLTDAERTSLLSSAA  VLTDAERTS         0.3668         944.6                32.00      Sequence
DRB1_0301   51  FYLRFRREAQNAAAL  FYLRFRREA         0.3651         962.7                32.00      Sequence
DRB1_0301  121  ACQALNFSHQNGIIH  CQALNFSHQ         0.3635         979.2                32.00      Sequence
DRB1_0301  204  VLYEVLTGEPPFTGD  LYEVLTGEP         0.3614        1002.2                32.00      Sequence
DRB1_0301  312  PRQDLDDTDRDRSIG  QDLDDTDRD         0.3610        1005.7                32.00      Sequence
DRB1_0301  292  RTSLLSSAAGNLSGP  RTSLLSSAA         0.3602        1014.5                32.00      Sequence
DRB1_0301  559  QFVMPDLSGMFWVDA  FVMPDLSGM         0.3580        1039.2                32.00      Sequence
DRB1_0301  236  SARHEGLSADLDAVV  LSADLDAVV         0.3551        1072.7                32.00      Sequence
DRB1_0301  190  DSVDARSDVYSLGCV  SVDARSDVY         0.3531        1095.4                32.00      Sequence
DRB1_0301  139  KPANIMISATNAVKV  IMISATNAV         0.3529        1097.7                32.00      Sequence
DRB1_0301  127  FSHQNGIIHRDVKPA  NGIIHRDVK         0.3522        1106.8                32.00      Sequence
DRB1_0301  481  NVVIIIVGSGPATKD  IIIVGSGPA         0.3521        1107.8                32.00      Sequence
DRB1_0301  427  EIPDVSTLTYAEAVK  IPDVSTLTY         0.3513        1116.9                32.00      Sequence
DRB1_0301  313  RQDLDDTDRDRSIGS  QDLDDTDRD         0.3513        1117.3                32.00      Sequence
DRB1_0301   93  YVDGVTLRDIVHTEG  GVTLRDIVH         0.3472        1167.9                32.00      Sequence
DRB1_0301  560  FVMPDLSGMFWVDAE  VMPDLSGMF         0.3450        1195.7                32.00      Sequence
DRB1_0301   44  DLARDPSFYLRFRRE  PSFYLRFRR         0.3424        1230.5                32.00      Sequence
DRB1_0301   99  LRDIVHTEGPMTPKR  IVHTEGPMT         0.3420        1236.0                32.00      Sequence
DRB1_0301  544  VPVDSVIELQVSKGN  VPVDSVIEL         0.3415        1243.0                32.00      Sequence
DRB1_0301  314  QDLDDTDRDRSIGSV  LDDTDRDRS         0.3393        1272.8                32.00      Sequence
DRB1_0301  310  PLPRQDLDDTDRDRS  LPRQDLDDT         0.3386        1281.7                32.00      Sequence
DRB1_0301   43  ADLARDPSFYLRFRR  DLARDPSFY         0.3361        1317.8                32.00      Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0301 | 187 | ARGDSVDARSDVYSL | ARGDSVDAR | 0.3340 | 1347.9 | 32.00 | Sequence |
| DRB1_0301 | 189 | GDSVDARSDVYSLGC | SVDARSDVY | 0.3320 | 1376.6 | 32.00 | Sequence |
| DRB1_0301 | 209 | LTGEPPFTGDSPVSV | EPPFTGDSP | 0.3319 | 1377.7 | 32.00 | Sequence |
| DRB1_0301 | 120 | DACQALNFSHQNGII | CQALNFSHQ | 0.3319 | 1379.0 | 32.00 | Sequence |
| DRB1_0301 | 608 | PAGTGVNRDGIITLR | GTGVNRDGI | 0.3312 | 1388.9 | 32.00 | Sequence |
| DRB1_0301 | 261 | RYQTAAEMRADLVRV | RYQTAAEMR | 0.3312 | 1389.2 | 32.00 | Sequence |
| DRB1_0301 | 291 | ERTSLLSSAAGNLSG | RTSLLSSAA | 0.3310 | 1391.2 | 32.00 | Sequence |
| DRB1_0301 | 100 | RDIVHTEGPMTPKRA | RDIVHTEGP | 0.3307 | 1395.8 | 32.00 | Sequence |
| DRB1_0301 | 98 | TLRDIVHTEGPMTPK | RDIVHTEGP | 0.3300 | 1407.4 | 32.00 | Sequence |
| DRB1_0301 | 17 | GFGGMSEVHLARDLR | GMSEVHLAR | 0.3294 | 1415.5 | 32.00 | Sequence |
| DRB1_0301 | 426 | REIPDVSTLTYAEAV | IPDVSTLTY | 0.3277 | 1442.8 | 32.00 | Sequence |
| DRB1_0301 | 203 | CVLYEVLTGEPPFTG | LYEVLTGEP | 0.3270 | 1452.8 | 32.00 | Sequence |
| DRB1_0301 | 543 | TVPVDSVIELQVSKG | VPVDSVIEL | 0.3250 | 1484.5 | 32.00 | Sequence |
| DRB1_0301 | 266 | AEMRADLVRVHNGEP | MRADLVRVH | 0.3241 | 1500.3 | 32.00 | Sequence |
| DRB1_0301 | 146 | SATNAVKVMDFGIAR | KVMDFGIAR | 0.3222 | 1531.6 | 32.00 | Sequence |
| DRB1_0301 | 214 | PFTGDSPVSVAYQHV | FTGDSPVSV | 0.3204 | 1561.7 | 32.00 | Sequence |
| DRB1_0301 | 348 | AINTFGGITRDVQVP | INTFGGITR | 0.3174 | 1612.7 | 32.00 | Sequence |
| DRB1_0301 | 485 | IIVGSGPATKDIPDV | IVGSGPATK | 0.3173 | 1614.3 | 32.00 | Sequence |
| DRB1_0301 | 188 | RGDSVDARSDVYSLG | SVDARSDVY | 0.3135 | 1681.2 | 32.00 | Sequence |
| DRB1_0301 | 158 | IARAIADSGNSVTQT | IARAIADSG | 0.3127 | 1697.5 | 32.00 | Sequence |
| DRB1_0301 | 554 | VSKGNQFVMPDLSGM | NQFVMPDLS | 0.3121 | 1707.3 | 32.00 | Sequence |
| DRB1_0301 | 545 | PVDSVIELQVSKGNQ | VDSVIELQV | 0.3114 | 1720.6 | 32.00 | Sequence |
| DRB1_0301 | 391 | STIPPDHVIGTDPAA | DHVIGTDPA | 0.3113 | 1721.8 | 32.00 | Sequence |
| DRB1_0301 | 315 | DLDDTDRDRSIGSVG | LDDTDRDRS | 0.3095 | 1756.2 | 32.00 | Sequence |
| DRB1_0301 | 82 | PAGPLPYIVMEYVDG | LPYIVMEYV | 0.3090 | 1766.1 | 32.00 | Sequence |
| DRB1_0301 | 186 | QARGDSVDARSDVYS | ARGDSVDAR | 0.3088 | 1769.9 | 32.00 | Sequence |
| DRB1_0301 | 433 | TLTYAEAVKKLTAAG | LTYAEAVKK | 0.3077 | 1791.4 | 32.00 | Sequence |
| DRB1_0301 | 97 | VTLRDIVHTEGPMTP | RDIVHTEGP | 0.3072 | 1801.6 | 32.00 | Sequence |
| DRB1_0301 | 119 | ADACQALNFSHQNGI | CQALNFSHQ | 0.3064 | 1816.7 | 32.00 | Sequence |
| DRB1_0301 | 354 | GITRDVQVPDVRGQS | RDVQVPDVR | 0.3061 | 1822.4 | 32.00 | Sequence |
| DRB1_0301 | 260 | NRYQTAAEMRADLVR | RYQTAAEMR | 0.3048 | 1848.2 | 32.00 | Sequence |
| DRB1_0301 | 2 | TPSHLSDRYELGEIL | TPSHLSDRY | 0.3003 | 1940.6 | 32.00 | Sequence |
| DRB1_0301 | 267 | EMRADLVRVHNGEPP | EMRADLVRV | 0.2999 | 1948.3 | 50.00 | Sequence |
| DRB1_0301 | 611 | TGVNRDGIITLRFGQ | VNRDGIITL | 0.2986 | 1975.9 | 50.00 | Sequence |
| DRB1_0301 | 96 | GVTLRDIVHTEGPMT | GVTLRDIVH | 0.2983 | 1981.8 | 50.00 | Sequence |
| DRB1_0301 | 425 | QREIPDVSTLTYAEA | IPDVSTLTY | 0.2979 | 1990.5 | 50.00 | Sequence |
| DRB1_0301 | 290 | AERTSLLSSAAGNLS | RTSLLSSAA | 0.2970 | 2010.6 | 50.00 | Sequence |
| DRB1_0301 | 542 | TTVPVDSVIELQVSK | VPVDSVIEL | 0.2950 | 2055.4 | 50.00 | Sequence |
| DRB1_0301 | 357 | RDVQVPDVRGQSSAD | RDVQVPDVR | 0.2946 | 2063.6 | 50.00 | Sequence |
| DRB1_0301 | 243 | SADLDAVVLKALAKN | SADLDAVVL | 0.2944 | 2067.5 | 50.00 | Sequence |
| DRB1_0301 | 316 | LDDTDRDRSIGSVGR | LDDTDRDRS | 0.2943 | 2071.3 | 50.00 | Sequence |
| DRB1_0301 | 607 | PPAGTGVNRDGIITL | GTGVNRDGI | 0.2917 | 2130.1 | 50.00 | Sequence |
| DRB1_0301 | 480 | TNVVIIIVGSGPATK | VIIIVGSGP | 0.2909 | 2148.7 | 50.00 | Sequence |
| DRB1_0301 | 356 | TRDVQVPDVRGQSSA | RDVQVPDVR | 0.2907 | 2151.6 | 50.00 | Sequence |
| DRB1_0301 | 202 | GCVLYEVLTGEPPFT | LYEVLTGEP | 0.2905 | 2156.7 | 50.00 | Sequence |
| DRB1_0301 | 355 | ITRDVQVPDVRGQSS | RDVQVPDVR | 0.2902 | 2165.1 | 50.00 | Sequence |
| DRB1_0301 | 496 | IPDVAGQTVDVAQKN | IPDVAGQTV | 0.2888 | 2196.6 | 50.00 | Sequence |
| DRB1_0301 | 220 | PVSVAYQHVREDPIP | VSVAYQHVR | 0.2883 | 2208.5 | 50.00 | Sequence |
| DRB1_0301 | 309 | DPLPRQDLDDTDRDR | LPRQDLDDT | 0.2882 | 2212.3 | 50.00 | Sequence |
| DRB1_0301 | 138 | VKPANIMISATNAVK | IMISATNAV | 0.2882 | 2212.9 | 50.00 | Sequence |
| DRB1_0301 | 155 | DFGIARAIADSGNSV | IARAIADSG | 0.2870 | 2241.5 | 50.00 | Sequence |
| DRB1_0301 | 195 | RSDVYSLGCVLYEVL | RSDVYSLGC | 0.2864 | 2256.0 | 50.00 | Sequence |
| DRB1_0301 | 518 | KFSQASVDSPRPAGE | FSQASVDSP | 0.2838 | 2319.2 | 50.00 | Sequence |
| DRB1_0301 | 221 | VSVAYQHVREDPIPP | VSVAYQHVR | 0.2811 | 2388.6 | 50.00 | Sequence |
| DRB1_0301 | 519 | FSQASVDSPRPAGEV | FSQASVDSP | 0.2804 | 2406.1 | 50.00 | Sequence |
| DRB1_0301 | 154 | MDFGIARAIADSGNS | DFGIARAIA | 0.2802 | 2411.7 | 50.00 | Sequence |
| DRB1_0301 | 197 | DVYSLGCVLYEVLTG | LGCVLYEVL | 0.2794 | 2432.6 | 50.00 | Sequence |
| DRB1_0301 | 198 | VYSLGCVLYEVLTGE | LGCVLYEVL | 0.2779 | 2472.8 | 50.00 | Sequence |
| DRB1_0301 | 201 | LGCVLYEVLTGEPPF | LGCVLYEVL | 0.2776 | 2480.6 | 50.00 | Sequence |
| DRB1_0301 | 259 | ENRYQTAAEMRADLV | RYQTAAEMR | 0.2773 | 2487.3 | 50.00 | Sequence |
| DRB1_0301 | 157 | GIARAIADSGNSVTQ | IARAIADSG | 0.2750 | 2551.4 | 50.00 | Sequence |
| DRB1_0301 | 1 | TTPSHLSDRYELGEI | TPSHLSDRY | 0.2743 | 2570.8 | 50.00 | Sequence |
| DRB1_0301 | 185 | EQARGDSVDARSDVY | ARGDSVDAR | 0.2740 | 2579.3 | 50.00 | Sequence |
| DRB1_0301 | 463 | VGKVIGTNPPANQTS | VIGTNPPAN | 0.2737 | 2588.5 | 50.00 | Sequence |
| DRB1_0301 | 498 | DVAGQTVDVAQKNLN | VAGQTVDVA | 0.2736 | 2590.6 | 50.00 | Sequence |
| DRB1_0301 | 398 | VIGTDPAANTSVSAG | VIGTDPAAN | 0.2735 | 2592.7 | 50.00 | Sequence |

```
DRB1_0301  219  SPVSVAYQHVREDPI  VSVAYQHVR        0.2735        2594.3                50.00     Sequence
DRB1_0301  194  ARSDVYSLGCVLYEV  RSDVYSLGC        0.2722        2629.4                50.00     Sequence
DRB1_0301  499  VAGQTVDVAQKNLNV  VAGQTVDVA        0.2704        2681.9                50.00     Sequence
DRB1_0301  215  FTGDSPVSVAYQHVR  FTGDSPVSV        0.2702        2686.6                50.00     Sequence
DRB1_0301  279  EPPEAPKVLTDAERT  APKVLTDAE        0.2697        2701.7                50.00     Sequence
DRB1_0301  156  FGIARAIADSGNSVT  IARAIADSG        0.2695        2708.0                50.00     Sequence
DRB1_0301  424  EQREIPDVSTLTYAE  EIPDVSTLT        0.2663        2803.4                50.00     Sequence
DRB1_0301  179  AQYLSPEQARGDSVD  AQYLSPEQA        0.2660        2812.7                50.00     Sequence
DRB1_0301  196  SDVYSLGCVLYEVLT  LGCVLYEVL        0.2657        2821.1                50.00     Sequence
DRB1_0301  192  VDARSDVYSLGCVLY  ARSDVYSLG        0.2649        2847.3                50.00     Sequence
DRB1_0301  412  GDEITVNVSTGPEQR  GDEITVNVS        0.2644        2861.6                50.00     Sequence
DRB1_0301   81  TPAGPLPYIVMEYVD  LPYIVMEYV        0.2641        2870.4                50.00     Sequence
DRB1_0301  375  TLQNRGFKIRTLQKP  LQNRGFKIR        0.2634        2892.3                50.00     Sequence
DRB1_0301  206  YEVLTGEPPFTGDSP  YEVLTGEPP        0.2630        2905.4                50.00     Sequence
DRB1_0301  193  DARSDVYSLGCVLYE  RSDVYSLGC        0.2618        2944.1                50.00     Sequence
DRB1_0301  126  NFSHQNGIIHRDVKP  NGIIHRDVK        0.2615        2951.4                50.00     Sequence
DRB1_0301  541  GTTVPVDSVIELQVS  VPVDSVIEL        0.2609        2970.9                50.00     Sequence
DRB1_0301  517  TKFSQASVDSPRPAG  FSQASVDSP        0.2609        2972.1                50.00     Sequence
DRB1_0301  178  TAQYLSPEQARGDSV  AQYLSPEQA        0.2607        2979.1                50.00     Sequence
DRB1_0301  347  IAINTFGGITRDVQV  INTFGGITR        0.2605        2985.0                50.00     Sequence
DRB1_0301  289  DAERTSLLSSAAGNL  RTSLLSSAA        0.2600        3001.2                50.00     Sequence
DRB1_0301  364  VRGQSSADAIATLQN  RGQSSADAI        0.2588        3038.6                50.00     Sequence
DRB1_0301  365  RGQSSADAIATLQNR  RGQSSADAI        0.2582        3060.2                50.00     Sequence
DRB1_0301  293  TSLLSSAAGNLSGPR  SLLSSAAGN        0.2571        3098.1                50.00     Sequence
DRB1_0301  258  PENRYQTAAEMRADL  RYQTAAEMR        0.2561        3129.1                50.00     Sequence
DRB1_0301  495  DIPDVAGQTVDVAQK  IPDVAGQTV        0.2551        3165.4                50.00     Sequence
DRB1_0301  462  LVGKVIGTNPPANQT  VGKVIGTNP        0.2531        3233.2                50.00     Sequence
DRB1_0301   52  YLRFRREAQNAAALN  YLRFRREAQ        0.2515        3290.1                50.00     Sequence
DRB1_0301  584  GMLDKGADVDAGGSQ  GMLDKGADV        0.2515        3290.7                50.00     Sequence
DRB1_0301  372  AIATLQNRGFKIRTL  AIATLQNRG        0.2509        3311.0                50.00     Sequence
DRB1_0301  552  LQVSKGNQFVMPDLS  LQVSKGNQF        0.2508        3313.2                50.00     Sequence
DRB1_0301  583  TGMLDKGADVDAGGS  GMLDKGADV        0.2506        3320.6                50.00     Sequence
DRB1_0301  562  MPDLSGMFWVDAEPR  MFWVDAEPR        0.2501        3340.1                50.00     Sequence
DRB1_0301  497  PDVAGQTVDVAQKNL  VAGQTVDVA        0.2494        3366.5                50.00     Sequence
DRB1_0301  407  TSVSAGDEITVNVST  TSVSAGDEI        0.2489        3384.2                50.00     Sequence
DRB1_0301  376  LQNRGFKIRTLQKPD  LQNRGFKIR        0.2485        3398.3                50.00     Sequence
DRB1_0301  582  WTGMLDKGADVDAGG  GMLDKGADV        0.2471        3450.2                50.00     Sequence
DRB1_0301   16  LGFGGMSEVHLARDL  GMSEVHLAR        0.2471        3451.6                50.00     Sequence
DRB1_0301  218  DSPVSVAYQHVREDP  VSVAYQHVR        0.2465        3473.8                50.00     Sequence
DRB1_0301    0  MTTPSHLSDRYELGE  TPSHLSDRY        0.2462        3483.9                50.00     Sequence
DRB1_0301  516  FTKFSQASVDSPRPA  FSQASVDSP        0.2436        3581.7                50.00     Sequence
DRB1_0301  184  PEQARGDSVDARSDV  ARGDSVDAR        0.2434        3591.6                50.00     Sequence
DRB1_0301  464  GKVIGTNPPANQTSA  GKVIGTNPP        0.2431        3601.1                50.00     Sequence
DRB1_0301  374  ATLQNRGFKIRTLQK  LQNRGFKIR        0.2415        3663.8                50.00     Sequence
DRB1_0301  561  VMPDLSGMFWVDAEP  VMPDLSGMF        0.2404        3709.2                50.00     Sequence
DRB1_0301  101  DIVHTEGPMTPKRAI  IVHTEGPMT        0.2398        3732.6                50.00     Sequence
DRB1_0301  118  IADACQALNFSHQNG  CQALNFSHQ        0.2398        3734.0                50.00     Sequence
DRB1_0301  177  GTAQYLSPEQARGDS  AQYLSPEQA        0.2394        3751.3                50.00     Sequence
DRB1_0301  200  SLGCVLYEVLTGEPP  LGCVLYEVL        0.2380        3809.3                50.00     Sequence
DRB1_0301  294  SLLSSAAGNLSGPRT  SLLSSAAGN        0.2372        3838.9                50.00     Sequence
DRB1_0301  434  LTYAEAVKKLTAAGF  LTYAEAVKK        0.2370        3848.2                50.00     Sequence
DRB1_0301  371  DAIATLQNRGFKIRT  AIATLQNRG        0.2370        3849.5                50.00     Sequence
DRB1_0301  380  GFKIRTLQKPDSTIP  IRTLQKPDS        0.2361        3888.3                50.00     Sequence
DRB1_0301  244  ADLDAVVLKALAKNP  LDAVVLKAL        0.2356        3907.4                50.00     Sequence
DRB1_0301  308  TDPLPRQDLDDTDRD  LPRQDLDDT        0.2355        3909.9                50.00     Sequence
DRB1_0301  159  ARAIADSGNSVTQTA  AIADSGNSV        0.2350        3932.9                50.00     Sequence
DRB1_0301  160  RAIADSGNSVTQTAA  AIADSGNSV        0.2317        4076.8                50.00     Sequence
DRB1_0301  134  IHRDVKPANIMISAT  IHRDVKPAN        0.2310        4104.8                50.00     Sequence
DRB1_0301  125  LNFSHQNGIIHRDVK  LNFSHQNGI        0.2304        4134.6                50.00     Sequence
DRB1_0301  411  AGDEITVNVSTGPEQ  GDEITVNVS        0.2299        4155.3                50.00     Sequence
DRB1_0301  409  VSAGDEITVNVSTGP  GDEITVNVS        0.2294        4179.9                50.00     Sequence
DRB1_0301  379  RGFKIRTLQKPDSTI  IRTLQKPDS        0.2281        4235.5                50.00     Sequence
DRB1_0301  390  DSTIPPDHVIGTDPA  DSTIPPDHV        0.2274        4270.3                50.00     Sequence
DRB1_0301  486  IVGSGPATKDIPDVA  IVGSGPATK        0.2265        4309.9                50.00     Sequence
DRB1_0301  199  YSLGCVLYEVLTGEP  LGCVLYEVL        0.2265        4311.7                50.00     Sequence
DRB1_0301  406  NTSVSAGDEITVNVS  TSVSAGDEI        0.2264        4317.9                50.00     Sequence
```

```
DRB1_0301   69  AIVAVYDTGEAETPA  IVAVYDTGE        0.2262       4324.9              50.00     Sequence
DRB1_0301  423  PEQREIPDVSTLTYA  EQREIPDVS        0.2258       4342.8              50.00     Sequence
DRB1_0301  363  DVRGQSSADAIATLQ  RGQSSADAI        0.2258       4346.5              50.00     Sequence
DRB1_0301  461  ELVGKVIGTNPPANQ  VGKVIGTNP        0.2257       4346.9              50.00     Sequence
DRB1_0301   70  IVAVYDTGEAETPAG  VAVYDTGEA        0.2251       4379.2              50.00     Sequence
DRB1_0301  581  GWTGMLDKGADVDAG  GMLDKGADV        0.2250       4382.1              50.00     Sequence
DRB1_0301    4  SHLSDRYELGEILGF  HLSDRYELG        0.2241       4423.1              50.00     Sequence
DRB1_0301   14  EILGFGGMSEVHLAR  LGFGGMSEV        0.2219       4534.0              50.00     Sequence
DRB1_0301   15  ILGFGGMSEVHLARD  LGFGGMSEV        0.2218       4538.9              50.00     Sequence
DRB1_0301  580  LGWTGMLDKGADVDA  GMLDKGADV        0.2213       4559.5              50.00     Sequence
DRB1_0301  246  LDAVVLKALAKNPEN  LDAVVLKAL        0.2213       4561.3              50.00     Sequence
DRB1_0301  268  MRADLVRVHNGEPPE  MRADLVRVH        0.2211       4570.7              50.00     Sequence
DRB1_0301  408  SVSAGDEITVNVSTG  VSAGDEITV        0.2203       4612.1              50.00     Sequence
DRB1_0301  225  YQHVREDPIPPSARH  YQHVREDPI        0.2198       4638.3              50.00     Sequence
DRB1_0301  540  AGTTVPVDSVIELQV  VPVDSVIEL        0.2186       4697.8              50.00     Sequence
DRB1_0301  381  FKIRTLQKPDSTIPP  IRTLQKPDS        0.2183       4711.5              50.00     Sequence
DRB1_0301  514  YGFTKFSQASVDSPR  YGFTKFSQA        0.2182       4715.4              50.00     Sequence
DRB1_0301  513  VYGFTKFSQASVDSP  YGFTKFSQA        0.2180       4727.2              50.00     Sequence
DRB1_0301  414  EITVNVSTGPEQREI  EITVNVSTG        0.2177       4740.0              50.00     Sequence
DRB1_0301   68  PAIVAVYDTGEAETP  IVAVYDTGE        0.2167       4795.2              50.00     Sequence
DRB1_0301   71  VAVYDTGEAETPAGP  VAVYDTGEA        0.2163       4815.3              50.00     Sequence
DRB1_0301  494  KDIPDVAGQTVDVAQ  IPDVAGQTV        0.2162       4820.3              50.00     Sequence
DRB1_0301  500  AGQTVDVAQKNLNVY  GQTVDVAQK        0.2162       4820.6              50.00     Sequence
DRB1_0301  176  IGTAQYLSPEQARGD  AQYLSPEQA        0.2158       4838.8              50.00     Sequence
DRB1_0301  257  NPENRYQTAAEMRAD  RYQTAAEMR        0.2157       4847.4              50.00     Sequence
DRB1_0301  245  DLDAVVLKALAKNPE  LDAVVLKAL        0.2137       4951.9              50.00     Sequence
DRB1_0301  373  IATLQNRGFKIRTLQ  LQNRGFKIR        0.2136       4956.7              50.00     Sequence
DRB1_0301  208  VLTGEPPFTGDSPVS  EPPFTGDSP        0.2122       5032.4              50.00     Sequence
DRB1_0301    3  PSHLSDRYELGEILG  HLSDRYELG        0.2118       5055.3              50.00     Sequence
DRB1_0301  410  SAGDEITVNVSTGPE  GDEITVNVS        0.2115       5073.1              50.00     Sequence
DRB1_0301  321  RDRSIGSVGRWVAVV  DRSIGSVGR        0.2114       5079.5              50.00     Sequence
DRB1_0301  102  IVHTEGPMTPKRAIE  IVHTEGPMT        0.2107       5113.0              50.00     Sequence
DRB1_0301  161  AIADSGNSVTQTAAV  AIADSGNSV        0.2106       5118.8              50.00     Sequence
DRB1_0301  378  NRGFKIRTLQKPDST  RGFKIRTLQ        0.2101       5147.6              50.00     Sequence
DRB1_0301  217  GDSPVSVAYQHVRED  VSVAYQHVR        0.2101       5149.0              50.00     Sequence
DRB1_0301  110  TPKRAIEVIADACQA  AIEVIADAC        0.2084       5244.7              50.00     Sequence
DRB1_0301  413  DEITVNVSTGPEQRE  EITVNVSTG        0.2081       5262.7              50.00     Sequence
DRB1_0301  597  SQHNRVVYQNPPAGT  SQHNRVVYQ        0.2077       5282.1              50.00     Sequence
DRB1_0301  322  DRSIGSVGRWVAVVA  DRSIGSVGR        0.2068       5338.3              50.00     Sequence
DRB1_0301   67  HPAIVAVYDTGEAET  IVAVYDTGE        0.2067       5343.3              50.00     Sequence
DRB1_0301  360  QVPDVRGQSSADAIA  VPDVRGQSS        0.2059       5387.7              50.00     Sequence
DRB1_0301  501  GQTVDVAQKNLNVYG  GQTVDVAQK        0.2054       5414.7              50.00     Sequence
DRB1_0301  359  VQVPDVRGQSSADAI  VPDVRGQSS        0.2053       5421.8              50.00     Sequence
DRB1_0301  405  ANTSVSAGDEITVNV  TSVSAGDEI        0.2046       5465.6              50.00     Sequence
DRB1_0301  511  LNVYGFTKFSQASVD  YGFTKFSQA        0.2043       5482.6              50.00     Sequence
DRB1_0301  596  GSQHNRVVYQNPPAG  GSQHNRVVY        0.2037       5519.3              50.00     Sequence
DRB1_0301  577  LRALGWTGMLDKGAD  LRALGWTGM        0.2034       5538.4              50.00     Sequence
DRB1_0301  370  ADAIATLQNRGFKIR  AIATLQNRG        0.2033       5540.6              50.00     Sequence
DRB1_0301  175  VIGTAQYLSPEQARG  AQYLSPEQA        0.2031       5554.0              50.00     Sequence
DRB1_0301  510  NLNVYGFTKFSQASV  YGFTKFSQA        0.2024       5598.7              50.00     Sequence
DRB1_0301  512  NVYGFTKFSQASVDS  YGFTKFSQA        0.2016       5645.0              50.00     Sequence
DRB1_0301  224  AYQHVREDPIPPSAR  YQHVREDPI        0.2013       5661.0              50.00     Sequence
DRB1_0301  553  QVSKGNQFVMPDLSG  NQFVMPDLS        0.2011       5677.8              50.00     Sequence
DRB1_0301  222  SVAYQHVREDPIPPS  YQHVREDPI        0.2003       5727.8              50.00     Sequence
DRB1_0301  599  HNRVVYQNPPAGTGV  VVYQNPPAG        0.1988       5818.6              50.00     Sequence
DRB1_0301  515  GFTKFSQASVDSPRP  FSQASVDSP        0.1983       5847.8              50.00     Sequence
DRB1_0301  415  ITVNVSTGPEQREIP  NVSTGPEQR        0.1961       5989.8              50.00     Sequence
DRB1_0301  137  DVKPANIMISATNAV  IMISATNAV        0.1961       5990.6              50.00     Sequence
DRB1_0301  579  ALGWTGMLDKGADVD  GMLDKGADV        0.1943       6106.4              50.00     Sequence
DRB1_0301  416  TVNVSTGPEQREIPD  VNVSTGPEQ        0.1942       6117.8              50.00     Sequence
DRB1_0301  377  QNRGFKIRTLQKPDS  GFKIRTLQK        0.1940       6126.5              50.00     Sequence
DRB1_0301  249  VVLKALAKNPENRYQ  VVLKALAKN        0.1939       6132.4              50.00     Sequence
DRB1_0301    5  HLSDRYELGEILGFG  HLSDRYELG        0.1937       6147.0              50.00     Sequence
DRB1_0301  465  KVIGTNPPANQTSAI  VIGTNPPAN        0.1936       6152.4              50.00     Sequence
DRB1_0301  362  PDVRGQSSADAIATL  RGQSSADAI        0.1933       6173.8              50.00     Sequence
DRB1_0301  440  VKKLTAAGFGRFKQA  VKKLTAAGF        0.1933       6173.9              50.00     Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0301 | 248 | AVVLKALAKNPENRY | VVLKALAKN | 0.1931 | 6186.6 | 50.00 | Sequence |
| DRB1_0301 | 475 | QTSAITNVVIIIVGS | TSAITNVVI | 0.1928 | 6210.0 | 50.00 | Sequence |
| DRB1_0301 | 320 | DRDRSIGSVGRWVAV | DRSIGSVGR | 0.1914 | 6305.9 | 50.00 | Sequence |
| DRB1_0301 | 460 | PELVGKVIGTNPPAN | VGKVIGTNP | 0.1900 | 6397.8 | 50.00 | Sequence |
| DRB1_0301 | 383 | IRTLQKPDSTIPPDH | RTLQKPDST | 0.1897 | 6421.2 | 50.00 | Sequence |
| DRB1_0301 | 479 | ITNVVIIIVGSGPAT | IIIVGSGPA | 0.1888 | 6484.5 | 50.00 | Sequence |
| DRB1_0301 | 319 | TDRDRSIGSVGRWVA | DRSIGSVGR | 0.1879 | 6547.0 | 50.00 | Sequence |
| DRB1_0301 | 223 | VAYQHVREDPIPPSA | YQHVREDPI | 0.1876 | 6569.4 | 50.00 | Sequence |
| DRB1_0301 | 358 | DVQVPDVRGQSSADA | VPDVRGQSS | 0.1872 | 6593.1 | 50.00 | Sequence |
| DRB1_0301 | 598 | QHNRVVYQNPPAGTG | VVYQNPPAG | 0.1869 | 6614.9 | 50.00 | Sequence |
| DRB1_0301 | 174 | AVIGTAQYLSPEQAR | AQYLSPEQA | 0.1868 | 6622.1 | 50.00 | Sequence |
| DRB1_0301 | 368 | SSADAIATLQNRGFK | SSADAIATL | 0.1863 | 6660.5 | 50.00 | Sequence |
| DRB1_0301 | 13 | GEILGFGGMSEVHLA | LGFGGMSEV | 0.1863 | 6663.9 | 50.00 | Sequence |
| DRB1_0301 | 172 | TAAVIGTAQYLSPEQ | AAVIGTAQY | 0.1857 | 6705.8 | 50.00 | Sequence |
| DRB1_0301 | 417 | VNVSTGPEQREIPDV | NVSTGPEQR | 0.1856 | 6710.1 | 50.00 | Sequence |
| DRB1_0301 | 303 | LSGPRTDPLPRQDLD | GPRTDPLPR | 0.1855 | 6721.1 | 50.00 | Sequence |
| DRB1_0301 | 247 | DAVVLKALAKNPENR | VVLKALAKN | 0.1850 | 6752.9 | 50.00 | Sequence |
| DRB1_0301 | 207 | EVLTGEPPFTGDSPV | EVLTGEPPF | 0.1850 | 6756.1 | 50.00 | Sequence |
| DRB1_0301 | 80 | ETPAGPLPYIVMEYV | LPYIVMEYV | 0.1849 | 6765.9 | 50.00 | Sequence |
| DRB1_0301 | 600 | NRVVYQNPPAGTGVN | NRVVYQNPP | 0.1848 | 6768.5 | 50.00 | Sequence |
| DRB1_0301 | 382 | KIRTLQKPDSTIPPD | IRTLQKPDS | 0.1847 | 6775.8 | 50.00 | Sequence |
| DRB1_0301 | 492 | ATKDIPDVAGQTVDV | ATKDIPDVA | 0.1840 | 6831.6 | 50.00 | Sequence |
| DRB1_0301 | 585 | MLDKGADVDAGGSQH | MLDKGADVD | 0.1839 | 6835.2 | 50.00 | Sequence |
| DRB1_0301 | 305 | GPRTDPLPRQDLDDT | GPRTDPLPR | 0.1838 | 6840.8 | 50.00 | Sequence |
| DRB1_0301 | 216 | TGDSPVSVAYQHVRE | VSVAYQHVR | 0.1829 | 6910.2 | 50.00 | Sequence |
| DRB1_0301 | 12 | LGEILGFGGMSEVHL | ILGFGGMSE | 0.1829 | 6910.7 | 50.00 | Sequence |
| DRB1_0301 | 250 | VLKALAKNPENRYQT | VLKALAKNP | 0.1826 | 6932.7 | 50.00 | Sequence |
| DRB1_0301 | 489 | SGPATKDIPDVAGQT | ATKDIPDVA | 0.1821 | 6968.7 | 50.00 | Sequence |
| DRB1_0301 | 578 | RALGWTGMLDKGADV | GMLDKGADV | 0.1819 | 6987.1 | 50.00 | Sequence |
| DRB1_0301 | 72 | AVYDTGEAETPAGPL | AVYDTGEAE | 0.1818 | 6994.3 | 50.00 | Sequence |
| DRB1_0301 | 550 | IELQVSKGNQFVMPD | LQVSKGNQF | 0.1818 | 6994.6 | 50.00 | Sequence |
| DRB1_0301 | 235 | PSARHEGLSADLDAV | HEGLSADLD | 0.1812 | 7041.5 | 50.00 | Sequence |
| DRB1_0301 | 346 | TIAINTFGGITRDVQ | INTFGGITR | 0.1809 | 7059.6 | 50.00 | Sequence |
| DRB1_0301 | 367 | QSSADAIATLQNRGF | SSADAIATL | 0.1807 | 7074.3 | 50.00 | Sequence |
| DRB1_0301 | 361 | VPDVRGQSSADAIAT | VPDVRGQSS | 0.1801 | 7119.7 | 50.00 | Sequence |
| DRB1_0301 | 256 | KNPENRYQTAAEMRA | RYQTAAEMR | 0.1799 | 7137.4 | 50.00 | Sequence |
| DRB1_0301 | 173 | AAVIGTAQYLSPEQA | AAVIGTAQY | 0.1798 | 7147.8 | 50.00 | Sequence |
| DRB1_0301 | 491 | PATKDIPDVAGQTVD | ATKDIPDVA | 0.1784 | 7258.0 | 50.00 | Sequence |
| DRB1_0301 | 295 | LLSSAAGNLSGPRTD | LLSSAAGNL | 0.1780 | 7287.5 | 50.00 | Sequence |
| DRB1_0301 | 576 | RLRALGWTGMLDKGA | LRALGWTGM | 0.1779 | 7293.1 | 50.00 | Sequence |
| DRB1_0301 | 520 | SQASVDSPRPAGEVT | SQASVDSPR | 0.1773 | 7345.3 | 50.00 | Sequence |
| DRB1_0301 | 474 | NQTSAITNVVIIIVG | TSAITNVVI | 0.1764 | 7410.5 | 50.00 | Sequence |
| DRB1_0301 | 317 | DDTDRDRSIGSVGRW | DDTDRDRSI | 0.1762 | 7430.3 | 50.00 | Sequence |
| DRB1_0301 | 183 | SPEQARGDSVDARSD | ARGDSVDAR | 0.1761 | 7437.1 | 50.00 | Sequence |
| DRB1_0301 | 422 | GPEQREIPDVSTLTY | EIPDVSTLT | 0.1749 | 7538.3 | 50.00 | Sequence |
| DRB1_0301 | 369 | SADAIATLQNRGFKI | AIATLQNRG | 0.1748 | 7543.6 | 50.00 | Sequence |
| DRB1_0301 | 307 | RTDPLPRQDLDDTDR | PLPRQDLDD | 0.1737 | 7636.5 | 50.00 | Sequence |
| DRB1_0301 | 473 | ANQTSAITNVVIIIV | ANQTSAITN | 0.1731 | 7687.7 | 50.00 | Sequence |
| DRB1_0301 | 551 | ELQVSKGNQFVMPDL | LQVSKGNQF | 0.1728 | 7706.1 | 50.00 | Sequence |
| DRB1_0301 | 606 | NPPAGTGVNRDGIIT | GTGVNRDGI | 0.1726 | 7725.3 | 50.00 | Sequence |
| DRB1_0301 | 399 | IGTDPAANTSVSAGD | DPAANTSVS | 0.1724 | 7739.7 | 50.00 | Sequence |
| DRB1_0301 | 8 | DRYELGEILGFGGMS | DRYELGEIL | 0.1721 | 7765.3 | 50.00 | Sequence |
| DRB1_0301 | 490 | GPATKDIPDVAGQTV | ATKDIPDVA | 0.1719 | 7780.6 | 50.00 | Sequence |
| DRB1_0301 | 340 | VLTVVVTIAINTFGG | VVVTIAINT | 0.1712 | 7840.3 | 50.00 | Sequence |
| DRB1_0301 | 402 | DPAANTSVSAGDEIT | DPAANTSVS | 0.1712 | 7844.9 | 50.00 | Sequence |
| DRB1_0301 | 595 | GGSQHNRVVYQNPPA | GSQHNRVVY | 0.1704 | 7913.0 | 50.00 | Sequence |
| DRB1_0301 | 124 | ALNFSHQNGIIHRDV | LNFSHQNGI | 0.1688 | 8048.4 | 50.00 | Sequence |
| DRB1_0301 | 366 | GQSSADAIATLQNRG | SSADAIATL | 0.1688 | 8052.9 | 50.00 | Sequence |
| DRB1_0301 | 304 | SGPRTDPLPRQDLDD | GPRTDPLPR | 0.1685 | 8077.7 | 50.00 | Sequence |
| DRB1_0301 | 171 | QTAAVIGTAQYLSPE | AAVIGTAQY | 0.1684 | 8085.6 | 50.00 | Sequence |
| DRB1_0301 | 123 | QALNFSHQNGIIHRD | LNFSHQNGI | 0.1683 | 8092.9 | 50.00 | Sequence |
| DRB1_0301 | 66 | NHPAIVAVYDTGEAE | AIVAVYDTG | 0.1680 | 8117.9 | 50.00 | Sequence |
| DRB1_0301 | 493 | TKDIPDVAGQTVDVA | IPDVAGQTV | 0.1678 | 8141.5 | 50.00 | Sequence |
| DRB1_0301 | 388 | KPDSTIPPDHVIGTD | DSTIPPDHV | 0.1670 | 8204.9 | 50.00 | Sequence |
| DRB1_0301 | 109 | MTPKRAIEVIADACQ | AIEVIADAC | 0.1670 | 8211.6 | 50.00 | Sequence |
| DRB1_0301 | 509 | KNLNVYGFTKFSQAS | YGFTKFSQA | 0.1650 | 8383.1 | 50.00 | Sequence |

```
DRB1_0301  439  AVKKLTAAGFGRFKQ  VKKLTAAGF        0.1645       8435.4              50.00     Sequence
DRB1_0301  389  PDSTIPPDHVIGTDP  DSTIPPDHV        0.1643       8450.6              50.00     Sequence
DRB1_0301  539  PAGTTVPVDSVIELQ  VPVDSVIEL        0.1643       8451.1              50.00     Sequence
DRB1_0301  287  LTDAERTSLLSSAAG  LTDAERTSL        0.1629       8578.9              50.00     Sequence
DRB1_0301    7  SDRYELGEILGFGGM  DRYELGEIL        0.1627       8596.7              50.00     Sequence
DRB1_0301  302  NLSGPRTDPLPRQDL  GPRTDPLPR        0.1625       8616.6              50.00     Sequence
DRB1_0301   60  QNAAALNHPAIVAVY  NAAALNHPA        0.1624       8626.8              50.00     Sequence
DRB1_0301  404  AANTSVSAGDEITVN  TSVSAGDEI        0.1621       8655.8              50.00     Sequence
DRB1_0301  594  AGGSQHNRVVYQNPP  AGGSQHNRV        0.1608       8778.8              50.00     Sequence
DRB1_0301  442  KLTAAGFGRFKQANS  LTAAGFGRF        0.1599       8859.7              50.00     Sequence
DRB1_0301  338  LAVLTVVVTIAINTF  LAVLTVVVT        0.1598       8875.7              50.00     Sequence
DRB1_0301  570  WVDAEPRLRALGWTG  WVDAEPRLR        0.1572       9129.2              50.00     Sequence
DRB1_0301    6  LSDRYELGEILGFGG  DRYELGEIL        0.1569       9153.9              50.00     Sequence
DRB1_0301  476  TSAITNVVIIIVGSG  TSAITNVVI        0.1569       9160.8              50.00     Sequence
DRB1_0301  318  DTDRDRSIGSVGRWV  DRSIGSVGR        0.1566       9186.1              50.00     Sequence
DRB1_0301  343  VVVTIAINTFGGITR  VVVTIAINT        0.1564       9209.4              50.00     Sequence
DRB1_0301  443  LTAAGFGRFKQANSP  LTAAGFGRF        0.1562       9225.1              50.00     Sequence
DRB1_0301  251  LKALAKNPENRYQTA  LKALAKNPE        0.1558       9262.0              50.00     Sequence
DRB1_0301  300  AGNLSGPRTDPLPRQ  AGNLSGPRT        0.1555       9295.9              50.00     Sequence
DRB1_0301  334  VVAVLAVLTVVVTIA  VVAVLAVLT        0.1553       9316.4              50.00     Sequence
DRB1_0301  401  TDPAANTSVSAGDEI  DPAANTSVS        0.1544       9405.6              50.00     Sequence
DRB1_0301  339  AVLTVVVTIAINTFG  VLTVVVTIA        0.1543       9413.5              50.00     Sequence
DRB1_0301  575  PRLRALGWTGMLDKG  LRALGWTGM        0.1532       9528.2              50.00     Sequence
DRB1_0301  448  FGRFKQANSPSTPEL  FKQANSPST        0.1528       9570.9              50.00     Sequence
DRB1_0301  288  TDAERTSLLSSAAGN  RTSLLSSAA        0.1526       9594.5              50.00     Sequence
DRB1_0301  459  TPELVGKVIGTNPPA  LVGKVIGTN        0.1524       9616.2              50.00     Sequence
DRB1_0301  342  TVVVTIAINTFGGIT  VVVTIAINT        0.1520       9653.1              50.00     Sequence
DRB1_0301  106  EGPMTPKRAIEVIAD  EGPMTPKRA        0.1512       9741.8              50.00     Sequence
DRB1_0301  387  QKPDSTIPPDHVIGT  DSTIPPDHV        0.1510       9756.6              50.00     Sequence
DRB1_0301  488  GSGPATKDIPDVAGQ  ATKDIPDVA        0.1503       9832.3              50.00     Sequence
DRB1_0301   73  VYDTGEAETPAGPLP  VYDTGEAET        0.1501       9855.7              50.00     Sequence
DRB1_0301  403  PAANTSVSAGDEITV  PAANTSVSA        0.1489       9984.7              50.00     Sequence
DRB1_0301  337  VLAVLTVVVTIAINT  VLAVLTVVV        0.1488       9999.3              50.00     Sequence
DRB1_0301  170  TQTAAVIGTAQYLSP  AAVIGTAQY        0.1485      10032.1              50.00     Sequence
DRB1_0301  306  PRTDPLPRQDLDDTD  LPRQDLDDT        0.1482      10064.7              50.00     Sequence
DRB1_0301    9  RYELGEILGFGGMSE  RYELGEILG        0.1478      10106.0              50.00     Sequence
DRB1_0301   11  ELGEILGFGGMSEVH  GEILGFGGM        0.1468      10214.8              50.00     Sequence
DRB1_0301   59  AQNAAALNHPAIVAV  QNAAALNHP        0.1467      10219.8              50.00     Sequence
DRB1_0301  446  AGFGRFKQANSPSTP  AGFGRFKQA        0.1467      10225.2              50.00     Sequence
DRB1_0301  182  LSPEQARGDSVDARS  ARGDSVDAR        0.1466      10236.9              50.00     Sequence
DRB1_0301  418  NVSTGPEQREIPDVS  NVSTGPEQR        0.1465      10245.3              50.00     Sequence
DRB1_0301  278  GEPPEAPKVLTDAER  PKVLTDAER        0.1464      10259.7              50.00     Sequence
DRB1_0301  162  IADSGNSVTQTAAVI  IADSGNSVT        0.1463      10266.3              50.00     Sequence
DRB1_0301  341  LTVVVTIAINTFGGI  VVVTIAINT        0.1454      10363.5              50.00     Sequence
DRB1_0301   61  NAAALNHPAIVAVYD  NAAALNHPA        0.1450      10415.7              50.00     Sequence
DRB1_0301  449  GRFKQANSPSTPELV  FKQANSPST        0.1450      10417.5              50.00     Sequence
DRB1_0301  103  VHTEGPMTPKRAIEV  VHTEGPMTP        0.1449      10430.6              50.00     Sequence
DRB1_0301  299  AAGNLSGPRTDPLPR  AGNLSGPRT        0.1448      10437.1              50.00     Sequence
DRB1_0301  336  AVLAVLTVVVTIAIN  VLAVLTVVV        0.1447      10442.9              50.00     Sequence
DRB1_0301  165  SGNSVTQTAAVIGTA  NSVTQTAAV        0.1445      10468.6              50.00     Sequence
DRB1_0301  450  RFKQANSPSTPELVG  FKQANSPST        0.1445      10471.2              50.00     Sequence
DRB1_0301  466  VIGTNPPANQTSAIT  VIGTNPPAN        0.1445      10473.7              50.00     Sequence
DRB1_0301   65  LNHPAIVAVYDTGEA  LNHPAIVAV        0.1443      10496.1              50.00     Sequence
DRB1_0301  521  QASVDSPRPAGEVTG  QASVDSPRP        0.1440      10531.5              50.00     Sequence
DRB1_0301  438  EAVKKLTAAGFGRFK  VKKLTAAGF        0.1439      10541.5              50.00     Sequence
DRB1_0301  502  QTVDVAQKNLNVYGF  QTVDVAQKN        0.1438      10554.1              50.00     Sequence
DRB1_0301  508  QKNLNVYGFTKFSQA  LNVYGFTKF        0.1437      10564.4              50.00     Sequence
DRB1_0301  586  LDKGADVDAGGSQHN  DKGADVDAG        0.1436      10567.3              50.00     Sequence
DRB1_0301  269  RADLVRVHNGEPPEA  RADLVRVHN        0.1431      10628.0              50.00     Sequence
DRB1_0301  344  VVTIAINTFGGITRD  VVTIAINTF        0.1423      10720.3              50.00     Sequence
DRB1_0301  105  TEGPMTPKRAIEVIA  EGPMTPKRA        0.1421      10745.4              50.00     Sequence
DRB1_0301  574  EPRLRALGWTGMLDK  LRALGWTGM        0.1406      10923.5              50.00     Sequence
DRB1_0301  400  GTDPAANTSVSAGDE  PAANTSVSA        0.1402      10969.7              50.00     Sequence
DRB1_0301  451  FKQANSPSTPELVGK  FKQANSPST        0.1398      11011.9              50.00     Sequence
DRB1_0301  472  PANQTSAITNVVIII  ANQTSAITN        0.1393      11078.9              50.00     Sequence
DRB1_0301  329  GRWVAVVAVLAVLTV  GRWVAVVAV        0.1392      11089.0              50.00     Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0301 | 384 | RTLQKPDSTIPPDHV | RTLQKPDST | 0.1390 | 11116.7 | 50.00 | Sequence |
| DRB1_0301 | 593 | DAGGSQHNRVVYQNP | AGGSQHNRV | 0.1386 | 11159.8 | 50.00 | Sequence |
| DRB1_0301 | 345 | VTIAINTFGGITRDV | INTFGGITR | 0.1385 | 11172.7 | 50.00 | Sequence |
| DRB1_0301 | 386 | LQKPDSTIPPDHVIG | DSTIPPDHV | 0.1375 | 11291.4 | 50.00 | Sequence |
| DRB1_0301 | 538 | PPAGTTVPVDSVIEL | VPVDSVIEL | 0.1371 | 11346.5 | 50.00 | Sequence |
| DRB1_0301 | 441 | KKLTAAGFGRFKQAN | LTAAGFGRF | 0.1369 | 11372.3 | 50.00 | Sequence |
| DRB1_0301 | 335 | VAVLAVLTVVVTIAI | VLAVLTVVV | 0.1369 | 11373.1 | 50.00 | Sequence |
| DRB1_0301 | 487 | VGSGPATKDIPDVAG | SGPATKDIP | 0.1354 | 11559.7 | 50.00 | Sequence |
| DRB1_0301 | 445 | AAGFGRFKQANSPST | AGFGRFKQA | 0.1348 | 11624.6 | 50.00 | Sequence |
| DRB1_0301 | 328 | VGRWVAVVAVLAVLT | GRWVAVVAV | 0.1348 | 11633.5 | 50.00 | Sequence |
| DRB1_0301 | 447 | GFGRFKQANSPSTPE | FKQANSPST | 0.1342 | 11711.0 | 50.00 | Sequence |
| DRB1_0301 | 108 | PMTPKRAIEVIADAC | MTPKRAIEV | 0.1339 | 11747.3 | 50.00 | Sequence |
| DRB1_0301 | 164 | DSGNSVTQTAAVIGT | SGNSVTQTA | 0.1336 | 11782.7 | 50.00 | Sequence |
| DRB1_0301 | 605 | QNPPAGTGVNRDGII | GTGVNRDGI | 0.1330 | 11858.4 | 50.00 | Sequence |
| DRB1_0301 | 166 | GNSVTQTAAVIGTAQ | NSVTQTAAV | 0.1329 | 11874.1 | 50.00 | Sequence |
| DRB1_0301 | 53 | LRFRREAQNAAALNH | LRFRREAQN | 0.1318 | 12010.8 | 50.00 | Sequence |
| DRB1_0301 | 272 | LVRVHNGEPPEAPKV | LVRVHNGEP | 0.1314 | 12064.4 | 50.00 | Sequence |
| DRB1_0301 | 270 | ADLVRVHNGEPPEAP | ADLVRVHNG | 0.1309 | 12133.4 | 50.00 | Sequence |
| DRB1_0301 | 421 | TGPEQREIPDVSTLT | EQREIPDVS | 0.1307 | 12151.9 | 50.00 | Sequence |
| DRB1_0301 | 62 | AAALNHPAIVAVYDT | AAALNHPAI | 0.1303 | 12207.7 | 50.00 | Sequence |
| DRB1_0301 | 10 | YELGEILGFGGMSEV | GEILGFGGM | 0.1294 | 12333.1 | 50.00 | Sequence |
| DRB1_0301 | 301 | GNLSGPRTDPLPRQD | LSGPRTDPL | 0.1293 | 12342.4 | 50.00 | Sequence |
| DRB1_0301 | 504 | VDVAQKNLNVYGFTK | VDVAQKNLN | 0.1293 | 12348.4 | 50.00 | Sequence |
| DRB1_0301 | 333 | AVVAVLAVLTVVVTI | VVAVLAVLT | 0.1292 | 12353.2 | 50.00 | Sequence |
| DRB1_0301 | 252 | KALAKNPENRYQTAA | ALAKNPENR | 0.1287 | 12423.7 | 50.00 | Sequence |
| DRB1_0301 | 331 | WVAVVAVLAVLTVVV | WVAVVAVLA | 0.1286 | 12439.8 | 50.00 | Sequence |
| DRB1_0301 | 167 | NSVTQTAAVIGTAQY | NSVTQTAAV | 0.1281 | 12498.0 | 50.00 | Sequence |
| DRB1_0301 | 104 | HTEGPMTPKRAIEVI | EGPMTPKRA | 0.1273 | 12614.0 | 50.00 | Sequence |
| DRB1_0301 | 64 | ALNHPAIVAVYDTGE | LNHPAIVAV | 0.1267 | 12691.3 | 50.00 | Sequence |
| DRB1_0301 | 587 | DKGADVDAGGSQHNR | GADVDAGGS | 0.1264 | 12740.9 | 50.00 | Sequence |
| DRB1_0301 | 181 | YLSPEQARGDSVDAR | PEQARGDSV | 0.1262 | 12757.4 | 50.00 | Sequence |
| DRB1_0301 | 503 | TVDVAQKNLNVYGFT | VDVAQKNLN | 0.1261 | 12775.9 | 50.00 | Sequence |
| DRB1_0301 | 330 | RWVAVVAVLAVLTVV | AVVAVLAVL | 0.1257 | 12828.6 | 50.00 | Sequence |
| DRB1_0301 | 271 | DLVRVHNGEPPEAPK | LVRVHNGEP | 0.1253 | 12883.6 | 50.00 | Sequence |
| DRB1_0301 | 226 | QHVREDPIPPSARHE | HVREDPIPP | 0.1252 | 12908.5 | 50.00 | Sequence |
| DRB1_0301 | 437 | AEAVKKLTAAGFGRF | VKKLTAAGF | 0.1244 | 13017.2 | 50.00 | Sequence |
| DRB1_0301 | 601 | RVVYQNPPAGTGVNR | VVYQNPPAG | 0.1237 | 13110.7 | 50.00 | Sequence |
| DRB1_0301 | 169 | VTQTAAVIGTAQYLS | AVIGTAQYL | 0.1233 | 13168.9 | 50.00 | Sequence |
| DRB1_0301 | 530 | AGEVTGTNPPAGTTV | GEVTGTNPP | 0.1220 | 13362.4 | 50.00 | Sequence |
| DRB1_0301 | 180 | QYLSPEQARGDSVDA | QYLSPEQAR | 0.1217 | 13399.0 | 50.00 | Sequence |
| DRB1_0301 | 477 | SAITNVVIIIVGSGP | SAITNVVII | 0.1216 | 13414.5 | 50.00 | Sequence |
| DRB1_0301 | 255 | AKNPENRYQTAAEMR | RYQTAAEMR | 0.1215 | 13426.0 | 50.00 | Sequence |
| DRB1_0301 | 589 | GADVDAGGSQHNRVV | GADVDAGGS | 0.1215 | 13434.4 | 50.00 | Sequence |
| DRB1_0301 | 298 | SAAGNLSGPRTDPLP | AGNLSGPRT | 0.1214 | 13436.8 | 50.00 | Sequence |
| DRB1_0301 | 107 | GPMTPKRAIEVIADA | PMTPKRAIE | 0.1214 | 13444.0 | 50.00 | Sequence |
| DRB1_0301 | 227 | HVREDPIPPSARHEG | HVREDPIPP | 0.1212 | 13471.4 | 50.00 | Sequence |
| DRB1_0301 | 588 | KGADVDAGGSQHNRV | GADVDAGGS | 0.1201 | 13626.8 | 50.00 | Sequence |
| DRB1_0301 | 332 | VAVVAVLAVLTVVVT | VVAVLAVLT | 0.1197 | 13698.8 | 50.00 | Sequence |
| DRB1_0301 | 385 | TLQKPDSTIPPDHVI | DSTIPPDHV | 0.1187 | 13847.5 | 50.00 | Sequence |
| DRB1_0301 | 592 | VDAGGSQHNRVVYQN | AGGSQHNRV | 0.1185 | 13866.4 | 50.00 | Sequence |
| DRB1_0301 | 234 | PPSARHEGLSADLDA | HEGLSADLD | 0.1180 | 13954.3 | 50.00 | Sequence |
| DRB1_0301 | 505 | DVAQKNLNVYGFTKF | VAQKNLNVY | 0.1171 | 14078.2 | 50.00 | Sequence |
| DRB1_0301 | 531 | GEVTGTNPPAGTTVP | GEVTGTNPP | 0.1171 | 14090.4 | 50.00 | Sequence |
| DRB1_0301 | 58 | EAQNAAALNHPAIVA | QNAAALNHP | 0.1170 | 14105.3 | 50.00 | Sequence |
| DRB1_0301 | 591 | DVDAGGSQHNRVVYQ | AGGSQHNRV | 0.1157 | 14300.0 | 50.00 | Sequence |
| DRB1_0301 | 478 | AITNVVIIIVGSGPA | IIIVGSGPA | 0.1157 | 14305.7 | 50.00 | Sequence |
| DRB1_0301 | 507 | AQKNLNVYGFTKFSQ | LNVYGFTKF | 0.1137 | 14616.3 | 50.00 | Sequence |
| DRB1_0301 | 529 | PAGEVTGTNPPAGTT | GEVTGTNPP | 0.1129 | 14738.4 | 50.00 | Sequence |
| DRB1_0301 | 163 | ADSGNSVTQTAAVIG | SGNSVTQTA | 0.1128 | 14746.9 | 50.00 | Sequence |
| DRB1_0301 | 253 | ALAKNPENRYQTAAE | ALAKNPENR | 0.1119 | 14891.4 | 50.00 | Sequence |
| DRB1_0301 | 327 | SVGRWVAVVAVLAVL | GRWVAVVAV | 0.1113 | 14988.3 | 50.00 | Sequence |
| DRB1_0301 | 63 | AALNHPAIVAVYDTG | LNHPAIVAV | 0.1112 | 15014.2 | 50.00 | Sequence |
| DRB1_0301 | 458 | STPELVGKVIGTNPP | TPELVGKVI | 0.1103 | 15163.7 | 50.00 | Sequence |
| DRB1_0301 | 323 | RSIGSVGRWVAVVAV | RSIGSVGRW | 0.1093 | 15324.3 | 50.00 | Sequence |
| DRB1_0301 | 506 | VAQKNLNVYGFTKFS | VAQKNLNVY | 0.1092 | 15335.0 | 50.00 | Sequence |
| DRB1_0301 | 444 | TAAGFGRFKQANSPS | AGFGRFKQA | 0.1091 | 15361.4 | 50.00 | Sequence |

```
  DRB1_0301  471  PPANQTSAITNVVII  ANQTSAITN        0.1074      15647.9                50.00     Sequence
  DRB1_0301  273  VRVHNGEPPEAPKVL  VRVHNGEPP        0.1064      15819.1                50.00     Sequence
  DRB1_0301  135  HRDVKPANIMISATN  HRDVKPANI        0.1057      15940.1                50.00     Sequence
  DRB1_0301   57  REAQNAAALNHPAIV  QNAAALNHP        0.1052      16021.2                50.00     Sequence
  DRB1_0301  325  IGSVGRWVAVVAVLA  GRWVAVVAV        0.1029      16414.8                50.00     Sequence
  DRB1_0301  297  SSAAGNLSGPRTDPL  AGNLSGPRT        0.1027      16460.3                50.00     Sequence
  DRB1_0301  528  RPAGEVTGTNPPAGT  GEVTGTNPP        0.1026      16483.8                50.00     Sequence
  DRB1_0301  228  VREDPIPPSARHEGL  VREDPIPPS        0.1013      16709.0                50.00     Sequence
  DRB1_0301  590  ADVDAGGSQHNRVVY  AGGSQHNRV        0.0987      17178.1                50.00     Sequence
  DRB1_0301  522  ASVDSPRPAGEVTGT  ASVDSPRPA        0.0971      17492.8                50.00     Sequence
  DRB1_0301  571  VDAEPRLRALGWTGM  VDAEPRLRA        0.0970      17502.1                50.00     Sequence
  DRB1_0301  324  SIGSVGRWVAVVAVL  SIGSVGRWV        0.0965      17595.3                50.00     Sequence
  DRB1_0301  452  KQANSPSTPELVGKV  KQANSPSTP        0.0960      17699.0                50.00     Sequence
  DRB1_0301  136  RDVKPANIMISATNA  VKPANIMIS        0.0930      18278.2                50.00     Sequence
  DRB1_0301  326  GSVGRWVAVVAVLAV  GRWVAVVAV        0.0925      18382.1                50.00     Sequence
  DRB1_0301  233  IPPSARHEGLSADLD  IPPSARHEG        0.0904      18793.8                50.00     Sequence
  DRB1_0301  573  AEPRLRALGWTGMLD  LRALGWTGM        0.0901      18865.1                50.00     Sequence
  DRB1_0301  602  VVYQNPPAGTGVNRD  VVYQNPPAG        0.0900      18878.6                50.00     Sequence
  DRB1_0301  296  LSSAAGNLSGPRTDP  LSSAAGNLS        0.0876      19381.9                50.00     Sequence
  DRB1_0301  435  TYAEAVKKLTAAGFG  AEAVKKLTA        0.0874      19429.8                50.00     Sequence
  DRB1_0301  254  LAKNPENRYQTAAEM  LAKNPENRY        0.0866      19587.5                50.00     Sequence
  DRB1_0301  168  SVTQTAAVIGTAQYL  SVTQTAAVI        0.0864      19622.7                50.00     Sequence
  DRB1_0301  537  NPPAGTTVPVDSVIE  AGTTVPVDS        0.0859      19743.2                50.00     Sequence
  DRB1_0301   54  RFRREAQNAAALNHP  RFRREAQNA        0.0858      19763.5                50.00     Sequence
  DRB1_0301  470  NPPANQTSAITNVVI  ANQTSAITN        0.0840      20145.4                50.00     Sequence
  DRB1_0301  436  YAEAVKKLTAAGFGR  AEAVKKLTA        0.0837      20206.1                50.00     Sequence
  DRB1_0301  457  PSTPELVGKVIGTNP  TPELVGKVI        0.0833      20297.3                50.00     Sequence
  DRB1_0301  274  RVHNGEPPEAPKVLT  RVHNGEPPE        0.0828      20406.3                50.00     Sequence
  DRB1_0301   56  RREAQNAAALNHPAI  RREAQNAAA        0.0798      21095.7                50.00     Sequence
  DRB1_0301  527  PRPAGEVTGTNPPAG  GEVTGTNPP        0.0796      21141.4                50.00     Sequence
  DRB1_0301  277  NGEPPEAPKVLTDAE  APKVLTDAE        0.0786      21356.8                50.00     Sequence
  DRB1_0301   55  FRREAQNAAALNHPA  RREAQNAAA        0.0757      22049.3                50.00     Sequence
  DRB1_0301  604  YQNPPAGTGVNRDGI  PPAGTGVNR        0.0742      22406.4                50.00     Sequence
  DRB1_0301  229  REDPIPPSARHEGLS  IPPSARHEG        0.0708      23239.2                50.00     Sequence
  DRB1_0301  532  EVTGTNPPAGTTVPV  VTGTNPPAG        0.0707      23270.4                50.00     Sequence
  DRB1_0301  456  SPSTPELVGKVIGTN  TPELVGKVI        0.0655      24605.5                50.00     Sequence
  DRB1_0301   79  AETPAGPLPYIVMEY  GPLPYIVME        0.0646      24852.2                50.00     Sequence
  DRB1_0301  536  TNPPAGTTVPVDSVI  NPPAGTTVP        0.0632      25236.2                50.00     Sequence
  DRB1_0301  526  SPRPAGEVTGTNPPA  GEVTGTNPP        0.0627      25370.6                50.00     Sequence
  DRB1_0301  230  EDPIPPSARHEGLSA  IPPSARHEG        0.0618      25627.7                50.00     Sequence
  DRB1_0301  572  DAEPRLRALGWTGML  LRALGWTGM        0.0606      25950.3                50.00     Sequence
  DRB1_0301  232  PIPPSARHEGLSADL  IPPSARHEG        0.0596      26228.6                50.00     Sequence
  DRB1_0301  420  STGPEQREIPDVSTL  EQREIPDVS        0.0587      26493.9                50.00     Sequence
  DRB1_0301  469  TNPPANQTSAITNVV  ANQTSAITN        0.0567      27071.7                50.00     Sequence
  DRB1_0301  419  VSTGPEQREIPDVST  VSTGPEQRE        0.0557      27380.7                50.00     Sequence
  DRB1_0301   74  YDTGEAETPAGPLPY  YDTGEAETP        0.0555      27436.7                50.00     Sequence
  DRB1_0301  523  SVDSPRPAGEVTGTN  VDSPRPAGE        0.0554      27442.7                50.00     Sequence
  DRB1_0301  467  IGTNPPANQTSAITN  IGTNPPANQ        0.0554      27461.7                50.00     Sequence
  DRB1_0301  231  DPIPPSARHEGLSAD  IPPSARHEG        0.0535      28040.2                50.00     Sequence
  DRB1_0301  455  NSPSTPELVGKVIGT  NSPSTPELV        0.0533      28092.2                50.00     Sequence
  DRB1_0301   75  DTGEAETPAGPLPYI  GEAETPAGP        0.0527      28260.5                50.00     Sequence
  DRB1_0301  603  VYQNPPAGTGVNRDG  VYQNPPAGT        0.0504      28978.8                50.00     Sequence
  DRB1_0301  533  VTGTNPPAGTTVPVD  VTGTNPPAG        0.0497      29211.8                50.00     Sequence
  DRB1_0301  454  ANSPSTPELVGKVIG  NSPSTPELV        0.0485      29583.0                50.00     Sequence
  DRB1_0301  453  QANSPSTPELVGKVI  NSPSTPELV        0.0482      29667.6                50.00     Sequence
  DRB1_0301  524  VDSPRPAGEVTGTNP  VDSPRPAGE        0.0476      29862.8                50.00     Sequence
  DRB1_0301   77  GEAETPAGPLPYIVM  GEAETPAGP        0.0461      30374.4                50.00     Sequence
  DRB1_0301  525  DSPRPAGEVTGTNPP  RPAGEVTGT        0.0452      30648.0                50.00     Sequence
  DRB1_0301  535  GTNPPAGTTVPVDSV  NPPAGTTVP        0.0445      30907.8                50.00     Sequence
  DRB1_0301  468  GTNPPANQTSAITNV  ANQTSAITN        0.0423      31637.3                50.00     Sequence
  DRB1_0301  275  VHNGEPPEAPKVLTD  VHNGEPPEA        0.0421      31710.3                50.00     Sequence
  DRB1_0301   76  TGEAETPAGPLPYIV  GEAETPAGP        0.0402      32373.8                50.00     Sequence
  DRB1_0301  534  TGTNPPAGTTVPVDS  NPPAGTTVP        0.0358      33942.7                50.00     Sequence
  DRB1_0301   78  EAETPAGPLPYIVME  AETPAGPLP        0.0307      35874.6                50.00     Sequence
  DRB1_0301  276  HNGEPPEAPKVLTDA  HNGEPPEAP        0.0254      37982.1                50.00     Sequence
-------------------------------------------------------------------------------------------------------
```

```
Allele: DRB1_0301. Number of high binders 15. Number of weak binders 71. Number of peptides 612

-----------------------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------------------
      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
-----------------------------------------------------------------------------------------------------
   DRB1_0401   38  VKVLRADLARDPSFY  KVLRADLAR         0.7082         23.5         SB     2.00     Sequence
   DRB1_0401   37  AVKVLRADLARDPSF  VKVLRADLA         0.6967         26.6         SB     2.00     Sequence
   DRB1_0401   29  DLRLHRDVAVKVLRA  LHRDVAVKV         0.6869         29.6         SB     2.00     Sequence
   DRB1_0401   30  LRLHRDVAVKVLRAD  LHRDVAVKV         0.6857         30.0         SB     2.00     Sequence
   DRB1_0401   36  VAVKVLRADLARDPS  KVLRADLAR         0.6707         35.3         SB     4.00     Sequence
   DRB1_0401   28  RDLRLHRDVAVKVLR  LRLHRDVAV         0.6608         39.3         SB     4.00     Sequence
   DRB1_0401   52  YLRFRREAQNAAALN  RFRREAQNA         0.6364         51.1         WB     4.00     Sequence
   DRB1_0401   53  LRFRREAQNAAALNH  RFRREAQNA         0.6342         52.4         WB     4.00     Sequence
   DRB1_0401  448  FGRFKQANSPSTPEL  RFKQANSPS         0.6279         56.1         WB     8.00     Sequence
   DRB1_0401   51  FYLRFRREAQNAAAL  RFRREAQNA         0.6191         61.6         WB     8.00     Sequence
   DRB1_0401   27  ARDLRLHRDVAVKVL  LRLHRDVAV         0.6189         61.7         WB     8.00     Sequence
   DRB1_0401  447  GFGRFKQANSPSTPE  FGRFKQANS         0.6154         64.2         WB     8.00     Sequence
   DRB1_0401   35  DVAVKVLRADLARDP  VKVLRADLA         0.6143         64.9         WB     8.00     Sequence
   DRB1_0401  558  NQFVMPDLSGMFWVD  QFVMPDLSG         0.6134         65.5         WB     8.00     Sequence
   DRB1_0401   26  LARDLRLHRDVAVKV  LRLHRDVAV         0.6130         65.8         WB     8.00     Sequence
   DRB1_0401  557  GNQFVMPDLSGMFWV  QFVMPDLSG         0.6109         67.4         WB     8.00     Sequence
   DRB1_0401  556  KGNQFVMPDLSGMFW  QFVMPDLSG         0.6071         70.2         WB     8.00     Sequence
   DRB1_0401   50  SFYLRFRREAQNAAA  RFRREAQNA         0.5944         80.5         WB     8.00     Sequence
   DRB1_0401   31  RLHRDVAVKVLRADL  LHRDVAVKV         0.5897         84.7         WB     8.00     Sequence
   DRB1_0401  446  AGFGRFKQANSPSTP  FGRFKQANS         0.5794         94.7         WB     8.00     Sequence
   DRB1_0401  378  NRGFKIRTLQKPDST  GFKIRTLQK         0.5770         97.2         WB     8.00     Sequence
   DRB1_0401  141  ANIMISATNAVKVMD  IMISATNAV         0.5759         98.4         WB     8.00     Sequence
   DRB1_0401  449  GRFKQANSPSTPELV  RFKQANSPS         0.5705        104.3         WB     8.00     Sequence
   DRB1_0401  380  GFKIRTLQKPDSTIP  GFKIRTLQK         0.5699        105.0         WB     8.00     Sequence
   DRB1_0401  142  NIMISATNAVKVMDF  IMISATNAV         0.5694        105.5         WB     8.00     Sequence
   DRB1_0401  140  PANIMISATNAVKVM  IMISATNAV         0.5632        112.9         WB    16.00     Sequence
   DRB1_0401  559  QFVMPDLSGMFWVDA  QFVMPDLSG         0.5605        116.2         WB    16.00     Sequence
   DRB1_0401   54  RFRREAQNAAALNHP  RFRREAQNA         0.5590        118.1         WB    16.00     Sequence
   DRB1_0401  379  RGFKIRTLQKPDSTI  GFKIRTLQK         0.5574        120.1         WB    16.00     Sequence
   DRB1_0401  555  SKGNQFVMPDLSGMF  QFVMPDLSG         0.5556        122.6         WB    16.00     Sequence
   DRB1_0401  377  QNRGFKIRTLQKPDS  GFKIRTLQK         0.5526        126.5         WB    16.00     Sequence
   DRB1_0401  599  HNRVVYQNPPAGTGV  RVVYQNPPA         0.5502        129.8         WB    16.00     Sequence
   DRB1_0401   34  RDVAVKVLRADLARD  VKVLRADLA         0.5473        134.0         WB    16.00     Sequence
   DRB1_0401  598  QHNRVVYQNPPAGTG  RVVYQNPPA         0.5464        135.4         WB    16.00     Sequence
   DRB1_0401  516  FTKFSQASVDSPRPA  KFSQASVDS         0.5436        139.5         WB    16.00     Sequence
   DRB1_0401  600  NRVVYQNPPAGTGVN  RVVYQNPPA         0.5431        140.3         WB    16.00     Sequence
   DRB1_0401  445  AAGFGRFKQANSPST  FGRFKQANS         0.5421        141.7         WB    16.00     Sequence
   DRB1_0401   32  LHRDVAVKVLRADLA  LHRDVAVKV         0.5419        142.1         WB    16.00     Sequence
   DRB1_0401   25  HLARDLRLHRDVAVK  LRLHRDVAV         0.5417        142.4         WB    16.00     Sequence
   DRB1_0401   49  PSFYLRFRREAQNAA  LRFRREAQN         0.5353        152.6         WB    16.00     Sequence
   DRB1_0401   15  ILGFGGMSEVHLARD  FGGMSEVHL         0.5330        156.5         WB    16.00     Sequence
   DRB1_0401  601  RVVYQNPPAGTGVNR  RVVYQNPPA         0.5325        157.4         WB    16.00     Sequence
   DRB1_0401  139  KPANIMISATNAVKV  NIMISATNA         0.5296        162.4         WB    16.00     Sequence
   DRB1_0401  151  VKVMDFGIARAIADS  KVMDFGIAR         0.5276        165.9         WB    16.00     Sequence
   DRB1_0401  515  GFTKFSQASVDSPRP  KFSQASVDS         0.5267        167.5         WB    16.00     Sequence
   DRB1_0401  450  RFKQANSPSTPELVG  RFKQANSPS         0.5260        168.8         WB    16.00     Sequence
   DRB1_0401   16  LGFGGMSEVHLARDL  FGGMSEVHL         0.5254        169.9         WB    16.00     Sequence
   DRB1_0401   24  VHLARDLRLHRDVAV  LRLHRDVAV         0.5243        171.9         WB    16.00     Sequence
   DRB1_0401  517  TKFSQASVDSPRPAG  KFSQASVDS         0.5203        179.4         WB    16.00     Sequence
   DRB1_0401   14  EILGFGGMSEVHLAR  FGGMSEVHL         0.5202        179.8         WB    16.00     Sequence
   DRB1_0401   17  GFGGMSEVHLARDLR  FGGMSEVHL         0.5171        185.9         WB    16.00     Sequence
   DRB1_0401  518  KFSQASVDSPRPAGE  KFSQASVDS         0.5141        192.0         WB    16.00     Sequence
   DRB1_0401  565  LSGMFWVDAEPRLRA  MFWVDAEPR         0.5133        193.7         WB    16.00     Sequence
   DRB1_0401  150  AVKVMDFGIARAIAD  KVMDFGIAR         0.5120        196.4         WB    16.00     Sequence
   DRB1_0401  376  LQNRGFKIRTLQKPD  GFKIRTLQK         0.5095        201.7         WB    16.00     Sequence
   DRB1_0401   33  HRDVAVKVLRADLAR  VKVLRADLA         0.5083        204.4         WB    16.00     Sequence
   DRB1_0401  381  FKIRTLQKPDSTIPP  RTLQKPDST         0.5057        210.2         WB    16.00     Sequence
   DRB1_0401   39  KVLRADLARDPSFYL  KVLRADLAR         0.5051        211.6         WB    16.00     Sequence
   DRB1_0401  260  NRYQTAAEMRADLVR  RYQTAAEMR         0.4985        227.4         WB    16.00     Sequence
```

```
DRB1_0401  567  GMFWVDAEPRLRALG  MFWVDAEPR        0.4981        228.4          WB    16.00      Sequence
DRB1_0401   90  VMEYVDGVTLRDIVH  MEYVDGVTL        0.4959        233.8          WB    16.00      Sequence
DRB1_0401  566  SGMFWVDAEPRLRAL  MFWVDAEPR        0.4956        234.6          WB    16.00      Sequence
DRB1_0401  597  SQHNRVVYQNPPAGT  RVVYQNPPA        0.4954        234.9          WB    16.00      Sequence
DRB1_0401  259  ENRYQTAAEMRADLV  RYQTAAEMR        0.4897        249.9          WB    16.00      Sequence
DRB1_0401   91  MEYVDGVTLRDIVHT  MEYVDGVTL        0.4880        254.7          WB    32.00      Sequence
DRB1_0401   88  YIVMEYVDGVTLRDI  MEYVDGVTL        0.4879        254.9          WB    32.00      Sequence
DRB1_0401   13  GEILGFGGMSEVHLA  FGGMSEVHL        0.4873        256.6          WB    32.00      Sequence
DRB1_0401  152  KVMDFGIARAIADSG  KVMDFGIAR        0.4869        257.7          WB    32.00      Sequence
DRB1_0401  143  IMISATNAVKVMDFG  IMISATNAV        0.4860        260.3          WB    32.00      Sequence
DRB1_0401  149  NAVKVMDFGIARAIA  KVMDFGIAR        0.4857        261.2          WB    32.00      Sequence
DRB1_0401  564  DLSGMFWVDAEPRLR  GMFWVDAEP        0.4849        263.4          WB    32.00      Sequence
DRB1_0401  340  VLTVVVTIAINTFGG  LTVVVTIAI        0.4811        274.4          WB    32.00      Sequence
DRB1_0401  554  VSKGNQFVMPDLSGM  QFVMPDLSG        0.4799        277.8          WB    32.00      Sequence
DRB1_0401   87  PYIVMEYVDGVTLRD  MEYVDGVTL        0.4781        283.4          WB    32.00      Sequence
DRB1_0401  375  TLQNRGFKIRTLQKP  NRGFKIRTL        0.4774        285.4          WB    32.00      Sequence
DRB1_0401  514  YGFTKFSQASVDSPR  KFSQASVDS        0.4770        286.7          WB    32.00      Sequence
DRB1_0401   89  IVMEYVDGVTLRDIV  MEYVDGVTL        0.4749        293.3          WB    32.00      Sequence
DRB1_0401  341  LTVVVTIAINTFGGI  LTVVVTIAI        0.4726        300.7          WB    32.00      Sequence
DRB1_0401  444  TAAGFGRFKQANSPS  FGRFKQANS        0.4716        304.0          WB    32.00      Sequence
DRB1_0401  258  PENRYQTAAEMRADL  NRYQTAAEM        0.4716        304.1          WB    32.00      Sequence
DRB1_0401  124  ALNFSHQNGIIHRDV  FSHQNGIIH        0.4704        308.1          WB    32.00      Sequence
DRB1_0401  138  VKPANIMISATNAVK  NIMISATNA        0.4700        309.2          WB    32.00      Sequence
DRB1_0401  425  QREIPDVSTLTYAEA  QREIPDVST        0.4687        313.7          WB    32.00      Sequence
DRB1_0401   23  EVHLARDLRLHRDVA  VHLARDLRL        0.4683        314.9          WB    32.00      Sequence
DRB1_0401  213  PPFTGDSPVSVAYQH  FTGDSPVSV        0.4667        320.5          WB    32.00      Sequence
DRB1_0401  513  VYGFTKFSQASVDSP  GFTKFSQAS        0.4645        328.5          WB    32.00      Sequence
DRB1_0401   18  FGGMSEVHLARDLRL  FGGMSEVHL        0.4618        337.9          WB    32.00      Sequence
DRB1_0401  382  KIRTLQKPDSTIPPD  RTLQKPDST        0.4596        346.0          WB    32.00      Sequence
DRB1_0401  212  EPPFTGDSPVSVAYQ  FTGDSPVSV        0.4576        353.6          WB    32.00      Sequence
DRB1_0401  383  IRTLQKPDSTIPPDH  RTLQKPDST        0.4561        359.4          WB    32.00      Sequence
DRB1_0401   48  DPSFYLRFRREAQNA  RFRREAQNA        0.4553        362.6          WB    32.00      Sequence
DRB1_0401  424  EQREIPDVSTLTYAE  QREIPDVST        0.4552        363.2          WB    32.00      Sequence
DRB1_0401  214  PFTGDSPVSVAYQHV  FTGDSPVSV        0.4539        368.4          WB    32.00      Sequence
DRB1_0401  339  AVLTVVVTIAINTFG  LTVVVTIAI        0.4534        370.4          WB    32.00      Sequence
DRB1_0401   12  LGEILGFGGMSEVHL  FGGMSEVHL        0.4511        379.5          WB    32.00      Sequence
DRB1_0401  261  RYQTAAEMRADLVRV  YQTAAEMRA        0.4504        382.6          WB    32.00      Sequence
DRB1_0401  433  TLTYAEAVKKLTAAG  LTYAEAVKK        0.4495        386.3          WB    32.00      Sequence
DRB1_0401   22  SEVHLARDLRLHRDV  VHLARDLRL        0.4482        391.6          WB    32.00      Sequence
DRB1_0401  125  LNFSHQNGIIHRDVK  FSHQNGIIH        0.4481        392.2          WB    32.00      Sequence
DRB1_0401  291  ERTSLLSSAAGNLSG  TSLLSSAAG        0.4472        395.7          WB    32.00      Sequence
DRB1_0401  123  QALNFSHQNGIIHRD  FSHQNGIIH        0.4463        399.8          WB    32.00      Sequence
DRB1_0401  290  AERTSLLSSAAGNLS  RTSLLSSAA        0.4462        400.3          WB    32.00      Sequence
DRB1_0401   55  FRREAQNAAALNHPA  FRREAQNAA        0.4426        416.0          WB    32.00      Sequence
DRB1_0401  384  RTLQKPDSTIPPDHV  RTLQKPDST        0.4399        428.3          WB    32.00      Sequence
DRB1_0401  512  NVYGFTKFSQASVDS  FTKFSQASV        0.4372        441.2          WB    32.00      Sequence
DRB1_0401  292  RTSLLSSAAGNLSGP  TSLLSSAAG        0.4343        455.0          WB    32.00      Sequence
DRB1_0401  432  STLTYAEAVKKLTAA  LTYAEAVKK        0.4337        458.3          WB    32.00      Sequence
DRB1_0401  148  TNAVKVMDFGIARAI  KVMDFGIAR        0.4334        459.6          WB    32.00      Sequence
DRB1_0401   86  LPYIVMEYVDGVTLR  MEYVDGVTL        0.4331        461.0          WB    32.00      Sequence
DRB1_0401  328  VGRWVAVVAVLAVLT  GRWVAVVAV        0.4320        466.7          WB    32.00      Sequence
DRB1_0401  596  GSQHNRVVYQNPPAG  RVVYQNPPA        0.4313        470.0          WB    32.00      Sequence
DRB1_0401  257  NPENRYQTAAEMRAD  RYQTAAEMR        0.4301        476.1          WB    32.00      Sequence
DRB1_0401  289  DAERTSLLSSAAGNL  RTSLLSSAA        0.4288        482.9          WB    32.00      Sequence
DRB1_0401  547  DSVIELQVSKGNQFV  SVIELQVSK        0.4275        490.2          WB    32.00      Sequence
DRB1_0401  423  PEQREIPDVSTLTYA  QREIPDVST        0.4269        493.4          WB    32.00      Sequence
DRB1_0401  327  SVGRWVAVVAVLAVL  GRWVAVVAV        0.4268        493.6          WB    32.00      Sequence
DRB1_0401  342  TVVVTIAINTFGGIT  VVVTIAINT        0.4259        498.3          WB    32.00      Sequence
DRB1_0401  575  PRLRALGWTGMLDKG  RLRALGWTG        0.4248        504.6                32.00      Sequence
DRB1_0401   21  MSEVHLARDLRLHRD  VHLARDLRL        0.4242        507.8                32.00      Sequence
DRB1_0401  153  VMDFGIARAIADSGN  FGIARAIAD        0.4240        508.9                32.00      Sequence
DRB1_0401  126  NFSHQNGIIHRDVKP  FSHQNGIIH        0.4218        521.3                32.00      Sequence
DRB1_0401  563  PDLSGMFWVDAEPRL  MFWVDAEPR        0.4213        523.8                32.00      Sequence
DRB1_0401  574  EPRLRALGWTGMLDK  RLRALGWTG        0.4207        527.6                32.00      Sequence
DRB1_0401  154  MDFGIARAIADSGNS  FGIARAIAD        0.4194        534.6                32.00      Sequence
DRB1_0401  326  GSVGRWVAVVAVLAV  GRWVAVVAV        0.4187        539.2                32.00      Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0401 | 211 | GEPPFTGDSPVSVAY | FTGDSPVSV | 0.4186 | 539.3 | 32.00 | Sequence |
| DRB1_0401 | 20 | GMSEVHLARDLRLHR | VHLARDLRL | 0.4177 | 544.9 | 32.00 | Sequence |
| DRB1_0401 | 155 | DFGIARAIADSGNSV | FGIARAIAD | 0.4172 | 548.0 | 32.00 | Sequence |
| DRB1_0401 | 362 | PDVRGQSSADAIATL | VRGQSSADA | 0.4158 | 556.2 | 32.00 | Sequence |
| DRB1_0401 | 434 | LTYAEAVKKLTAAGF | LTYAEAVKK | 0.4138 | 568.1 | 32.00 | Sequence |
| DRB1_0401 | 122 | CQALNFSHQNGIIHR | FSHQNGIIH | 0.4135 | 570.1 | 32.00 | Sequence |
| DRB1_0401 | 548 | SVIELQVSKGNQFVM | SVIELQVSK | 0.4131 | 572.6 | 32.00 | Sequence |
| DRB1_0401 | 338 | LAVLTVVVTIAINTF | LTVVVTIAI | 0.4130 | 573.2 | 32.00 | Sequence |
| DRB1_0401 | 431 | VSTLTYAEAVKKLTA | LTYAEAVKK | 0.4086 | 601.2 | 32.00 | Sequence |
| DRB1_0401 | 553 | QVSKGNQFVMPDLSG | QFVMPDLSG | 0.4063 | 616.4 | 32.00 | Sequence |
| DRB1_0401 | 127 | FSHQNGIIHRDVKPA | FSHQNGIIH | 0.4052 | 623.7 | 32.00 | Sequence |
| DRB1_0401 | 576 | RLRALGWTGMLDKGA | RLRALGWTG | 0.4052 | 623.8 | 32.00 | Sequence |
| DRB1_0401 | 361 | VPDVRGQSSADAIAT | VRGQSSADA | 0.4046 | 627.8 | 32.00 | Sequence |
| DRB1_0401 | 343 | VVVTIAINTFGGITR | VVVTIAINT | 0.4041 | 631.3 | 32.00 | Sequence |
| DRB1_0401 | 132 | GIIHRDVKPANIMIS | IHRDVKPAN | 0.4034 | 635.9 | 32.00 | Sequence |
| DRB1_0401 | 133 | IIHRDVKPANIMISA | IHRDVKPAN | 0.4009 | 653.1 | 32.00 | Sequence |
| DRB1_0401 | 546 | VDSVIELQVSKGNQF | SVIELQVSK | 0.3947 | 699.0 | 32.00 | Sequence |
| DRB1_0401 | 137 | DVKPANIMISATNAV | NIMISATNA | 0.3920 | 719.6 | 32.00 | Sequence |
| DRB1_0401 | 85 | PLPYIVMEYVDGVTL | MEYVDGVTL | 0.3917 | 721.9 | 32.00 | Sequence |
| DRB1_0401 | 461 | ELVGKVIGTNPPANQ | ELVGKVIGT | 0.3911 | 726.2 | 32.00 | Sequence |
| DRB1_0401 | 293 | TSLLSSAAGNLSGPR | TSLLSSAAG | 0.3900 | 735.2 | 32.00 | Sequence |
| DRB1_0401 | 225 | YQHVREDPIPPSARH | HVREDPIPP | 0.3884 | 748.1 | 32.00 | Sequence |
| DRB1_0401 | 266 | AEMRADLVRVHNGEP | EMRADLVRV | 0.3865 | 763.8 | 50.00 | Sequence |
| DRB1_0401 | 460 | PELVGKVIGTNPPAN | ELVGKVIGT | 0.3857 | 770.2 | 50.00 | Sequence |
| DRB1_0401 | 288 | TDAERTSLLSSAAGN | RTSLLSSAA | 0.3827 | 795.4 | 50.00 | Sequence |
| DRB1_0401 | 562 | MPDLSGMFWVDAEPR | MFWVDAEPR | 0.3820 | 801.7 | 50.00 | Sequence |
| DRB1_0401 | 156 | FGIARAIADSGNSVT | FGIARAIAD | 0.3817 | 804.3 | 50.00 | Sequence |
| DRB1_0401 | 573 | AEPRLRALGWTGMLD | RLRALGWTG | 0.3813 | 807.8 | 50.00 | Sequence |
| DRB1_0401 | 256 | KNPENRYQTAAEMRA | RYQTAAEMR | 0.3794 | 824.5 | 50.00 | Sequence |
| DRB1_0401 | 215 | FTGDSPVSVAYQHVR | FTGDSPVSV | 0.3793 | 825.5 | 50.00 | Sequence |
| DRB1_0401 | 147 | ATNAVKVMDFGIARA | KVMDFGIAR | 0.3763 | 852.2 | 50.00 | Sequence |
| DRB1_0401 | 325 | IGSVGRWVAVVAVLA | VGRWVAVVA | 0.3742 | 872.2 | 50.00 | Sequence |
| DRB1_0401 | 131 | NGIIHRDVKPANIMI | IHRDVKPAN | 0.3737 | 876.6 | 50.00 | Sequence |
| DRB1_0401 | 374 | ATLQNRGFKIRTLQK | NRGFKIRTL | 0.3726 | 887.3 | 50.00 | Sequence |
| DRB1_0401 | 595 | GGSQHNRVVYQNPPA | RVVYQNPPA | 0.3721 | 891.9 | 50.00 | Sequence |
| DRB1_0401 | 329 | GRWVAVVAVLAVLTV | WVAVVAVLA | 0.3718 | 895.3 | 50.00 | Sequence |
| DRB1_0401 | 422 | GPEQREIPDVSTLTY | QREIPDVST | 0.3715 | 897.9 | 50.00 | Sequence |
| DRB1_0401 | 224 | AYQHVREDPIPPSAR | HVREDPIPP | 0.3714 | 898.6 | 50.00 | Sequence |
| DRB1_0401 | 396 | DHVIGTDPAANTSVS | VIGTDPAAN | 0.3710 | 902.6 | 50.00 | Sequence |
| DRB1_0401 | 511 | LNVYGFTKFSQASVD | VYGFTKFSQ | 0.3709 | 904.0 | 50.00 | Sequence |
| DRB1_0401 | 568 | MFWVDAEPRLRALGW | MFWVDAEPR | 0.3708 | 905.3 | 50.00 | Sequence |
| DRB1_0401 | 337 | VLAVLTVVVTIAINT | LTVVVTIAI | 0.3703 | 909.3 | 50.00 | Sequence |
| DRB1_0401 | 426 | REIPDVSTLTYAEAV | EIPDVSTLT | 0.3696 | 916.3 | 50.00 | Sequence |
| DRB1_0401 | 121 | ACQALNFSHQNGIIH | FSHQNGIIH | 0.3695 | 917.7 | 50.00 | Sequence |
| DRB1_0401 | 363 | DVRGQSSADAIATLQ | VRGQSSADA | 0.3673 | 940.0 | 50.00 | Sequence |
| DRB1_0401 | 134 | IHRDVKPANIMISAT | IHRDVKPAN | 0.3655 | 958.6 | 50.00 | Sequence |
| DRB1_0401 | 267 | EMRADLVRVHNGEPP | EMRADLVRV | 0.3648 | 965.2 | 50.00 | Sequence |
| DRB1_0401 | 47 | RDPSFYLRFRREAQN | LRFRREAQN | 0.3636 | 978.6 | 50.00 | Sequence |
| DRB1_0401 | 430 | DVSTLTYAEAVKKLT | LTYAEAVKK | 0.3627 | 987.4 | 50.00 | Sequence |
| DRB1_0401 | 92 | EYVDGVTLRDIVHTE | YVDGVTLRD | 0.3619 | 995.9 | 50.00 | Sequence |
| DRB1_0401 | 459 | TPELVGKVIGTNPPA | ELVGKVIGT | 0.3605 | 1011.0 | 50.00 | Sequence |
| DRB1_0401 | 545 | PVDSVIELQVSKGNQ | SVIELQVSK | 0.3593 | 1024.6 | 50.00 | Sequence |
| DRB1_0401 | 395 | PDHVIGTDPAANTSV | VIGTDPAAN | 0.3574 | 1046.4 | 50.00 | Sequence |
| DRB1_0401 | 265 | AAEMRADLVRVHNGE | EMRADLVRV | 0.3559 | 1063.6 | 50.00 | Sequence |
| DRB1_0401 | 397 | HVIGTDPAANTSVSA | VIGTDPAAN | 0.3545 | 1079.0 | 50.00 | Sequence |
| DRB1_0401 | 360 | QVPDVRGQSSADAIA | VRGQSSADA | 0.3543 | 1081.9 | 50.00 | Sequence |
| DRB1_0401 | 442 | KLTAAGFGRFKQANS | FGRFKQANS | 0.3532 | 1094.8 | 50.00 | Sequence |
| DRB1_0401 | 210 | TGEPPFTGDSPVSVA | FTGDSPVSV | 0.3530 | 1096.6 | 50.00 | Sequence |
| DRB1_0401 | 364 | VRGQSSADAIATLQN | VRGQSSADA | 0.3525 | 1103.1 | 50.00 | Sequence |
| DRB1_0401 | 510 | NLNVYGFTKFSQASV | VYGFTKFSQ | 0.3523 | 1106.0 | 50.00 | Sequence |
| DRB1_0401 | 223 | VAYQHVREDPIPPSA | YQHVREDPI | 0.3509 | 1122.3 | 50.00 | Sequence |
| DRB1_0401 | 226 | QHVREDPIPPSARHE | HVREDPIPP | 0.3477 | 1162.0 | 50.00 | Sequence |
| DRB1_0401 | 578 | RALGWTGMLDKGADV | LGWTGMLDK | 0.3474 | 1165.4 | 50.00 | Sequence |
| DRB1_0401 | 577 | LRALGWTGMLDKGAD | LGWTGMLDK | 0.3474 | 1165.7 | 50.00 | Sequence |
| DRB1_0401 | 19 | GGMSEVHLARDLRLH | VHLARDLRL | 0.3452 | 1193.9 | 50.00 | Sequence |
| DRB1_0401 | 443 | LTAAGFGRFKQANSP | FGRFKQANS | 0.3436 | 1214.4 | 50.00 | Sequence |

```
DRB1_0401  262  YQTAAEMRADLVRVH  YQTAAEMRA        0.3376       1296.6              50.00     Sequence
DRB1_0401  144  MISATNAVKVMDFGI  MISATNAVK        0.3340       1347.6              50.00     Sequence
DRB1_0401  572  DAEPRLRALGWTGML  RLRALGWTG        0.3333       1358.1              50.00     Sequence
DRB1_0401  136  RDVKPANIMISATNA  NIMISATNA        0.3321       1376.0              50.00     Sequence
DRB1_0401  130  QNGIIHRDVKPANIM  GIIHRDVKP        0.3316       1382.2              50.00     Sequence
DRB1_0401  112  KRAIEVIADACQALN  RAIEVIADA        0.3291       1421.4              50.00     Sequence
DRB1_0401   42  RADLARDPSFYLRFR  LARDPSFYL        0.3260       1469.1              50.00     Sequence
DRB1_0401   93  YVDGVTLRDIVHTEG  YVDGVTLRD        0.3258       1472.6              50.00     Sequence
DRB1_0401  157  GIARAIADSGNSVTQ  RAIADSGNS        0.3252       1482.1              50.00     Sequence
DRB1_0401  412  GDEITVNVSTGPEQR  DEITVNVST        0.3249       1486.6              50.00     Sequence
DRB1_0401  111  PKRAIEVIADACQAL  RAIEVIADA        0.3248       1487.7              50.00     Sequence
DRB1_0401  330  RWVAVVAVLAVLTVV  WVAVVAVLA        0.3242       1497.5              50.00     Sequence
DRB1_0401  394  PPDHVIGTDPAANTS  HVIGTDPAA        0.3236       1507.9              50.00     Sequence
DRB1_0401  294  SLLSSAAGNLSGPRT  SLLSSAAGN        0.3217       1539.2              50.00     Sequence
DRB1_0401  287  LTDAERTSLLSSAAG  RTSLLSSAA        0.3207       1555.6              50.00     Sequence
DRB1_0401  209  LTGEPPFTGDSPVSV  FTGDSPVSV        0.3198       1570.4              50.00     Sequence
DRB1_0401  549  VIELQVSKGNQFVMP  IELQVSKGN        0.3198       1571.0              50.00     Sequence
DRB1_0401  336  AVLAVLTVVVTIAIN  LTVVVTIAI        0.3196       1575.3              50.00     Sequence
DRB1_0401  264  TAAEMRADLVRVHNG  EMRADLVRV        0.3189       1586.1              50.00     Sequence
DRB1_0401  248  AVVLKALAKNPENRY  AVVLKALAK        0.3181       1600.5              50.00     Sequence
DRB1_0401  413  DEITVNVSTGPEQRE  DEITVNVST        0.3178       1605.6              50.00     Sequence
DRB1_0401  451  FKQANSPSTPELVGK  FKQANSPST        0.3169       1620.6              50.00     Sequence
DRB1_0401  222  SVAYQHVREDPIPPS  YQHVREDPI        0.3158       1641.4              50.00     Sequence
DRB1_0401  115  IEVIADACQALNFSH  EVIADACQA        0.3153       1649.7              50.00     Sequence
DRB1_0401  146  SATNAVKVMDFGIAR  KVMDFGIAR        0.3144       1665.9              50.00     Sequence
DRB1_0401  458  STPELVGKVIGTNPP  ELVGKVIGT        0.3140       1672.1              50.00     Sequence
DRB1_0401  113  RAIEVIADACQALNF  RAIEVIADA        0.3134       1683.8              50.00     Sequence
DRB1_0401  550  IELQVSKGNQFVMPD  IELQVSKGN        0.3124       1701.9              50.00     Sequence
DRB1_0401  579  ALGWTGMLDKGADVD  ALGWTGMLD        0.3123       1704.5              50.00     Sequence
DRB1_0401  438  EAVKKLTAAGFGRFK  EAVKKLTAA        0.3121       1708.2              50.00     Sequence
DRB1_0401   56  RREAQNAAALNHPAI  RREAQNAAA        0.3097       1752.5              50.00     Sequence
DRB1_0401  160  RAIADSGNSVTQTAA  RAIADSGNS        0.3094       1758.6              50.00     Sequence
DRB1_0401   11  ELGEILGFGGMSEVH  ILGFGGMSE        0.3092       1761.7              50.00     Sequence
DRB1_0401  195  RSDVYSLGCVLYEVL  VYSLGCVLY        0.3091       1763.7              50.00     Sequence
DRB1_0401  544  VPVDSVIELQVSKGN  SVIELQVSK        0.3091       1764.7              50.00     Sequence
DRB1_0401  427  EIPDVSTLTYAEAVK  EIPDVSTLT        0.3082       1780.7              50.00     Sequence
DRB1_0401  196  SDVYSLGCVLYEVLT  VYSLGCVLY        0.3079       1787.2              50.00     Sequence
DRB1_0401  359  VQVPDVRGQSSADAI  VRGQSSADA        0.3069       1806.1              50.00     Sequence
DRB1_0401  158  IARAIADSGNSVTQT  RAIADSGNS        0.3067       1810.4              50.00     Sequence
DRB1_0401  437  AEAVKKLTAAGFGRF  VKKLTAAGF        0.3055       1834.2              50.00     Sequence
DRB1_0401  110  TPKRAIEVIADACQA  RAIEVIADA        0.3047       1850.8              50.00     Sequence
DRB1_0401  247  DAVVLKALAKNPENR  VVLKALAKN        0.3038       1867.7              50.00     Sequence
DRB1_0401  203  CVLYEVLTGEPPFTG  YEVLTGEPP        0.3036       1871.8              50.00     Sequence
DRB1_0401    9  RYELGEILGFGGMSE  RYELGEILG        0.3020       1904.2              50.00     Sequence
DRB1_0401  611  TGVNRDGIITLRFGQ  GVNRDGIIT        0.3019       1906.8              50.00     Sequence
DRB1_0401  239  HEGLSADLDAVVLKA  HEGLSADLD        0.3016       1912.8              50.00     Sequence
DRB1_0401  135  HRDVKPANIMISATN  HRDVKPANI        0.3013       1919.4              50.00     Sequence
DRB1_0401  114  AIEVIADACQALNFS  EVIADACQA        0.3004       1937.5              50.00     Sequence
DRB1_0401  159  ARAIADSGNSVTQTA  RAIADSGNS        0.3003       1939.5              50.00     Sequence
DRB1_0401  335  VAVLAVLTVVVTIAI  LTVVVTIAI        0.2995       1956.8              50.00     Sequence
DRB1_0401  429  PDVSTLTYAEAVKKL  LTYAEAVKK        0.2992       1964.0              50.00     Sequence
DRB1_0401  249  VVLKALAKNPENRYQ  VVLKALAKN        0.2992       1964.0              50.00     Sequence
DRB1_0401  331  WVAVVAVLAVLTVVV  WVAVVAVLA        0.2989       1970.6              50.00     Sequence
DRB1_0401  411  AGDEITVNVSTGPEQ  DEITVNVST        0.2983       1982.4              50.00     Sequence
DRB1_0401   41  LRADLARDPSFYLRF  LARDPSFYL        0.2979       1992.2              50.00     Sequence
DRB1_0401    7  SDRYELGEILGFGGM  RYELGEILG        0.2960       2032.8              50.00     Sequence
DRB1_0401  561  VMPDLSGMFWVDAEP  GMFWVDAEP        0.2950       2054.0              50.00     Sequence
DRB1_0401  202  GCVLYEVLTGEPPFT  CVLYEVLTG        0.2946       2063.3              50.00     Sequence
DRB1_0401  502  QTVDVAQKNLNVYGF  QTVDVAQKN        0.2943       2069.9              50.00     Sequence
DRB1_0401  238  RHEGLSADLDAVVLK  GLSADLDAV        0.2943       2071.3              50.00     Sequence
DRB1_0401  552  LQVSKGNQFVMPDLS  LQVSKGNQF        0.2942       2073.5              50.00     Sequence
DRB1_0401    8  DRYELGEILGFGGMS  RYELGEILG        0.2933       2093.7              50.00     Sequence
DRB1_0401  246  LDAVVLKALAKNPEN  VVLKALAKN        0.2923       2114.7              50.00     Sequence
DRB1_0401  268  MRADLVRVHNGEPPE  RADLVRVHN        0.2895       2181.4              50.00     Sequence
DRB1_0401   44  DLARDPSFYLRFRRE  LARDPSFYL        0.2890       2192.0              50.00     Sequence
DRB1_0401  462  LVGKVIGTNPPANQT  KVIGTNPPA        0.2881       2214.2              50.00     Sequence
```

```
DRB1_0401   84  GPLPYIVMEYVDGVT  YIVMEYVDG         0.2866        2249.7               50.00      Sequence
DRB1_0401  240  EGLSADLDAVVLKAL  LSADLDAVV         0.2864        2255.0               50.00      Sequence
DRB1_0401   45  LARDPSFYLRFRREA  LARDPSFYL         0.2864        2255.5               50.00      Sequence
DRB1_0401  358  DVQVPDVRGQSSADA  VRGQSSADA         0.2860        2265.6               50.00      Sequence
DRB1_0401  286  VLTDAERTSLLSSAA  RTSLLSSAA         0.2859        2267.5               50.00      Sequence
DRB1_0401  245  DLDAVVLKALAKNPE  AVVLKALAK         0.2858        2269.4               50.00      Sequence
DRB1_0401  352  FGGITRDVQVPDVRG  ITRDVQVPD         0.2856        2275.0               50.00      Sequence
DRB1_0401  436  YAEAVKKLTAAGFGR  EAVKKLTAA         0.2853        2281.8               50.00      Sequence
DRB1_0401  129  HQNGIIHRDVKPANI  GIIHRDVKP         0.2852        2284.4               50.00      Sequence
DRB1_0401  501  GQTVDVAQKNLNVYG  QTVDVAQKN         0.2848        2294.3               50.00      Sequence
DRB1_0401  324  SIGSVGRWVAVVAVL  VGRWVAVVA         0.2847        2296.7               50.00      Sequence
DRB1_0401  198  VYSLGCVLYEVLTGE  YSLGCVLYE         0.2840        2314.7               50.00      Sequence
DRB1_0401  236  SARHEGLSADLDAVV  SARHEGLSA         0.2837        2321.4               50.00      Sequence
DRB1_0401  145  ISATNAVKVMDFGIA  ISATNAVKV         0.2828        2344.0               50.00      Sequence
DRB1_0401  398  VIGTDPAANTSVSAG  VIGTDPAAN         0.2826        2350.5               50.00      Sequence
DRB1_0401  194  ARSDVYSLGCVLYEV  VYSLGCVLY         0.2824        2355.8               50.00      Sequence
DRB1_0401  571  VDAEPRLRALGWTGM  RLRALGWTG         0.2811        2387.1               50.00      Sequence
DRB1_0401  367  QSSADAIATLQNRGF  QSSADAIAT         0.2808        2395.0               50.00      Sequence
DRB1_0401  263  QTAAEMRADLVRVHN  EMRADLVRV         0.2807        2399.1               50.00      Sequence
DRB1_0401  241  GLSADLDAVVLKALA  LSADLDAVV         0.2806        2401.8               50.00      Sequence
DRB1_0401  610  GTGVNRDGIITLRFG  GVNRDGIIT         0.2800        2416.3               50.00      Sequence
DRB1_0401  237  ARHEGLSADLDAVVL  HEGLSADLD         0.2794        2431.6               50.00      Sequence
DRB1_0401    6  LSDRYELGEILGFGG  RYELGEILG         0.2794        2433.9               50.00      Sequence
DRB1_0401  393  IPPDHVIGTDPAANT  HVIGTDPAA         0.2794        2433.9               50.00      Sequence
DRB1_0401   40  VLRADLARDPSFYLR  LARDPSFYL         0.2790        2444.1               50.00      Sequence
DRB1_0401  410  SAGDEITVNVSTGPE  DEITVNVST         0.2782        2465.7               50.00      Sequence
DRB1_0401  204  VLYEVLTGEPPFTGD  YEVLTGEPP         0.2778        2475.1               50.00      Sequence
DRB1_0401  116  EVIADACQALNFSHQ  EVIADACQA         0.2758        2530.4               50.00      Sequence
DRB1_0401  484  IIIVGSGPATKDIPD  IIIVGSGPA         0.2755        2536.8               50.00      Sequence
DRB1_0401  483  VIIIVGSGPATKDIP  IIIVGSGPA         0.2750        2550.1               50.00      Sequence
DRB1_0401  197  DVYSLGCVLYEVLTG  VYSLGCVLY         0.2750        2552.6               50.00      Sequence
DRB1_0401  421  TGPEQREIPDVSTLT  QREIPDVST         0.2749        2553.3               50.00      Sequence
DRB1_0401  284  PKVLTDAERTSLLSS  KVLTDAERT         0.2747        2559.1               50.00      Sequence
DRB1_0401  428  IPDVSTLTYAEAVKK  VSTLTYAEA         0.2732        2600.4               50.00      Sequence
DRB1_0401  221  VSVAYQHVREDPIPP  YQHVREDPI         0.2731        2604.2               50.00      Sequence
DRB1_0401  285  KVLTDAERTSLLSSA  KVLTDAERT         0.2725        2621.8               50.00      Sequence
DRB1_0401  373  IATLQNRGFKIRTLQ  NRGFKIRTL         0.2721        2631.9               50.00      Sequence
DRB1_0401   43  ADLARDPSFYLRFRR  LARDPSFYL         0.2718        2642.2               50.00      Sequence
DRB1_0401  353  GGITRDVQVPDVRGQ  ITRDVQVPD         0.2713        2654.9               50.00      Sequence
DRB1_0401  602  VVYQNPPAGTGVNRD  VVYQNPPAG         0.2713        2656.5               50.00      Sequence
DRB1_0401  482  VVIIIVGSGPATKDI  IIIVGSGPA         0.2707        2673.6               50.00      Sequence
DRB1_0401  509  KNLNVYGFTKFSQAS  VYGFTKFSQ         0.2706        2675.0               50.00      Sequence
DRB1_0401  120  DACQALNFSHQNGII  QALNFSHQN         0.2704        2682.1               50.00      Sequence
DRB1_0401  201  LGCVLYEVLTGEPPF  CVLYEVLTG         0.2703        2682.9               50.00      Sequence
DRB1_0401  109  MTPKRAIEVIADACQ  RAIEVIADA         0.2703        2683.2               50.00      Sequence
DRB1_0401  200  SLGCVLYEVLTGEPP  SLGCVLYEV         0.2700        2693.6               50.00      Sequence
DRB1_0401  519  FSQASVDSPRPAGEV  FSQASVDSP         0.2693        2714.0               50.00      Sequence
DRB1_0401   96  GVTLRDIVHTEGPMT  VTLRDIVHT         0.2682        2746.8               50.00      Sequence
DRB1_0401  175  VIGTAQYLSPEQARG  VIGTAQYLS         0.2678        2757.1               50.00      Sequence
DRB1_0401  464  GKVIGTNPPANQTSA  KVIGTNPPA         0.2673        2772.6               50.00      Sequence
DRB1_0401  481  NVVIIIVGSGPATKD  IIIVGSGPA         0.2667        2791.5               50.00      Sequence
DRB1_0401  255  AKNPENRYQTAAEMR  RYQTAAEMR         0.2660        2813.0               50.00      Sequence
DRB1_0401  351  TFGGITRDVQVPDVR  GITRDVQVP         0.2654        2830.6               50.00      Sequence
DRB1_0401  235  PSARHEGLSADLDAV  SARHEGLSA         0.2653        2833.4               50.00      Sequence
DRB1_0401   65  LNHPAIVAVYDTGEA  PAIVAVYDT         0.2652        2837.7               50.00      Sequence
DRB1_0401  409  VSAGDEITVNVSTGP  DEITVNVST         0.2644        2862.3               50.00      Sequence
DRB1_0401  205  LYEVLTGEPPFTGDS  YEVLTGEPP         0.2641        2870.2               50.00      Sequence
DRB1_0401  186  QARGDSVDARSDVYS  QARGDSVDA         0.2641        2871.8               50.00      Sequence
DRB1_0401    5  HLSDRYELGEILGFG  RYELGEILG         0.2622        2929.3               50.00      Sequence
DRB1_0401   95  DGVTLRDIVHTEGPM  VTLRDIVHT         0.2622        2930.6               50.00      Sequence
DRB1_0401   68  PAIVAVYDTGEAETP  VAVYDTGEA         0.2608        2974.2               50.00      Sequence
DRB1_0401  193  DARSDVYSLGCVLYE  VYSLGCVLY         0.2604        2989.3               50.00      Sequence
DRB1_0401  199  YSLGCVLYEVLTGEP  YSLGCVLYE         0.2602        2994.0               50.00      Sequence
DRB1_0401  269  RADLVRVHNGEPPEA  RADLVRVHN         0.2602        2994.1               50.00      Sequence
DRB1_0401  185  EQARGDSVDARSDVY  QARGDSVDA         0.2601        2997.8               50.00      Sequence
DRB1_0401  435  TYAEAVKKLTAAGFG  EAVKKLTAA         0.2600        3000.4               50.00      Sequence
```

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| DRB1_0401 | 66 | NHPAIVAVYDTGEAE | PAIVAVYDT | 0.2599 | 3003.8 | 50.00 | Sequence |
| DRB1_0401 | 4 | SHLSDRYELGEILGF | RYELGEILG | 0.2599 | 3005.0 | 50.00 | Sequence |
| DRB1_0401 | 100 | RDIVHTEGPMTPKRA | IVHTEGPMT | 0.2582 | 3058.6 | 50.00 | Sequence |
| DRB1_0401 | 499 | VAGQTVDVAQKNLNV | QTVDVAQKN | 0.2577 | 3077.1 | 50.00 | Sequence |
| DRB1_0401 | 580 | LGWTGMLDKGADVDA | WTGMLDKGA | 0.2573 | 3088.9 | 50.00 | Sequence |
| DRB1_0401 | 101 | DIVHTEGPMTPKRAI | VHTEGPMTP | 0.2559 | 3137.3 | 50.00 | Sequence |
| DRB1_0401 | 179 | AQYLSPEQARGDSVD | QYLSPEQAR | 0.2557 | 3143.8 | 50.00 | Sequence |
| DRB1_0401 | 500 | AGQTVDVAQKNLNVY | QTVDVAQKN | 0.2550 | 3166.0 | 50.00 | Sequence |
| DRB1_0401 | 365 | RGQSSADAIATLQNR | QSSADAIAT | 0.2550 | 3167.5 | 50.00 | Sequence |
| DRB1_0401 | 463 | VGKVIGTNPPANQTS | KVIGTNPPA | 0.2550 | 3168.9 | 50.00 | Sequence |
| DRB1_0401 | 372 | AIATLQNRGFKIRTL | IATLQNRGF | 0.2549 | 3170.1 | 50.00 | Sequence |
| DRB1_0401 | 570 | WVDAEPRLRALGWTG | RLRALGWTG | 0.2536 | 3215.4 | 50.00 | Sequence |
| DRB1_0401 | 371 | DAIATLQNRGFKIRT | IATLQNRGF | 0.2515 | 3289.8 | 50.00 | Sequence |
| DRB1_0401 | 184 | PEQARGDSVDARSDV | QARGDSVDA | 0.2507 | 3318.9 | 50.00 | Sequence |
| DRB1_0401 | 354 | GITRDVQVPDVRGQS | ITRDVQVPD | 0.2507 | 3319.1 | 50.00 | Sequence |
| DRB1_0401 | 67 | HPAIVAVYDTGEAET | PAIVAVYDT | 0.2503 | 3333.7 | 50.00 | Sequence |
| DRB1_0401 | 102 | IVHTEGPMTPKRAIE | IVHTEGPMT | 0.2499 | 3347.5 | 50.00 | Sequence |
| DRB1_0401 | 344 | VVTIAINTFGGITRD | VVTIAINTF | 0.2496 | 3359.9 | 50.00 | Sequence |
| DRB1_0401 | 46 | ARDPSFYLRFRREAQ | PSFYLRFRR | 0.2488 | 3388.3 | 50.00 | Sequence |
| DRB1_0401 | 220 | PVSVAYQHVREDPIP | YQHVREDPI | 0.2487 | 3391.5 | 50.00 | Sequence |
| DRB1_0401 | 283 | APKVLTDAERTSLLS | KVLTDAERT | 0.2486 | 3393.4 | 50.00 | Sequence |
| DRB1_0401 | 94 | VDGVTLRDIVHTEGP | VTLRDIVHT | 0.2482 | 3410.3 | 50.00 | Sequence |
| DRB1_0401 | 323 | RSIGSVGRWVAVVAV | VGRWVAVVA | 0.2480 | 3417.7 | 50.00 | Sequence |
| DRB1_0401 | 180 | QYLSPEQARGDSVDA | QYLSPEQAR | 0.2475 | 3434.1 | 50.00 | Sequence |
| DRB1_0401 | 227 | HVREDPIPPSARHEG | HVREDPIPP | 0.2474 | 3441.0 | 50.00 | Sequence |
| DRB1_0401 | 609 | AGTGVNRDGIITLRF | GVNRDGIIT | 0.2471 | 3450.0 | 50.00 | Sequence |
| DRB1_0401 | 244 | ADLDAVVLKALAKNP | AVVLKALAK | 0.2463 | 3480.6 | 50.00 | Sequence |
| DRB1_0401 | 118 | IADACQALNFSHQNG | IADACQALN | 0.2452 | 3520.7 | 50.00 | Sequence |
| DRB1_0401 | 370 | ADAIATLQNRGFKIR | IATLQNRGF | 0.2447 | 3539.5 | 50.00 | Sequence |
| DRB1_0401 | 192 | VDARSDVYSLGCVLY | VYSLGCVLY | 0.2435 | 3588.7 | 50.00 | Sequence |
| DRB1_0401 | 97 | VTLRDIVHTEGPMTP | VTLRDIVHT | 0.2433 | 3594.8 | 50.00 | Sequence |
| DRB1_0401 | 480 | TNVVIIIVGSGPATK | NVVIIIVGS | 0.2432 | 3598.1 | 50.00 | Sequence |
| DRB1_0401 | 178 | TAQYLSPEQARGDSV | QYLSPEQAR | 0.2431 | 3603.5 | 50.00 | Sequence |
| DRB1_0401 | 119 | ADACQALNFSHQNGI | DACQALNFS | 0.2421 | 3640.2 | 50.00 | Sequence |
| DRB1_0401 | 366 | GQSSADAIATLQNRG | QSSADAIAT | 0.2419 | 3651.2 | 50.00 | Sequence |
| DRB1_0401 | 560 | FVMPDLSGMFWVDAE | FVMPDLSGM | 0.2418 | 3653.5 | 50.00 | Sequence |
| DRB1_0401 | 64 | ALNHPAIVAVYDTGE | ALNHPAIVA | 0.2415 | 3665.8 | 50.00 | Sequence |
| DRB1_0401 | 319 | TDRDRSIGSVGRWVA | TDRDRSIGS | 0.2402 | 3719.2 | 50.00 | Sequence |
| DRB1_0401 | 465 | KVIGTNPPANQTSAI | KVIGTNPPA | 0.2386 | 3783.0 | 50.00 | Sequence |
| DRB1_0401 | 234 | PPSARHEGLSADLDA | SARHEGLSA | 0.2370 | 3849.3 | 50.00 | Sequence |
| DRB1_0401 | 334 | VVAVLAVLTVVVTIA | VAVLAVLTV | 0.2364 | 3873.5 | 50.00 | Sequence |
| DRB1_0401 | 357 | RDVQVPDVRGQSSAD | RDVQVPDVR | 0.2361 | 3885.5 | 50.00 | Sequence |
| DRB1_0401 | 457 | PSTPELVGKVIGTNP | ELVGKVIGT | 0.2360 | 3889.5 | 50.00 | Sequence |
| DRB1_0401 | 206 | YEVLTGEPPFTGDSP | YEVLTGEPP | 0.2358 | 3897.3 | 50.00 | Sequence |
| DRB1_0401 | 349 | INTFGGITRDVQVPD | INTFGGITR | 0.2357 | 3903.7 | 50.00 | Sequence |
| DRB1_0401 | 10 | YELGEILGFGGMSEV | ILGFGGMSE | 0.2350 | 3933.7 | 50.00 | Sequence |
| DRB1_0401 | 176 | IGTAQYLSPEQARGD | QYLSPEQAR | 0.2347 | 3945.6 | 50.00 | Sequence |
| DRB1_0401 | 177 | GTAQYLSPEQARGDS | QYLSPEQAR | 0.2339 | 3980.5 | 50.00 | Sequence |
| DRB1_0401 | 103 | VHTEGPMTPKRAIEV | VHTEGPMTP | 0.2337 | 3988.2 | 50.00 | Sequence |
| DRB1_0401 | 3 | PSHLSDRYELGEILG | RYELGEILG | 0.2331 | 4014.9 | 50.00 | Sequence |
| DRB1_0401 | 503 | TVDVAQKNLNVYGFT | DVAQKNLNV | 0.2315 | 4085.3 | 50.00 | Sequence |
| DRB1_0401 | 128 | SHQNGIIHRDVKPAN | GIIHRDVKP | 0.2314 | 4088.1 | 50.00 | Sequence |
| DRB1_0401 | 117 | VIADACQALNFSHQN | DACQALNFS | 0.2314 | 4088.5 | 50.00 | Sequence |
| DRB1_0401 | 295 | LLSSAAGNLSGPRTD | LSSAAGNLS | 0.2312 | 4099.4 | 50.00 | Sequence |
| DRB1_0401 | 318 | DTDRDRSIGSVGRWV | TDRDRSIGS | 0.2295 | 4174.2 | 50.00 | Sequence |
| DRB1_0401 | 243 | SADLDAVVLKALAKN | VVLKALAKN | 0.2292 | 4185.9 | 50.00 | Sequence |
| DRB1_0401 | 369 | SADAIATLQNRGFKI | DAIATLQNR | 0.2287 | 4210.8 | 50.00 | Sequence |
| DRB1_0401 | 99 | LRDIVHTEGPMTPKR | IVHTEGPMT | 0.2278 | 4249.9 | 50.00 | Sequence |
| DRB1_0401 | 508 | QKNLNVYGFTKFSQA | VYGFTKFSQ | 0.2275 | 4264.3 | 50.00 | Sequence |
| DRB1_0401 | 282 | EAPKVLTDAERTSLL | KVLTDAERT | 0.2275 | 4266.4 | 50.00 | Sequence |
| DRB1_0401 | 569 | FWVDAEPRLRALGWT | FWVDAEPRL | 0.2268 | 4296.0 | 50.00 | Sequence |
| DRB1_0401 | 440 | VKKLTAAGFGRFKQA | KLTAAGFGR | 0.2266 | 4308.0 | 50.00 | Sequence |
| DRB1_0401 | 83 | AGPLPYIVMEYVDGV | YIVMEYVDG | 0.2264 | 4316.7 | 50.00 | Sequence |
| DRB1_0401 | 183 | SPEQARGDSVDARSD | QARGDSVDA | 0.2257 | 4349.0 | 50.00 | Sequence |
| DRB1_0401 | 439 | AVKKLTAAGFGRFKQ | KLTAAGFGR | 0.2255 | 4357.1 | 50.00 | Sequence |
| DRB1_0401 | 551 | ELQVSKGNQFVMPDL | LQVSKGNQF | 0.2255 | 4358.2 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0401 | 174 | AVIGTAQYLSPEQAR | VIGTAQYLS | 0.2254 | 4363.0 | 50.00 | Sequence |
| DRB1_0401 | 414 | EITVNVSTGPEQREI | ITVNVSTGP | 0.2254 | 4364.5 | 50.00 | Sequence |
| DRB1_0401 | 242 | LSADLDAVVLKALAK | LSADLDAVV | 0.2239 | 4436.5 | 50.00 | Sequence |
| DRB1_0401 | 219 | SPVSVAYQHVREDPI | YQHVREDPI | 0.2233 | 4464.9 | 50.00 | Sequence |
| DRB1_0401 | 498 | DVAGQTVDVAQKNLN | VAGQTVDVA | 0.2221 | 4520.4 | 50.00 | Sequence |
| DRB1_0401 | 472 | PANQTSAITNVVIII | QTSAITNVV | 0.2221 | 4523.8 | 50.00 | Sequence |
| DRB1_0401 | 317 | DDTDRDRSIGSVGRW | TDRDRSIGS | 0.2202 | 4616.0 | 50.00 | Sequence |
| DRB1_0401 | 485 | IIVGSGPATKDIPDV | IIVGSGPAT | 0.2198 | 4637.0 | 50.00 | Sequence |
| DRB1_0401 | 350 | NTFGGITRDVQVPDV | GITRDVQVP | 0.2196 | 4648.4 | 50.00 | Sequence |
| DRB1_0401 | 474 | NQTSAITNVVIIIVG | TSAITNVVI | 0.2193 | 4659.4 | 50.00 | Sequence |
| DRB1_0401 | 108 | PMTPKRAIEVIADAC | RAIEVIADA | 0.2192 | 4666.7 | 50.00 | Sequence |
| DRB1_0401 | 475 | QTSAITNVVIIIVGS | SAITNVVII | 0.2188 | 4683.9 | 50.00 | Sequence |
| DRB1_0401 | 356 | TRDVQVPDVRGQSSA | RDVQVPDVR | 0.2187 | 4690.5 | 50.00 | Sequence |
| DRB1_0401 | 333 | AVVAVLAVLTVVVTI | VAVLAVLTV | 0.2170 | 4776.0 | 50.00 | Sequence |
| DRB1_0401 | 399 | IGTDPAANTSVSAGD | IGTDPAANT | 0.2166 | 4800.2 | 50.00 | Sequence |
| DRB1_0401 | 473 | ANQTSAITNVVIIIV | TSAITNVVI | 0.2161 | 4827.8 | 50.00 | Sequence |
| DRB1_0401 | 504 | VDVAQKNLNVYGFTK | DVAQKNLNV | 0.2133 | 4974.2 | 50.00 | Sequence |
| DRB1_0401 | 207 | EVLTGEPPFTGDSPV | LTGEPPFTG | 0.2129 | 4995.2 | 50.00 | Sequence |
| DRB1_0401 | 505 | DVAQKNLNVYGFTKF | DVAQKNLNV | 0.2124 | 5024.3 | 50.00 | Sequence |
| DRB1_0401 | 476 | TSAITNVVIIIVGSG | TSAITNVVI | 0.2110 | 5101.6 | 50.00 | Sequence |
| DRB1_0401 | 497 | PDVAGQTVDVAQKNL | VAGQTVDVA | 0.2106 | 5123.5 | 50.00 | Sequence |
| DRB1_0401 | 479 | ITNVVIIIVGSGPAT | NVVIIIVGS | 0.2103 | 5136.2 | 50.00 | Sequence |
| DRB1_0401 | 322 | DRSIGSVGRWVAVVA | DRSIGSVGR | 0.2100 | 5156.5 | 50.00 | Sequence |
| DRB1_0401 | 355 | ITRDVQVPDVRGQSS | RDVQVPDVR | 0.2099 | 5161.5 | 50.00 | Sequence |
| DRB1_0401 | 250 | VLKALAKNPENRYQT | KALAKNPEN | 0.2095 | 5181.2 | 50.00 | Sequence |
| DRB1_0401 | 385 | TLQKPDSTIPPDHVI | QKPDSTIPP | 0.2091 | 5205.3 | 50.00 | Sequence |
| DRB1_0401 | 441 | KKLTAAGFGRFKQAN | KLTAAGFGR | 0.2088 | 5222.1 | 50.00 | Sequence |
| DRB1_0401 | 543 | TVPVDSVIELQVSKG | SVIELQVSK | 0.2085 | 5238.4 | 50.00 | Sequence |
| DRB1_0401 | 368 | SSADAIATLQNRGFK | DAIATLQNR | 0.2084 | 5244.6 | 50.00 | Sequence |
| DRB1_0401 | 348 | AINTFGGITRDVQVP | INTFGGITR | 0.2084 | 5246.4 | 50.00 | Sequence |
| DRB1_0401 | 332 | VAVVAVLAVLTVVVT | VAVLAVLTV | 0.2082 | 5255.1 | 50.00 | Sequence |
| DRB1_0401 | 63 | AALNHPAIVAVYDTG | ALNHPAIVA | 0.2077 | 5286.6 | 50.00 | Sequence |
| DRB1_0401 | 392 | TIPPDHVIGTDPAAN | HVIGTDPAA | 0.2076 | 5291.9 | 50.00 | Sequence |
| DRB1_0401 | 69 | AIVAVYDTGEAETPA | VAVYDTGEA | 0.2070 | 5326.7 | 50.00 | Sequence |
| DRB1_0401 | 173 | AAVIGTAQYLSPEQA | VIGTAQYLS | 0.2065 | 5352.2 | 50.00 | Sequence |
| DRB1_0401 | 98 | TLRDIVHTEGPMTPK | IVHTEGPMT | 0.2045 | 5472.1 | 50.00 | Sequence |
| DRB1_0401 | 581 | GWTGMLDKGADVDAG | WTGMLDKGA | 0.2036 | 5525.2 | 50.00 | Sequence |
| DRB1_0401 | 167 | NSVTQTAAVIGTAQY | NSVTQTAAV | 0.2033 | 5543.5 | 50.00 | Sequence |
| DRB1_0401 | 345 | VTIAINTFGGITRDV | VTIAINTFG | 0.2030 | 5558.8 | 50.00 | Sequence |
| DRB1_0401 | 471 | PPANQTSAITNVVII | PANQTSAIT | 0.2028 | 5574.8 | 50.00 | Sequence |
| DRB1_0401 | 191 | SVDARSDVYSLGCVL | RSDVYSLGC | 0.2026 | 5586.9 | 50.00 | Sequence |
| DRB1_0401 | 408 | SVSAGDEITVNVSTG | DEITVNVST | 0.2023 | 5604.9 | 50.00 | Sequence |
| DRB1_0401 | 57 | REAQNAAALNHPAIV | REAQNAAAL | 0.2015 | 5650.6 | 50.00 | Sequence |
| DRB1_0401 | 478 | AITNVVIIIVGSGPA | NVVIIIVGS | 0.1996 | 5769.7 | 50.00 | Sequence |
| DRB1_0401 | 271 | DLVRVHNGEPPEAPK | VRVHNGEPP | 0.1992 | 5795.1 | 50.00 | Sequence |
| DRB1_0401 | 60 | QNAAALNHPAIVAVY | NAAALNHPA | 0.1992 | 5796.4 | 50.00 | Sequence |
| DRB1_0401 | 251 | LKALAKNPENRYQTA | KALAKNPEN | 0.1986 | 5829.2 | 50.00 | Sequence |
| DRB1_0401 | 316 | LDDTDRDRSIGSVGR | TDRDRSIGS | 0.1968 | 5946.6 | 50.00 | Sequence |
| DRB1_0401 | 208 | VLTGEPPFTGDSPVS | LTGEPPFTG | 0.1961 | 5993.9 | 50.00 | Sequence |
| DRB1_0401 | 233 | IPPSARHEGLSADLD | SARHEGLSA | 0.1947 | 6083.2 | 50.00 | Sequence |
| DRB1_0401 | 496 | IPDVAGQTVDVAQKN | VAGQTVDVA | 0.1947 | 6083.3 | 50.00 | Sequence |
| DRB1_0401 | 270 | ADLVRVHNGEPPEAP | VRVHNGEPP | 0.1939 | 6136.4 | 50.00 | Sequence |
| DRB1_0401 | 346 | TIAINTFGGITRDVQ | INTFGGITR | 0.1933 | 6177.9 | 50.00 | Sequence |
| DRB1_0401 | 166 | GNSVTQTAAVIGTAQ | NSVTQTAAV | 0.1923 | 6244.7 | 50.00 | Sequence |
| DRB1_0401 | 272 | LVRVHNGEPPEAPKV | VRVHNGEPP | 0.1919 | 6269.5 | 50.00 | Sequence |
| DRB1_0401 | 281 | PEAPKVLTDAERTSL | KVLTDAERT | 0.1907 | 6351.8 | 50.00 | Sequence |
| DRB1_0401 | 296 | LSSAAGNLSGPRTDP | LSSAAGNLS | 0.1902 | 6384.6 | 50.00 | Sequence |
| DRB1_0401 | 70 | IVAVYDTGEAETPAG | VAVYDTGEA | 0.1896 | 6427.1 | 50.00 | Sequence |
| DRB1_0401 | 477 | SAITNVVIIIVGSGP | SAITNVVII | 0.1887 | 6487.3 | 50.00 | Sequence |
| DRB1_0401 | 62 | AAALNHPAIVAVYDT | ALNHPAIVA | 0.1881 | 6534.6 | 50.00 | Sequence |
| DRB1_0401 | 71 | VAVYDTGEAETPAGP | VAVYDTGEA | 0.1873 | 6586.2 | 50.00 | Sequence |
| DRB1_0401 | 582 | WTGMLDKGADVDAGG | GMLDKGADV | 0.1867 | 6631.7 | 50.00 | Sequence |
| DRB1_0401 | 420 | STGPEQREIPDVSTL | QREIPDVST | 0.1864 | 6657.2 | 50.00 | Sequence |
| DRB1_0401 | 190 | DSVDARSDVYSLGCV | DARSDVYSL | 0.1854 | 6725.1 | 50.00 | Sequence |
| DRB1_0401 | 59 | AQNAAALNHPAIVAV | NAAALNHPA | 0.1850 | 6752.3 | 50.00 | Sequence |
| DRB1_0401 | 181 | YLSPEQARGDSVDAR | QARGDSVDA | 0.1843 | 6806.9 | 50.00 | Sequence |

```
DRB1_0401  182  LSPEQARGDSVDARS  QARGDSVDA         0.1839       6833.2                 50.00     Sequence
DRB1_0401  320  DRDRSIGSVGRWVAV  DRSIGSVGR         0.1829       6908.9                 50.00     Sequence
DRB1_0401  456  SPSTPELVGKVIGTN  ELVGKVIGT         0.1824       6947.5                 50.00     Sequence
DRB1_0401  254  LAKNPENRYQTAAEM  LAKNPENRY         0.1817       7003.6                 50.00     Sequence
DRB1_0401  415  ITVNVSTGPEQREIP  ITVNVSTGP         0.1814       7027.1                 50.00     Sequence
DRB1_0401  165  SGNSVTQTAAVIGTA  NSVTQTAAV         0.1813       7029.0                 50.00     Sequence
DRB1_0401  470  NPPANQTSAITNVVI  PANQTSAIT         0.1806       7085.0                 50.00     Sequence
DRB1_0401  347  IAINTFGGITRDVQV  INTFGGITR         0.1797       7156.7                 50.00     Sequence
DRB1_0401  107  GPMTPKRAIEVIADA  RAIEVIADA         0.1795       7168.5                 50.00     Sequence
DRB1_0401  507  AQKNLNVYGFTKFSQ  VYGFTKFSQ         0.1790       7210.5                 50.00     Sequence
DRB1_0401  252  KALAKNPENRYQTAA  KALAKNPEN         0.1785       7245.3                 50.00     Sequence
DRB1_0401   58  EAQNAAALNHPAIVA  NAAALNHPA         0.1778       7305.8                 50.00     Sequence
DRB1_0401   61  NAAALNHPAIVAVYD  ALNHPAIVA         0.1775       7327.2                 50.00     Sequence
DRB1_0401    2  TPSHLSDRYELGEIL  SHLSDRYEL         0.1773       7343.8                 50.00     Sequence
DRB1_0401  401  TDPAANTSVSAGDEI  PAANTSVSA         0.1769       7375.2                 50.00     Sequence
DRB1_0401  218  DSPVSVAYQHVREDP  PVSVAYQHV         0.1750       7528.7                 50.00     Sequence
DRB1_0401  273  VRVHNGEPPEAPKVL  VRVHNGEPP         0.1740       7609.5                 50.00     Sequence
DRB1_0401  400  GTDPAANTSVSAGDE  PAANTSVSA         0.1738       7623.4                 50.00     Sequence
DRB1_0401  187  ARGDSVDARSDVYSL  ARGDSVDAR         0.1712       7840.0                 50.00     Sequence
DRB1_0401  407  TSVSAGDEITVNVST  VSAGDEITV         0.1708       7876.7                 50.00     Sequence
DRB1_0401  403  PAANTSVSAGDEITV  PAANTSVSA         0.1704       7915.0                 50.00     Sequence
DRB1_0401  164  DSGNSVTQTAAVIGT  NSVTQTAAV         0.1699       7952.0                 50.00     Sequence
DRB1_0401  608  PAGTGVNRDGIITLR  GVNRDGIIT         0.1695       7986.4                 50.00     Sequence
DRB1_0401  402  DPAANTSVSAGDEIT  PAANTSVSA         0.1691       8022.8                 50.00     Sequence
DRB1_0401  528  RPAGEVTGTNPPAGT  PAGEVTGTN         0.1664       8264.9                 50.00     Sequence
DRB1_0401  172  TAAVIGTAQYLSPEQ  VIGTAQYLS         0.1657       8328.3                 50.00     Sequence
DRB1_0401  280  PPEAPKVLTDAERTS  KVLTDAERT         0.1654       8348.9                 50.00     Sequence
DRB1_0401  168  SVTQTAAVIGTAQYL  SVTQTAAVI         0.1648       8408.8                 50.00     Sequence
DRB1_0401  321  RDRSIGSVGRWVAVV  DRSIGSVGR         0.1644       8442.2                 50.00     Sequence
DRB1_0401  529  PAGEVTGTNPPAGTT  EVTGTNPPA         0.1600       8855.5                 50.00     Sequence
DRB1_0401  542  TTVPVDSVIELQVSK  SVIELQVSK         0.1580       9047.4                 50.00     Sequence
DRB1_0401  520  SQASVDSPRPAGEVT  QASVDSPRP         0.1571       9140.6                 50.00     Sequence
DRB1_0401  594  AGGSQHNRVVYQNPP  QHNRVVYQN         0.1571       9140.8                 50.00     Sequence
DRB1_0401  386  LQKPDSTIPPDHVIG  QKPDSTIPP         0.1560       9246.4                 50.00     Sequence
DRB1_0401  217  GDSPVSVAYQHVRED  SPVSVAYQH         0.1552       9326.5                 50.00     Sequence
DRB1_0401  527  PRPAGEVTGTNPPAG  PAGEVTGTN         0.1544       9406.7                 50.00     Sequence
DRB1_0401  189  GDSVDARSDVYSLGC  VDARSDVYS         0.1537       9481.7                 50.00     Sequence
DRB1_0401  188  RGDSVDARSDVYSLG  RGDSVDARS         0.1534       9506.9                 50.00     Sequence
DRB1_0401  391  STIPPDHVIGTDPAA  HVIGTDPAA         0.1529       9560.5                 50.00     Sequence
DRB1_0401   82  PAGPLPYIVMEYVDG  YIVMEYVDG         0.1527       9578.5                 50.00     Sequence
DRB1_0401  253  ALAKNPENRYQTAAE  LAKNPENRY         0.1518       9678.4                 50.00     Sequence
DRB1_0401    1  TTPSHLSDRYELGEI  SHLSDRYEL         0.1472      10170.9                 50.00     Sequence
DRB1_0401  506  VAQKNLNVYGFTKFS  VAQKNLNVY         0.1469      10200.6                 50.00     Sequence
DRB1_0401  315  DLDDTDRDRSIGSVG  TDRDRSIGS         0.1463      10273.0                 50.00     Sequence
DRB1_0401  106  EGPMTPKRAIEVIAD  MTPKRAIEV         0.1459      10308.4                 50.00     Sequence
DRB1_0401  583  TGMLDKGADVDAGGS  GMLDKGADV         0.1457      10333.8                 50.00     Sequence
DRB1_0401  469  TNPPANQTSAITNVV  PANQTSAIT         0.1446      10457.1                 50.00     Sequence
DRB1_0401  170  TQTAAVIGTAQYLSP  TQTAAVIGT         0.1427      10681.0                 50.00     Sequence
DRB1_0401  161  AIADSGNSVTQTAAV  AIADSGNSV         0.1424      10711.1                 50.00     Sequence
DRB1_0401  163  ADSGNSVTQTAAVIG  NSVTQTAAV         0.1414      10825.3                 50.00     Sequence
DRB1_0401  171  QTAAVIGTAQYLSPE  VIGTAQYLS         0.1393      11080.4                 50.00     Sequence
DRB1_0401  526  SPRPAGEVTGTNPPA  PAGEVTGTN         0.1391      11102.1                 50.00     Sequence
DRB1_0401  495  DIPDVAGQTVDVAQK  DVAGQTVDV         0.1387      11146.7                 50.00     Sequence
DRB1_0401  162  IADSGNSVTQTAAVI  SGNSVTQTA         0.1376      11279.6                 50.00     Sequence
DRB1_0401  455  NSPSTPELVGKVIGT  ELVGKVIGT         0.1367      11389.8                 50.00     Sequence
DRB1_0401  466  VIGTNPPANQTSAIT  VIGTNPPAN         0.1356      11534.6                 50.00     Sequence
DRB1_0401  313  RQDLDDTDRDRSIGS  RQDLDDTDR         0.1354      11555.5                 50.00     Sequence
DRB1_0401  169  VTQTAAVIGTAQYLS  TQTAAVIGT         0.1340      11732.4                 50.00     Sequence
DRB1_0401  584  GMLDKGADVDAGGSQ  GMLDKGADV         0.1338      11760.4                 50.00     Sequence
DRB1_0401  406  NTSVSAGDEITVNVS  VSAGDEITV         0.1335      11790.7                 50.00     Sequence
DRB1_0401  274  RVHNGEPPEAPKVLT  RVHNGEPPE         0.1335      11793.6                 50.00     Sequence
DRB1_0401  521  QASVDSPRPAGEVTG  QASVDSPRP         0.1329      11874.3                 50.00     Sequence
DRB1_0401  310  PLPRQDLDDTDRDRS  LPRQDLDDT         0.1311      12108.2                 50.00     Sequence
DRB1_0401  232  PIPPSARHEGLSADL  SARHEGLSA         0.1305      12181.7                 50.00     Sequence
DRB1_0401  303  LSGPRTDPLPRQDLD  LSGPRTDPL         0.1304      12200.6                 50.00     Sequence
DRB1_0401  279  EPPEAPKVLTDAERT  KVLTDAERT         0.1293      12340.6                 50.00     Sequence
```

```
DRB1_0401  603  VYQNPPAGTGVNRDG  VYQNPPAGT        0.1292      12352.5               50.00     Sequence
DRB1_0401    0  MTTPSHLSDRYELGE  HLSDRYELG        0.1274      12605.4               50.00     Sequence
DRB1_0401  419  VSTGPEQREIPDVST  QREIPDVST        0.1272      12626.7               50.00     Sequence
DRB1_0401  314  QDLDDTDRDRSIGSV  TDRDRSIGS        0.1266      12704.0               50.00     Sequence
DRB1_0401  493  TKDIPDVAGQTVDVA  TKDIPDVAG        0.1264      12731.6               50.00     Sequence
DRB1_0401  302  NLSGPRTDPLPRQDL  LSGPRTDPL        0.1263      12749.4               50.00     Sequence
DRB1_0401  216  TGDSPVSVAYQHVRE  SPVSVAYQH        0.1262      12769.8               50.00     Sequence
DRB1_0401  494  KDIPDVAGQTVDVAQ  DVAGQTVDV        0.1262      12770.0               50.00     Sequence
DRB1_0401  531  GEVTGTNPPAGTTVP  GEVTGTNPP        0.1241      13055.1               50.00     Sequence
DRB1_0401  607  PPAGTGVNRDGIITL  GVNRDGIIT        0.1229      13224.3               50.00     Sequence
DRB1_0401  304  SGPRTDPLPRQDLDD  PRTDPLPRQ        0.1219      13374.7               50.00     Sequence
DRB1_0401  311  LPRQDLDDTDRDRSI  LPRQDLDDT        0.1187      13843.9               50.00     Sequence
DRB1_0401  301  GNLSGPRTDPLPRQD  LSGPRTDPL        0.1176      14011.5               50.00     Sequence
DRB1_0401  305  GPRTDPLPRQDLDDT  GPRTDPLPR        0.1164      14193.2               50.00     Sequence
DRB1_0401  486  IVGSGPATKDIPDVA  IVGSGPATK        0.1149      14426.1               50.00     Sequence
DRB1_0401  525  DSPRPAGEVTGTNPP  PAGEVTGTN        0.1144      14505.3               50.00     Sequence
DRB1_0401  593  DAGGSQHNRVVYQNP  QHNRVVYQN        0.1138      14591.5               50.00     Sequence
DRB1_0401  105  TEGPMTPKRAIEVIA  MTPKRAIEV        0.1131      14712.3               50.00     Sequence
DRB1_0401  309  DPLPRQDLDDTDRDR  PRQDLDDTD        0.1130      14727.3               50.00     Sequence
DRB1_0401  387  QKPDSTIPPDHVIGT  QKPDSTIPP        0.1123      14835.1               50.00     Sequence
DRB1_0401  530  AGEVTGTNPPAGTTV  GEVTGTNPP        0.1121      14863.2               50.00     Sequence
DRB1_0401   72  AVYDTGEAETPAGPL  AVYDTGEAE        0.1121      14866.9               50.00     Sequence
DRB1_0401  541  GTTVPVDSVIELQVS  TVPVDSVIE        0.1114      14974.4               50.00     Sequence
DRB1_0401  532  EVTGTNPPAGTTVPV  EVTGTNPPA        0.1109      15053.7               50.00     Sequence
DRB1_0401  297  SSAAGNLSGPRTDPL  SSAAGNLSG        0.1097      15263.9               50.00     Sequence
DRB1_0401  468  GTNPPANQTSAITNV  PANQTSAIT        0.1093      15330.3               50.00     Sequence
DRB1_0401   73  VYDTGEAETPAGPLP  YDTGEAETP        0.1089      15383.7               50.00     Sequence
DRB1_0401  492  ATKDIPDVAGQTVDV  TKDIPDVAG        0.1083      15486.2               50.00     Sequence
DRB1_0401  405  ANTSVSAGDEITVNV  VSAGDEITV        0.1081      15518.7               50.00     Sequence
DRB1_0401  300  AGNLSGPRTDPLPRQ  LSGPRTDPL        0.1080      15534.0               50.00     Sequence
DRB1_0401  467  IGTNPPANQTSAITN  IGTNPPANQ        0.1077      15595.2               50.00     Sequence
DRB1_0401  228  VREDPIPPSARHEGL  VREDPIPPS        0.1070      15706.2               50.00     Sequence
DRB1_0401  489  SGPATKDIPDVAGQT  ATKDIPDVA        0.1059      15901.2               50.00     Sequence
DRB1_0401  390  DSTIPPDHVIGTDPA  DHVIGTDPA        0.1058      15916.0               50.00     Sequence
DRB1_0401  299  AAGNLSGPRTDPLPR  LSGPRTDPL        0.1051      16031.4               50.00     Sequence
DRB1_0401  491  PATKDIPDVAGQTVD  TKDIPDVAG        0.1051      16045.0               50.00     Sequence
DRB1_0401  490  GPATKDIPDVAGQTV  TKDIPDVAG        0.1048      16085.8               50.00     Sequence
DRB1_0401  452  KQANSPSTPELVGKV  KQANSPSTP        0.1035      16309.6               50.00     Sequence
DRB1_0401  308  TDPLPRQDLDDTDRD  LPRQDLDDT        0.0980      17312.2               50.00     Sequence
DRB1_0401  298  SAAGNLSGPRTDPLP  AAGNLSGPR        0.0965      17605.2               50.00     Sequence
DRB1_0401  275  VHNGEPPEAPKVLTD  VHNGEPPEA        0.0963      17637.2               50.00     Sequence
DRB1_0401  312  PRQDLDDTDRDRSIG  RQDLDDTDR        0.0959      17712.0               50.00     Sequence
DRB1_0401  592  VDAGGSQHNRVVYQN  QHNRVVYQN        0.0955      17788.3               50.00     Sequence
DRB1_0401  540  AGTTVPVDSVIELQV  TVPVDSVIE        0.0952      17851.1               50.00     Sequence
DRB1_0401  539  PAGTTVPVDSVIELQ  GTTVPVDSV        0.0951      17864.1               50.00     Sequence
DRB1_0401  488  GSGPATKDIPDVAGQ  ATKDIPDVA        0.0927      18340.4               50.00     Sequence
DRB1_0401  104  HTEGPMTPKRAIEVI  MTPKRAIEV        0.0907      18733.3               50.00     Sequence
DRB1_0401  585  MLDKGADVDAGGSQH  LDKGADVDA        0.0903      18819.2               50.00     Sequence
DRB1_0401  404  AANTSVSAGDEITVN  VSAGDEITV        0.0901      18863.2               50.00     Sequence
DRB1_0401  524  VDSPRPAGEVTGTNP  PAGEVTGTN        0.0896      18961.9               50.00     Sequence
DRB1_0401  538  PPAGTTVPVDSVIEL  GTTVPVDSV        0.0892      19038.3               50.00     Sequence
DRB1_0401  606  NPPAGTGVNRDGIIT  GVNRDGIIT        0.0878      19339.2               50.00     Sequence
DRB1_0401   81  TPAGPLPYIVMEYVD  PLPYIVMEY        0.0874      19413.2               50.00     Sequence
DRB1_0401  533  VTGTNPPAGTTVPVD  VTGTNPPAG        0.0838      20201.5               50.00     Sequence
DRB1_0401  231  DPIPPSARHEGLSAD  SARHEGLSA        0.0835      20249.2               50.00     Sequence
DRB1_0401  306  PRTDPLPRQDLDDTD  PRTDPLPRQ        0.0833      20296.0               50.00     Sequence
DRB1_0401  487  VGSGPATKDIPDVAG  ATKDIPDVA        0.0827      20440.1               50.00     Sequence
DRB1_0401  586  LDKGADVDAGGSQHN  LDKGADVDA        0.0825      20478.2               50.00     Sequence
DRB1_0401  307  RTDPLPRQDLDDTDR  LPRQDLDDT        0.0813      20746.2               50.00     Sequence
DRB1_0401   80  ETPAGPLPYIVMEYV  ETPAGPLPY        0.0802      20990.1               50.00     Sequence
DRB1_0401  278  GEPPEAPKVLTDAER  PKVLTDAER        0.0769      21750.7               50.00     Sequence
DRB1_0401  591  DVDAGGSQHNRVVYQ  DAGGSQHNR        0.0768      21776.4               50.00     Sequence
DRB1_0401  537  NPPAGTTVPVDSVIE  AGTTVPVDS        0.0760      21974.0               50.00     Sequence
DRB1_0401  276  HNGEPPEAPKVLTDA  HNGEPPEAP        0.0755      22094.9               50.00     Sequence
DRB1_0401  522  ASVDSPRPAGEVTGT  ASVDSPRPA        0.0733      22628.4               50.00     Sequence
DRB1_0401   74  YDTGEAETPAGPLPY  YDTGEAETP        0.0731      22666.6               50.00     Sequence
```

```
   DRB1_0401  589  GADVDAGGSQHNRVV  DAGGSQHNR        0.0713      23117.6               50.00     Sequence
   DRB1_0401  523  SVDSPRPAGEVTGTN  PAGEVTGTN        0.0706      23296.1               50.00     Sequence
   DRB1_0401  590  ADVDAGGSQHNRVVY  DAGGSQHNR        0.0702      23389.1               50.00     Sequence
   DRB1_0401   77  GEAETPAGPLPYIVM  GEAETPAGP        0.0701      23412.9               50.00     Sequence
   DRB1_0401   79  AETPAGPLPYIVMEY  ETPAGPLPY        0.0698      23487.5               50.00     Sequence
   DRB1_0401  418  NVSTGPEQREIPDVS  EQREIPDVS        0.0696      23534.5               50.00     Sequence
   DRB1_0401  389  PDSTIPPDHVIGTDP  DSTIPPDHV        0.0693      23629.2               50.00     Sequence
   DRB1_0401  587  DKGADVDAGGSQHNR  DKGADVDAG        0.0689      23720.9               50.00     Sequence
   DRB1_0401  534  TGTNPPAGTTVPVDS  TGTNPPAGT        0.0680      23968.6               50.00     Sequence
   DRB1_0401   75  DTGEAETPAGPLPYI  DTGEAETPA        0.0674      24101.7               50.00     Sequence
   DRB1_0401  388  KPDSTIPPDHVIGTD  DSTIPPDHV        0.0669      24254.7               50.00     Sequence
   DRB1_0401  230  EDPIPPSARHEGLSA  SARHEGLSA        0.0654      24630.0               50.00     Sequence
   DRB1_0401   78  EAETPAGPLPYIVME  ETPAGPLPY        0.0621      25535.8               50.00     Sequence
   DRB1_0401  536  TNPPAGTTVPVDSVI  PAGTTVPVD        0.0606      25960.7               50.00     Sequence
   DRB1_0401  588  KGADVDAGGSQHNRV  KGADVDAGG        0.0605      25992.7               50.00     Sequence
   DRB1_0401  416  TVNVSTGPEQREIPD  TVNVSTGPE        0.0579      26726.8               50.00     Sequence
   DRB1_0401   76  TGEAETPAGPLPYIV  GEAETPAGP        0.0576      26807.6               50.00     Sequence
   DRB1_0401  535  GTNPPAGTTVPVDSV  PAGTTVPVD        0.0542      27824.2               50.00     Sequence
   DRB1_0401  453  QANSPSTPELVGKVI  QANSPSTPE        0.0534      28062.4               50.00     Sequence
   DRB1_0401  277  NGEPPEAPKVLTDAE  PPEAPKVLT        0.0528      28231.1               50.00     Sequence
   DRB1_0401  605  QNPPAGTGVNRDGII  TGVNRDGII        0.0515      28634.7               50.00     Sequence
   DRB1_0401  604  YQNPPAGTGVNRDGI  YQNPPAGTG        0.0505      28943.4               50.00     Sequence
   DRB1_0401  454  ANSPSTPELVGKVIG  NSPSTPELV        0.0485      29599.3               50.00     Sequence
   DRB1_0401  229  REDPIPPSARHEGLS  REDPIPPSA        0.0459      30444.8               50.00     Sequence
   DRB1_0401  417  VNVSTGPEQREIPDV  VNVSTGPEQ        0.0458      30462.2               50.00     Sequence
-------------------------------------------------------------------------------------------------

Allele: DRB1_0401. Number of high binders 6. Number of weak binders 111. Number of peptides 612

-------------------------------------------------------------------------------------------------
-------------------------------------------------------------------------------------------------
      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
-------------------------------------------------------------------------------------------------
   DRB1_0404  141  ANIMISATNAVKVMD  IMISATNAV        0.7698         12.1         SB     0.80     Sequence
   DRB1_0404  140  PANIMISATNAVKVM  NIMISATNA        0.7674         12.4         SB     0.80     Sequence
   DRB1_0404  142  NIMISATNAVKVMDF  IMISATNAV        0.7635         12.9         SB     0.80     Sequence
   DRB1_0404  139  KPANIMISATNAVKV  NIMISATNA        0.7456         15.7         SB     2.00     Sequence
   DRB1_0404  138  VKPANIMISATNAVK  NIMISATNA        0.7093         23.2         SB     4.00     Sequence
   DRB1_0404  342  TVVVTIAINTFGGIT  VVVTIAINT        0.6785         32.4         SB     4.00     Sequence
   DRB1_0404  343  VVVTIAINTFGGITR  VVVTIAINT        0.6654         37.3         SB     8.00     Sequence
   DRB1_0404  143  IMISATNAVKVMDFG  IMISATNAV        0.6649         37.6         SB     8.00     Sequence
   DRB1_0404  341  LTVVVTIAINTFGGI  VVVTIAINT        0.6644         37.8         SB     8.00     Sequence
   DRB1_0404  481  NVVIIIVGSGPATKD  VVIIIVGSG        0.6552         41.7         SB     8.00     Sequence
   DRB1_0404  137  DVKPANIMISATNAV  NIMISATNA        0.6479         45.1         SB     8.00     Sequence
   DRB1_0404  480  TNVVIIIVGSGPATK  VVIIIVGSG        0.6432         47.5         SB     8.00     Sequence
   DRB1_0404  340  VLTVVVTIAINTFGG  VVVTIAINT        0.6366         51.0         WB     8.00     Sequence
   DRB1_0404  482  VVIIIVGSGPATKDI  VVIIIVGSG        0.6305         54.5         WB     8.00     Sequence
   DRB1_0404  479  ITNVVIIIVGSGPAT  VVIIIVGSG        0.6151         64.4         WB     8.00     Sequence
   DRB1_0404  344  VVTIAINTFGGITRD  VVTIAINTF        0.6148         64.6         WB     8.00     Sequence
   DRB1_0404  339  AVLTVVVTIAINTFG  VVVTIAINT        0.6134         65.5         WB     8.00     Sequence
   DRB1_0404   68  PAIVAVYDTGEAETP  AIVAVYDTG        0.6124         66.3         WB     8.00     Sequence
   DRB1_0404  575  PRLRALGWTGMLDKG  RLRALGWTG        0.6093         68.5         WB     8.00     Sequence
   DRB1_0404   67  HPAIVAVYDTGEAET  AIVAVYDTG        0.6074         70.0         WB    16.00     Sequence
   DRB1_0404  576  RLRALGWTGMLDKGA  RALGWTGML        0.6072         70.1         WB    16.00     Sequence
   DRB1_0404  600  NRVVYQNPPAGTGVN  RVVYQNPPA        0.5948         80.2         WB    16.00     Sequence
   DRB1_0404   66  NHPAIVAVYDTGEAE  AIVAVYDTG        0.5929         81.9         WB    16.00     Sequence
   DRB1_0404  599  HNRVVYQNPPAGTGV  RVVYQNPPA        0.5891         85.3         WB    16.00     Sequence
   DRB1_0404  291  ERTSLLSSAAGNLSG  RTSLLSSAA        0.5889         85.5         WB    16.00     Sequence
   DRB1_0404  559  QFVMPDLSGMFWVDA  QFVMPDLSG        0.5877         86.5         WB    16.00     Sequence
   DRB1_0404  574  EPRLRALGWTGMLDK  RLRALGWTG        0.5871         87.1         WB    16.00     Sequence
   DRB1_0404   87  PYIVMEYVDGVTLRD  YIVMEYVDG        0.5858         88.3         WB    16.00     Sequence
   DRB1_0404  558  NQFVMPDLSGMFWVD  QFVMPDLSG        0.5827         91.4         WB    16.00     Sequence
   DRB1_0404  290  AERTSLLSSAAGNLS  RTSLLSSAA        0.5819         92.2         WB    16.00     Sequence
   DRB1_0404   88  YIVMEYVDGVTLRDI  YIVMEYVDG        0.5817         92.4         WB    16.00     Sequence
   DRB1_0404  333  AVVAVLAVLTVVVTI  AVVAVLAVL        0.5812         92.9         WB    16.00     Sequence
   DRB1_0404   69  AIVAVYDTGEAETPA  AIVAVYDTG        0.5769         97.3         WB    16.00     Sequence
```

```
DRB1_0404   86  LPYIVMEYVDGVTLR  YIVMEYVDG        0.5749         99.4          WB    16.00      Sequence
DRB1_0404  338  LAVLTVVVTIAINTF  AVLTVVVTI        0.5725        102.1          WB    16.00      Sequence
DRB1_0404   85  PLPYIVMEYVDGVTL  YIVMEYVDG        0.5710        103.8          WB    16.00      Sequence
DRB1_0404  332  VAVVAVLAVLTVVVT  AVVAVLAVL        0.5690        106.0          WB    16.00      Sequence
DRB1_0404  598  QHNRVVYQNPPAGTG  RVVYQNPPA        0.5680        107.1          WB    16.00      Sequence
DRB1_0404  478  AITNVVIIIVGSGPA  VVIIIVGSG        0.5675        107.7          WB    16.00      Sequence
DRB1_0404  483  VIIIVGSGPATKDIP  IIIVGSGPA        0.5663        109.1          WB    16.00      Sequence
DRB1_0404  557  GNQFVMPDLSGMFWV  QFVMPDLSG        0.5661        109.4          WB    16.00      Sequence
DRB1_0404  573  AEPRLRALGWTGMLD  RLRALGWTG        0.5628        113.3          WB    16.00      Sequence
DRB1_0404  345  VTIAINTFGGITRDV  IAINTFGGI        0.5593        117.7          WB    16.00      Sequence
DRB1_0404  289  DAERTSLLSSAAGNL  RTSLLSSAA        0.5562        121.7          WB    16.00      Sequence
DRB1_0404   36  VAVKVLRADLARDPS  VKVLRADLA        0.5557        122.3          WB    16.00      Sequence
DRB1_0404  292  RTSLLSSAAGNLSGP  LLSSAAGNL        0.5553        122.9          WB    16.00      Sequence
DRB1_0404  556  KGNQFVMPDLSGMFW  QFVMPDLSG        0.5549        123.4          WB    16.00      Sequence
DRB1_0404  331  WVAVVAVLAVLTVVV  AVVAVLAVL        0.5521        127.2          WB    16.00      Sequence
DRB1_0404  330  RWVAVVAVLAVLTVV  AVVAVLAVL        0.5516        128.0          WB    16.00      Sequence
DRB1_0404   35  DVAVKVLRADLARDP  VKVLRADLA        0.5447        137.9          WB    16.00      Sequence
DRB1_0404  560  FVMPDLSGMFWVDAE  FVMPDLSGM        0.5419        142.1          WB    16.00      Sequence
DRB1_0404  337  VLAVLTVVVTIAINT  AVLTVVVTI        0.5418        142.3          WB    16.00      Sequence
DRB1_0404  334  VVAVLAVLTVVVTIA  AVLAVLTVV        0.5397        145.6          WB    16.00      Sequence
DRB1_0404  136  RDVKPANIMISATNA  NIMISATNA        0.5349        153.2          WB    16.00      Sequence
DRB1_0404  577  LRALGWTGMLDKGAD  RALGWTGML        0.5342        154.4          WB    16.00      Sequence
DRB1_0404   65  LNHPAIVAVYDTGEA  AIVAVYDTG        0.5328        156.7          WB    16.00      Sequence
DRB1_0404  336  AVLAVLTVVVTIAIN  AVLTVVVTI        0.5318        158.5          WB    16.00      Sequence
DRB1_0404  601  RVVYQNPPAGTGVNR  RVVYQNPPA        0.5318        158.6          WB    16.00      Sequence
DRB1_0404   37  AVKVLRADLARDPSF  AVKVLRADL        0.5284        164.4          WB    16.00      Sequence
DRB1_0404  346  TIAINTFGGITRDVQ  IAINTFGGI        0.5278        165.5          WB    16.00      Sequence
DRB1_0404  329  GRWVAVVAVLAVLTV  RWVAVVAVL        0.5276        165.9          WB    16.00      Sequence
DRB1_0404   84  GPLPYIVMEYVDGVT  YIVMEYVDG        0.5273        166.4          WB    16.00      Sequence
DRB1_0404   34  RDVAVKVLRADLARD  AVKVLRADL        0.5245        171.5          WB    32.00      Sequence
DRB1_0404  448  FGRFKQANSPSTPEL  RFKQANSPS        0.5214        177.4          WB    32.00      Sequence
DRB1_0404  335  VAVLAVLTVVVTIAI  AVLAVLTVV        0.5176        184.9          WB    32.00      Sequence
DRB1_0404  447  GFGRFKQANSPSTPE  RFKQANSPS        0.5151        190.0          WB    32.00      Sequence
DRB1_0404  555  SKGNQFVMPDLSGMF  QFVMPDLSG        0.5121        196.1          WB    32.00      Sequence
DRB1_0404  597  SQHNRVVYQNPPAGT  RVVYQNPPA        0.5088        203.4          WB    32.00      Sequence
DRB1_0404  150  AVKVMDFGIARAIAD  KVMDFGIAR        0.5073        206.5          WB    32.00      Sequence
DRB1_0404  572  DAEPRLRALGWTGML  RLRALGWTG        0.5006        222.0          WB    32.00      Sequence
DRB1_0404  347  IAINTFGGITRDVQV  IAINTFGGI        0.4915        245.1          WB    32.00      Sequence
DRB1_0404   13  GEILGFGGMSEVHLA  EILGFGGMS        0.4907        247.4          WB    32.00      Sequence
DRB1_0404  449  GRFKQANSPSTPELV  FKQANSPST        0.4904        248.1          WB    32.00      Sequence
DRB1_0404  288  TDAERTSLLSSAAGN  ERTSLLSSA        0.4890        251.8          WB    32.00      Sequence
DRB1_0404  149  NAVKVMDFGIARAIA  VKVMDFGIA        0.4886        252.9          WB    32.00      Sequence
DRB1_0404   83  AGPLPYIVMEYVDGV  YIVMEYVDG        0.4849        263.4          WB    32.00      Sequence
DRB1_0404  477  SAITNVVIIIVGSGP  VVIIIVGSG        0.4844        264.8          WB    32.00      Sequence
DRB1_0404  446  AGFGRFKQANSPSTP  RFKQANSPS        0.4839        266.0          WB    32.00      Sequence
DRB1_0404  151  VKVMDFGIARAIADS  VKVMDFGIA        0.4835        267.2          WB    32.00      Sequence
DRB1_0404  293  TSLLSSAAGNLSGPR  LLSSAAGNL        0.4812        274.0          WB    32.00      Sequence
DRB1_0404  484  IIIVGSGPATKDIPD  IIIVGSGPA        0.4777        284.5          WB    32.00      Sequence
DRB1_0404   33  HRDVAVKVLRADLAR  AVKVLRADL        0.4754        291.7          WB    32.00      Sequence
DRB1_0404  395  PDHVIGTDPAANTSV  HVIGTDPAA        0.4725        300.9          WB    32.00      Sequence
DRB1_0404   12  LGEILGFGGMSEVHL  EILGFGGMS        0.4722        302.0          WB    32.00      Sequence
DRB1_0404  148  TNAVKVMDFGIARAI  VKVMDFGIA        0.4694        311.3          WB    32.00      Sequence
DRB1_0404   14  EILGFGGMSEVHLAR  EILGFGGMS        0.4694        311.4          WB    32.00      Sequence
DRB1_0404  396  DHVIGTDPAANTSVS  HVIGTDPAA        0.4690        312.7          WB    32.00      Sequence
DRB1_0404  460  PELVGKVIGTNPPAN  LVGKVIGTN        0.4684        314.7          WB    32.00      Sequence
DRB1_0404  328  VGRWVAVVAVLAVLT  RWVAVVAVL        0.4682        315.3          WB    32.00      Sequence
DRB1_0404  547  DSVIELQVSKGNQFV  SVIELQVSK        0.4678        316.8          WB    32.00      Sequence
DRB1_0404  546  VDSVIELQVSKGNQF  SVIELQVSK        0.4644        328.8          WB    32.00      Sequence
DRB1_0404  461  ELVGKVIGTNPPANQ  KVIGTNPPA        0.4643        329.1          WB    32.00      Sequence
DRB1_0404  394  PPDHVIGTDPAANTS  HVIGTDPAA        0.4559        360.3          WB    32.00      Sequence
DRB1_0404   64  ALNHPAIVAVYDTGE  AIVAVYDTG        0.4559        360.4          WB    32.00      Sequence
DRB1_0404  545  PVDSVIELQVSKGNQ  SVIELQVSK        0.4552        362.9          WB    32.00      Sequence
DRB1_0404  247  DAVVLKALAKNPENR  VLKALAKNP        0.4547        365.0          WB    32.00      Sequence
DRB1_0404  554  VSKGNQFVMPDLSGM  QFVMPDLSG        0.4542        366.9          WB    32.00      Sequence
DRB1_0404  381  FKIRTLQKPDSTIPP  KIRTLQKPD        0.4539        368.0          WB    32.00      Sequence
DRB1_0404  578  RALGWTGMLDKGADV  RALGWTGML        0.4529        372.2          WB    32.00      Sequence
```

```
DRB1_0404  561  VMPDLSGMFWVDAEP  VMPDLSGMF          0.4487          389.5          WB    32.00       Sequence
DRB1_0404  380  GFKIRTLQKPDSTIP  KIRTLQKPD          0.4450          405.4          WB    32.00       Sequence
DRB1_0404  462  LVGKVIGTNPPANQT  KVIGTNPPA          0.4450          405.5          WB    32.00       Sequence
DRB1_0404  564  DLSGMFWVDAEPRLR  LSGMFWVDA          0.4410          423.2          WB    32.00       Sequence
DRB1_0404  459  TPELVGKVIGTNPPA  LVGKVIGTN          0.4397          429.2          WB    32.00       Sequence
DRB1_0404  113  RAIEVIADACQALNF  EVIADACQA          0.4396          430.1          WB    32.00       Sequence
DRB1_0404  425  QREIPDVSTLTYAEA  REIPDVSTL          0.4395          430.3          WB    32.00       Sequence
DRB1_0404  397  HVIGTDPAANTSVSA  HVIGTDPAA          0.4394          430.8          WB    32.00       Sequence
DRB1_0404  445  AAGFGRFKQANSPST  RFKQANSPS          0.4394          430.8          WB    32.00       Sequence
DRB1_0404  248  AVVLKALAKNPENRY  VLKALAKNP          0.4379          437.7          WB    32.00       Sequence
DRB1_0404  563  PDLSGMFWVDAEPRL  LSGMFWVDA          0.4374          440.0          WB    32.00       Sequence
DRB1_0404  411  AGDEITVNVSTGPEQ  EITVNVSTG          0.4369          442.7          WB    32.00       Sequence
DRB1_0404  412  GDEITVNVSTGPEQR  EITVNVSTG          0.4344          454.6          WB    32.00       Sequence
DRB1_0404  548  SVIELQVSKGNQFVM  SVIELQVSK          0.4341          456.4          WB    32.00       Sequence
DRB1_0404   38  VKVLRADLARDPSFY  KVLRADLAR          0.4331          461.3          WB    32.00       Sequence
DRB1_0404   89  IVMEYVDGVTLRDIV  IVMEYVDGV          0.4330          461.8          WB    32.00       Sequence
DRB1_0404   11  ELGEILGFGGMSEVH  EILGFGGMS          0.4317          467.9          WB    32.00       Sequence
DRB1_0404  246  LDAVVLKALAKNPEN  VVLKALAKN          0.4314          469.5          WB    32.00       Sequence
DRB1_0404  379  RGFKIRTLQKPDSTI  KIRTLQKPD          0.4312          470.9          WB    32.00       Sequence
DRB1_0404  426  REIPDVSTLTYAEAV  REIPDVSTL          0.4296          479.1          WB    32.00       Sequence
DRB1_0404  596  GSQHNRVVYQNPPAG  RVVYQNPPA          0.4295          479.7          WB    32.00       Sequence
DRB1_0404  511  LNVYGFTKFSQASVD  LNVYGFTKF          0.4282          486.5          WB    32.00       Sequence
DRB1_0404  114  AIEVIADACQALNFS  EVIADACQA          0.4254          501.1                32.00       Sequence
DRB1_0404   82  PAGPLPYIVMEYVDG  YIVMEYVDG          0.4248          504.3                32.00       Sequence
DRB1_0404  510  NLNVYGFTKFSQASV  LNVYGFTKF          0.4235          511.8                32.00       Sequence
DRB1_0404  147  ATNAVKVMDFGIARA  VKVMDFGIA          0.4233          512.9                32.00       Sequence
DRB1_0404  413  DEITVNVSTGPEQRE  EITVNVSTG          0.4230          514.2                32.00       Sequence
DRB1_0404  201  LGCVLYEVLTGEPPF  CVLYEVLTG          0.4230          514.3                32.00       Sequence
DRB1_0404  112  KRAIEVIADACQALN  AIEVIADAC          0.4227          516.2                32.00       Sequence
DRB1_0404  450  RFKQANSPSTPELVG  FKQANSPST          0.4221          519.4                32.00       Sequence
DRB1_0404  202  GCVLYEVLTGEPPFT  CVLYEVLTG          0.4189          537.8                32.00       Sequence
DRB1_0404   30  LRLHRDVAVKVLRAD  LRLHRDVAV          0.4185          540.0                32.00       Sequence
DRB1_0404  287  LTDAERTSLLSSAAG  ERTSLLSSA          0.4184          540.7                32.00       Sequence
DRB1_0404  203  CVLYEVLTGEPPFTG  CVLYEVLTG          0.4174          546.6                32.00       Sequence
DRB1_0404  565  LSGMFWVDAEPRLRA  LSGMFWVDA          0.4172          547.8                32.00       Sequence
DRB1_0404  382  KIRTLQKPDSTIPPD  TLQKPDSTI          0.4161          554.3                32.00       Sequence
DRB1_0404  571  VDAEPRLRALGWTGM  RLRALGWTG          0.4140          566.7                32.00       Sequence
DRB1_0404  562  MPDLSGMFWVDAEPR  LSGMFWVDA          0.4138          568.0                32.00       Sequence
DRB1_0404  476  TSAITNVVIIIVGSG  NVVIIIVGS          0.4128          574.2                32.00       Sequence
DRB1_0404   29  DLRLHRDVAVKVLRA  LRLHRDVAV          0.4128          574.7                32.00       Sequence
DRB1_0404  294  SLLSSAAGNLSGPRT  LLSSAAGNL          0.4121          578.5                32.00       Sequence
DRB1_0404  327  SVGRWVAVVAVLAVL  RWVAVVAVL          0.4120          579.3                32.00       Sequence
DRB1_0404   28  RDLRLHRDVAVKVLR  LRLHRDVAV          0.4111          585.4                32.00       Sequence
DRB1_0404  326  GSVGRWVAVVAVLAV  SVGRWVAVV          0.4087          600.3                32.00       Sequence
DRB1_0404   32  LHRDVAVKVLRADLA  AVKVLRADL          0.4057          620.6                50.00       Sequence
DRB1_0404  249  VVLKALAKNPENRYQ  VLKALAKNP          0.4050          625.1                50.00       Sequence
DRB1_0404   96  GVTLRDIVHTEGPMT  TLRDIVHTE          0.4046          627.9                50.00       Sequence
DRB1_0404  458  STPELVGKVIGTNPP  ELVGKVIGT          0.4037          633.8                50.00       Sequence
DRB1_0404  370  ADAIATLQNRGFKIR  DAIATLQNR          0.4027          640.6                50.00       Sequence
DRB1_0404  474  NQTSAITNVVIIIVG  QTSAITNVV          0.4013          650.2                50.00       Sequence
DRB1_0404  152  KVMDFGIARAIADSG  KVMDFGIAR          0.4012          651.2                50.00       Sequence
DRB1_0404  509  KNLNVYGFTKFSQAS  LNVYGFTKF          0.4007          654.8                50.00       Sequence
DRB1_0404  200  SLGCVLYEVLTGEPP  CVLYEVLTG          0.4000          659.8                50.00       Sequence
DRB1_0404  393  IPPDHVIGTDPAANT  HVIGTDPAA          0.3993          664.4                50.00       Sequence
DRB1_0404  197  DVYSLGCVLYEVLTG  DVYSLGCVL          0.3989          667.7                50.00       Sequence
DRB1_0404   10  YELGEILGFGGMSEV  EILGFGGMS          0.3985          670.7                50.00       Sequence
DRB1_0404  371  DAIATLQNRGFKIRT  DAIATLQNR          0.3981          673.2                50.00       Sequence
DRB1_0404  473  ANQTSAITNVVIIIV  QTSAITNVV          0.3977          676.1                50.00       Sequence
DRB1_0404   97  VTLRDIVHTEGPMTP  TLRDIVHTE          0.3970          681.6                50.00       Sequence
DRB1_0404  544  VPVDSVIELQVSKGN  SVIELQVSK          0.3967          683.9                50.00       Sequence
DRB1_0404  514  YGFTKFSQASVDSPR  KFSQASVDS          0.3966          684.4                50.00       Sequence
DRB1_0404  475  QTSAITNVVIIIVGS  NVVIIIVGS          0.3953          693.9                50.00       Sequence
DRB1_0404  369  SADAIATLQNRGFKI  DAIATLQNR          0.3951          695.5                50.00       Sequence
DRB1_0404  463  VGKVIGTNPPANQTS  KVIGTNPPA          0.3938          705.3                50.00       Sequence
DRB1_0404  111  PKRAIEVIADACQAL  AIEVIADAC          0.3931          711.0                50.00       Sequence
DRB1_0404   27  ARDLRLHRDVAVKVL  LRLHRDVAV          0.3930          711.6                50.00       Sequence
```

```
DRB1_0404  378  NRGFKIRTLQKPDST  KIRTLQKPD        0.3916        722.5              50.00     Sequence
DRB1_0404  245  DLDAVVLKALAKNPE  AVVLKALAK        0.3912        726.0              50.00     Sequence
DRB1_0404  424  EQREIPDVSTLTYAE  REIPDVSTL        0.3861        766.7              50.00     Sequence
DRB1_0404  472  PANQTSAITNVVIII  QTSAITNVV        0.3854        772.6              50.00     Sequence
DRB1_0404  410  SAGDEITVNVSTGPE  EITVNVSTG        0.3832        791.0              50.00     Sequence
DRB1_0404  464  GKVIGTNPPANQTSA  KVIGTNPPA        0.3830        793.1              50.00     Sequence
DRB1_0404  512  NVYGFTKFSQASVDS  YGFTKFSQA        0.3826        796.5              50.00     Sequence
DRB1_0404  135  HRDVKPANIMISATN  VKPANIMIS        0.3820        801.4              50.00     Sequence
DRB1_0404   63  AALNHPAIVAVYDTG  AIVAVYDTG        0.3818        803.1              50.00     Sequence
DRB1_0404  167  NSVTQTAAVIGTAQY  SVTQTAAVI        0.3793        825.4              50.00     Sequence
DRB1_0404  414  EITVNVSTGPEQREI  EITVNVSTG        0.3792        826.1              50.00     Sequence
DRB1_0404  199  YSLGCVLYEVLTGEP  CVLYEVLTG        0.3782        835.1              50.00     Sequence
DRB1_0404  204  VLYEVLTGEPPFTGD  EVLTGEPPF        0.3769        847.5              50.00     Sequence
DRB1_0404   95  DGVTLRDIVHTEGPM  VTLRDIVHT        0.3763        852.7              50.00     Sequence
DRB1_0404  146  SATNAVKVMDFGIAR  VKVMDFGIA        0.3760        855.2              50.00     Sequence
DRB1_0404  437  AEAVKKLTAAGFGRF  AVKKLTAAG        0.3728        885.3              50.00     Sequence
DRB1_0404  543  TVPVDSVIELQVSKG  SVIELQVSK        0.3727        886.3              50.00     Sequence
DRB1_0404  513  VYGFTKFSQASVDSP  FTKFSQASV        0.3715        897.8              50.00     Sequence
DRB1_0404  515  GFTKFSQASVDSPRP  KFSQASVDS        0.3711        901.9              50.00     Sequence
DRB1_0404  156  FGIARAIADSGNSVT  FGIARAIAD        0.3707        905.7              50.00     Sequence
DRB1_0404  295  LLSSAAGNLSGPRTD  LLSSAAGNL        0.3704        909.3              50.00     Sequence
DRB1_0404  436  YAEAVKKLTAAGFGR  AVKKLTAAG        0.3703        909.8              50.00     Sequence
DRB1_0404  196  SDVYSLGCVLYEVLT  DVYSLGCVL        0.3700        912.5              50.00     Sequence
DRB1_0404  193  DARSDVYSLGCVLYE  DARSDVYSL        0.3677        936.2              50.00     Sequence
DRB1_0404  325  IGSVGRWVAVVAVLA  SVGRWVAVV        0.3667        946.1              50.00     Sequence
DRB1_0404  155  DFGIARAIADSGNSV  FGIARAIAD        0.3662        951.2              50.00     Sequence
DRB1_0404  166  GNSVTQTAAVIGTAQ  SVTQTAAVI        0.3658        954.8              50.00     Sequence
DRB1_0404  508  QKNLNVYGFTKFSQA  LNVYGFTKF        0.3658        955.2              50.00     Sequence
DRB1_0404  392  TIPPDHVIGTDPAAN  HVIGTDPAA        0.3656        957.1              50.00     Sequence
DRB1_0404  198  VYSLGCVLYEVLTGE  CVLYEVLTG        0.3656        957.2              50.00     Sequence
DRB1_0404  423  PEQREIPDVSTLTYA  REIPDVSTL        0.3617        998.8              50.00     Sequence
DRB1_0404  195  RSDVYSLGCVLYEVL  DVYSLGCVL        0.3594       1023.7              50.00     Sequence
DRB1_0404  368  SSADAIATLQNRGFK  DAIATLQNR        0.3594       1023.8              50.00     Sequence
DRB1_0404  383  IRTLQKPDSTIPPDH  TLQKPDSTI        0.3589       1028.8              50.00     Sequence
DRB1_0404  165  SGNSVTQTAAVIGTA  SVTQTAAVI        0.3588       1030.4              50.00     Sequence
DRB1_0404  457  PSTPELVGKVIGTNP  ELVGKVIGT        0.3580       1039.5              50.00     Sequence
DRB1_0404  485  IIVGSGPATKDIPDV  IIVGSGPAT        0.3576       1044.1              50.00     Sequence
DRB1_0404  438  EAVKKLTAAGFGRFK  AVKKLTAAG        0.3573       1047.3              50.00     Sequence
DRB1_0404  542  TTVPVDSVIELQVSK  SVIELQVSK        0.3565       1056.8              50.00     Sequence
DRB1_0404  168  SVTQTAAVIGTAQYL  SVTQTAAVI        0.3563       1058.5              50.00     Sequence
DRB1_0404  115  IEVIADACQALNFSH  EVIADACQA        0.3556       1066.3              50.00     Sequence
DRB1_0404  516  FTKFSQASVDSPRPA  KFSQASVDS        0.3537       1089.2              50.00     Sequence
DRB1_0404  444  TAAGFGRFKQANSPS  RFKQANSPS        0.3524       1104.7              50.00     Sequence
DRB1_0404   94  VDGVTLRDIVHTEGP  VTLRDIVHT        0.3515       1115.2              50.00     Sequence
DRB1_0404  154  MDFGIARAIADSGNS  FGIARAIAD        0.3500       1132.9              50.00     Sequence
DRB1_0404    9  RYELGEILGFGGMSE  EILGFGGMS        0.3490       1145.3              50.00     Sequence
DRB1_0404   26  LARDLRLHRDVAVKV  LRLHRDVAV        0.3489       1146.5              50.00     Sequence
DRB1_0404  192  VDARSDVYSLGCVLY  DARSDVYSL        0.3460       1183.2              50.00     Sequence
DRB1_0404  471  PPANQTSAITNVVII  NQTSAITNV        0.3445       1202.7              50.00     Sequence
DRB1_0404   31  RLHRDVAVKVLRADL  RLHRDVAVK        0.3445       1203.2              50.00     Sequence
DRB1_0404   51  FYLRFRREAQNAAAL  RFRREAQNA        0.3440       1209.2              50.00     Sequence
DRB1_0404  427  EIPDVSTLTYAEAVK  EIPDVSTLT        0.3429       1223.3              50.00     Sequence
DRB1_0404  377  QNRGFKIRTLQKPDS  KIRTLQKPD        0.3428       1224.7              50.00     Sequence
DRB1_0404   52  YLRFRREAQNAAALN  RFRREAQNA        0.3405       1256.4              50.00     Sequence
DRB1_0404  324  SIGSVGRWVAVVAVL  SVGRWVAVV        0.3404       1257.0              50.00     Sequence
DRB1_0404  244  ADLDAVVLKALAKNP  AVVLKALAK        0.3396       1267.6              50.00     Sequence
DRB1_0404  110  TPKRAIEVIADACQA  AIEVIADAC        0.3394       1271.6              50.00     Sequence
DRB1_0404  250  VLKALAKNPENRYQT  VLKALAKNP        0.3386       1281.5              50.00     Sequence
DRB1_0404   98  TLRDIVHTEGPMTPK  IVHTEGPMT        0.3374       1298.8              50.00     Sequence
DRB1_0404  435  TYAEAVKKLTAAGFG  EAVKKLTAA        0.3353       1328.2              50.00     Sequence
DRB1_0404  553  QVSKGNQFVMPDLSG  QFVMPDLSG        0.3345       1339.7              50.00     Sequence
DRB1_0404   15  ILGFGGMSEVHLARD  LGFGGMSEV        0.3342       1345.0              50.00     Sequence
DRB1_0404  116  EVIADACQALNFSHQ  EVIADACQA        0.3327       1366.9              50.00     Sequence
DRB1_0404  205  LYEVLTGEPPFTGDS  EVLTGEPPF        0.3307       1396.3              50.00     Sequence
DRB1_0404  566  SGMFWVDAEPRLRAL  MFWVDAEPR        0.3305       1398.8              50.00     Sequence
DRB1_0404  153  VMDFGIARAIADSGN  FGIARAIAD        0.3287       1426.8              50.00     Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0404 | 384 | RTLQKPDSTIPPDHV | TLQKPDSTI | 0.3268 | 1457.0 | 50.00 | Sequence |
| DRB1_0404 | 194 | ARSDVYSLGCVLYEV | DVYSLGCVL | 0.3266 | 1460.2 | 50.00 | Sequence |
| DRB1_0404 | 595 | GGSQHNRVVYQNPPA | RVVYQNPPA | 0.3263 | 1464.4 | 50.00 | Sequence |
| DRB1_0404 | 517 | TKFSQASVDSPRPAG | TKFSQASVD | 0.3246 | 1492.0 | 50.00 | Sequence |
| DRB1_0404 | 206 | YEVLTGEPPFTGDSP | EVLTGEPPF | 0.3245 | 1492.5 | 50.00 | Sequence |
| DRB1_0404 | 409 | VSAGDEITVNVSTGP | EITVNVSTG | 0.3234 | 1510.6 | 50.00 | Sequence |
| DRB1_0404 | 465 | KVIGTNPPANQTSAI | KVIGTNPPA | 0.3214 | 1544.9 | 50.00 | Sequence |
| DRB1_0404 | 145 | ISATNAVKVMDFGIA | VKVMDFGIA | 0.3175 | 1611.0 | 50.00 | Sequence |
| DRB1_0404 | 50 | SFYLRFRREAQNAAA | RFRREAQNA | 0.3159 | 1638.4 | 50.00 | Sequence |
| DRB1_0404 | 430 | DVSTLTYAEAVKKLT | STLTYAEAV | 0.3151 | 1652.6 | 50.00 | Sequence |
| DRB1_0404 | 157 | GIARAIADSGNSVTQ | RAIADSGNS | 0.3151 | 1653.4 | 50.00 | Sequence |
| DRB1_0404 | 53 | LRFRREAQNAAALNH | RFRREAQNA | 0.3147 | 1660.1 | 50.00 | Sequence |
| DRB1_0404 | 133 | IIHRDVKPANIMISA | IIHRDVKPA | 0.3147 | 1661.1 | 50.00 | Sequence |
| DRB1_0404 | 134 | IHRDVKPANIMISAT | DVKPANIMI | 0.3146 | 1661.7 | 50.00 | Sequence |
| DRB1_0404 | 164 | DSGNSVTQTAAVIGT | SVTQTAAVI | 0.3141 | 1671.9 | 50.00 | Sequence |
| DRB1_0404 | 429 | PDVSTLTYAEAVKKL | STLTYAEAV | 0.3135 | 1682.7 | 50.00 | Sequence |
| DRB1_0404 | 158 | IARAIADSGNSVTQT | RAIADSGNS | 0.3124 | 1701.8 | 50.00 | Sequence |
| DRB1_0404 | 422 | GPEQREIPDVSTLTY | REIPDVSTL | 0.3124 | 1702.1 | 50.00 | Sequence |
| DRB1_0404 | 25 | HLARDLRLHRDVAVK | LRLHRDVAV | 0.3123 | 1704.5 | 50.00 | Sequence |
| DRB1_0404 | 507 | AQKNLNVYGFTKFSQ | LNVYGFTKF | 0.3114 | 1721.4 | 50.00 | Sequence |
| DRB1_0404 | 93 | YVDGVTLRDIVHTEG | VTLRDIVHT | 0.3107 | 1734.0 | 50.00 | Sequence |
| DRB1_0404 | 385 | TLQKPDSTIPPDHVI | TLQKPDSTI | 0.3086 | 1773.4 | 50.00 | Sequence |
| DRB1_0404 | 173 | AAVIGTAQYLSPEQA | AAVIGTAQY | 0.3080 | 1785.7 | 50.00 | Sequence |
| DRB1_0404 | 431 | VSTLTYAEAVKKLTA | STLTYAEAV | 0.3078 | 1789.4 | 50.00 | Sequence |
| DRB1_0404 | 391 | STIPPDHVIGTDPAA | HVIGTDPAA | 0.3067 | 1810.8 | 50.00 | Sequence |
| DRB1_0404 | 144 | MISATNAVKVMDFGI | MISATNAVK | 0.3061 | 1821.6 | 50.00 | Sequence |
| DRB1_0404 | 267 | EMRADLVRVHNGEPP | EMRADLVRV | 0.3048 | 1848.7 | 50.00 | Sequence |
| DRB1_0404 | 367 | QSSADAIATLQNRGF | DAIATLQNR | 0.3038 | 1867.5 | 50.00 | Sequence |
| DRB1_0404 | 172 | TAAVIGTAQYLSPEQ | AAVIGTAQY | 0.3017 | 1911.8 | 50.00 | Sequence |
| DRB1_0404 | 207 | EVLTGEPPFTGDSPV | EVLTGEPPF | 0.3011 | 1924.5 | 50.00 | Sequence |
| DRB1_0404 | 100 | RDIVHTEGPMTPKRA | DIVHTEGPM | 0.3007 | 1931.4 | 50.00 | Sequence |
| DRB1_0404 | 123 | QALNFSHQNGIIHRD | LNFSHQNGI | 0.3006 | 1934.5 | 50.00 | Sequence |
| DRB1_0404 | 191 | SVDARSDVYSLGCVL | DARSDVYSL | 0.3000 | 1946.7 | 50.00 | Sequence |
| DRB1_0404 | 432 | STLTYAEAVKKLTAA | STLTYAEAV | 0.2985 | 1978.3 | 50.00 | Sequence |
| DRB1_0404 | 121 | ACQALNFSHQNGIIH | LNFSHQNGI | 0.2984 | 1980.5 | 50.00 | Sequence |
| DRB1_0404 | 428 | IPDVSTLTYAEAVKK | STLTYAEAV | 0.2975 | 1999.1 | 50.00 | Sequence |
| DRB1_0404 | 541 | GTTVPVDSVIELQVS | TVPVDSVIE | 0.2970 | 2010.8 | 50.00 | Sequence |
| DRB1_0404 | 540 | AGTTVPVDSVIELQV | TVPVDSVIE | 0.2954 | 2045.5 | 50.00 | Sequence |
| DRB1_0404 | 99 | LRDIVHTEGPMTPKR | IVHTEGPMT | 0.2951 | 2051.9 | 50.00 | Sequence |
| DRB1_0404 | 171 | QTAAVIGTAQYLSPE | AAVIGTAQY | 0.2939 | 2080.2 | 50.00 | Sequence |
| DRB1_0404 | 132 | GIIHRDVKPANIMIS | IIHRDVKPA | 0.2934 | 2090.7 | 50.00 | Sequence |
| DRB1_0404 | 434 | LTYAEAVKKLTAAGF | EAVKKLTAA | 0.2933 | 2091.9 | 50.00 | Sequence |
| DRB1_0404 | 348 | AINTFGGITRDVQVP | AINTFGGIT | 0.2923 | 2114.9 | 50.00 | Sequence |
| DRB1_0404 | 122 | CQALNFSHQNGIIHR | LNFSHQNGI | 0.2911 | 2143.8 | 50.00 | Sequence |
| DRB1_0404 | 101 | DIVHTEGPMTPKRAI | DIVHTEGPM | 0.2908 | 2150.5 | 50.00 | Sequence |
| DRB1_0404 | 456 | SPSTPELVGKVIGTN | ELVGKVIGT | 0.2899 | 2171.7 | 50.00 | Sequence |
| DRB1_0404 | 170 | TQTAAVIGTAQYLSP | AAVIGTAQY | 0.2889 | 2194.9 | 50.00 | Sequence |
| DRB1_0404 | 49 | PSFYLRFRREAQNAA | FYLRFRREA | 0.2887 | 2200.7 | 50.00 | Sequence |
| DRB1_0404 | 39 | KVLRADLARDPSFYL | KVLRADLAR | 0.2881 | 2214.4 | 50.00 | Sequence |
| DRB1_0404 | 16 | LGFGGMSEVHLARDL | LGFGGMSEV | 0.2879 | 2220.0 | 50.00 | Sequence |
| DRB1_0404 | 8 | DRYELGEILGFGGMS | EILGFGGMS | 0.2878 | 2221.1 | 50.00 | Sequence |
| DRB1_0404 | 286 | VLTDAERTSLLSSAA | RTSLLSSAA | 0.2868 | 2246.3 | 50.00 | Sequence |
| DRB1_0404 | 266 | AEMRADLVRVHNGEP | EMRADLVRV | 0.2866 | 2250.3 | 50.00 | Sequence |
| DRB1_0404 | 470 | NPPANQTSAITNVVI | NQTSAITNV | 0.2854 | 2279.4 | 50.00 | Sequence |
| DRB1_0404 | 159 | ARAIADSGNSVTQTA | RAIADSGNS | 0.2836 | 2324.8 | 50.00 | Sequence |
| DRB1_0404 | 124 | ALNFSHQNGIIHRDV | LNFSHQNGI | 0.2834 | 2329.0 | 50.00 | Sequence |
| DRB1_0404 | 160 | RAIADSGNSVTQTAA | RAIADSGNS | 0.2825 | 2352.1 | 50.00 | Sequence |
| DRB1_0404 | 439 | AVKKLTAAGFGRFKQ | AVKKLTAAG | 0.2819 | 2367.5 | 50.00 | Sequence |
| DRB1_0404 | 376 | LQNRGFKIRTLQKPD | KIRTLQKPD | 0.2810 | 2389.7 | 50.00 | Sequence |
| DRB1_0404 | 174 | AVIGTAQYLSPEQAR | AVIGTAQYL | 0.2807 | 2398.1 | 50.00 | Sequence |
| DRB1_0404 | 503 | TVDVAQKNLNVYGFT | TVDVAQKNL | 0.2804 | 2405.8 | 50.00 | Sequence |
| DRB1_0404 | 24 | VHLARDLRLHRDVAV | LRLHRDVAV | 0.2801 | 2414.1 | 50.00 | Sequence |
| DRB1_0404 | 372 | AIATLQNRGFKIRTL | AIATLQNRG | 0.2798 | 2421.6 | 50.00 | Sequence |
| DRB1_0404 | 81 | TPAGPLPYIVMEYVD | PLPYIVMEY | 0.2795 | 2431.2 | 50.00 | Sequence |
| DRB1_0404 | 433 | TLTYAEAVKKLTAAG | EAVKKLTAA | 0.2785 | 2457.7 | 50.00 | Sequence |
| DRB1_0404 | 117 | VIADACQALNFSHQN | VIADACQAL | 0.2783 | 2460.5 | 50.00 | Sequence |

```
DRB1_0404   90  VMEYVDGVTLRDIVH  MEYVDGVTL        0.2744       2568.5              50.00     Sequence
DRB1_0404  567  GMFWVDAEPRLRALG  MFWVDAEPR        0.2740       2577.9              50.00     Sequence
DRB1_0404  451  FKQANSPSTPELVGK  FKQANSPST        0.2732       2602.6              50.00     Sequence
DRB1_0404  265  AAEMRADLVRVHNGE  EMRADLVRV        0.2727       2616.2              50.00     Sequence
DRB1_0404   92  EYVDGVTLRDIVHTE  VTLRDIVHT        0.2723       2626.2              50.00     Sequence
DRB1_0404  323  RSIGSVGRWVAVVAV  SVGRWVAVV        0.2712       2657.4              50.00     Sequence
DRB1_0404  408  SVSAGDEITVNVSTG  EITVNVSTG        0.2703       2683.5              50.00     Sequence
DRB1_0404  109  MTPKRAIEVIADACQ  AIEVIADAC        0.2701       2689.0              50.00     Sequence
DRB1_0404  120  DACQALNFSHQNGII  LNFSHQNGI        0.2699       2695.5              50.00     Sequence
DRB1_0404  243  SADLDAVVLKALAKN  AVVLKALAK        0.2689       2725.7              50.00     Sequence
DRB1_0404  539  PAGTTVPVDSVIELQ  TVPVDSVIE        0.2677       2759.6              50.00     Sequence
DRB1_0404  505  DVAQKNLNVYGFTKF  DVAQKNLNV        0.2677       2760.7              50.00     Sequence
DRB1_0404   22  SEVHLARDLRLHRDV  VHLARDLRL        0.2664       2800.5              50.00     Sequence
DRB1_0404  502  QTVDVAQKNLNVYGF  TVDVAQKNL        0.2657       2820.0              50.00     Sequence
DRB1_0404   62  AAALNHPAIVAVYDT  NHPAIVAVY        0.2648       2848.3              50.00     Sequence
DRB1_0404   21  MSEVHLARDLRLHRD  VHLARDLRL        0.2646       2853.8              50.00     Sequence
DRB1_0404  125  LNFSHQNGIIHRDVK  LNFSHQNGI        0.2646       2855.4              50.00     Sequence
DRB1_0404  570  WVDAEPRLRALGWTG  RLRALGWTG        0.2642       2867.4              50.00     Sequence
DRB1_0404  421  TGPEQREIPDVSTLT  REIPDVSTL        0.2629       2908.7              50.00     Sequence
DRB1_0404  602  VVYQNPPAGTGVNRD  VVYQNPPAG        0.2626       2916.7              50.00     Sequence
DRB1_0404  506  VAQKNLNVYGFTKFS  LNVYGFTKF        0.2624       2924.2              50.00     Sequence
DRB1_0404  269  RADLVRVHNGEPPEA  DLVRVHNGE        0.2622       2930.2              50.00     Sequence
DRB1_0404  163  ADSGNSVTQTAAVIG  SVTQTAAVI        0.2600       3001.9              50.00     Sequence
DRB1_0404   17  GFGGMSEVHLARDLR  FGGMSEVHL        0.2593       3023.9              50.00     Sequence
DRB1_0404  518  KFSQASVDSPRPAGE  FSQASVDSP        0.2583       3056.6              50.00     Sequence
DRB1_0404  270  ADLVRVHNGEPPEAP  DLVRVHNGE        0.2579       3068.5              50.00     Sequence
DRB1_0404   48  DPSFYLRFRREAQNA  FYLRFRREA        0.2567       3110.4              50.00     Sequence
DRB1_0404   91  MEYVDGVTLRDIVHT  MEYVDGVTL        0.2567       3111.1              50.00     Sequence
DRB1_0404   20  GMSEVHLARDLRLHR  EVHLARDLR        0.2561       3128.6              50.00     Sequence
DRB1_0404   70  IVAVYDTGEAETPAG  IVAVYDTGE        0.2561       3131.4              50.00     Sequence
DRB1_0404  268  MRADLVRVHNGEPPE  DLVRVHNGE        0.2555       3150.1              50.00     Sequence
DRB1_0404   23  EVHLARDLRLHRDVA  VHLARDLRL        0.2547       3179.3              50.00     Sequence
DRB1_0404   54  RFRREAQNAAALNHP  RFRREAQNA        0.2543       3193.1              50.00     Sequence
DRB1_0404  504  VDVAQKNLNVYGFTK  DVAQKNLNV        0.2538       3209.4              50.00     Sequence
DRB1_0404  169  VTQTAAVIGTAQYLS  AAVIGTAQY        0.2528       3242.2              50.00     Sequence
DRB1_0404  238  RHEGLSADLDAVVLK  GLSADLDAV        0.2516       3287.2              50.00     Sequence
DRB1_0404   18  FGGMSEVHLARDLRL  FGGMSEVHL        0.2495       3363.5              50.00     Sequence
DRB1_0404   80  ETPAGPLPYIVMEYV  PLPYIVMEY        0.2491       3378.0              50.00     Sequence
DRB1_0404  119  ADACQALNFSHQNGI  ACQALNFSH        0.2487       3390.5              50.00     Sequence
DRB1_0404  264  TAAEMRADLVRVHNG  EMRADLVRV        0.2483       3407.4              50.00     Sequence
DRB1_0404  501  GQTVDVAQKNLNVYG  TVDVAQKNL        0.2482       3407.7              50.00     Sequence
DRB1_0404  190  DSVDARSDVYSLGCV  DARSDVYSL        0.2477       3426.8              50.00     Sequence
DRB1_0404  131  NGIIHRDVKPANIMI  IIHRDVKPA        0.2453       3517.8              50.00     Sequence
DRB1_0404  366  GQSSADAIATLQNRG  DAIATLQNR        0.2451       3526.1              50.00     Sequence
DRB1_0404  240  EGLSADLDAVVLKAL  GLSADLDAV        0.2444       3552.9              50.00     Sequence
DRB1_0404  611  TGVNRDGIITLRFGQ  VNRDGIITL        0.2433       3596.8              50.00     Sequence
DRB1_0404  552  LQVSKGNQFVMPDLS  LQVSKGNQF        0.2410       3684.0              50.00     Sequence
DRB1_0404  176  IGTAQYLSPEQARGD  IGTAQYLSP        0.2409       3688.4              50.00     Sequence
DRB1_0404  241  GLSADLDAVVLKALA  GLSADLDAV        0.2401       3719.8              50.00     Sequence
DRB1_0404  237  ARHEGLSADLDAVVL  GLSADLDAV        0.2368       3855.6              50.00     Sequence
DRB1_0404  239  HEGLSADLDAVVLKA  GLSADLDAV        0.2349       3936.8              50.00     Sequence
DRB1_0404  538  PPAGTTVPVDSVIEL  TVPVDSVIE        0.2337       3988.6              50.00     Sequence
DRB1_0404  212  EPPFTGDSPVSVAYQ  PFTGDSPVS        0.2335       3997.0              50.00     Sequence
DRB1_0404  175  VIGTAQYLSPEQARG  IGTAQYLSP        0.2326       4035.4              50.00     Sequence
DRB1_0404  568  MFWVDAEPRLRALGW  MFWVDAEPR        0.2322       4051.7              50.00     Sequence
DRB1_0404  108  PMTPKRAIEVIADAC  AIEVIADAC        0.2314       4088.0              50.00     Sequence
DRB1_0404  213  PPFTGDSPVSVAYQH  PFTGDSPVS        0.2314       4089.2              50.00     Sequence
DRB1_0404   61  NAAALNHPAIVAVYD  NAAALNHPA        0.2307       4121.4              50.00     Sequence
DRB1_0404  219  SPVSVAYQHVREDPI  SPVSVAYQH        0.2297       4163.6              50.00     Sequence
DRB1_0404   19  GGMSEVHLARDLRLH  EVHLARDLR        0.2294       4177.8              50.00     Sequence
DRB1_0404  102  IVHTEGPMTPKRAIE  IVHTEGPMT        0.2293       4181.0              50.00     Sequence
DRB1_0404  162  IADSGNSVTQTAAVI  SVTQTAAVI        0.2292       4188.8              50.00     Sequence
DRB1_0404  258  PENRYQTAAEMRADL  NRYQTAAEM        0.2276       4261.7              50.00     Sequence
DRB1_0404  443  LTAAGFGRFKQANSP  GFGRFKQAN        0.2274       4271.1              50.00     Sequence
DRB1_0404  211  GEPPFTGDSPVSVAY  PFTGDSPVS        0.2256       4351.6              50.00     Sequence
DRB1_0404  549  VIELQVSKGNQFVMP  VIELQVSKG        0.2254       4365.5              50.00     Sequence
```

```
DRB1_0404  322  DRSIGSVGRWVAVVA  SVGRWVAVV        0.2249       4389.1          50.00     Sequence
DRB1_0404  118  IADACQALNFSHQNG  ACQALNFSH        0.2245       4406.7          50.00     Sequence
DRB1_0404  579  ALGWTGMLDKGADVD  ALGWTGMLD        0.2244       4412.8          50.00     Sequence
DRB1_0404    7  SDRYELGEILGFGGM  YELGEILGF        0.2243       4415.5          50.00     Sequence
DRB1_0404  500  AGQTVDVAQKNLNVY  TVDVAQKNL        0.2242       4419.9          50.00     Sequence
DRB1_0404  321  RDRSIGSVGRWVAVV  SVGRWVAVV        0.2240       4428.2          50.00     Sequence
DRB1_0404  610  GTGVNRDGIITLRFG  VNRDGIITL        0.2235       4454.3          50.00     Sequence
DRB1_0404  224  AYQHVREDPIPPSAR  HVREDPIPP        0.2233       4462.6          50.00     Sequence
DRB1_0404  259  ENRYQTAAEMRADLV  NRYQTAAEM        0.2232       4467.5          50.00     Sequence
DRB1_0404  469  TNPPANQTSAITNVV  NQTSAITNV        0.2223       4510.1          50.00     Sequence
DRB1_0404   60  QNAAALNHPAIVAVY  NAAALNHPA        0.2223       4512.0          50.00     Sequence
DRB1_0404  271  DLVRVHNGEPPEAPK  DLVRVHNGE        0.2210       4574.5          50.00     Sequence
DRB1_0404  189  GDSVDARSDVYSLGC  DARSDVYSL        0.2205       4601.9          50.00     Sequence
DRB1_0404  130  QNGIIHRDVKPANIM  IIHRDVKPA        0.2197       4639.0          50.00     Sequence
DRB1_0404  362  PDVRGQSSADAIATL  DVRGQSSAD        0.2193       4662.5          50.00     Sequence
DRB1_0404  225  YQHVREDPIPPSARH  HVREDPIPP        0.2193       4662.8          50.00     Sequence
DRB1_0404  214  PFTGDSPVSVAYQHV  FTGDSPVSV        0.2189       4680.1          50.00     Sequence
DRB1_0404  236  SARHEGLSADLDAVV  GLSADLDAV        0.2189       4680.5          50.00     Sequence
DRB1_0404  455  NSPSTPELVGKVIGT  ELVGKVIGT        0.2166       4800.6          50.00     Sequence
DRB1_0404  285  KVLTDAERTSLLSSA  KVLTDAERT        0.2151       4878.5          50.00     Sequence
DRB1_0404  261  RYQTAAEMRADLVRV  EMRADLVRV        0.2141       4931.0          50.00     Sequence
DRB1_0404  551  ELQVSKGNQFVMPDL  LQVSKGNQF        0.2138       4946.4          50.00     Sequence
DRB1_0404  353  GGITRDVQVPDVRGQ  GITRDVQVP        0.2134       4969.8          50.00     Sequence
DRB1_0404  218  DSPVSVAYQHVREDP  SPVSVAYQH        0.2134       4970.9          50.00     Sequence
DRB1_0404  363  DVRGQSSADAIATLQ  DVRGQSSAD        0.2126       5010.3          50.00     Sequence
DRB1_0404  260  NRYQTAAEMRADLVR  NRYQTAAEM        0.2120       5045.3          50.00     Sequence
DRB1_0404  537  NPPAGTTVPVDSVIE  TVPVDSVIE        0.2116       5063.4          50.00     Sequence
DRB1_0404  223  VAYQHVREDPIPPSA  HVREDPIPP        0.2109       5105.6          50.00     Sequence
DRB1_0404  263  QTAAEMRADLVRVHN  EMRADLVRV        0.2107       5112.9          50.00     Sequence
DRB1_0404  257  NPENRYQTAAEMRAD  NRYQTAAEM        0.2097       5173.6          50.00     Sequence
DRB1_0404  282  EAPKVLTDAERTSLL  APKVLTDAE        0.2096       5178.2          50.00     Sequence
DRB1_0404  351  TFGGITRDVQVPDVR  GGITRDVQV        0.2094       5190.8          50.00     Sequence
DRB1_0404  361  VPDVRGQSSADAIAT  DVRGQSSAD        0.2077       5282.4          50.00     Sequence
DRB1_0404  281  PEAPKVLTDAERTSL  APKVLTDAE        0.2054       5420.4          50.00     Sequence
DRB1_0404   47  RDPSFYLRFRREAQN  FYLRFRREA        0.2043       5480.2          50.00     Sequence
DRB1_0404  550  IELQVSKGNQFVMPD  LQVSKGNQF        0.2043       5485.0          50.00     Sequence
DRB1_0404  352  FGGITRDVQVPDVRG  GITRDVQVP        0.2042       5489.2          50.00     Sequence
DRB1_0404   59  AQNAAALNHPAIVAV  NAAALNHPA        0.2033       5540.7          50.00     Sequence
DRB1_0404  499  VAGQTVDVAQKNLNV  TVDVAQKNL        0.2029       5566.4          50.00     Sequence
DRB1_0404  251  LKALAKNPENRYQTA  LKALAKNPE        0.2014       5657.4          50.00     Sequence
DRB1_0404   79  AETPAGPLPYIVMEY  PLPYIVMEY        0.2012       5671.7          50.00     Sequence
DRB1_0404  530  AGEVTGTNPPAGTTV  EVTGTNPPA        0.2004       5720.2          50.00     Sequence
DRB1_0404  398  VIGTDPAANTSVSAG  VIGTDPAAN        0.2003       5724.3          50.00     Sequence
DRB1_0404    6  LSDRYELGEILGFGG  YELGEILGF        0.2001       5739.5          50.00     Sequence
DRB1_0404  531  GEVTGTNPPAGTTVP  EVTGTNPPA        0.1998       5754.6          50.00     Sequence
DRB1_0404  498  DVAGQTVDVAQKNLN  DVAGQTVDV        0.1994       5778.8          50.00     Sequence
DRB1_0404  349  INTFGGITRDVQVPD  TFGGITRDV        0.1994       5784.0          50.00     Sequence
DRB1_0404  210  TGEPPFTGDSPVSVA  PPFTGDSPV        0.1990       5806.1          50.00     Sequence
DRB1_0404  221  VSVAYQHVREDPIPP  YQHVREDPI        0.1989       5813.5          50.00     Sequence
DRB1_0404  442  KLTAAGFGRFKQANS  GFGRFKQAN        0.1986       5829.1          50.00     Sequence
DRB1_0404  235  PSARHEGLSADLDAV  GLSADLDAV        0.1982       5858.9          50.00     Sequence
DRB1_0404  529  PAGEVTGTNPPAGTT  EVTGTNPPA        0.1976       5896.6          50.00     Sequence
DRB1_0404  420  STGPEQREIPDVSTL  REIPDVSTL        0.1969       5937.2          50.00     Sequence
DRB1_0404  375  TLQNRGFKIRTLQKP  FKIRTLQKP        0.1966       5959.9          50.00     Sequence
DRB1_0404  242  LSADLDAVVLKALAK  AVVLKALAK        0.1964       5968.5          50.00     Sequence
DRB1_0404  283  APKVLTDAERTSLLS  KVLTDAERT        0.1961       5989.5          50.00     Sequence
DRB1_0404  280  PPEAPKVLTDAERTS  APKVLTDAE        0.1959       6002.2          50.00     Sequence
DRB1_0404  320  DRDRSIGSVGRWVAV  RDRSIGSVG        0.1957       6019.6          50.00     Sequence
DRB1_0404  519  FSQASVDSPRPAGEV  FSQASVDSP        0.1952       6047.4          50.00     Sequence
DRB1_0404  220  PVSVAYQHVREDPIP  PVSVAYQHV        0.1939       6137.9          50.00     Sequence
DRB1_0404  222  SVAYQHVREDPIPPS  YQHVREDPI        0.1932       6179.9          50.00     Sequence
DRB1_0404  360  QVPDVRGQSSADAIA  DVRGQSSAD        0.1927       6212.4          50.00     Sequence
DRB1_0404  262  YQTAAEMRADLVRVH  EMRADLVRV        0.1920       6265.9          50.00     Sequence
DRB1_0404  497  PDVAGQTVDVAQKNL  DVAGQTVDV        0.1917       6281.6          50.00     Sequence
DRB1_0404  354  GITRDVQVPDVRGQS  GITRDVQVP        0.1916       6288.3          50.00     Sequence
DRB1_0404  386  LQKPDSTIPPDHVIG  LQKPDSTIP        0.1893       6449.7          50.00     Sequence
```

```
DRB1_0404  415  ITVNVSTGPEQREIP  ITVNVSTGP        0.1890       6472.4                50.00     Sequence
DRB1_0404  188  RGDSVDARSDVYSLG  DARSDVYSL        0.1889       6474.8                50.00     Sequence
DRB1_0404    5  HLSDRYELGEILGFG  RYELGEILG        0.1888       6482.6                50.00     Sequence
DRB1_0404  217  GDSPVSVAYQHVRED  SPVSVAYQH        0.1881       6530.4                50.00     Sequence
DRB1_0404  609  AGTGVNRDGIITLRF  VNRDGIITL        0.1869       6615.4                50.00     Sequence
DRB1_0404    4  SHLSDRYELGEILGF  SHLSDRYEL        0.1868       6625.1                50.00     Sequence
DRB1_0404  177  GTAQYLSPEQARGDS  GTAQYLSPE        0.1859       6692.0                50.00     Sequence
DRB1_0404  365  RGQSSADAIATLQNR  DAIATLQNR        0.1850       6756.1                50.00     Sequence
DRB1_0404  161  AIADSGNSVTQTAAV  AIADSGNSV        0.1842       6816.5                50.00     Sequence
DRB1_0404  129  HQNGIIHRDVKPANI  IIHRDVKPA        0.1827       6924.7                50.00     Sequence
DRB1_0404  350  NTFGGITRDVQVPDV  TFGGITRDV        0.1820       6980.5                50.00     Sequence
DRB1_0404  594  AGGSQHNRVVYQNPP  NRVVYQNPP        0.1814       7021.1                50.00     Sequence
DRB1_0404  256  KNPENRYQTAAEMRA  NRYQTAAEM        0.1812       7041.5                50.00     Sequence
DRB1_0404  466  VIGTNPPANQTSAIT  VIGTNPPAN        0.1810       7054.0                50.00     Sequence
DRB1_0404   55  FRREAQNAAALNHPA  FRREAQNAA        0.1803       7105.2                50.00     Sequence
DRB1_0404  390  DSTIPPDHVIGTDPA  TIPPDHVIG        0.1794       7177.7                50.00     Sequence
DRB1_0404  319  TDRDRSIGSVGRWVA  DRDRSIGSV        0.1784       7254.1                50.00     Sequence
DRB1_0404  536  TNPPAGTTVPVDSVI  NPPAGTTVP        0.1782       7272.2                50.00     Sequence
DRB1_0404  215  FTGDSPVSVAYQHVR  FTGDSPVSV        0.1780       7283.7                50.00     Sequence
DRB1_0404   58  EAQNAAALNHPAIVA  NAAALNHPA        0.1780       7289.5                50.00     Sequence
DRB1_0404  359  VQVPDVRGQSSADAI  DVRGQSSAD        0.1771       7354.6                50.00     Sequence
DRB1_0404  486  IVGSGPATKDIPDVA  IVGSGPATK        0.1765       7408.3                50.00     Sequence
DRB1_0404  284  PKVLTDAERTSLLSS  KVLTDAERT        0.1758       7460.0                50.00     Sequence
DRB1_0404  318  DTDRDRSIGSVGRWV  RDRSIGSVG        0.1758       7465.8                50.00     Sequence
DRB1_0404  272  LVRVHNGEPPEAPKV  RVHNGEPPE        0.1757       7470.1                50.00     Sequence
DRB1_0404  226  QHVREDPIPPSARHE  HVREDPIPP        0.1757       7470.7                50.00     Sequence
DRB1_0404  126  NFSHQNGIIHRDVKP  NFSHQNGII        0.1748       7545.4                50.00     Sequence
DRB1_0404  279  EPPEAPKVLTDAERT  APKVLTDAE        0.1747       7548.5                50.00     Sequence
DRB1_0404  364  VRGQSSADAIATLQN  VRGQSSADA        0.1727       7720.7                50.00     Sequence
DRB1_0404  496  IPDVAGQTVDVAQKN  DVAGQTVDV        0.1724       7743.0                50.00     Sequence
DRB1_0404  209  LTGEPPFTGDSPVSV  PPFTGDSPV        0.1709       7865.4                50.00     Sequence
DRB1_0404   40  VLRADLARDPSFYLR  ADLARDPSF        0.1709       7867.9                50.00     Sequence
DRB1_0404  528  RPAGEVTGTNPPAGT  EVTGTNPPA        0.1708       7878.3                50.00     Sequence
DRB1_0404    3  PSHLSDRYELGEILG  SHLSDRYEL        0.1683       8097.6                50.00     Sequence
DRB1_0404  387  QKPDSTIPPDHVIGT  TIPPDHVIG        0.1672       8192.7                50.00     Sequence
DRB1_0404  532  EVTGTNPPAGTTVPV  EVTGTNPPA        0.1669       8217.0                50.00     Sequence
DRB1_0404  227  HVREDPIPPSARHEG  HVREDPIPP        0.1663       8272.3                50.00     Sequence
DRB1_0404  389  PDSTIPPDHVIGTDP  TIPPDHVIG        0.1660       8293.4                50.00     Sequence
DRB1_0404   42  RADLARDPSFYLRFR  ADLARDPSF        0.1660       8295.8                50.00     Sequence
DRB1_0404  373  IATLQNRGFKIRTLQ  IATLQNRGF        0.1652       8367.8                50.00     Sequence
DRB1_0404  296  LSSAAGNLSGPRTDP  AAGNLSGPR        0.1647       8417.3                50.00     Sequence
DRB1_0404  216  TGDSPVSVAYQHVRE  SPVSVAYQH        0.1644       8446.7                50.00     Sequence
DRB1_0404  178  TAQYLSPEQARGDSV  QYLSPEQAR        0.1638       8499.3                50.00     Sequence
DRB1_0404  440  VKKLTAAGFGRFKQA  VKKLTAAGF        0.1633       8543.0                50.00     Sequence
DRB1_0404  388  KPDSTIPPDHVIGTD  TIPPDHVIG        0.1627       8599.2                50.00     Sequence
DRB1_0404  495  DIPDVAGQTVDVAQK  DVAGQTVDV        0.1624       8625.9                50.00     Sequence
DRB1_0404   41  LRADLARDPSFYLRF  ADLARDPSF        0.1613       8726.7                50.00     Sequence
DRB1_0404  569  FWVDAEPRLRALGWT  FWVDAEPRL        0.1605       8805.7                50.00     Sequence
DRB1_0404  107  GPMTPKRAIEVIADA  PKRAIEVIA        0.1604       8818.1                50.00     Sequence
DRB1_0404   43  ADLARDPSFYLRFRR  ADLARDPSF        0.1593       8920.1                50.00     Sequence
DRB1_0404  468  GTNPPANQTSAITNV  NQTSAITNV        0.1592       8926.5                50.00     Sequence
DRB1_0404  317  DDTDRDRSIGSVGRW  DRDRSIGSV        0.1583       9015.6                50.00     Sequence
DRB1_0404  358  DVQVPDVRGQSSADA  DVRGQSSAD        0.1573       9116.7                50.00     Sequence
DRB1_0404  355  ITRDVQVPDVRGQSS  TRDVQVPDV        0.1552       9324.5                50.00     Sequence
DRB1_0404  582  WTGMLDKGADVDAGG  MLDKGADVD        0.1543       9414.1                50.00     Sequence
DRB1_0404  356  TRDVQVPDVRGQSSA  TRDVQVPDV        0.1542       9430.9                50.00     Sequence
DRB1_0404  580  LGWTGMLDKGADVDA  GWTGMLDKG        0.1539       9453.1                50.00     Sequence
DRB1_0404   57  REAQNAAALNHPAIV  REAQNAAAL        0.1536       9484.2                50.00     Sequence
DRB1_0404  255  AKNPENRYQTAAEMR  NRYQTAAEM        0.1525       9603.1                50.00     Sequence
DRB1_0404   71  VAVYDTGEAETPAGP  VAVYDTGEA        0.1524       9608.4                50.00     Sequence
DRB1_0404  310  PLPRQDLDDTDRDRS  LPRQDLDDT        0.1520       9651.4                50.00     Sequence
DRB1_0404  581  GWTGMLDKGADVDAG  TGMLDKGAD        0.1520       9652.8                50.00     Sequence
DRB1_0404   78  EAETPAGPLPYIVME  AGPLPYIVM        0.1516       9694.5                50.00     Sequence
DRB1_0404  127  FSHQNGIIHRDVKPA  IIHRDVKPA        0.1511       9752.1                50.00     Sequence
DRB1_0404  608  PAGTGVNRDGIITLR  VNRDGIITL        0.1500       9861.7                50.00     Sequence
DRB1_0404  311  LPRQDLDDTDRDRSI  LPRQDLDDT        0.1496       9911.8                50.00     Sequence
```

```
DRB1_0404  187  ARGDSVDARSDVYSL  DARSDVYSL         0.1476      10123.6              50.00      Sequence
DRB1_0404   46  ARDPSFYLRFRREAQ  FYLRFRREA         0.1473      10152.9              50.00      Sequence
DRB1_0404  374  ATLQNRGFKIRTLQK  NRGFKIRTL         0.1470      10195.1              50.00      Sequence
DRB1_0404  309  DPLPRQDLDDTDRDR  LPRQDLDDT         0.1466      10236.1              50.00      Sequence
DRB1_0404  308  TDPLPRQDLDDTDRD  LPRQDLDDT         0.1461      10290.5              50.00      Sequence
DRB1_0404  407  TSVSAGDEITVNVST  DEITVNVST         0.1460      10306.5              50.00      Sequence
DRB1_0404  208  VLTGEPPFTGDSPVS  VLTGEPPFT         0.1458      10318.9              50.00      Sequence
DRB1_0404  273  VRVHNGEPPEAPKVL  RVHNGEPPE         0.1449      10421.9              50.00      Sequence
DRB1_0404  527  PRPAGEVTGTNPPAG  EVTGTNPPA         0.1448      10437.2              50.00      Sequence
DRB1_0404  494  KDIPDVAGQTVDVAQ  DVAGQTVDV         0.1417      10790.6              50.00      Sequence
DRB1_0404   56  RREAQNAAALNHPAI  REAQNAAAL         0.1416      10802.8              50.00      Sequence
DRB1_0404  278  GEPPEAPKVLTDAER  APKVLTDAE         0.1410      10874.3              50.00      Sequence
DRB1_0404  357  RDVQVPDVRGQSSAD  RDVQVPDVR         0.1401      10983.9              50.00      Sequence
DRB1_0404  128  SHQNGIIHRDVKPAN  IIHRDVKPA         0.1394      11063.2              50.00      Sequence
DRB1_0404  252  KALAKNPENRYQTAA  KALAKNPEN         0.1393      11070.8              50.00      Sequence
DRB1_0404  491  PATKDIPDVAGQTVD  PATKDIPDV         0.1388      11139.7              50.00      Sequence
DRB1_0404  316  LDDTDRDRSIGSVGR  RDRSIGSVG         0.1383      11198.5              50.00      Sequence
DRB1_0404  490  GPATKDIPDVAGQTV  PATKDIPDV         0.1361      11468.6              50.00      Sequence
DRB1_0404  535  GTNPPAGTTVPVDSV  NPPAGTTVP         0.1359      11487.0              50.00      Sequence
DRB1_0404  441  KKLTAAGFGRFKQAN  AGFGRFKQA         0.1353      11563.2              50.00      Sequence
DRB1_0404  297  SSAAGNLSGPRTDPL  AAGNLSGPR         0.1342      11702.1              50.00      Sequence
DRB1_0404  234  PPSARHEGLSADLDA  RHEGLSADL         0.1339      11746.3              50.00      Sequence
DRB1_0404   45  LARDPSFYLRFRREA  FYLRFRREA         0.1333      11818.6              50.00      Sequence
DRB1_0404  489  SGPATKDIPDVAGQT  PATKDIPDV         0.1323      11952.8              50.00      Sequence
DRB1_0404  416  TVNVSTGPEQREIPD  TVNVSTGPE         0.1317      12029.1              50.00      Sequence
DRB1_0404  179  AQYLSPEQARGDSVD  QYLSPEQAR         0.1290      12388.1              50.00      Sequence
DRB1_0404  307  RTDPLPRQDLDDTDR  LPRQDLDDT         0.1280      12519.6              50.00      Sequence
DRB1_0404    2  TPSHLSDRYELGEIL  SHLSDRYEL         0.1279      12531.0              50.00      Sequence
DRB1_0404  493  TKDIPDVAGQTVDVA  DIPDVAGQT         0.1274      12604.3              50.00      Sequence
DRB1_0404  583  TGMLDKGADVDAGGS  TGMLDKGAD         0.1249      12938.7              50.00      Sequence
DRB1_0404   77  GEAETPAGPLPYIVM  AGPLPYIVM         0.1228      13247.1              50.00      Sequence
DRB1_0404  534  TGTNPPAGTTVPVDS  NPPAGTTVP         0.1225      13285.2              50.00      Sequence
DRB1_0404    1  TTPSHLSDRYELGEI  SHLSDRYEL         0.1220      13355.1              50.00      Sequence
DRB1_0404  302  NLSGPRTDPLPRQDL  LSGPRTDPL         0.1218      13380.8              50.00      Sequence
DRB1_0404  533  VTGTNPPAGTTVPVD  VTGTNPPAG         0.1206      13558.1              50.00      Sequence
DRB1_0404  520  SQASVDSPRPAGEVT  SQASVDSPR         0.1205      13581.6              50.00      Sequence
DRB1_0404  488  GSGPATKDIPDVAGQ  PATKDIPDV         0.1204      13586.7              50.00      Sequence
DRB1_0404  401  TDPAANTSVSAGDEI  AANTSVSAG         0.1201      13627.5              50.00      Sequence
DRB1_0404  298  SAAGNLSGPRTDPLP  AAGNLSGPR         0.1197      13697.9              50.00      Sequence
DRB1_0404  106  EGPMTPKRAIEVIAD  TPKRAIEVI         0.1178      13971.7              50.00      Sequence
DRB1_0404  399  IGTDPAANTSVSAGD  TDPAANTSV         0.1175      14023.8              50.00      Sequence
DRB1_0404  607  PPAGTGVNRDGIITL  VNRDGIITL         0.1169      14112.7              50.00      Sequence
DRB1_0404  301  GNLSGPRTDPLPRQD  LSGPRTDPL         0.1154      14352.0              50.00      Sequence
DRB1_0404  103  VHTEGPMTPKRAIEV  VHTEGPMTP         0.1147      14458.1              50.00      Sequence
DRB1_0404  400  GTDPAANTSVSAGDE  PAANTSVSA         0.1130      14719.3              50.00      Sequence
DRB1_0404  299  AAGNLSGPRTDPLPR  NLSGPRTDP         0.1130      14721.5              50.00      Sequence
DRB1_0404  406  NTSVSAGDEITVNVS  SVSAGDEIT         0.1127      14770.2              50.00      Sequence
DRB1_0404  274  RVHNGEPPEAPKVLT  RVHNGEPPE         0.1124      14815.7              50.00      Sequence
DRB1_0404   44  DLARDPSFYLRFRRE  LARDPSFYL         0.1119      14903.4              50.00      Sequence
DRB1_0404  303  LSGPRTDPLPRQDLD  LSGPRTDPL         0.1111      15024.7              50.00      Sequence
DRB1_0404  492  ATKDIPDVAGQTVDV  DIPDVAGQT         0.1110      15042.0              50.00      Sequence
DRB1_0404  593  DAGGSQHNRVVYQNP  HNRVVYQNP         0.1109      15054.5              50.00      Sequence
DRB1_0404    0  MTTPSHLSDRYELGE  SHLSDRYEL         0.1109      15067.9              50.00      Sequence
DRB1_0404  306  PRTDPLPRQDLDDTD  LPRQDLDDT         0.1108      15073.1              50.00      Sequence
DRB1_0404  233  IPPSARHEGLSADLD  RHEGLSADL         0.1107      15099.0              50.00      Sequence
DRB1_0404  487  VGSGPATKDIPDVAG  PATKDIPDV         0.1104      15135.7              50.00      Sequence
DRB1_0404  180  QYLSPEQARGDSVDA  QYLSPEQAR         0.1094      15309.4              50.00      Sequence
DRB1_0404  300  AGNLSGPRTDPLPRQ  LSGPRTDPL         0.1091      15351.1              50.00      Sequence
DRB1_0404  467  IGTNPPANQTSAITN  NPPANQTSA         0.1087      15429.3              50.00      Sequence
DRB1_0404  402  DPAANTSVSAGDEIT  PAANTSVSA         0.1086      15441.5              50.00      Sequence
DRB1_0404  526  SPRPAGEVTGTNPPA  EVTGTNPPA         0.1081      15520.4              50.00      Sequence
DRB1_0404  403  PAANTSVSAGDEITV  PAANTSVSA         0.1079      15564.0              50.00      Sequence
DRB1_0404  186  QARGDSVDARSDVYS  QARGDSVDA         0.1078      15567.5              50.00      Sequence
DRB1_0404  404  AANTSVSAGDEITVN  SVSAGDEIT         0.1062      15848.6              50.00      Sequence
DRB1_0404  405  ANTSVSAGDEITVNV  SVSAGDEIT         0.1057      15927.7              50.00      Sequence
DRB1_0404  584  GMLDKGADVDAGGSQ  MLDKGADVD         0.1052      16016.9              50.00      Sequence
```

```
   DRB1_0404  105  TEGPMTPKRAIEVIA  MTPKRAIEV        0.1041      16213.5                 50.00     Sequence
   DRB1_0404  277  NGEPPEAPKVLTDAE  APKVLTDAE        0.1026      16471.5                 50.00     Sequence
   DRB1_0404  452  KQANSPSTPELVGKV  QANSPSTPE        0.1020      16589.9                 50.00     Sequence
   DRB1_0404  254  LAKNPENRYQTAAEM  NRYQTAAEM        0.1016      16655.7                 50.00     Sequence
   DRB1_0404  185  EQARGDSVDARSDVY  QARGDSVDA        0.0961      17677.6                 50.00     Sequence
   DRB1_0404  315  DLDDTDRDRSIGSVG  DRDRSIGSV        0.0944      17995.4                 50.00     Sequence
   DRB1_0404  305  GPRTDPLPRQDLDDT  LPRQDLDDT        0.0943      18027.6                 50.00     Sequence
   DRB1_0404  232  PIPPSARHEGLSADL  RHEGLSADL        0.0922      18429.7                 50.00     Sequence
   DRB1_0404  253  ALAKNPENRYQTAAE  ALAKNPENR        0.0918      18520.9                 50.00     Sequence
   DRB1_0404  417  VNVSTGPEQREIPDV  NVSTGPEQR        0.0918      18525.1                 50.00     Sequence
   DRB1_0404  453  QANSPSTPELVGKVI  QANSPSTPE        0.0917      18547.5                 50.00     Sequence
   DRB1_0404  104  HTEGPMTPKRAIEVI  TPKRAIEVI        0.0916      18549.9                 50.00     Sequence
   DRB1_0404  521  QASVDSPRPAGEVTG  SVDSPRPAG        0.0899      18904.1                 50.00     Sequence
   DRB1_0404  603  VYQNPPAGTGVNRDG  VYQNPPAGT        0.0895      18994.9                 50.00     Sequence
   DRB1_0404  183  SPEQARGDSVDARSD  QARGDSVDA        0.0885      19193.7                 50.00     Sequence
   DRB1_0404  606  NPPAGTGVNRDGIIT  TGVNRDGII        0.0875      19410.7                 50.00     Sequence
   DRB1_0404  312  PRQDLDDTDRDRSIG  PRQDLDDTD        0.0857      19782.1                 50.00     Sequence
   DRB1_0404  184  PEQARGDSVDARSDV  QARGDSVDA        0.0850      19926.7                 50.00     Sequence
   DRB1_0404  523  SVDSPRPAGEVTGTN  SVDSPRPAG        0.0836      20229.8                 50.00     Sequence
   DRB1_0404  522  ASVDSPRPAGEVTGT  SVDSPRPAG        0.0828      20409.8                 50.00     Sequence
   DRB1_0404  182  LSPEQARGDSVDARS  QARGDSVDA        0.0817      20649.0                 50.00     Sequence
   DRB1_0404  454  ANSPSTPELVGKVIG  PELVGKVIG        0.0816      20673.6                 50.00     Sequence
   DRB1_0404  418  NVSTGPEQREIPDVS  NVSTGPEQR        0.0810      20806.0                 50.00     Sequence
   DRB1_0404  605  QNPPAGTGVNRDGII  TGVNRDGII        0.0808      20855.8                 50.00     Sequence
   DRB1_0404  304  SGPRTDPLPRQDLDD  GPRTDPLPR        0.0794      21168.4                 50.00     Sequence
   DRB1_0404  181  YLSPEQARGDSVDAR  QARGDSVDA        0.0763      21905.4                 50.00     Sequence
   DRB1_0404  591  DVDAGGSQHNRVVYQ  DVDAGGSQH        0.0762      21924.9                 50.00     Sequence
   DRB1_0404  525  DSPRPAGEVTGTNPP  PRPAGEVTG        0.0757      22040.4                 50.00     Sequence
   DRB1_0404  419  VSTGPEQREIPDVST  EQREIPDVS        0.0754      22116.4                 50.00     Sequence
   DRB1_0404  585  MLDKGADVDAGGSQH  MLDKGADVD        0.0753      22139.6                 50.00     Sequence
   DRB1_0404  228  VREDPIPPSARHEGL  REDPIPPSA        0.0742      22397.0                 50.00     Sequence
   DRB1_0404  604  YQNPPAGTGVNRDGI  NPPAGTGVN        0.0736      22559.9                 50.00     Sequence
   DRB1_0404   76  TGEAETPAGPLPYIV  ETPAGPLPY        0.0726      22784.9                 50.00     Sequence
   DRB1_0404  592  VDAGGSQHNRVVYQN  QHNRVVYQN        0.0707      23255.8                 50.00     Sequence
   DRB1_0404  229  REDPIPPSARHEGLS  REDPIPPSA        0.0684      23860.2                 50.00     Sequence
   DRB1_0404  524  VDSPRPAGEVTGTNP  PRPAGEVTG        0.0669      24257.1                 50.00     Sequence
   DRB1_0404  590  ADVDAGGSQHNRVVY  DVDAGGSQH        0.0666      24335.7                 50.00     Sequence
   DRB1_0404  587  DKGADVDAGGSQHNR  DKGADVDAG        0.0661      24444.2                 50.00     Sequence
   DRB1_0404  231  DPIPPSARHEGLSAD  SARHEGLSA        0.0636      25134.2                 50.00     Sequence
   DRB1_0404  589  GADVDAGGSQHNRVV  DVDAGGSQH        0.0630      25289.5                 50.00     Sequence
   DRB1_0404  276  HNGEPPEAPKVLTDA  EAPKVLTDA        0.0630      25291.6                 50.00     Sequence
   DRB1_0404   72  AVYDTGEAETPAGPL  AVYDTGEAE        0.0630      25299.6                 50.00     Sequence
   DRB1_0404  586  LDKGADVDAGGSQHN  DKGADVDAG        0.0609      25867.0                 50.00     Sequence
   DRB1_0404   75  DTGEAETPAGPLPYI  TGEAETPAG        0.0594      26299.1                 50.00     Sequence
   DRB1_0404  588  KGADVDAGGSQHNRV  DVDAGGSQH        0.0590      26395.7                 50.00     Sequence
   DRB1_0404   74  YDTGEAETPAGPLPY  YDTGEAETP        0.0588      26473.5                 50.00     Sequence
   DRB1_0404   73  VYDTGEAETPAGPLP  VYDTGEAET        0.0576      26820.3                 50.00     Sequence
   DRB1_0404  313  RQDLDDTDRDRSIGS  RQDLDDTDR        0.0555      27437.3                 50.00     Sequence
   DRB1_0404  230  EDPIPPSARHEGLSA  PIPPSARHE        0.0547      27668.1                 50.00     Sequence
   DRB1_0404  275  VHNGEPPEAPKVLTD  VHNGEPPEA        0.0530      28169.5                 50.00     Sequence
   DRB1_0404  314  QDLDDTDRDRSIGSV  DRDRSIGSV        0.0491      29402.3                 50.00     Sequence
-----------------------------------------------------------------------------------------------

Allele: DRB1_0404. Number of high binders 12. Number of weak binders 109. Number of peptides 612

-----------------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------------
      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
-----------------------------------------------------------------------------------------------
   DRB1_0405  379  RGFKIRTLQKPDSTI  FKIRTLQKP        0.6747         33.8          SB     4.00     Sequence
   DRB1_0405  380  GFKIRTLQKPDSTIP  FKIRTLQKP        0.6664         37.0          SB     8.00     Sequence
   DRB1_0405  378  NRGFKIRTLQKPDST  FKIRTLQKP        0.6613         39.0          SB     8.00     Sequence
   DRB1_0405  447  GFGRFKQANSPSTPE  FKQANSPST        0.6493         44.5          SB     8.00     Sequence
   DRB1_0405  448  FGRFKQANSPSTPEL  FKQANSPST        0.6456         46.3          SB     8.00     Sequence
   DRB1_0405  514  YGFTKFSQASVDSPR  FTKFSQASV        0.6420         48.1          SB     8.00     Sequence
   DRB1_0405  513  VYGFTKFSQASVDSP  FTKFSQASV        0.6399         49.2          SB     8.00     Sequence
```

```
DRB1_0405  377  QNRGFKIRTLQKPDS  FKIRTLQKP       0.6344       52.2       WB    8.00     Sequence
DRB1_0405  515  GFTKFSQASVDSPRP  FTKFSQASV       0.6325       53.3       WB    8.00     Sequence
DRB1_0405  141  ANIMISATNAVKVMD  IMISATNAV       0.6266       56.8       WB   16.00     Sequence
DRB1_0405  446  AGFGRFKQANSPSTP  FKQANSPST       0.6261       57.2       WB   16.00     Sequence
DRB1_0405  326  GSVGRWVAVVAVLAV  GRWVAVVAV       0.6243       58.3       WB   16.00     Sequence
DRB1_0405  512  NVYGFTKFSQASVDS  FTKFSQASV       0.6174       62.8       WB   16.00     Sequence
DRB1_0405  516  FTKFSQASVDSPRPA  FTKFSQASV       0.6164       63.5       WB   16.00     Sequence
DRB1_0405  140  PANIMISATNAVKVM  IMISATNAV       0.6161       63.7       WB   16.00     Sequence
DRB1_0405  578  RALGWTGMLDKGADV  ALGWTGMLD       0.6152       64.3       WB   16.00     Sequence
DRB1_0405  142  NIMISATNAVKVMDF  IMISATNAV       0.6151       64.4       WB   16.00     Sequence
DRB1_0405  327  SVGRWVAVVAVLAVL  GRWVAVVAV       0.6148       64.6       WB   16.00     Sequence
DRB1_0405  449  GRFKQANSPSTPELV  FKQANSPST       0.6118       66.7       WB   16.00     Sequence
DRB1_0405  325  IGSVGRWVAVVAVLA  GRWVAVVAV       0.6091       68.7       WB   16.00     Sequence
DRB1_0405  381  FKIRTLQKPDSTIPP  FKIRTLQKP       0.6042       72.4       WB   16.00     Sequence
DRB1_0405  577  LRALGWTGMLDKGAD  ALGWTGMLD       0.6030       73.4       WB   16.00     Sequence
DRB1_0405  139  KPANIMISATNAVKV  IMISATNAV       0.5984       77.1       WB   16.00     Sequence
DRB1_0405  445  AAGFGRFKQANSPST  FGRFKQANS       0.5978       77.6       WB   16.00     Sequence
DRB1_0405  328  VGRWVAVVAVLAVLT  GRWVAVVAV       0.5949       80.1       WB   16.00     Sequence
DRB1_0405  511  LNVYGFTKFSQASVD  FTKFSQASV       0.5928       82.0       WB   16.00     Sequence
DRB1_0405  564  DLSGMFWVDAEPRLR  GMFWVDAEP       0.5911       83.4       WB   16.00     Sequence
DRB1_0405  576  RLRALGWTGMLDKGA  ALGWTGMLD       0.5884       85.9       WB   16.00     Sequence
DRB1_0405  565  LSGMFWVDAEPRLRA  GMFWVDAEP       0.5857       88.4       WB   16.00     Sequence
DRB1_0405  376  LQNRGFKIRTLQKPD  FKIRTLQKP       0.5848       89.3       WB   16.00     Sequence
DRB1_0405  450  RFKQANSPSTPELVG  FKQANSPST       0.5830       91.1       WB   16.00     Sequence
DRB1_0405  143  IMISATNAVKVMDFG  IMISATNAV       0.5820       92.0       WB   16.00     Sequence
DRB1_0405   90  VMEYVDGVTLRDIVH  MEYVDGVTL       0.5775       96.6       WB   16.00     Sequence
DRB1_0405  579  ALGWTGMLDKGADVD  ALGWTGMLD       0.5751       99.3       WB   16.00     Sequence
DRB1_0405  566  SGMFWVDAEPRLRAL  GMFWVDAEP       0.5724      102.2       WB   16.00     Sequence
DRB1_0405  353  GGITRDVQVPDVRGQ  ITRDVQVPD       0.5708      103.9       WB   16.00     Sequence
DRB1_0405  352  FGGITRDVQVPDVRG  ITRDVQVPD       0.5699      104.9       WB   16.00     Sequence
DRB1_0405   89  IVMEYVDGVTLRDIV  MEYVDGVTL       0.5682      107.0       WB   16.00     Sequence
DRB1_0405  138  VKPANIMISATNAVK  IMISATNAV       0.5669      108.4       WB   16.00     Sequence
DRB1_0405  563  PDLSGMFWVDAEPRL  GMFWVDAEP       0.5630      113.0       WB   32.00     Sequence
DRB1_0405   88  YIVMEYVDGVTLRDI  MEYVDGVTL       0.5622      114.1       WB   32.00     Sequence
DRB1_0405   91  MEYVDGVTLRDIVHT  YVDGVTLRD       0.5584      118.9       WB   32.00     Sequence
DRB1_0405  329  GRWVAVVAVLAVLTV  GRWVAVVAV       0.5539      124.8       WB   32.00     Sequence
DRB1_0405   29  DLRLHRDVAVKVLRA  LRLHRDVAV       0.5492      131.3       WB   32.00     Sequence
DRB1_0405   87  PYIVMEYVDGVTLRD  MEYVDGVTL       0.5452      137.1       WB   32.00     Sequence
DRB1_0405  202  GCVLYEVLTGEPPFT  CVLYEVLTG       0.5438      139.3       WB   32.00     Sequence
DRB1_0405   28  RDLRLHRDVAVKVLR  LRLHRDVAV       0.5427      140.9       WB   32.00     Sequence
DRB1_0405  562  MPDLSGMFWVDAEPR  GMFWVDAEP       0.5371      149.7       WB   32.00     Sequence
DRB1_0405  324  SIGSVGRWVAVVAVL  GRWVAVVAV       0.5365      150.7       WB   32.00     Sequence
DRB1_0405   27  ARDLRLHRDVAVKVL  LRLHRDVAV       0.5362      151.1       WB   32.00     Sequence
DRB1_0405  201  LGCVLYEVLTGEPPF  CVLYEVLTG       0.5350      153.1       WB   32.00     Sequence
DRB1_0405   50  SFYLRFRREAQNAAA  LRFRREAQN       0.5348      153.5       WB   32.00     Sequence
DRB1_0405   51  FYLRFRREAQNAAAL  LRFRREAQN       0.5333      155.9       WB   32.00     Sequence
DRB1_0405   92  EYVDGVTLRDIVHTE  YVDGVTLRD       0.5332      156.1       WB   32.00     Sequence
DRB1_0405  351  TFGGITRDVQVPDVR  ITRDVQVPD       0.5298      162.0       WB   32.00     Sequence
DRB1_0405   86  LPYIVMEYVDGVTLR  LPYIVMEYV       0.5292      163.0       WB   32.00     Sequence
DRB1_0405  510  NLNVYGFTKFSQASV  FTKFSQASV       0.5283      164.6       WB   32.00     Sequence
DRB1_0405  354  GITRDVQVPDVRGQS  ITRDVQVPD       0.5276      165.9       WB   32.00     Sequence
DRB1_0405  575  PRLRALGWTGMLDKG  ALGWTGMLD       0.5259      169.0       WB   32.00     Sequence
DRB1_0405  194  ARSDVYSLGCVLYEV  DVYSLGCVL       0.5256      169.4       WB   32.00     Sequence
DRB1_0405   84  GPLPYIVMEYVDGVT  LPYIVMEYV       0.5252      170.2       WB   32.00     Sequence
DRB1_0405   85  PLPYIVMEYVDGVTL  LPYIVMEYV       0.5239      172.7       WB   32.00     Sequence
DRB1_0405  193  DARSDVYSLGCVLYE  YSLGCVLYE       0.5232      173.9       WB   32.00     Sequence
DRB1_0405  599  HNRVVYQNPPAGTGV  RVVYQNPPA       0.5227      174.9       WB   32.00     Sequence
DRB1_0405   93  YVDGVTLRDIVHTEG  YVDGVTLRD       0.5215      177.2       WB   32.00     Sequence
DRB1_0405  199  YSLGCVLYEVLTGEP  YSLGCVLYE       0.5214      177.5       WB   32.00     Sequence
DRB1_0405  598  QHNRVVYQNPPAGTG  RVVYQNPPA       0.5205      179.2       WB   32.00     Sequence
DRB1_0405  200  SLGCVLYEVLTGEPP  CVLYEVLTG       0.5203      179.5       WB   32.00     Sequence
DRB1_0405   49  PSFYLRFRREAQNAA  LRFRREAQN       0.5181      183.8       WB   32.00     Sequence
DRB1_0405   52  YLRFRREAQNAAALN  LRFRREAQN       0.5177      184.7       WB   32.00     Sequence
DRB1_0405  203  CVLYEVLTGEPPFTG  LYEVLTGEP       0.5159      188.3       WB   32.00     Sequence
DRB1_0405   26  LARDLRLHRDVAVKV  LRLHRDVAV       0.5123      195.8       WB   32.00     Sequence
DRB1_0405  222  SVAYQHVREDPIPPS  VAYQHVRED       0.5078      205.5       WB   32.00     Sequence
```

```
DRB1_0405  223  VAYQHVREDPIPPSA  VAYQHVRED         0.5060         209.6          WB    32.00       Sequence
DRB1_0405   83  AGPLPYIVMEYVDGV  LPYIVMEYV         0.5059         209.7          WB    32.00       Sequence
DRB1_0405  375  TLQNRGFKIRTLQKP  FKIRTLQKP         0.5047         212.5          WB    32.00       Sequence
DRB1_0405  597  SQHNRVVYQNPPAGT  RVVYQNPPA         0.5039         214.5          WB    32.00       Sequence
DRB1_0405  137  DVKPANIMISATNAV  NIMISATNA         0.5033         215.7          WB    32.00       Sequence
DRB1_0405  196  SDVYSLGCVLYEVLT  YSLGCVLYE         0.5024         217.8          WB    32.00       Sequence
DRB1_0405   30  LRLHRDVAVKVLRAD  LRLHRDVAV         0.4993         225.3          WB    32.00       Sequence
DRB1_0405  198  VYSLGCVLYEVLTGE  YSLGCVLYE         0.4992         225.7          WB    32.00       Sequence
DRB1_0405  567  GMFWVDAEPRLRALG  GMFWVDAEP         0.4985         227.2          WB    32.00       Sequence
DRB1_0405  197  DVYSLGCVLYEVLTG  YSLGCVLYE         0.4982         228.1          WB    32.00       Sequence
DRB1_0405  355  ITRDVQVPDVRGQSS  ITRDVQVPD         0.4974         229.9          WB    32.00       Sequence
DRB1_0405   34  RDVAVKVLRADLARD  VAVKVLRAD         0.4973         230.2          WB    32.00       Sequence
DRB1_0405   35  DVAVKVLRADLARDP  VAVKVLRAD         0.4967         231.6          WB    32.00       Sequence
DRB1_0405  444  TAAGFGRFKQANSPS  FGRFKQANS         0.4948         236.5          WB    32.00       Sequence
DRB1_0405  451  FKQANSPSTPELVGK  FKQANSPST         0.4929         241.5          WB    32.00       Sequence
DRB1_0405  195  RSDVYSLGCVLYEVL  DVYSLGCVL         0.4922         243.2          WB    32.00       Sequence
DRB1_0405  350  NTFGGITRDVQVPDV  ITRDVQVPD         0.4912         245.9          WB    32.00       Sequence
DRB1_0405  289  DAERTSLLSSAAGNL  RTSLLSSAA         0.4894         250.7          WB    32.00       Sequence
DRB1_0405  471  PPANQTSAITNVVII  QTSAITNVV         0.4865         258.8          WB    32.00       Sequence
DRB1_0405  288  TDAERTSLLSSAAGN  RTSLLSSAA         0.4848         263.5          WB    32.00       Sequence
DRB1_0405  600  NRVVYQNPPAGTGVN  RVVYQNPPA         0.4831         268.5          WB    32.00       Sequence
DRB1_0405  574  EPRLRALGWTGMLDK  ALGWTGMLD         0.4820         271.6          WB    32.00       Sequence
DRB1_0405  221  VSVAYQHVREDPIPP  VAYQHVRED         0.4819         272.0          WB    32.00       Sequence
DRB1_0405  580  LGWTGMLDKGADVDA  LGWTGMLDK         0.4815         273.2          WB    32.00       Sequence
DRB1_0405  151  VKVMDFGIARAIADS  FGIARAIAD         0.4798         278.3          WB    32.00       Sequence
DRB1_0405  339  AVLTVVVTIAINTFG  TVVVTIAIN         0.4791         280.5          WB    32.00       Sequence
DRB1_0405  323  RSIGSVGRWVAVVAV  GRWVAVVAV         0.4785         282.2          WB    32.00       Sequence
DRB1_0405   31  RLHRDVAVKVLRADL  VAVKVLRAD         0.4784         282.6          WB    32.00       Sequence
DRB1_0405  596  GSQHNRVVYQNPPAG  RVVYQNPPA         0.4769         287.1          WB    32.00       Sequence
DRB1_0405  517  TKFSQASVDSPRPAG  FSQASVDSP         0.4767         287.7          WB    32.00       Sequence
DRB1_0405  369  SADAIATLQNRGFKI  DAIATLQNR         0.4749         293.4          WB    50.00       Sequence
DRB1_0405  338  LAVLTVVVTIAINTF  TVVVTIAIN         0.4749         293.4          WB    50.00       Sequence
DRB1_0405  472  PANQTSAITNVVIII  QTSAITNVV         0.4737         297.1          WB    50.00       Sequence
DRB1_0405  370  ADAIATLQNRGFKIR  DAIATLQNR         0.4737         297.2          WB    50.00       Sequence
DRB1_0405  220  PVSVAYQHVREDPIP  VAYQHVRED         0.4737         297.2          WB    50.00       Sequence
DRB1_0405   32  LHRDVAVKVLRADLA  VAVKVLRAD         0.4734         298.1          WB    50.00       Sequence
DRB1_0405  561  VMPDLSGMFWVDAEP  GMFWVDAEP         0.4733         298.5          WB    50.00       Sequence
DRB1_0405  340  VLTVVVTIAINTFGG  TVVVTIAIN         0.4717         303.6          WB    50.00       Sequence
DRB1_0405  249  VVLKALAKNPENRYQ  VVLKALAKN         0.4702         308.8          WB    50.00       Sequence
DRB1_0405  124  ALNFSHQNGIIHRDV  FSHQNGIIH         0.4700         309.3          WB    50.00       Sequence
DRB1_0405   82  PAGPLPYIVMEYVDG  LPYIVMEYV         0.4700         309.5          WB    50.00       Sequence
DRB1_0405   13  GEILGFGGMSEVHLA  FGGMSEVHL         0.4697         310.2          WB    50.00       Sequence
DRB1_0405  247  DAVVLKALAKNPENR  VVLKALAKN         0.4697         310.5          WB    50.00       Sequence
DRB1_0405   53  LRFRREAQNAAALNH  LRFRREAQN         0.4692         312.2          WB    50.00       Sequence
DRB1_0405  248  AVVLKALAKNPENRY  VVLKALAKN         0.4687         313.8          WB    50.00       Sequence
DRB1_0405   48  DPSFYLRFRREAQNA  LRFRREAQN         0.4680         316.1          WB    50.00       Sequence
DRB1_0405  473  ANQTSAITNVVIIIV  QTSAITNVV         0.4680         316.1          WB    50.00       Sequence
DRB1_0405  611  TGVNRDGIITLRFGQ  VNRDGIITL         0.4672         319.0          WB    50.00       Sequence
DRB1_0405  290  AERTSLLSSAAGNLS  RTSLLSSAA         0.4653         325.6          WB    50.00       Sequence
DRB1_0405  382  KIRTLQKPDSTIPPD  KIRTLQKPD         0.4652         325.7          WB    50.00       Sequence
DRB1_0405  337  VLAVLTVVVTIAINT  TVVVTIAIN         0.4645         328.2          WB    50.00       Sequence
DRB1_0405   33  HRDVAVKVLRADLAR  VAVKVLRAD         0.4642         329.6          WB    50.00       Sequence
DRB1_0405  368  SSADAIATLQNRGFK  DAIATLQNR         0.4616         338.8          WB    50.00       Sequence
DRB1_0405   36  VAVKVLRADLARDPS  VAVKVLRAD         0.4614         339.5          WB    50.00       Sequence
DRB1_0405  125  LNFSHQNGIIHRDVK  FSHQNGIIH         0.4608         341.7          WB    50.00       Sequence
DRB1_0405  204  VLYEVLTGEPPFTGD  LYEVLTGEP         0.4606         342.5          WB    50.00       Sequence
DRB1_0405  150  AVKVMDFGIARAIAD  FGIARAIAD         0.4583         351.1          WB    50.00       Sequence
DRB1_0405  246  LDAVVLKALAKNPEN  VVLKALAKN         0.4573         355.0          WB    50.00       Sequence
DRB1_0405   14  EILGFGGMSEVHLAR  FGGMSEVHL         0.4572         355.4          WB    50.00       Sequence
DRB1_0405  610  GTGVNRDGIITLRFG  VNRDGIITL         0.4564         358.4          WB    50.00       Sequence
DRB1_0405  470  NPPANQTSAITNVVI  NQTSAITNV         0.4548         364.5          WB    50.00       Sequence
DRB1_0405   12  LGEILGFGGMSEVHL  EILGFGGMS         0.4542         366.9          WB    50.00       Sequence
DRB1_0405  123  QALNFSHQNGIIHRD  FSHQNGIIH         0.4541         367.3          WB    50.00       Sequence
DRB1_0405   99  LRDIVHTEGPMTPKR  IVHTEGPMT         0.4540         367.9          WB    50.00       Sequence
DRB1_0405  336  AVLAVLTVVVTIAIN  LAVLTVVVT         0.4521         375.3          WB    50.00       Sequence
DRB1_0405  330  RWVAVVAVLAVLTVV  WVAVVAVLA         0.4520         375.9          WB    50.00       Sequence
```

```
DRB1_0405   25  HLARDLRLHRDVAVK  LRLHRDVAV        0.4515        377.9          WB    50.00      Sequence
DRB1_0405  342  TVVVTIAINTFGGIT  TVVVTIAIN        0.4503        382.9          WB    50.00      Sequence
DRB1_0405   96  GVTLRDIVHTEGPMT  IVHTEGPMT        0.4501        383.5          WB    50.00      Sequence
DRB1_0405  100  RDIVHTEGPMTPKRA  IVHTEGPMT        0.4494        386.5          WB    50.00      Sequence
DRB1_0405   94  VDGVTLRDIVHTEGP  VTLRDIVHT        0.4487        389.5          WB    50.00      Sequence
DRB1_0405  341  LTVVVTIAINTFGGI  TVVVTIAIN        0.4486        390.1          WB    50.00      Sequence
DRB1_0405  225  YQHVREDPIPPSARH  HVREDPIPP        0.4463        399.9          WB    50.00      Sequence
DRB1_0405  219  SPVSVAYQHVREDPI  VAYQHVRED        0.4444        408.0          WB    50.00      Sequence
DRB1_0405  152  KVMDFGIARAIADSG  FGIARAIAD        0.4443        408.5          WB    50.00      Sequence
DRB1_0405  474  NQTSAITNVVIIIVG  SAITNVVII        0.4440        410.1          WB    50.00      Sequence
DRB1_0405  224  AYQHVREDPIPPSAR  HVREDPIPP        0.4424        417.2          WB    50.00      Sequence
DRB1_0405  371  DAIATLQNRGFKIRT  DAIATLQNR        0.4397        429.4          WB    50.00      Sequence
DRB1_0405   97  VTLRDIVHTEGPMTP  IVHTEGPMT        0.4396        430.1          WB    50.00      Sequence
DRB1_0405  547  DSVIELQVSKGNQFV  VIELQVSKG        0.4394        430.9          WB    50.00      Sequence
DRB1_0405  101  DIVHTEGPMTPKRAI  IVHTEGPMT        0.4391        432.0          WB    50.00      Sequence
DRB1_0405  347  IAINTFGGITRDVQV  IAINTFGGI        0.4388        433.5          WB    50.00      Sequence
DRB1_0405  609  AGTGVNRDGIITLRF  GVNRDGIIT        0.4388        433.8          WB    50.00      Sequence
DRB1_0405  212  EPPFTGDSPVSVAYQ  FTGDSPVSV        0.4385        434.9          WB    50.00      Sequence
DRB1_0405  144  MISATNAVKVMDFGI  MISATNAVK        0.4364        444.9          WB    50.00      Sequence
DRB1_0405  136  RDVKPANIMISATNA  NIMISATNA        0.4355        449.1          WB    50.00      Sequence
DRB1_0405  546  VDSVIELQVSKGNQF  VIELQVSKG        0.4351        451.4          WB    50.00      Sequence
DRB1_0405   39  KVLRADLARDPSFYL  LARDPSFYL        0.4347        453.0          WB    50.00      Sequence
DRB1_0405  367  QSSADAIATLQNRGF  DAIATLQNR        0.4346        453.6          WB    50.00      Sequence
DRB1_0405  548  SVIELQVSKGNQFVM  VIELQVSKG        0.4344        454.8          WB    50.00      Sequence
DRB1_0405  475  QTSAITNVVIIIVGS  SAITNVVII        0.4327        463.3          WB    50.00      Sequence
DRB1_0405   11  ELGEILGFGGMSEVH  ILGFGGMSE        0.4303        475.3          WB    50.00      Sequence
DRB1_0405  153  VMDFGIARAIADSGN  FGIARAIAD        0.4295        479.2          WB    50.00      Sequence
DRB1_0405  555  SKGNQFVMPDLSGMF  FVMPDLSGM        0.4287        483.6          WB    50.00      Sequence
DRB1_0405  318  DTDRDRSIGSVGRWV  DRDRSIGSV        0.4286        484.3          WB    50.00      Sequence
DRB1_0405  556  KGNQFVMPDLSGMFW  FVMPDLSGM        0.4285        484.7          WB    50.00      Sequence
DRB1_0405  291  ERTSLLSSAAGNLSG  RTSLLSSAA        0.4285        484.8          WB    50.00      Sequence
DRB1_0405  213  PPFTGDSPVSVAYQH  FTGDSPVSV        0.4284        485.1          WB    50.00      Sequence
DRB1_0405   98  TLRDIVHTEGPMTPK  IVHTEGPMT        0.4283        485.7          WB    50.00      Sequence
DRB1_0405  335  VAVLAVLTVVVTIAI  LAVLTVVVT        0.4278        488.6          WB    50.00      Sequence
DRB1_0405   47  RDPSFYLRFRREAQN  LRFRREAQN        0.4275        489.9          WB    50.00      Sequence
DRB1_0405  287  LTDAERTSLLSSAAG  AERTSLLSS        0.4271        492.1          WB    50.00      Sequence
DRB1_0405  482  VVIIIVGSGPATKDI  IIIVGSGPA        0.4270        492.5          WB    50.00      Sequence
DRB1_0405  226  QHVREDPIPPSARHE  HVREDPIPP        0.4265        495.3          WB    50.00      Sequence
DRB1_0405  541  GTTVPVDSVIELQVS  VPVDSVIEL        0.4257        499.5          WB    50.00      Sequence
DRB1_0405  481  NVVIIIVGSGPATKD  IIIVGSGPA        0.4254        501.1                50.00      Sequence
DRB1_0405  554  VSKGNQFVMPDLSGM  GNQFVMPDL        0.4254        501.3                50.00      Sequence
DRB1_0405  126  NFSHQNGIIHRDVKP  FSHQNGIIH        0.4251        502.7                50.00      Sequence
DRB1_0405  211  GEPPFTGDSPVSVAY  FTGDSPVSV        0.4249        503.9                50.00      Sequence
DRB1_0405  601  RVVYQNPPAGTGVNR  RVVYQNPPA        0.4245        506.4                50.00      Sequence
DRB1_0405   95  DGVTLRDIVHTEGPM  VTLRDIVHT        0.4240        509.0                50.00      Sequence
DRB1_0405  595  GGSQHNRVVYQNPPA  RVVYQNPPA        0.4234        512.1                50.00      Sequence
DRB1_0405  174  AVIGTAQYLSPEQAR  AVIGTAQYL        0.4231        514.1                50.00      Sequence
DRB1_0405  426  REIPDVSTLTYAEAV  EIPDVSTLT        0.4220        519.9                50.00      Sequence
DRB1_0405   40  VLRADLARDPSFYLR  LARDPSFYL        0.4208        526.7                50.00      Sequence
DRB1_0405  245  DLDAVVLKALAKNPE  VVLKALAKN        0.4207        527.3                50.00      Sequence
DRB1_0405  346  TIAINTFGGITRDVQ  IAINTFGGI        0.4202        530.2                50.00      Sequence
DRB1_0405   81  TPAGPLPYIVMEYVD  LPYIVMEYV        0.4200        531.1                50.00      Sequence
DRB1_0405  443  LTAAGFGRFKQANSP  FGRFKQANS        0.4189        537.6                50.00      Sequence
DRB1_0405  173  AAVIGTAQYLSPEQA  AVIGTAQYL        0.4189        537.6                50.00      Sequence
DRB1_0405  192  VDARSDVYSLGCVLY  SDVYSLGCV        0.4188        538.6                50.00      Sequence
DRB1_0405  317  DDTDRDRSIGSVGRW  DRDRSIGSV        0.4172        547.9                50.00      Sequence
DRB1_0405   64  ALNHPAIVAVYDTGE  AIVAVYDTG        0.4165        551.7                50.00      Sequence
DRB1_0405  560  FVMPDLSGMFWVDAE  FVMPDLSGM        0.4163        552.9                50.00      Sequence
DRB1_0405  509  KNLNVYGFTKFSQAS  YGFTKFSQA        0.4160        555.0                50.00      Sequence
DRB1_0405   15  ILGFGGMSEVHLARD  FGGMSEVHL        0.4156        557.2                50.00      Sequence
DRB1_0405  205  LYEVLTGEPPFTGDS  LYEVLTGEP        0.4154        558.6                50.00      Sequence
DRB1_0405  319  TDRDRSIGSVGRWVA  DRDRSIGSV        0.4140        566.8                50.00      Sequence
DRB1_0405   24  VHLARDLRLHRDVAV  LRLHRDVAV        0.4139        567.6                50.00      Sequence
DRB1_0405  266  AEMRADLVRVHNGEP  EMRADLVRV        0.4135        570.0                50.00      Sequence
DRB1_0405  539  PAGTTVPVDSVIELQ  GTTVPVDSV        0.4130        573.5                50.00      Sequence
DRB1_0405   42  RADLARDPSFYLRFR  LARDPSFYL        0.4125        576.5                50.00      Sequence
```

```
DRB1_0405  424  EQREIPDVSTLTYAE  EIPDVSTLT       0.4109      586.3             50.00    Sequence
DRB1_0405   67  HPAIVAVYDTGEAET  AIVAVYDTG       0.4103      590.5             50.00    Sequence
DRB1_0405  542  TTVPVDSVIELQVSK  VPVDSVIEL       0.4102      590.6             50.00    Sequence
DRB1_0405   10  YELGEILGFGGMSEV  EILGFGGMS       0.4099      592.7             50.00    Sequence
DRB1_0405  122  CQALNFSHQNGIIHR  FSHQNGIIH       0.4090      598.3             50.00    Sequence
DRB1_0405  334  VVAVLAVLTVVVTIA  LAVLTVVVT       0.4089      599.0             50.00    Sequence
DRB1_0405   66  NHPAIVAVYDTGEAE  AIVAVYDTG       0.4088      599.9             50.00    Sequence
DRB1_0405  476  TSAITNVVIIIVGSG  SAITNVVII       0.4086      600.8             50.00    Sequence
DRB1_0405   63  AALNHPAIVAVYDTG  AALNHPAIV       0.4077      607.1             50.00    Sequence
DRB1_0405  425  QREIPDVSTLTYAEA  EIPDVSTLT       0.4075      608.6             50.00    Sequence
DRB1_0405  147  ATNAVKVMDFGIARA  VKVMDFGIA       0.4074      609.0             50.00    Sequence
DRB1_0405  148  TNAVKVMDFGIARAI  VKVMDFGIA       0.4072      610.1             50.00    Sequence
DRB1_0405  557  GNQFVMPDLSGMFWV  FVMPDLSGM       0.4064      615.6             50.00    Sequence
DRB1_0405  544  VPVDSVIELQVSKGN  VPVDSVIEL       0.4054      622.6             50.00    Sequence
DRB1_0405  540  AGTTVPVDSVIELQV  GTTVPVDSV       0.4053      623.1             50.00    Sequence
DRB1_0405   68  PAIVAVYDTGEAETP  AIVAVYDTG       0.4053      623.2             50.00    Sequence
DRB1_0405  545  PVDSVIELQVSKGNQ  SVIELQVSK       0.4052      623.8             50.00    Sequence
DRB1_0405  480  TNVVIIIVGSGPATK  VVIIIVGSG       0.4050      625.3             50.00    Sequence
DRB1_0405  573  AEPRLRALGWTGMLD  ALGWTGMLD       0.4040      632.0             50.00    Sequence
DRB1_0405  258  PENRYQTAAEMRADL  NRYQTAAEM       0.4031      637.8             50.00    Sequence
DRB1_0405  427  EIPDVSTLTYAEAVK  EIPDVSTLT       0.4021      645.0             50.00    Sequence
DRB1_0405  332  VAVVAVLAVLTVVVT  LAVLTVVVT       0.4017      647.5             50.00    Sequence
DRB1_0405  349  INTFGGITRDVQVPD  GGITRDVQV       0.4008      653.9             50.00    Sequence
DRB1_0405    9  RYELGEILGFGGMSE  YELGEILGF       0.4007      654.5             50.00    Sequence
DRB1_0405  265  AAEMRADLVRVHNGE  EMRADLVRV       0.4000      659.9             50.00    Sequence
DRB1_0405  257  NPENRYQTAAEMRAD  NRYQTAAEM       0.3999      660.4             50.00    Sequence
DRB1_0405  191  SVDARSDVYSLGCVL  ARSDVYSLG       0.3994      664.3             50.00    Sequence
DRB1_0405  333  AVVAVLAVLTVVVTI  LAVLTVVVT       0.3993      664.7             50.00    Sequence
DRB1_0405   41  LRADLARDPSFYLRF  LARDPSFYL       0.3992      665.6             50.00    Sequence
DRB1_0405  210  TGEPPFTGDSPVSVA  FTGDSPVSV       0.3992      665.7             50.00    Sequence
DRB1_0405   16  LGFGGMSEVHLARDL  FGGMSEVHL       0.3986      669.8             50.00    Sequence
DRB1_0405  154  MDFGIARAIADSGNS  FGIARAIAD       0.3980      674.0             50.00    Sequence
DRB1_0405  538  PPAGTTVPVDSVIEL  PAGTTVPVD       0.3973      679.1             50.00    Sequence
DRB1_0405  343  VVVTIAINTFGGITR  VVVTIAINT       0.3969      682.2             50.00    Sequence
DRB1_0405   65  LNHPAIVAVYDTGEA  AIVAVYDTG       0.3965      685.5             50.00    Sequence
DRB1_0405  286  VLTDAERTSLLSSAA  AERTSLLSS       0.3952      695.0             50.00    Sequence
DRB1_0405  581  GWTGMLDKGADVDAG  GWTGMLDKG       0.3952      695.1             50.00    Sequence
DRB1_0405  479  ITNVVIIIVGSGPAT  VVIIIVGSG       0.3947      698.7             50.00    Sequence
DRB1_0405  331  WVAVVAVLAVLTVVV  WVAVVAVLA       0.3946      699.6             50.00    Sequence
DRB1_0405  345  VTIAINTFGGITRDV  IAINTFGGI       0.3941      703.6             50.00    Sequence
DRB1_0405  267  EMRADLVRVHNGEPP  EMRADLVRV       0.3937      706.0             50.00    Sequence
DRB1_0405  264  TAAEMRADLVRVHNG  EMRADLVRV       0.3930      712.0             50.00    Sequence
DRB1_0405   43  ADLARDPSFYLRFRR  LARDPSFYL       0.3929      712.6             50.00    Sequence
DRB1_0405  549  VIELQVSKGNQFVMP  VIELQVSKG       0.3923      716.9             50.00    Sequence
DRB1_0405  316  LDDTDRDRSIGSVGR  DRDRSIGSV       0.3922      718.1             50.00    Sequence
DRB1_0405  462  LVGKVIGTNPPANQT  KVIGTNPPA       0.3919      720.2             50.00    Sequence
DRB1_0405  259  ENRYQTAAEMRADLV  NRYQTAAEM       0.3915      723.3             50.00    Sequence
DRB1_0405  477  SAITNVVIIIVGSGP  SAITNVVII       0.3913      725.1             50.00    Sequence
DRB1_0405  469  TNPPANQTSAITNVV  QTSAITNVV       0.3911      726.1             50.00    Sequence
DRB1_0405  478  AITNVVIIIVGSGPA  VVIIIVGSG       0.3903      732.5             50.00    Sequence
DRB1_0405  463  VGKVIGTNPPANQTS  VIGTNPPAN       0.3895      738.8             50.00    Sequence
DRB1_0405  172  TAAVIGTAQYLSPEQ  AVIGTAQYL       0.3895      739.2             50.00    Sequence
DRB1_0405   62  AAALNHPAIVAVYDT  LNHPAIVAV       0.3894      739.8             50.00    Sequence
DRB1_0405   37  AVKVLRADLARDPSF  VLRADLARD       0.3884      747.9             50.00    Sequence
DRB1_0405  344  VVTIAINTFGGITRD  IAINTFGGI       0.3883      748.9             50.00    Sequence
DRB1_0405  149  NAVKVMDFGIARAIA  KVMDFGIAR       0.3879      752.4             50.00    Sequence
DRB1_0405  176  IGTAQYLSPEQARGD  AQYLSPEQA       0.3875      755.4             50.00    Sequence
DRB1_0405  372  AIATLQNRGFKIRTL  AIATLQNRG       0.3872      757.6             50.00    Sequence
DRB1_0405  361  VPDVRGQSSADAIAT  DVRGQSSAD       0.3872      757.8             50.00    Sequence
DRB1_0405  483  VIIIVGSGPATKDIP  IIIVGSGPA       0.3864      764.0             50.00    Sequence
DRB1_0405  175  VIGTAQYLSPEQARG  AQYLSPEQA       0.3864      764.6             50.00    Sequence
DRB1_0405  484  IIIVGSGPATKDIPD  IIIVGSGPA       0.3861      767.1             50.00    Sequence
DRB1_0405  145  ISATNAVKVMDFGIA  ATNAVKVMD       0.3846      779.6             50.00    Sequence
DRB1_0405  423  PEQREIPDVSTLTYA  EQREIPDVS       0.3844      780.8             50.00    Sequence
DRB1_0405  543  TVPVDSVIELQVSKG  VPVDSVIEL       0.3840      784.5             50.00    Sequence
DRB1_0405  422  GPEQREIPDVSTLTY  EQREIPDVS       0.3838      786.5             50.00    Sequence
```

```
DRB1_0405  374  ATLQNRGFKIRTLQK  GFKIRTLQK         0.3835         788.5                50.00      Sequence
DRB1_0405  559  QFVMPDLSGMFWVDA  FVMPDLSGM         0.3829         793.8                50.00      Sequence
DRB1_0405  146  SATNAVKVMDFGIAR  VKVMDFGIA         0.3829         793.8                50.00      Sequence
DRB1_0405  362  PDVRGQSSADAIATL  DVRGQSSAD         0.3828         794.9                50.00      Sequence
DRB1_0405  366  GQSSADAIATLQNRG  ADAIATLQN         0.3827         795.6                50.00      Sequence
DRB1_0405  431  VSTLTYAEAVKKLTA  LTYAEAVKK         0.3825         797.4                50.00      Sequence
DRB1_0405  553  QVSKGNQFVMPDLSG  GNQFVMPDL         0.3818         803.7                50.00      Sequence
DRB1_0405  558  NQFVMPDLSGMFWVD  FVMPDLSGM         0.3816         805.0                50.00      Sequence
DRB1_0405  127  FSHQNGIIHRDVKPA  FSHQNGIIH         0.3816         805.5                50.00      Sequence
DRB1_0405  360  QVPDVRGQSSADAIA  DVRGQSSAD         0.3815         805.6                50.00      Sequence
DRB1_0405   17  GFGGMSEVHLARDLR  FGGMSEVHL         0.3807         812.7                50.00      Sequence
DRB1_0405  461  ELVGKVIGTNPPANQ  KVIGTNPPA         0.3802         817.8                50.00      Sequence
DRB1_0405  164  DSGNSVTQTAAVIGT  NSVTQTAAV         0.3800         819.1                50.00      Sequence
DRB1_0405  155  DFGIARAIADSGNSV  FGIARAIAD         0.3800         819.5                50.00      Sequence
DRB1_0405  432  STLTYAEAVKKLTAA  LTYAEAVKK         0.3799         819.6                50.00      Sequence
DRB1_0405  552  LQVSKGNQFVMPDLS  GNQFVMPDL         0.3795         823.6                50.00      Sequence
DRB1_0405  214  PFTGDSPVSVAYQHV  FTGDSPVSV         0.3785         832.9                50.00      Sequence
DRB1_0405  165  SGNSVTQTAAVIGTA  NSVTQTAAV         0.3775         841.3                50.00      Sequence
DRB1_0405  292  RTSLLSSAAGNLSGP  SLLSSAAGN         0.3762         853.8                50.00      Sequence
DRB1_0405  430  DVSTLTYAEAVKKLT  STLTYAEAV         0.3760         855.8                50.00      Sequence
DRB1_0405   80  ETPAGPLPYIVMEYV  LPYIVMEYV         0.3757         857.9                50.00      Sequence
DRB1_0405  508  QKNLNVYGFTKFSQA  YGFTKFSQA         0.3752         862.7                50.00      Sequence
DRB1_0405  132  GIIHRDVKPANIMIS  IIHRDVKPA         0.3745         869.7                50.00      Sequence
DRB1_0405    8  DRYELGEILGFGGMS  DRYELGEIL         0.3732         881.6                50.00      Sequence
DRB1_0405   69  AIVAVYDTGEAETPA  AIVAVYDTG         0.3730         884.0                50.00      Sequence
DRB1_0405  102  IVHTEGPMTPKRAIE  IVHTEGPMT         0.3726         887.4                50.00      Sequence
DRB1_0405  428  IPDVSTLTYAEAVKK  STLTYAEAV         0.3719         893.8                50.00      Sequence
DRB1_0405  156  FGIARAIADSGNSVT  FGIARAIAD         0.3719         894.3                50.00      Sequence
DRB1_0405   38  VKVLRADLARDPSFY  VLRADLARD         0.3714         899.2                50.00      Sequence
DRB1_0405  518  KFSQASVDSPRPAGE  FSQASVDSP         0.3703         909.8                50.00      Sequence
DRB1_0405  464  GKVIGTNPPANQTSA  KVIGTNPPA         0.3701         912.1                50.00      Sequence
DRB1_0405  256  KNPENRYQTAAEMRA  NRYQTAAEM         0.3699         913.5                50.00      Sequence
DRB1_0405  177  GTAQYLSPEQARGDS  AQYLSPEQA         0.3693         919.4                50.00      Sequence
DRB1_0405  121  ACQALNFSHQNGIIH  FSHQNGIIH         0.3682         930.7                50.00      Sequence
DRB1_0405  244  ADLDAVVLKALAKNP  VVLKALAKN         0.3681         931.3                50.00      Sequence
DRB1_0405  131  NGIIHRDVKPANIMI  IIHRDVKPA         0.3678         935.0                50.00      Sequence
DRB1_0405  236  SARHEGLSADLDAVV  ARHEGLSAD         0.3663         950.3                50.00      Sequence
DRB1_0405  263  QTAAEMRADLVRVHN  EMRADLVRV         0.3659         953.9                50.00      Sequence
DRB1_0405  227  HVREDPIPPSARHEG  VREDPIPPS         0.3655         958.4                50.00      Sequence
DRB1_0405   61  NAAALNHPAIVAVYD  AALNHPAIV         0.3654         959.8                50.00      Sequence
DRB1_0405  320  DRDRSIGSVGRWVAV  DRDRSIGSV         0.3649         964.5                50.00      Sequence
DRB1_0405  363  DVRGQSSADAIATLQ  DVRGQSSAD         0.3648         966.0                50.00      Sequence
DRB1_0405  429  PDVSTLTYAEAVKKL  STLTYAEAV         0.3643         971.1                50.00      Sequence
DRB1_0405  537  NPPAGTTVPVDSVIE  PAGTTVPVD         0.3635         978.8                50.00      Sequence
DRB1_0405   18  FGGMSEVHLARDLRL  FGGMSEVHL         0.3633         981.1                50.00      Sequence
DRB1_0405   23  EVHLARDLRLHRDVA  VHLARDLRL         0.3631         983.8                50.00      Sequence
DRB1_0405  209  LTGEPPFTGDSPVSV  FTGDSPVSV         0.3620         995.7                50.00      Sequence
DRB1_0405    7  SDRYELGEILGFGGM  YELGEILGF         0.3615        1000.8                50.00      Sequence
DRB1_0405  608  PAGTGVNRDGIITLR  VNRDGIITL         0.3602        1014.7                50.00      Sequence
DRB1_0405  110  TPKRAIEVIADACQA  KRAIEVIAD         0.3594        1024.1                50.00      Sequence
DRB1_0405  421  TGPEQREIPDVSTLT  EQREIPDVS         0.3587        1031.2                50.00      Sequence
DRB1_0405  171  QTAAVIGTAQYLSPE  AVIGTAQYL         0.3575        1044.4                50.00      Sequence
DRB1_0405  243  SADLDAVVLKALAKN  VVLKALAKN         0.3563        1058.4                50.00      Sequence
DRB1_0405  133  IIHRDVKPANIMISA  DVKPANIMI         0.3560        1061.9                50.00      Sequence
DRB1_0405  460  PELVGKVIGTNPPAN  LVGKVIGTN         0.3554        1068.8                50.00      Sequence
DRB1_0405  163  ADSGNSVTQTAAVIG  NSVTQTAAV         0.3553        1070.3                50.00      Sequence
DRB1_0405   22  SEVHLARDLRLHRDV  VHLARDLRL         0.3545        1079.3                50.00      Sequence
DRB1_0405  109  MTPKRAIEVIADACQ  KRAIEVIAD         0.3536        1090.0                50.00      Sequence
DRB1_0405   21  MSEVHLARDLRLHRD  VHLARDLRL         0.3532        1094.4                50.00      Sequence
DRB1_0405  178  TAQYLSPEQARGDSV  AQYLSPEQA         0.3531        1095.9                50.00      Sequence
DRB1_0405  359  VQVPDVRGQSSADAI  DVRGQSSAD         0.3527        1101.0                50.00      Sequence
DRB1_0405  465  KVIGTNPPANQTSAI  VIGTNPPAN         0.3525        1103.2                50.00      Sequence
DRB1_0405  551  ELQVSKGNQFVMPDL  GNQFVMPDL         0.3495        1139.8                50.00      Sequence
DRB1_0405  488  GSGPATKDIPDVAGQ  ATKDIPDVA         0.3493        1142.0                50.00      Sequence
DRB1_0405  206  YEVLTGEPPFTGDSP  VLTGEPPFT         0.3491        1144.4                50.00      Sequence
DRB1_0405  348  AINTFGGITRDVQVP  GGITRDVQV         0.3490        1145.9                50.00      Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0405 | 260 | NRYQTAAEMRADLVR | NRYQTAAEM | 0.3482 | 1155.9 | 50.00 | Sequence |
| DRB1_0405 | 489 | SGPATKDIPDVAGQT | ATKDIPDVA | 0.3480 | 1158.5 | 50.00 | Sequence |
| DRB1_0405 | 166 | GNSVTQTAAVIGTAQ | NSVTQTAAV | 0.3468 | 1172.8 | 50.00 | Sequence |
| DRB1_0405 | 218 | DSPVSVAYQHVREDP | VAYQHVRED | 0.3466 | 1175.4 | 50.00 | Sequence |
| DRB1_0405 | 44 | DLARDPSFYLRFRRE | LARDPSFYL | 0.3458 | 1185.6 | 50.00 | Sequence |
| DRB1_0405 | 130 | QNGIIHRDVKPANIM | IIHRDVKPA | 0.3451 | 1195.3 | 50.00 | Sequence |
| DRB1_0405 | 433 | TLTYAEAVKKLTAAG | LTYAEAVKK | 0.3448 | 1198.8 | 50.00 | Sequence |
| DRB1_0405 | 162 | IADSGNSVTQTAAVI | NSVTQTAAV | 0.3438 | 1211.8 | 50.00 | Sequence |
| DRB1_0405 | 135 | HRDVKPANIMISATN | VKPANIMIS | 0.3433 | 1218.4 | 50.00 | Sequence |
| DRB1_0405 | 268 | MRADLVRVHNGEPPE | LVRVHNGEP | 0.3432 | 1220.0 | 50.00 | Sequence |
| DRB1_0405 | 315 | DLDDTDRDRSIGSVG | DRDRSIGSV | 0.3426 | 1227.5 | 50.00 | Sequence |
| DRB1_0405 | 190 | DSVDARSDVYSLGCV | SDVYSLGCV | 0.3425 | 1228.9 | 50.00 | Sequence |
| DRB1_0405 | 235 | PSARHEGLSADLDAV | ARHEGLSAD | 0.3411 | 1248.5 | 50.00 | Sequence |
| DRB1_0405 | 490 | GPATKDIPDVAGQTV | ATKDIPDVA | 0.3388 | 1279.5 | 50.00 | Sequence |
| DRB1_0405 | 536 | TNPPAGTTVPVDSVI | PAGTTVPVD | 0.3377 | 1295.2 | 50.00 | Sequence |
| DRB1_0405 | 19 | GGMSEVHLARDLRLH | GGMSEVHLA | 0.3376 | 1295.4 | 50.00 | Sequence |
| DRB1_0405 | 365 | RGQSSADAIATLQNR | ADAIATLQN | 0.3374 | 1299.0 | 50.00 | Sequence |
| DRB1_0405 | 111 | PKRAIEVIADACQAL | KRAIEVIAD | 0.3358 | 1321.8 | 50.00 | Sequence |
| DRB1_0405 | 234 | PPSARHEGLSADLDA | SARHEGLSA | 0.3353 | 1328.6 | 50.00 | Sequence |
| DRB1_0405 | 519 | FSQASVDSPRPAGEV | FSQASVDSP | 0.3351 | 1331.1 | 50.00 | Sequence |
| DRB1_0405 | 550 | IELQVSKGNQFVMPD | LQVSKGNQF | 0.3349 | 1334.5 | 50.00 | Sequence |
| DRB1_0405 | 112 | KRAIEVIADACQALN | RAIEVIADA | 0.3348 | 1336.5 | 50.00 | Sequence |
| DRB1_0405 | 395 | PDHVIGTDPAANTSV | HVIGTDPAA | 0.3341 | 1346.1 | 50.00 | Sequence |
| DRB1_0405 | 6 | LSDRYELGEILGFGG | YELGEILGF | 0.3339 | 1348.3 | 50.00 | Sequence |
| DRB1_0405 | 356 | TRDVQVPDVRGQSSA | TRDVQVPDV | 0.3337 | 1352.4 | 50.00 | Sequence |
| DRB1_0405 | 20 | GMSEVHLARDLRLHR | VHLARDLRL | 0.3332 | 1358.9 | 50.00 | Sequence |
| DRB1_0405 | 107 | GPMTPKRAIEVIADA | PKRAIEVIA | 0.3331 | 1359.9 | 50.00 | Sequence |
| DRB1_0405 | 108 | PMTPKRAIEVIADAC | PKRAIEVIA | 0.3328 | 1365.3 | 50.00 | Sequence |
| DRB1_0405 | 358 | DVQVPDVRGQSSADA | DVRGQSSAD | 0.3326 | 1368.1 | 50.00 | Sequence |
| DRB1_0405 | 161 | AIADSGNSVTQTAAV | NSVTQTAAV | 0.3322 | 1374.1 | 50.00 | Sequence |
| DRB1_0405 | 129 | HQNGIIHRDVKPANI | IIHRDVKPA | 0.3317 | 1381.0 | 50.00 | Sequence |
| DRB1_0405 | 383 | IRTLQKPDSTIPPDH | TLQKPDSTI | 0.3304 | 1401.7 | 50.00 | Sequence |
| DRB1_0405 | 262 | YQTAAEMRADLVRVH | EMRADLVRV | 0.3303 | 1402.1 | 50.00 | Sequence |
| DRB1_0405 | 237 | ARHEGLSADLDAVVL | ARHEGLSAD | 0.3295 | 1414.6 | 50.00 | Sequence |
| DRB1_0405 | 55 | FRREAQNAAALNHPA | FRREAQNAA | 0.3293 | 1417.4 | 50.00 | Sequence |
| DRB1_0405 | 434 | LTYAEAVKKLTAAGF | YAEAVKKLT | 0.3291 | 1420.7 | 50.00 | Sequence |
| DRB1_0405 | 54 | RFRREAQNAAALNHP | FRREAQNAA | 0.3289 | 1424.2 | 50.00 | Sequence |
| DRB1_0405 | 45 | LARDPSFYLRFRREA | LARDPSFYL | 0.3280 | 1438.0 | 50.00 | Sequence |
| DRB1_0405 | 413 | DEITVNVSTGPEQRE | DEITVNVST | 0.3277 | 1442.9 | 50.00 | Sequence |
| DRB1_0405 | 394 | PPDHVIGTDPAANTS | HVIGTDPAA | 0.3274 | 1447.0 | 50.00 | Sequence |
| DRB1_0405 | 487 | VGSGPATKDIPDVAG | ATKDIPDVA | 0.3271 | 1452.2 | 50.00 | Sequence |
| DRB1_0405 | 167 | NSVTQTAAVIGTAQY | NSVTQTAAV | 0.3269 | 1454.6 | 50.00 | Sequence |
| DRB1_0405 | 412 | GDEITVNVSTGPEQR | DEITVNVST | 0.3269 | 1454.9 | 50.00 | Sequence |
| DRB1_0405 | 215 | FTGDSPVSVAYQHVR | FTGDSPVSV | 0.3268 | 1457.3 | 50.00 | Sequence |
| DRB1_0405 | 285 | KVLTDAERTSLLSSA | AERTSLLSS | 0.3266 | 1459.7 | 50.00 | Sequence |
| DRB1_0405 | 134 | IHRDVKPANIMISAT | DVKPANIMI | 0.3259 | 1471.1 | 50.00 | Sequence |
| DRB1_0405 | 435 | TYAEAVKKLTAAGFG | YAEAVKKLT | 0.3247 | 1490.7 | 50.00 | Sequence |
| DRB1_0405 | 170 | TQTAAVIGTAQYLSP | AVIGTAQYL | 0.3246 | 1492.1 | 50.00 | Sequence |
| DRB1_0405 | 582 | WTGMLDKGADVDAGG | GMLDKGADV | 0.3239 | 1502.9 | 50.00 | Sequence |
| DRB1_0405 | 420 | STGPEQREIPDVSTL | EQREIPDVS | 0.3234 | 1510.4 | 50.00 | Sequence |
| DRB1_0405 | 5 | HLSDRYELGEILGFG | YELGEILGF | 0.3217 | 1539.9 | 50.00 | Sequence |
| DRB1_0405 | 396 | DHVIGTDPAANTSVS | HVIGTDPAA | 0.3212 | 1548.4 | 50.00 | Sequence |
| DRB1_0405 | 436 | YAEAVKKLTAAGFGR | EAVKKLTAA | 0.3209 | 1553.5 | 50.00 | Sequence |
| DRB1_0405 | 60 | QNAAALNHPAIVAVY | AALNHPAIV | 0.3207 | 1556.8 | 50.00 | Sequence |
| DRB1_0405 | 485 | IIVGSGPATKDIPDV | IIVGSGPAT | 0.3204 | 1560.7 | 50.00 | Sequence |
| DRB1_0405 | 250 | VLKALAKNPENRYQT | VLKALAKNP | 0.3203 | 1562.0 | 50.00 | Sequence |
| DRB1_0405 | 179 | AQYLSPEQARGDSVD | AQYLSPEQA | 0.3195 | 1575.5 | 50.00 | Sequence |
| DRB1_0405 | 233 | IPPSARHEGLSADLD | ARHEGLSAD | 0.3195 | 1576.9 | 50.00 | Sequence |
| DRB1_0405 | 468 | GTNPPANQTSAITNV | ANQTSAITN | 0.3184 | 1595.0 | 50.00 | Sequence |
| DRB1_0405 | 217 | GDSPVSVAYQHVRED | VAYQHVRED | 0.3166 | 1626.8 | 50.00 | Sequence |
| DRB1_0405 | 271 | DLVRVHNGEPPEAPK | LVRVHNGEP | 0.3154 | 1647.3 | 50.00 | Sequence |
| DRB1_0405 | 269 | RADLVRVHNGEPPEA | LVRVHNGEP | 0.3138 | 1675.8 | 50.00 | Sequence |
| DRB1_0405 | 113 | RAIEVIADACQALNF | RAIEVIADA | 0.3138 | 1677.1 | 50.00 | Sequence |
| DRB1_0405 | 506 | VAQKNLNVYGFTKFS | VAQKNLNVY | 0.3134 | 1683.0 | 50.00 | Sequence |
| DRB1_0405 | 411 | AGDEITVNVSTGPEQ | DEITVNVST | 0.3123 | 1704.7 | 50.00 | Sequence |
| DRB1_0405 | 486 | IVGSGPATKDIPDVA | ATKDIPDVA | 0.3119 | 1711.7 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0405 | 169 | VTQTAAVIGTAQYLS | AVIGTAQYL | 0.3116 | 1717.4 | 50.00 | Sequence |
| DRB1_0405 | 364 | VRGQSSADAIATLQN | VRGQSSADA | 0.3114 | 1720.3 | 50.00 | Sequence |
| DRB1_0405 | 397 | HVIGTDPAANTSVSA | HVIGTDPAA | 0.3111 | 1726.1 | 50.00 | Sequence |
| DRB1_0405 | 270 | ADLVRVHNGEPPEAP | LVRVHNGEP | 0.3107 | 1734.6 | 50.00 | Sequence |
| DRB1_0405 | 507 | AQKNLNVYGFTKFSQ | LNVYGFTKF | 0.3106 | 1735.2 | 50.00 | Sequence |
| DRB1_0405 | 255 | AKNPENRYQTAAEMR | NRYQTAAEM | 0.3102 | 1743.1 | 50.00 | Sequence |
| DRB1_0405 | 442 | KLTAAGFGRFKQANS | FGRFKQANS | 0.3101 | 1745.2 | 50.00 | Sequence |
| DRB1_0405 | 594 | AGGSQHNRVVYQNPP | SQHNRVVYQ | 0.3100 | 1747.4 | 50.00 | Sequence |
| DRB1_0405 | 106 | EGPMTPKRAIEVIAD | GPMTPKRAI | 0.3094 | 1757.5 | 50.00 | Sequence |
| DRB1_0405 | 568 | MFWVDAEPRLRALGW | FWVDAEPRL | 0.3094 | 1759.3 | 50.00 | Sequence |
| DRB1_0405 | 373 | IATLQNRGFKIRTLQ | IATLQNRGF | 0.3092 | 1762.5 | 50.00 | Sequence |
| DRB1_0405 | 466 | VIGTNPPANQTSAIT | VIGTNPPAN | 0.3088 | 1770.0 | 50.00 | Sequence |
| DRB1_0405 | 293 | TSLLSSAAGNLSGPR | SLLSSAAGN | 0.3080 | 1785.0 | 50.00 | Sequence |
| DRB1_0405 | 410 | SAGDEITVNVSTGPE | DEITVNVST | 0.3077 | 1791.8 | 50.00 | Sequence |
| DRB1_0405 | 505 | DVAQKNLNVYGFTKF | AQKNLNVYG | 0.3073 | 1798.4 | 50.00 | Sequence |
| DRB1_0405 | 128 | SHQNGIIHRDVKPAN | IIHRDVKPA | 0.3047 | 1850.5 | 50.00 | Sequence |
| DRB1_0405 | 504 | VDVAQKNLNVYGFTK | AQKNLNVYG | 0.3042 | 1860.8 | 50.00 | Sequence |
| DRB1_0405 | 272 | LVRVHNGEPPEAPKV | LVRVHNGEP | 0.3011 | 1924.0 | 50.00 | Sequence |
| DRB1_0405 | 414 | EITVNVSTGPEQREI | TVNVSTGPE | 0.3004 | 1937.3 | 50.00 | Sequence |
| DRB1_0405 | 207 | EVLTGEPPFTGDSPV | EVLTGEPPF | 0.3001 | 1945.5 | 50.00 | Sequence |
| DRB1_0405 | 160 | RAIADSGNSVTQTAA | RAIADSGNS | 0.2994 | 1959.0 | 50.00 | Sequence |
| DRB1_0405 | 385 | TLQKPDSTIPPDHVI | KPDSTIPPD | 0.2994 | 1959.5 | 50.00 | Sequence |
| DRB1_0405 | 393 | IPPDHVIGTDPAANT | HVIGTDPAA | 0.2985 | 1979.2 | 50.00 | Sequence |
| DRB1_0405 | 459 | TPELVGKVIGTNPPA | LVGKVIGTN | 0.2982 | 1985.0 | 50.00 | Sequence |
| DRB1_0405 | 572 | DAEPRLRALGWTGML | RLRALGWTG | 0.2981 | 1986.1 | 50.00 | Sequence |
| DRB1_0405 | 384 | RTLQKPDSTIPPDHV | TLQKPDSTI | 0.2975 | 2000.9 | 50.00 | Sequence |
| DRB1_0405 | 4 | SHLSDRYELGEILGF | YELGEILGF | 0.2970 | 2010.0 | 50.00 | Sequence |
| DRB1_0405 | 409 | VSAGDEITVNVSTGP | DEITVNVST | 0.2970 | 2011.7 | 50.00 | Sequence |
| DRB1_0405 | 607 | PPAGTGVNRDGIITL | GVNRDGIIT | 0.2967 | 2016.9 | 50.00 | Sequence |
| DRB1_0405 | 46 | ARDPSFYLRFRREAQ | SFYLRFRRE | 0.2960 | 2032.8 | 50.00 | Sequence |
| DRB1_0405 | 254 | LAKNPENRYQTAAEM | NRYQTAAEM | 0.2951 | 2052.4 | 50.00 | Sequence |
| DRB1_0405 | 242 | LSADLDAVVLKALAK | LSADLDAVV | 0.2935 | 2088.2 | 50.00 | Sequence |
| DRB1_0405 | 59 | AQNAAALNHPAIVAV | AALNHPAIV | 0.2917 | 2128.5 | 50.00 | Sequence |
| DRB1_0405 | 503 | TVDVAQKNLNVYGFT | AQKNLNVYG | 0.2916 | 2131.5 | 50.00 | Sequence |
| DRB1_0405 | 239 | HEGLSADLDAVVLKA | LSADLDAVV | 0.2905 | 2156.9 | 50.00 | Sequence |
| DRB1_0405 | 238 | RHEGLSADLDAVVLK | GLSADLDAV | 0.2893 | 2185.1 | 50.00 | Sequence |
| DRB1_0405 | 419 | VSTGPEQREIPDVST | PEQREIPDV | 0.2889 | 2194.8 | 50.00 | Sequence |
| DRB1_0405 | 261 | RYQTAAEMRADLVRV | YQTAAEMRA | 0.2881 | 2215.2 | 50.00 | Sequence |
| DRB1_0405 | 491 | PATKDIPDVAGQTVD | ATKDIPDVA | 0.2862 | 2260.4 | 50.00 | Sequence |
| DRB1_0405 | 408 | SVSAGDEITVNVSTG | DEITVNVST | 0.2853 | 2281.2 | 50.00 | Sequence |
| DRB1_0405 | 158 | IARAIADSGNSVTQT | RAIADSGNS | 0.2851 | 2286.8 | 50.00 | Sequence |
| DRB1_0405 | 189 | GDSVDARSDVYSLGC | VDARSDVYS | 0.2848 | 2293.7 | 50.00 | Sequence |
| DRB1_0405 | 569 | FWVDAEPRLRALGWT | FWVDAEPRL | 0.2847 | 2296.4 | 50.00 | Sequence |
| DRB1_0405 | 357 | RDVQVPDVRGQSSAD | DVRGQSSAD | 0.2842 | 2309.1 | 50.00 | Sequence |
| DRB1_0405 | 159 | ARAIADSGNSVTQTA | RAIADSGNS | 0.2818 | 2370.0 | 50.00 | Sequence |
| DRB1_0405 | 157 | GIARAIADSGNSVTQ | RAIADSGNS | 0.2803 | 2409.5 | 50.00 | Sequence |
| DRB1_0405 | 437 | AEAVKKLTAAGFGRF | AVKKLTAAG | 0.2793 | 2436.0 | 50.00 | Sequence |
| DRB1_0405 | 241 | GLSADLDAVVLKALA | LSADLDAVV | 0.2783 | 2461.6 | 50.00 | Sequence |
| DRB1_0405 | 602 | VVYQNPPAGTGVNRD | VVYQNPPAG | 0.2780 | 2469.6 | 50.00 | Sequence |
| DRB1_0405 | 114 | AIEVIADACQALNFS | AIEVIADAC | 0.2775 | 2482.4 | 50.00 | Sequence |
| DRB1_0405 | 284 | PKVLTDAERTSLLSS | AERTSLLSS | 0.2767 | 2504.0 | 50.00 | Sequence |
| DRB1_0405 | 240 | EGLSADLDAVVLKAL | LSADLDAVV | 0.2751 | 2549.4 | 50.00 | Sequence |
| DRB1_0405 | 583 | TGMLDKGADVDAGGS | GMLDKGADV | 0.2751 | 2549.5 | 50.00 | Sequence |
| DRB1_0405 | 294 | SLLSSAAGNLSGPRT | SLLSSAAGN | 0.2745 | 2563.7 | 50.00 | Sequence |
| DRB1_0405 | 535 | GTNPPAGTTVPVDSV | PAGTTVPVD | 0.2738 | 2584.2 | 50.00 | Sequence |
| DRB1_0405 | 407 | TSVSAGDEITVNVST | VSAGDEITV | 0.2719 | 2639.6 | 50.00 | Sequence |
| DRB1_0405 | 58 | EAQNAAALNHPAIVA | AALNHPAIV | 0.2696 | 2703.7 | 50.00 | Sequence |
| DRB1_0405 | 392 | TIPPDHVIGTDPAAN | HVIGTDPAA | 0.2695 | 2708.1 | 50.00 | Sequence |
| DRB1_0405 | 314 | QDLDDTDRDRSIGSV | DRDRSIGSV | 0.2678 | 2757.5 | 50.00 | Sequence |
| DRB1_0405 | 458 | STPELVGKVIGTNPP | LVGKVIGTN | 0.2677 | 2762.4 | 50.00 | Sequence |
| DRB1_0405 | 120 | DACQALNFSHQNGII | LNFSHQNGI | 0.2670 | 2782.3 | 50.00 | Sequence |
| DRB1_0405 | 502 | QTVDVAQKNLNVYGF | AQKNLNVYG | 0.2667 | 2792.4 | 50.00 | Sequence |
| DRB1_0405 | 115 | IEVIADACQALNFSH | EVIADACQA | 0.2658 | 2817.5 | 50.00 | Sequence |
| DRB1_0405 | 438 | EAVKKLTAAGFGRFK | EAVKKLTAA | 0.2636 | 2885.4 | 50.00 | Sequence |
| DRB1_0405 | 188 | RGDSVDARSDVYSLG | DARSDVYSL | 0.2622 | 2929.9 | 50.00 | Sequence |
| DRB1_0405 | 57 | REAQNAAALNHPAIV | AALNHPAIV | 0.2616 | 2948.3 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0405 | 415 | ITVNVSTGPEQREIP | TVNVSTGPE | 0.2607 | 2978.1 | 50.00 | Sequence |
| DRB1_0405 | 185 | EQARGDSVDARSDVY | QARGDSVDA | 0.2599 | 3003.6 | 50.00 | Sequence |
| DRB1_0405 | 321 | RDRSIGSVGRWVAVV | RDRSIGSVG | 0.2589 | 3037.7 | 50.00 | Sequence |
| DRB1_0405 | 322 | DRSIGSVGRWVAVVA | VGRWVAVVA | 0.2585 | 3048.7 | 50.00 | Sequence |
| DRB1_0405 | 70 | IVAVYDTGEAETPAG | AVYDTGEAE | 0.2582 | 3058.3 | 50.00 | Sequence |
| DRB1_0405 | 168 | SVTQTAAVIGTAQYL | SVTQTAAVI | 0.2577 | 3075.0 | 50.00 | Sequence |
| DRB1_0405 | 467 | IGTNPPANQTSAITN | ANQTSAITN | 0.2569 | 3104.2 | 50.00 | Sequence |
| DRB1_0405 | 184 | PEQARGDSVDARSDV | QARGDSVDA | 0.2559 | 3138.5 | 50.00 | Sequence |
| DRB1_0405 | 501 | GQTVDVAQKNLNVYG | AQKNLNVYG | 0.2548 | 3175.3 | 50.00 | Sequence |
| DRB1_0405 | 104 | HTEGPMTPKRAIEVI | GPMTPKRAI | 0.2547 | 3177.2 | 50.00 | Sequence |
| DRB1_0405 | 251 | LKALAKNPENRYQTA | KALAKNPEN | 0.2533 | 3227.0 | 50.00 | Sequence |
| DRB1_0405 | 105 | TEGPMTPKRAIEVIA | GPMTPKRAI | 0.2519 | 3276.2 | 50.00 | Sequence |
| DRB1_0405 | 208 | VLTGEPPFTGDSPVS | PPFTGDSPV | 0.2516 | 3287.9 | 50.00 | Sequence |
| DRB1_0405 | 232 | PIPPSARHEGLSADL | ARHEGLSAD | 0.2512 | 3300.0 | 50.00 | Sequence |
| DRB1_0405 | 186 | QARGDSVDARSDVYS | QARGDSVDA | 0.2499 | 3346.9 | 50.00 | Sequence |
| DRB1_0405 | 116 | EVIADACQALNFSHQ | EVIADACQA | 0.2484 | 3401.2 | 50.00 | Sequence |
| DRB1_0405 | 500 | AGQTVDVAQKNLNVY | DVAQKNLNV | 0.2473 | 3441.3 | 50.00 | Sequence |
| DRB1_0405 | 497 | PDVAGQTVDVAQKNL | VAGQTVDVA | 0.2472 | 3446.0 | 50.00 | Sequence |
| DRB1_0405 | 386 | LQKPDSTIPPDHVIG | KPDSTIPPD | 0.2464 | 3477.9 | 50.00 | Sequence |
| DRB1_0405 | 498 | DVAGQTVDVAQKNLN | GQTVDVAQK | 0.2456 | 3508.1 | 50.00 | Sequence |
| DRB1_0405 | 492 | ATKDIPDVAGQTVDV | ATKDIPDVA | 0.2447 | 3539.4 | 50.00 | Sequence |
| DRB1_0405 | 499 | VAGQTVDVAQKNLNV | GQTVDVAQK | 0.2444 | 3552.1 | 50.00 | Sequence |
| DRB1_0405 | 183 | SPEQARGDSVDARSD | QARGDSVDA | 0.2439 | 3571.5 | 50.00 | Sequence |
| DRB1_0405 | 3 | PSHLSDRYELGEILG | PSHLSDRYE | 0.2426 | 3621.7 | 50.00 | Sequence |
| DRB1_0405 | 571 | VDAEPRLRALGWTGM | PRLRALGWT | 0.2405 | 3704.0 | 50.00 | Sequence |
| DRB1_0405 | 180 | QYLSPEQARGDSVDA | YLSPEQARG | 0.2404 | 3707.9 | 50.00 | Sequence |
| DRB1_0405 | 496 | IPDVAGQTVDVAQKN | DVAGQTVDV | 0.2390 | 3765.1 | 50.00 | Sequence |
| DRB1_0405 | 187 | ARGDSVDARSDVYSL | RGDSVDARS | 0.2385 | 3786.9 | 50.00 | Sequence |
| DRB1_0405 | 418 | NVSTGPEQREIPDVS | PEQREIPDV | 0.2374 | 3832.8 | 50.00 | Sequence |
| DRB1_0405 | 56 | RREAQNAAALNHPAI | EAQNAAALN | 0.2349 | 3935.8 | 50.00 | Sequence |
| DRB1_0405 | 79 | AETPAGPLPYIVMEY | GPLPYIVME | 0.2345 | 3954.1 | 50.00 | Sequence |
| DRB1_0405 | 584 | GMLDKGADVDAGGSQ | GMLDKGADV | 0.2334 | 4001.0 | 50.00 | Sequence |
| DRB1_0405 | 119 | ADACQALNFSHQNGI | LNFSHQNGI | 0.2322 | 4054.5 | 50.00 | Sequence |
| DRB1_0405 | 593 | DAGGSQHNRVVYQNP | SQHNRVVYQ | 0.2311 | 4100.4 | 50.00 | Sequence |
| DRB1_0405 | 103 | VHTEGPMTPKRAIEV | GPMTPKRAI | 0.2300 | 4150.1 | 50.00 | Sequence |
| DRB1_0405 | 495 | DIPDVAGQTVDVAQK | DVAGQTVDV | 0.2278 | 4252.4 | 50.00 | Sequence |
| DRB1_0405 | 216 | TGDSPVSVAYQHVRE | SPVSVAYQH | 0.2277 | 4254.4 | 50.00 | Sequence |
| DRB1_0405 | 416 | TVNVSTGPEQREIPD | TVNVSTGPE | 0.2267 | 4300.8 | 50.00 | Sequence |
| DRB1_0405 | 406 | NTSVSAGDEITVNVS | VSAGDEITV | 0.2263 | 4323.0 | 50.00 | Sequence |
| DRB1_0405 | 228 | VREDPIPPSARHEGL | VREDPIPPS | 0.2250 | 4380.1 | 50.00 | Sequence |
| DRB1_0405 | 403 | PAANTSVSAGDEITV | PAANTSVSA | 0.2248 | 4393.0 | 50.00 | Sequence |
| DRB1_0405 | 391 | STIPPDHVIGTDPAA | HVIGTDPAA | 0.2247 | 4394.9 | 50.00 | Sequence |
| DRB1_0405 | 606 | NPPAGTGVNRDGIIT | GVNRDGIIT | 0.2245 | 4405.4 | 50.00 | Sequence |
| DRB1_0405 | 2 | TPSHLSDRYELGEIL | PSHLSDRYE | 0.2238 | 4440.1 | 50.00 | Sequence |
| DRB1_0405 | 301 | GNLSGPRTDPLPRQD | GNLSGPRTD | 0.2235 | 4455.3 | 50.00 | Sequence |
| DRB1_0405 | 117 | VIADACQALNFSHQN | VIADACQAL | 0.2234 | 4458.1 | 50.00 | Sequence |
| DRB1_0405 | 570 | WVDAEPRLRALGWTG | PRLRALGWT | 0.2229 | 4483.1 | 50.00 | Sequence |
| DRB1_0405 | 309 | DPLPRQDLDDTDRDR | LPRQDLDDT | 0.2203 | 4612.7 | 50.00 | Sequence |
| DRB1_0405 | 283 | APKVLTDAERTSLLS | KVLTDAERT | 0.2197 | 4638.6 | 50.00 | Sequence |
| DRB1_0405 | 252 | KALAKNPENRYQTAA | KALAKNPEN | 0.2194 | 4656.5 | 50.00 | Sequence |
| DRB1_0405 | 417 | VNVSTGPEQREIPDV | PEQREIPDV | 0.2179 | 4732.9 | 50.00 | Sequence |
| DRB1_0405 | 307 | RTDPLPRQDLDDTDR | LPRQDLDDT | 0.2175 | 4750.3 | 50.00 | Sequence |
| DRB1_0405 | 387 | QKPDSTIPPDHVIGT | KPDSTIPPD | 0.2170 | 4777.3 | 50.00 | Sequence |
| DRB1_0405 | 398 | VIGTDPAANTSVSAG | VIGTDPAAN | 0.2167 | 4796.3 | 50.00 | Sequence |
| DRB1_0405 | 304 | SGPRTDPLPRQDLDD | SGPRTDPLP | 0.2163 | 4814.5 | 50.00 | Sequence |
| DRB1_0405 | 310 | PLPRQDLDDTDRDRS | LPRQDLDDT | 0.2159 | 4836.5 | 50.00 | Sequence |
| DRB1_0405 | 402 | DPAANTSVSAGDEIT | PAANTSVSA | 0.2150 | 4883.0 | 50.00 | Sequence |
| DRB1_0405 | 308 | TDPLPRQDLDDTDRD | LPRQDLDDT | 0.2148 | 4893.7 | 50.00 | Sequence |
| DRB1_0405 | 71 | VAVYDTGEAETPAGP | AVYDTGEAE | 0.2146 | 4906.6 | 50.00 | Sequence |
| DRB1_0405 | 305 | GPRTDPLPRQDLDDT | GPRTDPLPR | 0.2134 | 4971.0 | 50.00 | Sequence |
| DRB1_0405 | 457 | PSTPELVGKVIGTNP | LVGKVIGTN | 0.2129 | 4995.7 | 50.00 | Sequence |
| DRB1_0405 | 281 | PEAPKVLTDAERTSL | KVLTDAERT | 0.2124 | 5023.9 | 50.00 | Sequence |
| DRB1_0405 | 401 | TDPAANTSVSAGDEI | PAANTSVSA | 0.2110 | 5098.0 | 50.00 | Sequence |
| DRB1_0405 | 306 | PRTDPLPRQDLDDTD | LPRQDLDDT | 0.2100 | 5152.5 | 50.00 | Sequence |
| DRB1_0405 | 452 | KQANSPSTPELVGKV | QANSPSTPE | 0.2100 | 5153.1 | 50.00 | Sequence |
| DRB1_0405 | 280 | PPEAPKVLTDAERTS | APKVLTDAE | 0.2100 | 5155.2 | 50.00 | Sequence |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| DRB1_0405 | 529 | PAGEVTGTNPPAGTT | GEVTGTNPP | 0.2093 | 5192.3 | 50.00 | Sequence |
| DRB1_0405 | 311 | LPRQDLDDTDRDRSI | LPRQDLDDT | 0.2088 | 5221.3 | 50.00 | Sequence |
| DRB1_0405 | 273 | VRVHNGEPPEAPKVL | RVHNGEPPE | 0.2077 | 5284.7 | 50.00 | Sequence |
| DRB1_0405 | 181 | YLSPEQARGDSVDAR | YLSPEQARG | 0.2072 | 5315.5 | 50.00 | Sequence |
| DRB1_0405 | 534 | TGTNPPAGTTVPVDS | PAGTTVPVD | 0.2056 | 5405.6 | 50.00 | Sequence |
| DRB1_0405 | 530 | AGEVTGTNPPAGTTV | GEVTGTNPP | 0.2054 | 5415.0 | 50.00 | Sequence |
| DRB1_0405 | 282 | EAPKVLTDAERTSLL | KVLTDAERT | 0.2036 | 5525.6 | 50.00 | Sequence |
| DRB1_0405 | 295 | LLSSAAGNLSGPRTD | LSSAAGNLS | 0.2031 | 5551.9 | 50.00 | Sequence |
| DRB1_0405 | 78 | EAETPAGPLPYIVME | GPLPYIVME | 0.2031 | 5553.1 | 50.00 | Sequence |
| DRB1_0405 | 231 | DPIPPSARHEGLSAD | SARHEGLSA | 0.2030 | 5559.8 | 50.00 | Sequence |
| DRB1_0405 | 253 | ALAKNPENRYQTAAE | LAKNPENRY | 0.2026 | 5583.4 | 50.00 | Sequence |
| DRB1_0405 | 182 | LSPEQARGDSVDARS | QARGDSVDA | 0.2024 | 5596.0 | 50.00 | Sequence |
| DRB1_0405 | 400 | GTDPAANTSVSAGDE | PAANTSVSA | 0.2023 | 5602.9 | 50.00 | Sequence |
| DRB1_0405 | 274 | RVHNGEPPEAPKVLT | RVHNGEPPE | 0.2016 | 5645.7 | 50.00 | Sequence |
| DRB1_0405 | 279 | EPPEAPKVLTDAERT | APKVLTDAE | 0.2006 | 5704.2 | 50.00 | Sequence |
| DRB1_0405 | 303 | LSGPRTDPLPRQDLD | GPRTDPLPR | 0.2004 | 5721.5 | 50.00 | Sequence |
| DRB1_0405 | 404 | AANTSVSAGDEITVN | AANTSVSAG | 0.1995 | 5771.6 | 50.00 | Sequence |
| DRB1_0405 | 300 | AGNLSGPRTDPLPRQ | GNLSGPRTD | 0.1995 | 5777.3 | 50.00 | Sequence |
| DRB1_0405 | 118 | IADACQALNFSHQNG | IADACQALN | 0.1992 | 5791.1 | 50.00 | Sequence |
| DRB1_0405 | 494 | KDIPDVAGQTVDVAQ | DVAGQTVDV | 0.1985 | 5837.5 | 50.00 | Sequence |
| DRB1_0405 | 531 | GEVTGTNPPAGTTVP | GEVTGTNPP | 0.1981 | 5861.8 | 50.00 | Sequence |
| DRB1_0405 | 388 | KPDSTIPPDHVIGTD | KPDSTIPPD | 0.1972 | 5922.1 | 50.00 | Sequence |
| DRB1_0405 | 302 | NLSGPRTDPLPRQDL | GPRTDPLPR | 0.1967 | 5952.3 | 50.00 | Sequence |
| DRB1_0405 | 1 | TTPSHLSDRYELGEI | PSHLSDRYE | 0.1962 | 5982.7 | 50.00 | Sequence |
| DRB1_0405 | 0 | MTTPSHLSDRYELGE | PSHLSDRYE | 0.1927 | 6214.1 | 50.00 | Sequence |
| DRB1_0405 | 528 | RPAGEVTGTNPPAGT | GEVTGTNPP | 0.1922 | 6247.6 | 50.00 | Sequence |
| DRB1_0405 | 399 | IGTDPAANTSVSAGD | IGTDPAANT | 0.1908 | 6344.6 | 50.00 | Sequence |
| DRB1_0405 | 456 | SPSTPELVGKVIGTN | LVGKVIGTN | 0.1887 | 6488.9 | 50.00 | Sequence |
| DRB1_0405 | 405 | ANTSVSAGDEITVNV | TSVSAGDEI | 0.1857 | 6705.2 | 50.00 | Sequence |
| DRB1_0405 | 453 | QANSPSTPELVGKVI | QANSPSTPE | 0.1845 | 6791.0 | 50.00 | Sequence |
| DRB1_0405 | 533 | VTGTNPPAGTTVPVD | PAGTTVPVD | 0.1806 | 7083.3 | 50.00 | Sequence |
| DRB1_0405 | 72 | AVYDTGEAETPAGPL | AVYDTGEAE | 0.1789 | 7218.3 | 50.00 | Sequence |
| DRB1_0405 | 299 | AAGNLSGPRTDPLPR | GNLSGPRTD | 0.1783 | 7262.4 | 50.00 | Sequence |
| DRB1_0405 | 390 | DSTIPPDHVIGTDPA | DHVIGTDPA | 0.1779 | 7295.8 | 50.00 | Sequence |
| DRB1_0405 | 527 | PRPAGEVTGTNPPAG | GEVTGTNPP | 0.1766 | 7395.3 | 50.00 | Sequence |
| DRB1_0405 | 592 | VDAGGSQHNRVVYQN | SQHNRVVYQ | 0.1762 | 7428.1 | 50.00 | Sequence |
| DRB1_0405 | 439 | AVKKLTAAGFGRFKQ | AVKKLTAAG | 0.1761 | 7441.1 | 50.00 | Sequence |
| DRB1_0405 | 455 | NSPSTPELVGKVIGT | NSPSTPELV | 0.1719 | 7781.1 | 50.00 | Sequence |
| DRB1_0405 | 493 | TKDIPDVAGQTVDVA | DVAGQTVDV | 0.1711 | 7852.0 | 50.00 | Sequence |
| DRB1_0405 | 296 | LSSAAGNLSGPRTDP | GNLSGPRTD | 0.1666 | 8239.2 | 50.00 | Sequence |
| DRB1_0405 | 298 | SAAGNLSGPRTDPLP | GNLSGPRTD | 0.1638 | 8498.5 | 50.00 | Sequence |
| DRB1_0405 | 454 | ANSPSTPELVGKVIG | NSPSTPELV | 0.1613 | 8732.8 | 50.00 | Sequence |
| DRB1_0405 | 532 | EVTGTNPPAGTTVPV | EVTGTNPPA | 0.1606 | 8797.5 | 50.00 | Sequence |
| DRB1_0405 | 526 | SPRPAGEVTGTNPPA | GEVTGTNPP | 0.1568 | 9162.7 | 50.00 | Sequence |
| DRB1_0405 | 297 | SSAAGNLSGPRTDPL | GNLSGPRTD | 0.1504 | 9820.2 | 50.00 | Sequence |
| DRB1_0405 | 591 | DVDAGGSQHNRVVYQ | SQHNRVVYQ | 0.1497 | 9892.9 | 50.00 | Sequence |
| DRB1_0405 | 389 | PDSTIPPDHVIGTDP | IPPDHVIGT | 0.1480 | 10082.0 | 50.00 | Sequence |
| DRB1_0405 | 278 | GEPPEAPKVLTDAER | APKVLTDAE | 0.1458 | 10321.8 | 50.00 | Sequence |
| DRB1_0405 | 75 | DTGEAETPAGPLPYI | EAETPAGPL | 0.1458 | 10326.3 | 50.00 | Sequence |
| DRB1_0405 | 277 | NGEPPEAPKVLTDAE | PPEAPKVLT | 0.1445 | 10473.8 | 50.00 | Sequence |
| DRB1_0405 | 520 | SQASVDSPRPAGEVT | SQASVDSPR | 0.1440 | 10528.1 | 50.00 | Sequence |
| DRB1_0405 | 77 | GEAETPAGPLPYIVM | TPAGPLPYI | 0.1421 | 10745.5 | 50.00 | Sequence |
| DRB1_0405 | 76 | TGEAETPAGPLPYIV | TPAGPLPYI | 0.1391 | 11104.6 | 50.00 | Sequence |
| DRB1_0405 | 441 | KKLTAAGFGRFKQAN | AGFGRFKQA | 0.1385 | 11170.0 | 50.00 | Sequence |
| DRB1_0405 | 313 | RQDLDDTDRDRSIGS | QDLDDTDRD | 0.1359 | 11488.6 | 50.00 | Sequence |
| DRB1_0405 | 275 | VHNGEPPEAPKVLTD | NGEPPEAPK | 0.1348 | 11634.2 | 50.00 | Sequence |
| DRB1_0405 | 585 | MLDKGADVDAGGSQH | MLDKGADVD | 0.1325 | 11921.4 | 50.00 | Sequence |
| DRB1_0405 | 312 | PRQDLDDTDRDRSIG | PRQDLDDTD | 0.1307 | 12160.4 | 50.00 | Sequence |
| DRB1_0405 | 605 | QNPPAGTGVNRDGII | PAGTGVNRD | 0.1269 | 12663.1 | 50.00 | Sequence |
| DRB1_0405 | 276 | HNGEPPEAPKVLTDA | NGEPPEAPK | 0.1257 | 12835.5 | 50.00 | Sequence |
| DRB1_0405 | 73 | VYDTGEAETPAGPLP | GEAETPAGP | 0.1235 | 13140.4 | 50.00 | Sequence |
| DRB1_0405 | 603 | VYQNPPAGTGVNRDG | VYQNPPAGT | 0.1218 | 13385.2 | 50.00 | Sequence |
| DRB1_0405 | 230 | EDPIPPSARHEGLSA | SARHEGLSA | 0.1212 | 13472.3 | 50.00 | Sequence |
| DRB1_0405 | 440 | VKKLTAAGFGRFKQA | VKKLTAAGF | 0.1211 | 13483.1 | 50.00 | Sequence |
| DRB1_0405 | 525 | DSPRPAGEVTGTNPP | GEVTGTNPP | 0.1202 | 13623.5 | 50.00 | Sequence |
| DRB1_0405 | 74 | YDTGEAETPAGPLPY | GEAETPAGP | 0.1195 | 13724.3 | 50.00 | Sequence |

```
   DRB1_0405  521  QASVDSPRPAGEVTG  ASVDSPRPA        0.1120      14890.4               50.00     Sequence
   DRB1_0405  590  ADVDAGGSQHNRVVY  GGSQHNRVV        0.1092      15347.4               50.00     Sequence
   DRB1_0405  522  ASVDSPRPAGEVTGT  ASVDSPRPA        0.1041      16208.3               50.00     Sequence
   DRB1_0405  587  DKGADVDAGGSQHNR  GADVDAGGS        0.0975      17412.8               50.00     Sequence
   DRB1_0405  229  REDPIPPSARHEGLS  REDPIPPSA        0.0971      17487.5               50.00     Sequence
   DRB1_0405  586  LDKGADVDAGGSQHN  DKGADVDAG        0.0969      17526.9               50.00     Sequence
   DRB1_0405  589  GADVDAGGSQHNRVV  DVDAGGSQH        0.0937      18136.5               50.00     Sequence
   DRB1_0405  604  YQNPPAGTGVNRDGI  PAGTGVNRD        0.0907      18748.9               50.00     Sequence
   DRB1_0405  588  KGADVDAGGSQHNRV  KGADVDAGG        0.0880      19295.9               50.00     Sequence
   DRB1_0405  523  SVDSPRPAGEVTGTN  SVDSPRPAG        0.0833      20297.7               50.00     Sequence
   DRB1_0405  524  VDSPRPAGEVTGTNP  AGEVTGTNP        0.0772      21680.5               50.00     Sequence
-------------------------------------------------------------------------------------------------

Allele: DRB1_0405. Number of high binders 7. Number of weak binders 171. Number of peptides 612

-------------------------------------------------------------------------------------------------
-------------------------------------------------------------------------------------------------
      Allele  pos            peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
-------------------------------------------------------------------------------------------------
   DRB1_0701   18  FGGMSEVHLARDLRL  VHLARDLRL        0.9255          2.2          SB     0.15     Sequence
   DRB1_0701   19  GGMSEVHLARDLRLH  VHLARDLRL        0.9164          2.5          SB     0.30     Sequence
   DRB1_0701  289  DAERTSLLSSAAGNL  LLSSAAGNL        0.9052          2.8          SB     0.40     Sequence
   DRB1_0701  290  AERTSLLSSAAGNLS  LLSSAAGNL        0.9018          2.9          SB     0.40     Sequence
   DRB1_0701   20  GMSEVHLARDLRLHR  VHLARDLRL        0.8999          3.0          SB     0.80     Sequence
   DRB1_0701  139  KPANIMISATNAVKV  ISATNAVKV        0.8971          3.0          SB     0.80     Sequence
   DRB1_0701  140  PANIMISATNAVKVM  ISATNAVKV        0.8915          3.2          SB     0.80     Sequence
   DRB1_0701  291  ERTSLLSSAAGNLSG  LLSSAAGNL        0.8863          3.4          SB     0.80     Sequence
   DRB1_0701  141  ANIMISATNAVKVMD  ISATNAVKV        0.8746          3.9          SB     1.00     Sequence
   DRB1_0701   21  MSEVHLARDLRLHRD  VHLARDLRL        0.8724          4.0          SB     1.00     Sequence
   DRB1_0701  292  RTSLLSSAAGNLSGP  LLSSAAGNL        0.8630          4.4          SB     2.00     Sequence
   DRB1_0701  142  NIMISATNAVKVMDF  ISATNAVKV        0.8614          4.5          SB     2.00     Sequence
   DRB1_0701   22  SEVHLARDLRLHRDV  VHLARDLRL        0.8545          4.8          SB     2.00     Sequence
   DRB1_0701  143  IMISATNAVKVMDFG  ISATNAVKV        0.8462          5.3          SB     2.00     Sequence
   DRB1_0701  293  TSLLSSAAGNLSGPR  LLSSAAGNL        0.8450          5.3          SB     2.00     Sequence
   DRB1_0701   24  VHLARDLRLHRDVAV  VHLARDLRL        0.8320          6.2          SB     2.00     Sequence
   DRB1_0701   23  EVHLARDLRLHRDVA  VHLARDLRL        0.8314          6.2          SB     2.00     Sequence
   DRB1_0701  294  SLLSSAAGNLSGPRT  LLSSAAGNL        0.8299          6.3          SB     2.00     Sequence
   DRB1_0701  144  MISATNAVKVMDFGI  ISATNAVKV        0.8274          6.5          SB     4.00     Sequence
   DRB1_0701  295  LLSSAAGNLSGPRTD  LLSSAAGNL        0.8087          7.9          SB     4.00     Sequence
   DRB1_0701   27  ARDLRLHRDVAVKVL  LHRDVAVKV        0.8004          8.7          SB     4.00     Sequence
   DRB1_0701  145  ISATNAVKVMDFGIA  ISATNAVKV        0.7995          8.8          SB     4.00     Sequence
   DRB1_0701   26  LARDLRLHRDVAVKV  LHRDVAVKV        0.7808         10.7          SB     4.00     Sequence
   DRB1_0701   28  RDLRLHRDVAVKVLR  LHRDVAVKV        0.7638         12.9          SB     8.00     Sequence
   DRB1_0701   39  KVLRADLARDPSFYL  LARDPSFYL        0.7443         15.9          SB     8.00     Sequence
   DRB1_0701  119  ADACQALNFSHQNGI  LNFSHQNGI        0.7440         16.0          SB     8.00     Sequence
   DRB1_0701  120  DACQALNFSHQNGII  LNFSHQNGI        0.7293         18.7          SB     8.00     Sequence
   DRB1_0701   29  DLRLHRDVAVKVLRA  LHRDVAVKV        0.7224         20.2          SB     8.00     Sequence
   DRB1_0701   40  VLRADLARDPSFYLR  LARDPSFYL        0.7206         20.6          SB     8.00     Sequence
   DRB1_0701  103  VHTEGPMTPKRAIEV  MTPKRAIEV        0.7123         22.5          SB     8.00     Sequence
   DRB1_0701  138  VKPANIMISATNAVK  IMISATNAV        0.7101         23.0          SB     8.00     Sequence
   DRB1_0701  121  ACQALNFSHQNGIIH  LNFSHQNGI        0.7064         24.0          SB     8.00     Sequence
   DRB1_0701  547  DSVIELQVSKGNQFV  LQVSKGNQF        0.7054         24.2          SB     8.00     Sequence
   DRB1_0701  548  SVIELQVSKGNQFVM  LQVSKGNQF        0.6993         25.9          SB    16.00     Sequence
   DRB1_0701  137  DVKPANIMISATNAV  IMISATNAV        0.6983         26.2          SB    16.00     Sequence
   DRB1_0701   41  LRADLARDPSFYLRF  LARDPSFYL        0.6944         27.3          SB    16.00     Sequence
   DRB1_0701  104  HTEGPMTPKRAIEVI  MTPKRAIEV        0.6910         28.3          SB    16.00     Sequence
   DRB1_0701   30  LRLHRDVAVKVLRAD  LHRDVAVKV        0.6870         29.6          SB    16.00     Sequence
   DRB1_0701  326  GSVGRWVAVVAVLAV  WVAVVAVLA        0.6852         30.2          SB    16.00     Sequence
   DRB1_0701  325  IGSVGRWVAVVAVLA  WVAVVAVLA        0.6808         31.6          SB    16.00     Sequence
   DRB1_0701  564  DLSGMFWVDAEPRLR  WVDAEPRLR        0.6705         35.4          SB    16.00     Sequence
   DRB1_0701  327  SVGRWVAVVAVLAVL  WVAVVAVLA        0.6679         36.3          SB    16.00     Sequence
   DRB1_0701  328  VGRWVAVVAVLAVLT  VVAVLAVLT        0.6635         38.1          SB    16.00     Sequence
   DRB1_0701  329  GRWVAVVAVLAVLTV  VVAVLAVLT        0.6632         38.2          SB    16.00     Sequence
   DRB1_0701  105  TEGPMTPKRAIEVIA  MTPKRAIEV        0.6582         40.4          SB    16.00     Sequence
   DRB1_0701  338  LAVLTVVVTIAINTF  VVTIAINTF        0.6555         41.6          SB    16.00     Sequence
   DRB1_0701  219  SPVSVAYQHVREDPI  YQHVREDPI        0.6522         43.1          SB    16.00     Sequence
```

```
DRB1_0701   32  LHRDVAVKVLRADLA  LHRDVAVKV        0.6499          44.2          SB    16.00      Sequence
DRB1_0701   42  RADLARDPSFYLRFR  LARDPSFYL        0.6488          44.7          SB    16.00      Sequence
DRB1_0701  122  CQALNFSHQNGIIHR  LNFSHQNGI        0.6484          44.9          SB    16.00      Sequence
DRB1_0701  565  LSGMFWVDAEPRLRA  WVDAEPRLR        0.6456          46.3          SB    16.00      Sequence
DRB1_0701  330  RWVAVVAVLAVLTVV  WVAVVAVLA        0.6433          47.4          SB    16.00      Sequence
DRB1_0701  470  NPPANQTSAITNVVI  QTSAITNVV        0.6425          47.8          SB    16.00      Sequence
DRB1_0701  549  VIELQVSKGNQFVMP  LQVSKGNQF        0.6415          48.4          SB    16.00      Sequence
DRB1_0701   25  HLARDLRLHRDVAVK  LRLHRDVAV        0.6397          49.3          SB    16.00      Sequence
DRB1_0701  478  AITNVVIIIVGSGPA  IIIVGSGPA        0.6352          51.8          WB    16.00      Sequence
DRB1_0701  546  VDSVIELQVSKGNQF  LQVSKGNQF        0.6320          53.6          WB    16.00      Sequence
DRB1_0701  339  AVLTVVVTIAINTFG  VVTIAINTF        0.6302          54.7          WB    16.00      Sequence
DRB1_0701  215  FTGDSPVSVAYQHVR  PVSVAYQHV        0.6254          57.6          WB    16.00      Sequence
DRB1_0701   31  RLHRDVAVKVLRADL  LHRDVAVKV        0.6252          57.7          WB    16.00      Sequence
DRB1_0701  566  SGMFWVDAEPRLRAL  WVDAEPRLR        0.6227          59.3          WB    16.00      Sequence
DRB1_0701  331  WVAVVAVLAVLTVVV  WVAVVAVLA        0.6217          59.9          WB    16.00      Sequence
DRB1_0701   43  ADLARDPSFYLRFRR  LARDPSFYL        0.6192          61.5          WB    16.00      Sequence
DRB1_0701  471  PPANQTSAITNVVII  QTSAITNVV        0.6186          62.0          WB    16.00      Sequence
DRB1_0701  123  QALNFSHQNGIIHRD  LNFSHQNGI        0.6170          63.0          WB    16.00      Sequence
DRB1_0701  220  PVSVAYQHVREDPIP  YQHVREDPI        0.6050          71.8          WB    16.00      Sequence
DRB1_0701  550  IELQVSKGNQFVMPD  LQVSKGNQF        0.6025          73.7          WB    16.00      Sequence
DRB1_0701  124  ALNFSHQNGIIHRDV  LNFSHQNGI        0.6004          75.4          WB    32.00      Sequence
DRB1_0701  106  EGPMTPKRAIEVIAD  MTPKRAIEV        0.5989          76.7          WB    32.00      Sequence
DRB1_0701  479  ITNVVIIIVGSGPAT  IIIVGSGPA        0.5956          79.5          WB    32.00      Sequence
DRB1_0701   44  DLARDPSFYLRFRRE  LARDPSFYL        0.5928          81.9          WB    32.00      Sequence
DRB1_0701  472  PANQTSAITNVVIII  TSAITNVVI        0.5904          84.1          WB    32.00      Sequence
DRB1_0701   45  LARDPSFYLRFRREA  LARDPSFYL        0.5884          85.9          WB    32.00      Sequence
DRB1_0701  214  PFTGDSPVSVAYQHV  FTGDSPVSV        0.5863          87.9          WB    32.00      Sequence
DRB1_0701  209  LTGEPPFTGDSPVSV  FTGDSPVSV        0.5840          90.1          WB    32.00      Sequence
DRB1_0701  337  VLAVLTVVVTIAINT  VVVTIAINT        0.5827          91.3          WB    32.00      Sequence
DRB1_0701  473  ANQTSAITNVVIIIV  QTSAITNVV        0.5816          92.5          WB    32.00      Sequence
DRB1_0701  445  AAGFGRFKQANSPST  FKQANSPST        0.5794          94.7          WB    32.00      Sequence
DRB1_0701  567  GMFWVDAEPRLRALG  WVDAEPRLR        0.5764          97.8          WB    32.00      Sequence
DRB1_0701  551  ELQVSKGNQFVMPDL  LQVSKGNQF        0.5763          97.9          WB    32.00      Sequence
DRB1_0701  335  VAVLAVLTVVVTIAI  LTVVVTIAI        0.5755          98.7          WB    32.00      Sequence
DRB1_0701  210  TGEPPFTGDSPVSVA  FTGDSPVSV        0.5754          98.9          WB    32.00      Sequence
DRB1_0701  340  VLTVVVTIAINTFGG  VVTIAINTF        0.5718         102.8          WB    32.00      Sequence
DRB1_0701  163  ADSGNSVTQTAAVIG  VTQTAAVIG        0.5706         104.2          WB    32.00      Sequence
DRB1_0701  107  GPMTPKRAIEVIADA  MTPKRAIEV        0.5697         105.2          WB    32.00      Sequence
DRB1_0701  125  LNFSHQNGIIHRDVK  LNFSHQNGI        0.5665         108.9          WB    32.00      Sequence
DRB1_0701  469  TNPPANQTSAITNVV  QTSAITNVV        0.5640         111.8          WB    32.00      Sequence
DRB1_0701  568  MFWVDAEPRLRALGW  WVDAEPRLR        0.5583         119.0          WB    32.00      Sequence
DRB1_0701  148  TNAVKVMDFGIARAI  MDFGIARAI        0.5541         124.6          WB    32.00      Sequence
DRB1_0701  480  TNVVIIIVGSGPATK  IIIVGSGPA        0.5540         124.7          WB    32.00      Sequence
DRB1_0701  332  VAVVAVLAVLTVVVT  VLAVLTVVV        0.5499         130.3          WB    32.00      Sequence
DRB1_0701  333  AVVAVLAVLTVVVTI  VVAVLAVLT        0.5480         133.0          WB    32.00      Sequence
DRB1_0701  474  NQTSAITNVVIIIVG  QTSAITNVV        0.5471         134.3          WB    32.00      Sequence
DRB1_0701  552  LQVSKGNQFVMPDLS  LQVSKGNQF        0.5465         135.3          WB    32.00      Sequence
DRB1_0701   59  AQNAAALNHPAIVAV  LNHPAIVAV        0.5460         136.0          WB    32.00      Sequence
DRB1_0701  221  VSVAYQHVREDPIPP  YQHVREDPI        0.5442         138.6          WB    32.00      Sequence
DRB1_0701  446  AGFGRFKQANSPSTP  FKQANSPST        0.5398         145.3          WB    32.00      Sequence
DRB1_0701  211  GEPPFTGDSPVSVAY  FTGDSPVSV        0.5388         146.9          WB    32.00      Sequence
DRB1_0701  131  NGIIHRDVKPANIMI  RDVKPANIM        0.5385         147.4          WB    32.00      Sequence
DRB1_0701  341  LTVVVTIAINTFGGI  VVTIAINTF        0.5379         148.4          WB    32.00      Sequence
DRB1_0701  108  PMTPKRAIEVIADAC  MTPKRAIEV        0.5376         148.9          WB    32.00      Sequence
DRB1_0701  164  DSGNSVTQTAAVIGT  VTQTAAVIG        0.5306         160.6          WB    32.00      Sequence
DRB1_0701  540  AGTTVPVDSVIELQV  VDSVIELQV        0.5306         160.7          WB    32.00      Sequence
DRB1_0701  336  AVLAVLTVVVTIAIN  LTVVVTIAI        0.5297         162.1          WB    32.00      Sequence
DRB1_0701  130  QNGIIHRDVKPANIM  RDVKPANIM        0.5292         163.0          WB    32.00      Sequence
DRB1_0701   12  LGEILGFGGMSEVHL  FGGMSEVHL        0.5272         166.5          WB    32.00      Sequence
DRB1_0701  569  FWVDAEPRLRALGWT  WVDAEPRLR        0.5238         172.8          WB    32.00      Sequence
DRB1_0701  111  PKRAIEVIADACQAL  VIADACQAL        0.5231         174.2          WB    32.00      Sequence
DRB1_0701  150  AVKVMDFGIARAIAD  MDFGIARAI        0.5222         175.8          WB    32.00      Sequence
DRB1_0701   85  PLPYIVMEYVDGVTL  MEYVDGVTL        0.5211         177.9          WB    32.00      Sequence
DRB1_0701  334  VVAVLAVLTVVVTIA  VVAVLAVLT        0.5209         178.4          WB    32.00      Sequence
DRB1_0701  428  IPDVSTLTYAEAVKK  LTYAEAVKK        0.5175         185.0          WB    32.00      Sequence
DRB1_0701  429  PDVSTLTYAEAVKKL  LTYAEAVKK        0.5171         185.9          WB    32.00      Sequence
```

```
DRB1_0701  510  NLNVYGFTKFSQASV  FTKFSQASV         0.5102         200.2          WB    32.00       Sequence
DRB1_0701  475  QTSAITNVVIIIVGS  QTSAITNVV         0.5100         200.7          WB    32.00       Sequence
DRB1_0701  109  MTPKRAIEVIADACQ  MTPKRAIEV         0.5075         206.2          WB    32.00       Sequence
DRB1_0701  570  WVDAEPRLRALGWTG  WVDAEPRLR         0.5072         206.9          WB    32.00       Sequence
DRB1_0701  511  LNVYGFTKFSQASVD  FTKFSQASV         0.5067         207.9          WB    32.00       Sequence
DRB1_0701  342  TVVVTIAINTFGGIT  VVTIAINTF         0.5064         208.5          WB    32.00       Sequence
DRB1_0701   60  QNAAALNHPAIVAVY  LNHPAIVAV         0.5063         208.8          WB    32.00       Sequence
DRB1_0701  169  VTQTAAVIGTAQYLS  AVIGTAQYL         0.5030         216.5          WB    32.00       Sequence
DRB1_0701  430  DVSTLTYAEAVKKLT  LTYAEAVKK         0.5020         218.8          WB    32.00       Sequence
DRB1_0701  216  TGDSPVSVAYQHVRE  PVSVAYQHV         0.5003         222.8          WB    32.00       Sequence
DRB1_0701  447  GFGRFKQANSPSTPE  FKQANSPST         0.4982         227.9          WB    32.00       Sequence
DRB1_0701  448  FGRFKQANSPSTPEL  FKQANSPST         0.4976         229.4          WB    32.00       Sequence
DRB1_0701  132  GIIHRDVKPANIMIS  RDVKPANIM         0.4920         243.7          WB    32.00       Sequence
DRB1_0701  481  NVVIIIVGSGPATKD  IIIVGSGPA         0.4912         245.9          WB    32.00       Sequence
DRB1_0701  112  KRAIEVIADACQALN  VIADACQAL         0.4905         247.7          WB    32.00       Sequence
DRB1_0701  222  SVAYQHVREDPIPPS  YQHVREDPI         0.4890         251.8          WB    32.00       Sequence
DRB1_0701  168  SVTQTAAVIGTAQYL  AVIGTAQYL         0.4871         257.0          WB    32.00       Sequence
DRB1_0701  343  VVVTIAINTFGGITR  VVTIAINTF         0.4853         262.1          WB    32.00       Sequence
DRB1_0701  541  GTTVPVDSVIELQVS  VDSVIELQV         0.4852         262.4          WB    32.00       Sequence
DRB1_0701  165  SGNSVTQTAAVIGTA  VTQTAAVIG         0.4841         265.5          WB    32.00       Sequence
DRB1_0701  212  EPPFTGDSPVSVAYQ  FTGDSPVSV         0.4836         267.1          WB    32.00       Sequence
DRB1_0701  437  AEAVKKLTAAGFGRF  LTAAGFGRF         0.4834         267.7          WB    32.00       Sequence
DRB1_0701   13  GEILGFGGMSEVHLA  FGGMSEVHL         0.4829         269.0          WB    32.00       Sequence
DRB1_0701  256  KNPENRYQTAAEMRA  YQTAAEMRA         0.4787         281.7          WB    32.00       Sequence
DRB1_0701  482  VVIIIVGSGPATKDI  IIIVGSGPA         0.4755         291.6          WB    32.00       Sequence
DRB1_0701   33  HRDVAVKVLRADLAR  VKVLRADLA         0.4748         293.7          WB    32.00       Sequence
DRB1_0701   96  GVTLRDIVHTEGPMT  IVHTEGPMT         0.4746         294.2          WB    32.00       Sequence
DRB1_0701  324  SIGSVGRWVAVVAVL  GRWVAVVAV         0.4743         295.3          WB    32.00       Sequence
DRB1_0701  449  GRFKQANSPSTPELV  FKQANSPST         0.4735         297.7          WB    32.00       Sequence
DRB1_0701  434  LTYAEAVKKLTAAGF  VKKLTAAGF         0.4721         302.5          WB    32.00       Sequence
DRB1_0701  555  SKGNQFVMPDLSGMF  FVMPDLSGM         0.4709         306.2          WB    32.00       Sequence
DRB1_0701   86  LPYIVMEYVDGVTLR  MEYVDGVTL         0.4645         328.2          WB    32.00       Sequence
DRB1_0701  113  RAIEVIADACQALNF  VIADACQAL         0.4591         347.9          WB    32.00       Sequence
DRB1_0701  213  PPFTGDSPVSVAYQH  FTGDSPVSV         0.4580         352.3          WB    32.00       Sequence
DRB1_0701  323  RSIGSVGRWVAVVAV  GRWVAVVAV         0.4579         352.8          WB    32.00       Sequence
DRB1_0701  438  EAVKKLTAAGFGRFK  LTAAGFGRF         0.4575         354.0          WB    32.00       Sequence
DRB1_0701  223  VAYQHVREDPIPPSA  YQHVREDPI         0.4566         357.5          WB    32.00       Sequence
DRB1_0701  151  VKVMDFGIARAIADS  MDFGIARAI         0.4534         370.1          WB    50.00       Sequence
DRB1_0701  149  NAVKVMDFGIARAIA  MDFGIARAI         0.4527         373.1          WB    50.00       Sequence
DRB1_0701  512  NVYGFTKFSQASVDS  FTKFSQASV         0.4517         377.3          WB    50.00       Sequence
DRB1_0701  133  IIHRDVKPANIMISA  RDVKPANIM         0.4503         382.9          WB    50.00       Sequence
DRB1_0701   61  NAAALNHPAIVAVYD  LNHPAIVAV         0.4496         385.7          WB    50.00       Sequence
DRB1_0701  369  SADAIATLQNRGFKI  TLQNRGFKI         0.4479         392.8          WB    50.00       Sequence
DRB1_0701  450  RFKQANSPSTPELVG  FKQANSPST         0.4460         400.9          WB    50.00       Sequence
DRB1_0701   97  VTLRDIVHTEGPMTP  IVHTEGPMT         0.4439         410.4          WB    50.00       Sequence
DRB1_0701   88  YIVMEYVDGVTLRDI  MEYVDGVTL         0.4430         414.4          WB    50.00       Sequence
DRB1_0701  431  VSTLTYAEAVKKLTA  LTYAEAVKK         0.4418         419.7          WB    50.00       Sequence
DRB1_0701  435  TYAEAVKKLTAAGFG  VKKLTAAGF         0.4414         421.6          WB    50.00       Sequence
DRB1_0701  483  VIIIVGSGPATKDIP  IIIVGSGPA         0.4362         446.1          WB    50.00       Sequence
DRB1_0701  217  GDSPVSVAYQHVRED  VSVAYQHVR         0.4340         456.9          WB    50.00       Sequence
DRB1_0701   14  EILGFGGMSEVHLAR  FGGMSEVHL         0.4338         457.6          WB    50.00       Sequence
DRB1_0701  379  RGFKIRTLQKPDSTI  TLQKPDSTI         0.4337         458.0          WB    50.00       Sequence
DRB1_0701  556  KGNQFVMPDLSGMFW  FVMPDLSGM         0.4296         478.8          WB    50.00       Sequence
DRB1_0701  224  AYQHVREDPIPPSAR  YQHVREDPI         0.4280         487.5          WB    50.00       Sequence
DRB1_0701  257  NPENRYQTAAEMRAD  YQTAAEMRA         0.4278         488.5          WB    50.00       Sequence
DRB1_0701  166  GNSVTQTAAVIGTAQ  VTQTAAVIG         0.4256         500.2                50.00       Sequence
DRB1_0701   62  AAALNHPAIVAVYDT  LNHPAIVAV         0.4235         511.4                50.00       Sequence
DRB1_0701  266  AEMRADLVRVHNGEP  LVRVHNGEP         0.4219         520.4                50.00       Sequence
DRB1_0701  439  AVKKLTAAGFGRFKQ  LTAAGFGRF         0.4217         521.9                50.00       Sequence
DRB1_0701   87  PYIVMEYVDGVTLRD  MEYVDGVTL         0.4185         540.2                50.00       Sequence
DRB1_0701  170  TQTAAVIGTAQYLSP  AVIGTAQYL         0.4184         540.6                50.00       Sequence
DRB1_0701  152  KVMDFGIARAIADSG  MDFGIARAI         0.4166         551.6                50.00       Sequence
DRB1_0701  380  GFKIRTLQKPDSTIP  TLQKPDSTI         0.4128         574.3                50.00       Sequence
DRB1_0701  114  AIEVIADACQALNFS  VIADACQAL         0.4124         576.7                50.00       Sequence
DRB1_0701  542  TTVPVDSVIELQVSK  VDSVIELQV         0.4124         577.1                50.00       Sequence
DRB1_0701  370  ADAIATLQNRGFKIR  TLQNRGFKI         0.4119         580.3                50.00       Sequence
```

```
DRB1_0701  134  IHRDVKPANIMISAT  RDVKPANIM        0.4097        593.8            50.00     Sequence
DRB1_0701  451  FKQANSPSTPELVGK  FKQANSPST        0.4080        605.0            50.00     Sequence
DRB1_0701  297  SSAAGNLSGPRTDPL  LSGPRTDPL        0.4067        613.7            50.00     Sequence
DRB1_0701  282  EAPKVLTDAERTSLL  TDAERTSLL        0.4067        613.8            50.00     Sequence
DRB1_0701  607  PPAGTGVNRDGIITL  VNRDGIITL        0.4056        621.2            50.00     Sequence
DRB1_0701  484  IIIVGSGPATKDIPD  IIIVGSGPA        0.4053        623.2            50.00     Sequence
DRB1_0701  167  NSVTQTAAVIGTAQY  VTQTAAVIG        0.4041        631.2            50.00     Sequence
DRB1_0701   89  IVMEYVDGVTLRDIV  MEYVDGVTL        0.4025        642.1            50.00     Sequence
DRB1_0701  432  STLTYAEAVKKLTAA  LTYAEAVKK        0.4013        650.5            50.00     Sequence
DRB1_0701   90  VMEYVDGVTLRDIVH  MEYVDGVTL        0.3984        671.2            50.00     Sequence
DRB1_0701  225  YQHVREDPIPPSARH  YQHVREDPI        0.3983        672.0            50.00     Sequence
DRB1_0701  554  VSKGNQFVMPDLSGM  FVMPDLSGM        0.3951        695.3            50.00     Sequence
DRB1_0701  513  VYGFTKFSQASVDSP  FTKFSQASV        0.3942        702.1            50.00     Sequence
DRB1_0701  258  PENRYQTAAEMRADL  YQTAAEMRA        0.3936        707.1            50.00     Sequence
DRB1_0701  436  YAEAVKKLTAAGFGR  VKKLTAAGF        0.3914        724.5            50.00     Sequence
DRB1_0701   63  AALNHPAIVAVYDTG  LNHPAIVAV        0.3899        736.0            50.00     Sequence
DRB1_0701  344  VVTIAINTFGGITRD  VVTIAINTF        0.3899        736.3            50.00     Sequence
DRB1_0701  319  TDRDRSIGSVGRWVA  IGSVGRWVA        0.3891        742.0            50.00     Sequence
DRB1_0701   64  ALNHPAIVAVYDTGE  LNHPAIVAV        0.3870        759.2            50.00     Sequence
DRB1_0701   98  TLRDIVHTEGPMTPK  IVHTEGPMT        0.3868        761.1            50.00     Sequence
DRB1_0701  553  QVSKGNQFVMPDLSG  QVSKGNQFV        0.3864        764.7            50.00     Sequence
DRB1_0701  440  VKKLTAAGFGRFKQA  LTAAGFGRF        0.3853        773.2            50.00     Sequence
DRB1_0701  557  GNQFVMPDLSGMFWV  FVMPDLSGM        0.3853        773.8            50.00     Sequence
DRB1_0701  115  IEVIADACQALNFSH  VIADACQAL        0.3845        780.2            50.00     Sequence
DRB1_0701  135  HRDVKPANIMISATN  RDVKPANIM        0.3836        788.2            50.00     Sequence
DRB1_0701  129  HQNGIIHRDVKPANI  HRDVKPANI        0.3818        802.9            50.00     Sequence
DRB1_0701  218  DSPVSVAYQHVREDP  PVSVAYQHV        0.3811        809.9            50.00     Sequence
DRB1_0701  146  SATNAVKVMDFGIAR  TNAVKVMDF        0.3808        812.1            50.00     Sequence
DRB1_0701  259  ENRYQTAAEMRADLV  YQTAAEMRA        0.3803        816.3            50.00     Sequence
DRB1_0701  563  PDLSGMFWVDAEPRL  FWVDAEPRL        0.3784        833.1            50.00     Sequence
DRB1_0701  240  EGLSADLDAVVLKAL  LDAVVLKAL        0.3723        890.8            50.00     Sequence
DRB1_0701   91  MEYVDGVTLRDIVHT  MEYVDGVTL        0.3705        907.4            50.00     Sequence
DRB1_0701  171  QTAAVIGTAQYLSPE  VIGTAQYLS        0.3700        913.2            50.00     Sequence
DRB1_0701  371  DAIATLQNRGFKIRT  TLQNRGFKI        0.3697        915.9            50.00     Sequence
DRB1_0701   15  ILGFGGMSEVHLARD  FGGMSEVHL        0.3686        926.8            50.00     Sequence
DRB1_0701  153  VMDFGIARAIADSGN  MDFGIARAI        0.3659        954.5            50.00     Sequence
DRB1_0701   34  RDVAVKVLRADLARD  VKVLRADLA        0.3657        956.2            50.00     Sequence
DRB1_0701  298  SAAGNLSGPRTDPLP  LSGPRTDPL        0.3634        980.8            50.00     Sequence
DRB1_0701  267  EMRADLVRVHNGEPP  LVRVHNGEP        0.3629        985.2            50.00     Sequence
DRB1_0701  283  APKVLTDAERTSLLS  LTDAERTSL        0.3620        995.0            50.00     Sequence
DRB1_0701  320  DRDRSIGSVGRWVAV  IGSVGRWVA        0.3596       1021.4            50.00     Sequence
DRB1_0701  116  EVIADACQALNFSHQ  VIADACQAL        0.3582       1037.1            50.00     Sequence
DRB1_0701  514  YGFTKFSQASVDSPR  FTKFSQASV        0.3571       1049.3            50.00     Sequence
DRB1_0701  608  PAGTGVNRDGIITLR  VNRDGIITL        0.3515       1114.9            50.00     Sequence
DRB1_0701  433  TLTYAEAVKKLTAAG  LTYAEAVKK        0.3514       1115.7            50.00     Sequence
DRB1_0701  609  AGTGVNRDGIITLRF  VNRDGIITL        0.3498       1135.8            50.00     Sequence
DRB1_0701  536  TNPPAGTTVPVDSVI  GTTVPVDSV        0.3490       1145.8            50.00     Sequence
DRB1_0701  476  TSAITNVVIIIVGSG  TSAITNVVI        0.3489       1147.2            50.00     Sequence
DRB1_0701  260  NRYQTAAEMRADLVR  YQTAAEMRA        0.3481       1156.7            50.00     Sequence
DRB1_0701  261  RYQTAAEMRADLVRV  YQTAAEMRA        0.3475       1163.9            50.00     Sequence
DRB1_0701  381  FKIRTLQKPDSTIPP  TLQKPDSTI        0.3459       1184.4            50.00     Sequence
DRB1_0701  403  PAANTSVSAGDEITV  TSVSAGDEI        0.3457       1186.9            50.00     Sequence
DRB1_0701  156  FGIARAIADSGNSVT  IADSGNSVT        0.3455       1189.8            50.00     Sequence
DRB1_0701  497  PDVAGQTVDVAQKNL  TVDVAQKNL        0.3451       1194.7            50.00     Sequence
DRB1_0701  571  VDAEPRLRALGWTGM  RLRALGWTG        0.3445       1202.5            50.00     Sequence
DRB1_0701  162  IADSGNSVTQTAAVI  SVTQTAAVI        0.3441       1208.2            50.00     Sequence
DRB1_0701  154  MDFGIARAIADSGNS  MDFGIARAI        0.3425       1229.0            50.00     Sequence
DRB1_0701   16  LGFGGMSEVHLARDL  FGGMSEVHL        0.3404       1257.4            50.00     Sequence
DRB1_0701   65  LNHPAIVAVYDTGEA  LNHPAIVAV        0.3401       1261.3            50.00     Sequence
DRB1_0701  147  ATNAVKVMDFGIARA  TNAVKVMDF        0.3400       1262.1            50.00     Sequence
DRB1_0701  572  DAEPRLRALGWTGML  RLRALGWTG        0.3393       1272.9            50.00     Sequence
DRB1_0701  558  NQFVMPDLSGMFWVD  FVMPDLSGM        0.3390       1276.3            50.00     Sequence
DRB1_0701  281  PEAPKVLTDAERTSL  LTDAERTSL        0.3380       1290.6            50.00     Sequence
DRB1_0701  372  AIATLQNRGFKIRTL  TLQNRGFKI        0.3379       1291.3            50.00     Sequence
DRB1_0701  136  RDVKPANIMISATNA  RDVKPANIM        0.3374       1298.3            50.00     Sequence
DRB1_0701  241  GLSADLDAVVLKALA  LDAVVLKAL        0.3369       1305.8            50.00     Sequence
```

```
DRB1_0701  321  RDRSIGSVGRWVAVV  IGSVGRWVA         0.3365        1311.9                  50.00      Sequence
DRB1_0701  543  TVPVDSVIELQVSKG  VDSVIELQV         0.3332        1358.9                  50.00      Sequence
DRB1_0701  127  FSHQNGIIHRDVKPA  IIHRDVKPA         0.3316        1382.4                  50.00      Sequence
DRB1_0701  385  TLQKPDSTIPPDHVI  STIPPDHVI         0.3308        1394.3                  50.00      Sequence
DRB1_0701   83  AGPLPYIVMEYVDGV  IVMEYVDGV         0.3298        1409.7                  50.00      Sequence
DRB1_0701   99  LRDIVHTEGPMTPKR  IVHTEGPMT         0.3297        1412.1                  50.00      Sequence
DRB1_0701  101  DIVHTEGPMTPKRAI  IVHTEGPMT         0.3285        1429.3                  50.00      Sequence
DRB1_0701  172  TAAVIGTAQYLSPEQ  VIGTAQYLS         0.3281        1435.5                  50.00      Sequence
DRB1_0701  299  AAGNLSGPRTDPLPR  LSGPRTDPL         0.3243        1496.3                  50.00      Sequence
DRB1_0701  117  VIADACQALNFSHQN  VIADACQAL         0.3242        1498.6                  50.00      Sequence
DRB1_0701  498  DVAGQTVDVAQKNLN  TVDVAQKNL         0.3201        1566.7                  50.00      Sequence
DRB1_0701   72  AVYDTGEAETPAGPL  EAETPAGPL         0.3168        1623.3                  50.00      Sequence
DRB1_0701  537  NPPAGTTVPVDSVIE  GTTVPVDSV         0.3147        1660.3                  50.00      Sequence
DRB1_0701  242  LSADLDAVVLKALAK  LDAVVLKAL         0.3140        1673.1                  50.00      Sequence
DRB1_0701  559  QFVMPDLSGMFWVDA  VMPDLSGMF         0.3131        1688.5                  50.00      Sequence
DRB1_0701  284  PKVLTDAERTSLLSS  LTDAERTSL         0.3130        1691.6                  50.00      Sequence
DRB1_0701  515  GFTKFSQASVDSPRP  FTKFSQASV         0.3111        1725.7                  50.00      Sequence
DRB1_0701  262  YQTAAEMRADLVRVH  YQTAAEMRA         0.3106        1735.3                  50.00      Sequence
DRB1_0701  173  AAVIGTAQYLSPEQA  VIGTAQYLS         0.3104        1738.7                  50.00      Sequence
DRB1_0701  441  KKLTAAGFGRFKQAN  LTAAGFGRF         0.3103        1740.9                  50.00      Sequence
DRB1_0701  268  MRADLVRVHNGEPPE  LVRVHNGEP         0.3080        1784.6                  50.00      Sequence
DRB1_0701  544  VPVDSVIELQVSKGN  VDSVIELQV         0.3074        1795.9                  50.00      Sequence
DRB1_0701  244  ADLDAVVLKALAKNP  VLKALAKNP         0.3073        1798.1                  50.00      Sequence
DRB1_0701  538  PPAGTTVPVDSVIEL  TTVPVDSVI         0.3068        1808.7                  50.00      Sequence
DRB1_0701  401  TDPAANTSVSAGDEI  TSVSAGDEI         0.3042        1859.7                  50.00      Sequence
DRB1_0701  322  DRSIGSVGRWVAVVA  IGSVGRWVA         0.3042        1860.7                  50.00      Sequence
DRB1_0701   17  GFGGMSEVHLARDLR  FGGMSEVHL         0.3026        1891.6                  50.00      Sequence
DRB1_0701  102  IVHTEGPMTPKRAIE  IVHTEGPMT         0.3020        1905.8                  50.00      Sequence
DRB1_0701  404  AANTSVSAGDEITVN  TSVSAGDEI         0.3007        1931.4                  50.00      Sequence
DRB1_0701   35  DVAVKVLRADLARDP  VKVLRADLA         0.3006        1933.3                  50.00      Sequence
DRB1_0701   84  GPLPYIVMEYVDGVT  IVMEYVDGV         0.3002        1941.7                  50.00      Sequence
DRB1_0701  373  IATLQNRGFKIRTLQ  TLQNRGFKI         0.2994        1958.4                  50.00      Sequence
DRB1_0701  384  RTLQKPDSTIPPDHV  TLQKPDSTI         0.2972        2006.7                  50.00      Sequence
DRB1_0701  573  AEPRLRALGWTGMLD  RLRALGWTG         0.2961        2030.2                  50.00      Sequence
DRB1_0701  499  VAGQTVDVAQKNLNV  TVDVAQKNL         0.2955        2044.7                  50.00      Sequence
DRB1_0701  100  RDIVHTEGPMTPKRA  IVHTEGPMT         0.2948        2058.6                  50.00      Sequence
DRB1_0701  560  FVMPDLSGMFWVDAE  VMPDLSGMF         0.2935        2087.9                  50.00      Sequence
DRB1_0701  174  AVIGTAQYLSPEQAR  VIGTAQYLS         0.2926        2108.4                  50.00      Sequence
DRB1_0701  236  SARHEGLSADLDAVV  LSADLDAVV         0.2903        2161.9                  50.00      Sequence
DRB1_0701  245  DLDAVVLKALAKNPE  VLKALAKNP         0.2901        2166.5                  50.00      Sequence
DRB1_0701  402  DPAANTSVSAGDEIT  TSVSAGDEI         0.2886        2203.1                  50.00      Sequence
DRB1_0701  155  DFGIARAIADSGNSV  FGIARAIAD         0.2872        2236.1                  50.00      Sequence
DRB1_0701  426  REIPDVSTLTYAEAV  STLTYAEAV         0.2872        2236.5                  50.00      Sequence
DRB1_0701   49  PSFYLRFRREAQNAA  FRREAQNAA         0.2857        2272.0                  50.00      Sequence
DRB1_0701  610  GTGVNRDGIITLRFG  VNRDGIITL         0.2854        2279.7                  50.00      Sequence
DRB1_0701  382  KIRTLQKPDSTIPPD  TLQKPDSTI         0.2846        2298.3                  50.00      Sequence
DRB1_0701  367  QSSADAIATLQNRGF  IATLQNRGF         0.2846        2300.3                  50.00      Sequence
DRB1_0701  300  AGNLSGPRTDPLPRQ  LSGPRTDPL         0.2841        2311.1                  50.00      Sequence
DRB1_0701  203  CVLYEVLTGEPPFTG  LTGEPPFTG         0.2836        2324.9                  50.00      Sequence
DRB1_0701  285  KVLTDAERTSLLSSA  LTDAERTSL         0.2831        2336.3                  50.00      Sequence
DRB1_0701  535  GTNPPAGTTVPVDSV  GTTVPVDSV         0.2826        2349.2                  50.00      Sequence
DRB1_0701  545  PVDSVIELQVSKGNQ  VDSVIELQV         0.2820        2366.0                  50.00      Sequence
DRB1_0701  516  FTKFSQASVDSPRPA  FTKFSQASV         0.2791        2441.4                  50.00      Sequence
DRB1_0701   92  EYVDGVTLRDIVHTE  VDGVTLRDI         0.2767        2504.1                  50.00      Sequence
DRB1_0701  237  ARHEGLSADLDAVVL  LSADLDAVV         0.2749        2553.1                  50.00      Sequence
DRB1_0701  128  SHQNGIIHRDVKPAN  IIHRDVKPA         0.2696        2706.1                  50.00      Sequence
DRB1_0701  405  ANTSVSAGDEITVNV  TSVSAGDEI         0.2690        2721.7                  50.00      Sequence
DRB1_0701  442  KLTAAGFGRFKQANS  LTAAGFGRF         0.2690        2721.8                  50.00      Sequence
DRB1_0701   37  AVKVLRADLARDPSF  VKVLRADLA         0.2687        2732.5                  50.00      Sequence
DRB1_0701   73  VYDTGEAETPAGPLP  EAETPAGPL         0.2684        2739.9                  50.00      Sequence
DRB1_0701  347  IAINTFGGITRDVQV  GGITRDVQV         0.2680        2753.2                  50.00      Sequence
DRB1_0701   36  VAVKVLRADLARDPS  VKVLRADLA         0.2674        2768.8                  50.00      Sequence
DRB1_0701  318  DTDRDRSIGSVGRWV  SIGSVGRWV         0.2669        2784.5                  50.00      Sequence
DRB1_0701  574  EPRLRALGWTGMLDK  RLRALGWTG         0.2669        2785.1                  50.00      Sequence
DRB1_0701  301  GNLSGPRTDPLPRQD  LSGPRTDPL         0.2663        2803.5                  50.00      Sequence
DRB1_0701  192  VDARSDVYSLGCVLY  VYSLGCVLY         0.2635        2890.6                  50.00      Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0701 | 500 | AGQTVDVAQKNLNVY | TVDVAQKNL | 0.2629 | 2907.4 | 50.00 | Sequence |
| DRB1_0701 | 157 | GIARAIADSGNSVTQ | IADSGNSVT | 0.2629 | 2909.4 | 50.00 | Sequence |
| DRB1_0701 | 58 | EAQNAAALNHPAIVA | ALNHPAIVA | 0.2623 | 2927.7 | 50.00 | Sequence |
| DRB1_0701 | 185 | EQARGDSVDARSDVY | SVDARSDVY | 0.2619 | 2938.3 | 50.00 | Sequence |
| DRB1_0701 | 246 | LDAVVLKALAKNPEN | VLKALAKNP | 0.2606 | 2982.9 | 50.00 | Sequence |
| DRB1_0701 | 539 | PAGTTVPVDSVIELQ | TTVPVDSVI | 0.2590 | 3033.7 | 50.00 | Sequence |
| DRB1_0701 | 269 | RADLVRVHNGEPPEA | LVRVHNGEP | 0.2585 | 3051.3 | 50.00 | Sequence |
| DRB1_0701 | 611 | TGVNRDGIITLRFGQ | VNRDGIITL | 0.2581 | 3064.6 | 50.00 | Sequence |
| DRB1_0701 | 93 | YVDGVTLRDIVHTEG | VDGVTLRDI | 0.2557 | 3142.7 | 50.00 | Sequence |
| DRB1_0701 | 296 | LSSAAGNLSGPRTDP | LSSAAGNLS | 0.2532 | 3228.2 | 50.00 | Sequence |
| DRB1_0701 | 186 | QARGDSVDARSDVYS | SVDARSDVY | 0.2528 | 3242.8 | 50.00 | Sequence |
| DRB1_0701 | 193 | DARSDVYSLGCVLYE | VYSLGCVLY | 0.2523 | 3260.5 | 50.00 | Sequence |
| DRB1_0701 | 286 | VLTDAERTSLLSSAA | LTDAERTSL | 0.2520 | 3273.5 | 50.00 | Sequence |
| DRB1_0701 | 248 | AVVLKALAKNPENRY | LAKNPENRY | 0.2496 | 3358.9 | 50.00 | Sequence |
| DRB1_0701 | 74 | YDTGEAETPAGPLPY | EAETPAGPL | 0.2493 | 3369.1 | 50.00 | Sequence |
| DRB1_0701 | 383 | IRTLQKPDSTIPPDH | TLQKPDSTI | 0.2485 | 3397.2 | 50.00 | Sequence |
| DRB1_0701 | 50 | SFYLRFRREAQNAAA | FRREAQNAA | 0.2482 | 3409.1 | 50.00 | Sequence |
| DRB1_0701 | 368 | SSADAIATLQNRGFK | IATLQNRGF | 0.2476 | 3431.8 | 50.00 | Sequence |
| DRB1_0701 | 345 | VTIAINTFGGITRDV | VTIAINTFG | 0.2463 | 3478.7 | 50.00 | Sequence |
| DRB1_0701 | 191 | SVDARSDVYSLGCVL | DVYSLGCVL | 0.2452 | 3522.4 | 50.00 | Sequence |
| DRB1_0701 | 204 | VLYEVLTGEPPFTGD | LTGEPPFTG | 0.2450 | 3530.5 | 50.00 | Sequence |
| DRB1_0701 | 302 | NLSGPRTDPLPRQDL | LSGPRTDPL | 0.2439 | 3570.8 | 50.00 | Sequence |
| DRB1_0701 | 194 | ARSDVYSLGCVLYEV | VYSLGCVLY | 0.2439 | 3572.3 | 50.00 | Sequence |
| DRB1_0701 | 386 | LQKPDSTIPPDHVIG | STIPPDHVI | 0.2438 | 3576.9 | 50.00 | Sequence |
| DRB1_0701 | 443 | LTAAGFGRFKQANSP | LTAAGFGRF | 0.2431 | 3602.3 | 50.00 | Sequence |
| DRB1_0701 | 175 | VIGTAQYLSPEQARG | VIGTAQYLS | 0.2416 | 3662.6 | 50.00 | Sequence |
| DRB1_0701 | 348 | AINTFGGITRDVQVP | GGITRDVQV | 0.2412 | 3679.1 | 50.00 | Sequence |
| DRB1_0701 | 427 | EIPDVSTLTYAEAVK | STLTYAEAV | 0.2408 | 3695.6 | 50.00 | Sequence |
| DRB1_0701 | 575 | PRLRALGWTGMLDKG | RLRALGWTG | 0.2391 | 3763.1 | 50.00 | Sequence |
| DRB1_0701 | 243 | SADLDAVVLKALAKN | LDAVVLKAL | 0.2388 | 3774.1 | 50.00 | Sequence |
| DRB1_0701 | 187 | ARGDSVDARSDVYSL | SVDARSDVY | 0.2373 | 3835.8 | 50.00 | Sequence |
| DRB1_0701 | 598 | QHNRVVYQNPPAGTG | YQNPPAGTG | 0.2367 | 3860.2 | 50.00 | Sequence |
| DRB1_0701 | 38 | VKVLRADLARDPSFY | VKVLRADLA | 0.2358 | 3897.6 | 50.00 | Sequence |
| DRB1_0701 | 202 | GCVLYEVLTGEPPFT | VLTGEPPFT | 0.2354 | 3916.9 | 50.00 | Sequence |
| DRB1_0701 | 590 | ADVDAGGSQHNRVVY | VDAGGSQHN | 0.2351 | 3928.0 | 50.00 | Sequence |
| DRB1_0701 | 238 | RHEGLSADLDAVVLK | LSADLDAVV | 0.2344 | 3959.3 | 50.00 | Sequence |
| DRB1_0701 | 375 | TLQNRGFKIRTLQKP | TLQNRGFKI | 0.2340 | 3973.7 | 50.00 | Sequence |
| DRB1_0701 | 406 | NTSVSAGDEITVNVS | TSVSAGDEI | 0.2340 | 3975.7 | 50.00 | Sequence |
| DRB1_0701 | 287 | LTDAERTSLLSSAAG | LTDAERTSL | 0.2337 | 3987.9 | 50.00 | Sequence |
| DRB1_0701 | 589 | GADVDAGGSQHNRVV | GGSQHNRVV | 0.2335 | 3997.3 | 50.00 | Sequence |
| DRB1_0701 | 158 | IARAIADSGNSVTQT | IADSGNSVT | 0.2329 | 4021.1 | 50.00 | Sequence |
| DRB1_0701 | 195 | RSDVYSLGCVLYEVL | VYSLGCVLY | 0.2321 | 4059.0 | 50.00 | Sequence |
| DRB1_0701 | 599 | HNRVVYQNPPAGTGV | YQNPPAGTG | 0.2318 | 4070.4 | 50.00 | Sequence |
| DRB1_0701 | 374 | ATLQNRGFKIRTLQK | TLQNRGFKI | 0.2312 | 4100.0 | 50.00 | Sequence |
| DRB1_0701 | 576 | RLRALGWTGMLDKGA | RLRALGWTG | 0.2293 | 4183.0 | 50.00 | Sequence |
| DRB1_0701 | 561 | VMPDLSGMFWVDAEP | VMPDLSGMF | 0.2277 | 4255.8 | 50.00 | Sequence |
| DRB1_0701 | 501 | GQTVDVAQKNLNVYG | TVDVAQKNL | 0.2266 | 4308.9 | 50.00 | Sequence |
| DRB1_0701 | 51 | FYLRFRREAQNAAAL | FRREAQNAA | 0.2257 | 4348.4 | 50.00 | Sequence |
| DRB1_0701 | 303 | LSGPRTDPLPRQDLD | LSGPRTDPL | 0.2243 | 4413.9 | 50.00 | Sequence |
| DRB1_0701 | 270 | ADLVRVHNGEPPEAP | LVRVHNGEP | 0.2243 | 4417.4 | 50.00 | Sequence |
| DRB1_0701 | 76 | TGEAETPAGPLPYIV | EAETPAGPL | 0.2240 | 4429.2 | 50.00 | Sequence |
| DRB1_0701 | 126 | NFSHQNGIIHRDVKP | FSHQNGIIH | 0.2239 | 4433.4 | 50.00 | Sequence |
| DRB1_0701 | 75 | DTGEAETPAGPLPYI | EAETPAGPL | 0.2210 | 4578.5 | 50.00 | Sequence |
| DRB1_0701 | 578 | RALGWTGMLDKGADV | GMLDKGADV | 0.2198 | 4637.2 | 50.00 | Sequence |
| DRB1_0701 | 196 | SDVYSLGCVLYEVLT | VYSLGCVLY | 0.2167 | 4793.5 | 50.00 | Sequence |
| DRB1_0701 | 407 | TSVSAGDEITVNVST | TSVSAGDEI | 0.2163 | 4816.0 | 50.00 | Sequence |
| DRB1_0701 | 477 | SAITNVVIIIVGSGP | ITNVVIIIV | 0.2155 | 4855.5 | 50.00 | Sequence |
| DRB1_0701 | 160 | RAIADSGNSVTQTAA | IADSGNSVT | 0.2147 | 4899.7 | 50.00 | Sequence |
| DRB1_0701 | 94 | VDGVTLRDIVHTEGP | VDGVTLRDI | 0.2135 | 4960.9 | 50.00 | Sequence |
| DRB1_0701 | 249 | VVLKALAKNPENRYQ | LAKNPENRY | 0.2133 | 4972.5 | 50.00 | Sequence |
| DRB1_0701 | 205 | LYEVLTGEPPFTGDS | LTGEPPFTG | 0.2129 | 4994.3 | 50.00 | Sequence |
| DRB1_0701 | 161 | AIADSGNSVTQTAAV | IADSGNSVT | 0.2092 | 5197.3 | 50.00 | Sequence |
| DRB1_0701 | 189 | GDSVDARSDVYSLGC | SVDARSDVY | 0.2080 | 5267.7 | 50.00 | Sequence |
| DRB1_0701 | 207 | EVLTGEPPFTGDSPV | PPFTGDSPV | 0.2079 | 5270.5 | 50.00 | Sequence |
| DRB1_0701 | 47 | RDPSFYLRFRREAQN | FYLRFRREA | 0.2078 | 5280.5 | 50.00 | Sequence |
| DRB1_0701 | 159 | ARAIADSGNSVTQTA | IADSGNSVT | 0.2062 | 5370.6 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0701 | 579 | ALGWTGMLDKGADVD | GMLDKGADV | 0.2056 | 5408.7 | 50.00 | Sequence |
| DRB1_0701 | 490 | GPATKDIPDVAGQTV | IPDVAGQTV | 0.2053 | 5423.6 | 50.00 | Sequence |
| DRB1_0701 | 502 | QTVDVAQKNLNVYGF | TVDVAQKNL | 0.2043 | 5479.8 | 50.00 | Sequence |
| DRB1_0701 | 606 | NPPAGTGVNRDGIIT | GTGVNRDGI | 0.2020 | 5620.8 | 50.00 | Sequence |
| DRB1_0701 | 591 | DVDAGGSQHNRVVYQ | VDAGGSQHN | 0.2017 | 5637.0 | 50.00 | Sequence |
| DRB1_0701 | 600 | NRVVYQNPPAGTGVN | YQNPPAGTG | 0.2016 | 5645.8 | 50.00 | Sequence |
| DRB1_0701 | 530 | AGEVTGTNPPAGTTV | TNPPAGTTV | 0.2015 | 5651.0 | 50.00 | Sequence |
| DRB1_0701 | 263 | QTAAEMRADLVRVHN | EMRADLVRV | 0.2007 | 5701.1 | 50.00 | Sequence |
| DRB1_0701 | 77 | GEAETPAGPLPYIVM | EAETPAGPL | 0.1993 | 5787.6 | 50.00 | Sequence |
| DRB1_0701 | 271 | DLVRVHNGEPPEAPK | LVRVHNGEP | 0.1978 | 5882.8 | 50.00 | Sequence |
| DRB1_0701 | 349 | INTFGGITRDVQVPD | GGITRDVQV | 0.1962 | 5982.7 | 50.00 | Sequence |
| DRB1_0701 | 46 | ARDPSFYLRFRREAQ | FYLRFRREA | 0.1960 | 5998.4 | 50.00 | Sequence |
| DRB1_0701 | 562 | MPDLSGMFWVDAEPR | MFWVDAEPR | 0.1951 | 6057.3 | 50.00 | Sequence |
| DRB1_0701 | 604 | YQNPPAGTGVNRDGI | GTGVNRDGI | 0.1950 | 6061.3 | 50.00 | Sequence |
| DRB1_0701 | 239 | HEGLSADLDAVVLKA | LSADLDAVV | 0.1949 | 6071.0 | 50.00 | Sequence |
| DRB1_0701 | 387 | QKPDSTIPPDHVIGT | STIPPDHVI | 0.1911 | 6323.8 | 50.00 | Sequence |
| DRB1_0701 | 188 | RGDSVDARSDVYSLG | SVDARSDVY | 0.1902 | 6385.6 | 50.00 | Sequence |
| DRB1_0701 | 197 | DVYSLGCVLYEVLTG | VYSLGCVLY | 0.1898 | 6412.4 | 50.00 | Sequence |
| DRB1_0701 | 588 | KGADVDAGGSQHNRV | VDAGGSQHN | 0.1887 | 6493.3 | 50.00 | Sequence |
| DRB1_0701 | 272 | LVRVHNGEPPEAPKV | LVRVHNGEP | 0.1886 | 6498.7 | 50.00 | Sequence |
| DRB1_0701 | 190 | DSVDARSDVYSLGCV | SVDARSDVY | 0.1884 | 6512.5 | 50.00 | Sequence |
| DRB1_0701 | 395 | PDHVIGTDPAANTSV | TDPAANTSV | 0.1875 | 6572.9 | 50.00 | Sequence |
| DRB1_0701 | 605 | QNPPAGTGVNRDGII | GTGVNRDGI | 0.1875 | 6576.8 | 50.00 | Sequence |
| DRB1_0701 | 10 | YELGEILGFGGMSEV | LGFGGMSEV | 0.1870 | 6608.2 | 50.00 | Sequence |
| DRB1_0701 | 485 | IIVGSGPATKDIPDV | IVGSGPATK | 0.1868 | 6622.6 | 50.00 | Sequence |
| DRB1_0701 | 247 | DAVVLKALAKNPENR | VLKALAKNP | 0.1856 | 6714.7 | 50.00 | Sequence |
| DRB1_0701 | 250 | VLKALAKNPENRYQT | LAKNPENRY | 0.1854 | 6725.4 | 50.00 | Sequence |
| DRB1_0701 | 350 | NTFGGITRDVQVPDV | GGITRDVQV | 0.1828 | 6917.7 | 50.00 | Sequence |
| DRB1_0701 | 206 | YEVLTGEPPFTGDSP | VLTGEPPFT | 0.1819 | 6982.4 | 50.00 | Sequence |
| DRB1_0701 | 346 | TIAINTFGGITRDVQ | AINTFGGIT | 0.1813 | 7032.7 | 50.00 | Sequence |
| DRB1_0701 | 361 | VPDVRGQSSADAIAT | RGQSSADAI | 0.1797 | 7153.0 | 50.00 | Sequence |
| DRB1_0701 | 592 | VDAGGSQHNRVVYQN | VDAGGSQHN | 0.1795 | 7172.0 | 50.00 | Sequence |
| DRB1_0701 | 503 | TVDVAQKNLNVYGFT | TVDVAQKNL | 0.1784 | 7254.4 | 50.00 | Sequence |
| DRB1_0701 | 601 | RVVYQNPPAGTGVNR | YQNPPAGTG | 0.1759 | 7458.1 | 50.00 | Sequence |
| DRB1_0701 | 52 | YLRFRREAQNAAALN | FRREAQNAA | 0.1757 | 7473.4 | 50.00 | Sequence |
| DRB1_0701 | 201 | LGCVLYEVLTGEPPF | EVLTGEPPF | 0.1739 | 7615.5 | 50.00 | Sequence |
| DRB1_0701 | 78 | EAETPAGPLPYIVME | EAETPAGPL | 0.1738 | 7622.9 | 50.00 | Sequence |
| DRB1_0701 | 580 | LGWTGMLDKGADVDA | GMLDKGADV | 0.1737 | 7634.4 | 50.00 | Sequence |
| DRB1_0701 | 53 | LRFRREAQNAAALNH | FRREAQNAA | 0.1725 | 7732.5 | 50.00 | Sequence |
| DRB1_0701 | 491 | PATKDIPDVAGQTVD | IPDVAGQTV | 0.1725 | 7735.6 | 50.00 | Sequence |
| DRB1_0701 | 359 | VQVPDVRGQSSADAI | RGQSSADAI | 0.1719 | 7781.3 | 50.00 | Sequence |
| DRB1_0701 | 95 | DGVTLRDIVHTEGPM | DIVHTEGPM | 0.1719 | 7783.8 | 50.00 | Sequence |
| DRB1_0701 | 48 | DPSFYLRFRREAQNA | FYLRFRREA | 0.1718 | 7789.1 | 50.00 | Sequence |
| DRB1_0701 | 531 | GEVTGTNPPAGTTVP | TNPPAGTTV | 0.1715 | 7816.4 | 50.00 | Sequence |
| DRB1_0701 | 208 | VLTGEPPFTGDSPVS | VLTGEPPFT | 0.1713 | 7838.1 | 50.00 | Sequence |
| DRB1_0701 | 57 | REAQNAAALNHPAIV | AALNHPAIV | 0.1713 | 7838.4 | 50.00 | Sequence |
| DRB1_0701 | 422 | GPEQREIPDVSTLTY | IPDVSTLTY | 0.1710 | 7858.3 | 50.00 | Sequence |
| DRB1_0701 | 235 | PSARHEGLSADLDAV | GLSADLDAV | 0.1708 | 7879.2 | 50.00 | Sequence |
| DRB1_0701 | 232 | PIPPSARHEGLSADL | RHEGLSADL | 0.1707 | 7888.8 | 50.00 | Sequence |
| DRB1_0701 | 67 | HPAIVAVYDTGEAET | VYDTGEAET | 0.1705 | 7900.8 | 50.00 | Sequence |
| DRB1_0701 | 360 | QVPDVRGQSSADAIA | RGQSSADAI | 0.1691 | 8027.8 | 50.00 | Sequence |
| DRB1_0701 | 264 | TAAEMRADLVRVHNG | EMRADLVRV | 0.1681 | 8108.8 | 50.00 | Sequence |
| DRB1_0701 | 362 | PDVRGQSSADAIATL | RGQSSADAI | 0.1664 | 8259.0 | 50.00 | Sequence |
| DRB1_0701 | 396 | DHVIGTDPAANTSVS | TDPAANTSV | 0.1652 | 8373.2 | 50.00 | Sequence |
| DRB1_0701 | 486 | IVGSGPATKDIPDVA | IVGSGPATK | 0.1627 | 8600.2 | 50.00 | Sequence |
| DRB1_0701 | 452 | KQANSPSTPELVGKV | ANSPSTPEL | 0.1626 | 8608.7 | 50.00 | Sequence |
| DRB1_0701 | 351 | TFGGITRDVQVPDVR | GGITRDVQV | 0.1618 | 8681.4 | 50.00 | Sequence |
| DRB1_0701 | 519 | FSQASVDSPRPAGEV | DSPRPAGEV | 0.1618 | 8683.5 | 50.00 | Sequence |
| DRB1_0701 | 279 | EPPEAPKVLTDAERT | KVLTDAERT | 0.1604 | 8812.1 | 50.00 | Sequence |
| DRB1_0701 | 66 | NHPAIVAVYDTGEAE | IVAVYDTGE | 0.1603 | 8826.9 | 50.00 | Sequence |
| DRB1_0701 | 586 | LDKGADVDAGGSQHN | VDAGGSQHN | 0.1599 | 8863.2 | 50.00 | Sequence |
| DRB1_0701 | 492 | ATKDIPDVAGQTVDV | IPDVAGQTV | 0.1599 | 8864.2 | 50.00 | Sequence |
| DRB1_0701 | 54 | RFRREAQNAAALNHP | FRREAQNAA | 0.1595 | 8901.5 | 50.00 | Sequence |
| DRB1_0701 | 288 | TDAERTSLLSSAAGN | TDAERTSLL | 0.1595 | 8903.3 | 50.00 | Sequence |
| DRB1_0701 | 462 | LVGKVIGTNPPANQT | GTNPPANQT | 0.1590 | 8954.1 | 50.00 | Sequence |
| DRB1_0701 | 280 | PPEAPKVLTDAERTS | KVLTDAERT | 0.1577 | 9073.3 | 50.00 | Sequence |

```
DRB1_0701  602  VVYQNPPAGTGVNRD  YQNPPAGTG        0.1562      9221.8             50.00     Sequence
DRB1_0701  532  EVTGTNPPAGTTVPV  TNPPAGTTV        0.1554      9307.5             50.00     Sequence
DRB1_0701   11  ELGEILGFGGMSEVH  LGFGGMSEV        0.1551      9337.0             50.00     Sequence
DRB1_0701  408  SVSAGDEITVNVSTG  VSAGDEITV        0.1548      9364.2             50.00     Sequence
DRB1_0701   68  PAIVAVYDTGEAETP  IVAVYDTGE        0.1532      9534.0             50.00     Sequence
DRB1_0701  460  PELVGKVIGTNPPAN  VIGTNPPAN        0.1529      9559.8             50.00     Sequence
DRB1_0701  265  AAEMRADLVRVHNGE  EMRADLVRV        0.1529      9565.1             50.00     Sequence
DRB1_0701  468  GTNPPANQTSAITNV  NQTSAITNV        0.1528      9572.5             50.00     Sequence
DRB1_0701  409  VSAGDEITVNVSTGP  VSAGDEITV        0.1527      9583.7             50.00     Sequence
DRB1_0701  411  AGDEITVNVSTGPEQ  VNVSTGPEQ        0.1522      9635.7             50.00     Sequence
DRB1_0701  388  KPDSTIPPDHVIGTD  DSTIPPDHV        0.1518      9671.3             50.00     Sequence
DRB1_0701   80  ETPAGPLPYIVMEYV  LPYIVMEYV        0.1516      9694.6             50.00     Sequence
DRB1_0701  454  ANSPSTPELVGKVIG  ANSPSTPEL        0.1491      9963.0             50.00     Sequence
DRB1_0701  233  IPPSARHEGLSADLD  RHEGLSADL        0.1489      9987.3             50.00     Sequence
DRB1_0701  453  QANSPSTPELVGKVI  ANSPSTPEL        0.1489      9989.0             50.00     Sequence
DRB1_0701  198  VYSLGCVLYEVLTGE  VYSLGCVLY        0.1487     10001.2             50.00     Sequence
DRB1_0701  410  SAGDEITVNVSTGPE  TVNVSTGPE        0.1482     10062.9             50.00     Sequence
DRB1_0701  363  DVRGQSSADAIATLQ  RGQSSADAI        0.1481     10071.8             50.00     Sequence
DRB1_0701  587  DKGADVDAGGSQHNR  VDAGGSQHN        0.1467     10223.5             50.00     Sequence
DRB1_0701  397  HVIGTDPAANTSVSA  TDPAANTSV        0.1458     10324.5             50.00     Sequence
DRB1_0701  423  PEQREIPDVSTLTYA  IPDVSTLTY        0.1443     10493.3             50.00     Sequence
DRB1_0701  412  GDEITVNVSTGPEQR  VNVSTGPEQ        0.1434     10595.1             50.00     Sequence
DRB1_0701  603  VYQNPPAGTGVNRDG  YQNPPAGTG        0.1433     10609.8             50.00     Sequence
DRB1_0701  467  IGTNPPANQTSAITN  ANQTSAITN        0.1430     10637.5             50.00     Sequence
DRB1_0701  352  FGGITRDVQVPDVRG  GGITRDVQV        0.1428     10667.9             50.00     Sequence
DRB1_0701   55  FRREAQNAAALNHPA  FRREAQNAA        0.1403     10957.4             50.00     Sequence
DRB1_0701  110  TPKRAIEVIADACQA  EVIADACQA        0.1399     11002.2             50.00     Sequence
DRB1_0701  178  TAQYLSPEQARGDSV  PEQARGDSV        0.1398     11011.8             50.00     Sequence
DRB1_0701   56  RREAQNAAALNHPAI  AAALNHPAI        0.1390     11118.4             50.00     Sequence
DRB1_0701  463  VGKVIGTNPPANQTS  GTNPPANQT        0.1385     11176.1             50.00     Sequence
DRB1_0701  414  EITVNVSTGPEQREI  STGPEQREI        0.1383     11200.7             50.00     Sequence
DRB1_0701  493  TKDIPDVAGQTVDVA  IPDVAGQTV        0.1382     11207.7             50.00     Sequence
DRB1_0701  364  VRGQSSADAIATLQN  RGQSSADAI        0.1362     11456.0             50.00     Sequence
DRB1_0701  520  SQASVDSPRPAGEVT  DSPRPAGEV        0.1356     11524.5             50.00     Sequence
DRB1_0701  505  DVAQKNLNVYGFTKF  LNVYGFTKF        0.1352     11575.7             50.00     Sequence
DRB1_0701  581  GWTGMLDKGADVDAG  GMLDKGADV        0.1352     11577.4             50.00     Sequence
DRB1_0701  461  ELVGKVIGTNPPANQ  VIGTNPPAN        0.1349     11620.1             50.00     Sequence
DRB1_0701  376  LQNRGFKIRTLQKPD  FKIRTLQKP        0.1349     11620.4             50.00     Sequence
DRB1_0701   69  AIVAVYDTGEAETPA  IVAVYDTGE        0.1332     11829.8             50.00     Sequence
DRB1_0701   81  TPAGPLPYIVMEYVD  LPYIVMEYV        0.1331     11841.0             50.00     Sequence
DRB1_0701  533  VTGTNPPAGTTVPVD  TNPPAGTTV        0.1327     11892.2             50.00     Sequence
DRB1_0701  255  AKNPENRYQTAAEMR  RYQTAAEMR        0.1324     11930.2             50.00     Sequence
DRB1_0701  317  DDTDRDRSIGSVGRW  RDRSIGSVG        0.1323     11954.4             50.00     Sequence
DRB1_0701  179  AQYLSPEQARGDSVD  PEQARGDSV        0.1301     12232.9             50.00     Sequence
DRB1_0701  529  PAGEVTGTNPPAGTT  GTNPPAGTT        0.1297     12288.5             50.00     Sequence
DRB1_0701  413  DEITVNVSTGPEQRE  NVSTGPEQR        0.1290     12377.0             50.00     Sequence
DRB1_0701  389  PDSTIPPDHVIGTDP  DSTIPPDHV        0.1278     12537.4             50.00     Sequence
DRB1_0701  234  PPSARHEGLSADLDA  RHEGLSADL        0.1278     12546.6             50.00     Sequence
DRB1_0701  494  KDIPDVAGQTVDVAQ  IPDVAGQTV        0.1268     12679.5             50.00     Sequence
DRB1_0701    4  SHLSDRYELGEILGF  YELGEILGF        0.1266     12713.9             50.00     Sequence
DRB1_0701  464  GKVIGTNPPANQTSA  GTNPPANQT        0.1252     12906.7             50.00     Sequence
DRB1_0701  254  LAKNPENRYQTAAEM  NRYQTAAEM        0.1237     13113.9             50.00     Sequence
DRB1_0701  398  VIGTDPAANTSVSAG  TDPAANTSV        0.1221     13345.5             50.00     Sequence
DRB1_0701  415  ITVNVSTGPEQREIP  STGPEQREI        0.1220     13355.3             50.00     Sequence
DRB1_0701  424  EQREIPDVSTLTYAE  IPDVSTLTY        0.1220     13361.8             50.00     Sequence
DRB1_0701  353  GGITRDVQVPDVRGQ  GGITRDVQV        0.1215     13434.6             50.00     Sequence
DRB1_0701  400  GTDPAANTSVSAGDE  TDPAANTSV        0.1212     13471.8             50.00     Sequence
DRB1_0701  593  DAGGSQHNRVVYQNP  GGSQHNRVV        0.1211     13484.4             50.00     Sequence
DRB1_0701  517  TKFSQASVDSPRPAG  FSQASVDSP        0.1210     13500.0             50.00     Sequence
DRB1_0701  199  YSLGCVLYEVLTGEP  LYEVLTGEP        0.1209     13509.2             50.00     Sequence
DRB1_0701  180  QYLSPEQARGDSVDA  PEQARGDSV        0.1204     13584.8             50.00     Sequence
DRB1_0701  495  DIPDVAGQTVDVAQK  IPDVAGQTV        0.1204     13596.4             50.00     Sequence
DRB1_0701    0  MTTPSHLSDRYELGE  SHLSDRYEL        0.1203     13603.7             50.00     Sequence
DRB1_0701  534  TGTNPPAGTTVPVDS  TNPPAGTTV        0.1201     13632.8             50.00     Sequence
DRB1_0701  421  TGPEQREIPDVSTLT  EIPDVSTLT        0.1192     13772.3             50.00     Sequence
DRB1_0701  582  WTGMLDKGADVDAGG  GMLDKGADV        0.1191     13782.2             50.00     Sequence
```

```
DRB1_0701  506  VAQKNLNVYGFTKFS  LNVYGFTKF         0.1183      13906.4              50.00      Sequence
DRB1_0701  176  IGTAQYLSPEQARGD  YLSPEQARG         0.1179      13958.7              50.00      Sequence
DRB1_0701    2  TPSHLSDRYELGEIL  DRYELGEIL         0.1173      14060.5              50.00      Sequence
DRB1_0701  508  QKNLNVYGFTKFSQA  YGFTKFSQA         0.1170      14106.1              50.00      Sequence
DRB1_0701  594  AGGSQHNRVVYQNPP  GGSQHNRVV         0.1161      14239.7              50.00      Sequence
DRB1_0701  251  LKALAKNPENRYQTA  LAKNPENRY         0.1157      14297.2              50.00      Sequence
DRB1_0701  521  QASVDSPRPAGEVTG  DSPRPAGEV         0.1154      14345.0              50.00      Sequence
DRB1_0701  377  QNRGFKIRTLQKPDS  FKIRTLQKP         0.1150      14414.0              50.00      Sequence
DRB1_0701   82  PAGPLPYIVMEYVDG  LPYIVMEYV         0.1147      14448.7              50.00      Sequence
DRB1_0701   70  IVAVYDTGEAETPAG  IVAVYDTGE         0.1133      14681.1              50.00      Sequence
DRB1_0701  366  GQSSADAIATLQNRG  AIATLQNRG         0.1125      14803.8              50.00      Sequence
DRB1_0701  316  LDDTDRDRSIGSVGR  RDRSIGSVG         0.1125      14804.4              50.00      Sequence
DRB1_0701  390  DSTIPPDHVIGTDPA  DSTIPPDHV         0.1120      14875.4              50.00      Sequence
DRB1_0701  399  IGTDPAANTSVSAGD  TDPAANTSV         0.1116      14947.9              50.00      Sequence
DRB1_0701  465  KVIGTNPPANQTSAI  GTNPPANQT         0.1114      14982.8              50.00      Sequence
DRB1_0701  466  VIGTNPPANQTSAIT  GTNPPANQT         0.1112      15009.9              50.00      Sequence
DRB1_0701  496  IPDVAGQTVDVAQKN  IPDVAGQTV         0.1104      15143.0              50.00      Sequence
DRB1_0701  228  VREDPIPPSARHEGL  PPSARHEGL         0.1102      15183.2              50.00      Sequence
DRB1_0701  358  DVQVPDVRGQSSADA  VRGQSSADA         0.1096      15269.7              50.00      Sequence
DRB1_0701  597  SQHNRVVYQNPPAGT  VYQNPPAGT         0.1089      15392.1              50.00      Sequence
DRB1_0701  425  QREIPDVSTLTYAEA  IPDVSTLTY         0.1084      15467.6              50.00      Sequence
DRB1_0701  458  STPELVGKVIGTNPP  GKVIGTNPP         0.1079      15559.1              50.00      Sequence
DRB1_0701  183  SPEQARGDSVDARSD  GDSVDARSD         0.1076      15611.2              50.00      Sequence
DRB1_0701  181  YLSPEQARGDSVDAR  PEQARGDSV         0.1061      15856.8              50.00      Sequence
DRB1_0701  365  RGQSSADAIATLQNR  RGQSSADAI         0.1058      15909.9              50.00      Sequence
DRB1_0701  378  NRGFKIRTLQKPDST  KIRTLQKPD         0.1051      16043.2              50.00      Sequence
DRB1_0701    3  PSHLSDRYELGEILG  SHLSDRYEL         0.1047      16108.3              50.00      Sequence
DRB1_0701  416  TVNVSTGPEQREIPD  STGPEQREI         0.1035      16316.8              50.00      Sequence
DRB1_0701  509  KNLNVYGFTKFSQAS  YGFTKFSQA         0.1030      16412.1              50.00      Sequence
DRB1_0701  583  TGMLDKGADVDAGGS  GMLDKGADV         0.1026      16474.7              50.00      Sequence
DRB1_0701    1  TTPSHLSDRYELGEI  SHLSDRYEL         0.1021      16573.8              50.00      Sequence
DRB1_0701  177  GTAQYLSPEQARGDS  YLSPEQARG         0.1013      16702.7              50.00      Sequence
DRB1_0701   79  AETPAGPLPYIVMEY  ETPAGPLPY         0.1005      16851.7              50.00      Sequence
DRB1_0701  522  ASVDSPRPAGEVTGT  DSPRPAGEV         0.0999      16958.7              50.00      Sequence
DRB1_0701  394  PPDHVIGTDPAANTS  GTDPAANTS         0.0997      16995.8              50.00      Sequence
DRB1_0701  518  KFSQASVDSPRPAGE  FSQASVDSP         0.0993      17081.7              50.00      Sequence
DRB1_0701  504  VDVAQKNLNVYGFTK  VAQKNLNVY         0.0991      17109.8              50.00      Sequence
DRB1_0701  184  PEQARGDSVDARSDV  GDSVDARSD         0.0991      17113.3              50.00      Sequence
DRB1_0701  577  LRALGWTGMLDKGAD  RALGWTGML         0.0990      17130.8              50.00      Sequence
DRB1_0701  226  QHVREDPIPPSARHE  PIPPSARHE         0.0989      17142.3              50.00      Sequence
DRB1_0701  252  KALAKNPENRYQTAA  LAKNPENRY         0.0989      17148.0              50.00      Sequence
DRB1_0701  487  VGSGPATKDIPDVAG  GSGPATKDI         0.0988      17158.4              50.00      Sequence
DRB1_0701  274  RVHNGEPPEAPKVLT  GEPPEAPKV         0.0984      17245.3              50.00      Sequence
DRB1_0701  507  AQKNLNVYGFTKFSQ  LNVYGFTKF         0.0978      17356.9              50.00      Sequence
DRB1_0701  392  TIPPDHVIGTDPAAN  VIGTDPAAN         0.0964      17624.1              50.00      Sequence
DRB1_0701  229  REDPIPPSARHEGLS  PPSARHEGL         0.0952      17842.6              50.00      Sequence
DRB1_0701  393  IPPDHVIGTDPAANT  VIGTDPAAN         0.0951      17860.2              50.00      Sequence
DRB1_0701  527  PRPAGEVTGTNPPAG  VTGTNPPAG         0.0951      17873.0              50.00      Sequence
DRB1_0701  584  GMLDKGADVDAGGSQ  GMLDKGADV         0.0947      17942.1              50.00      Sequence
DRB1_0701  459  TPELVGKVIGTNPPA  GKVIGTNPP         0.0933      18220.7              50.00      Sequence
DRB1_0701  273  VRVHNGEPPEAPKVL  GEPPEAPKV         0.0920      18486.4              50.00      Sequence
DRB1_0701  200  SLGCVLYEVLTGEPP  LYEVLTGEP         0.0917      18539.5              50.00      Sequence
DRB1_0701  523  SVDSPRPAGEVTGTN  DSPRPAGEV         0.0912      18648.3              50.00      Sequence
DRB1_0701  456  SPSTPELVGKVIGTN  LVGKVIGTN         0.0911      18666.3              50.00      Sequence
DRB1_0701  488  GSGPATKDIPDVAGQ  GSGPATKDI         0.0908      18728.8              50.00      Sequence
DRB1_0701  275  VHNGEPPEAPKVLTD  GEPPEAPKV         0.0907      18740.0              50.00      Sequence
DRB1_0701  595  GGSQHNRVVYQNPPA  GGSQHNRVV         0.0889      19112.0              50.00      Sequence
DRB1_0701  420  STGPEQREIPDVSTL  REIPDVSTL         0.0882      19243.6              50.00      Sequence
DRB1_0701  525  DSPRPAGEVTGTNPP  DSPRPAGEV         0.0882      19256.3              50.00      Sequence
DRB1_0701  315  DLDDTDRDRSIGSVG  RDRSIGSVG         0.0862      19683.7              50.00      Sequence
DRB1_0701  253  ALAKNPENRYQTAAE  LAKNPENRY         0.0856      19811.0              50.00      Sequence
DRB1_0701  118  IADACQALNFSHQNG  ADACQALNF         0.0854      19847.9              50.00      Sequence
DRB1_0701  227  HVREDPIPPSARHEG  PIPPSARHE         0.0852      19893.5              50.00      Sequence
DRB1_0701    9  RYELGEILGFGGMSE  ILGFGGMSE         0.0846      20014.2              50.00      Sequence
DRB1_0701  596  GSQHNRVVYQNPPAG  VVYQNPPAG         0.0844      20052.6              50.00      Sequence
DRB1_0701  182  LSPEQARGDSVDARS  PEQARGDSV         0.0844      20055.4              50.00      Sequence
```

```
   DRB1_0701  230  EDPIPPSARHEGLSA  PPSARHEGL        0.0844      20067.8                50.00     Sequence
   DRB1_0701  417  VNVSTGPEQREIPDV  VNVSTGPEQ        0.0843      20094.5                50.00     Sequence
   DRB1_0701    5  HLSDRYELGEILGFG  YELGEILGF        0.0839      20169.6                50.00     Sequence
   DRB1_0701  455  NSPSTPELVGKVIGT  NSPSTPELV        0.0832      20316.4                50.00     Sequence
   DRB1_0701  528  RPAGEVTGTNPPAGT  VTGTNPPAG        0.0829      20384.7                50.00     Sequence
   DRB1_0701  354  GITRDVQVPDVRGQS  TRDVQVPDV        0.0825      20468.0                50.00     Sequence
   DRB1_0701  457  PSTPELVGKVIGTNP  LVGKVIGTN        0.0809      20828.1                50.00     Sequence
   DRB1_0701  391  STIPPDHVIGTDPAA  STIPPDHVI        0.0808      20854.3                50.00     Sequence
   DRB1_0701  524  VDSPRPAGEVTGTNP  DSPRPAGEV        0.0805      20919.3                50.00     Sequence
   DRB1_0701  276  HNGEPPEAPKVLTDA  GEPPEAPKV        0.0770      21746.0                50.00     Sequence
   DRB1_0701  231  DPIPPSARHEGLSAD  PPSARHEGL        0.0760      21966.9                50.00     Sequence
   DRB1_0701  526  SPRPAGEVTGTNPPA  GEVTGTNPP        0.0692      23641.7                50.00     Sequence
   DRB1_0701    6  LSDRYELGEILGFGG  YELGEILGF        0.0692      23656.8                50.00     Sequence
   DRB1_0701  277  NGEPPEAPKVLTDAE  GEPPEAPKV        0.0677      24034.8                50.00     Sequence
   DRB1_0701  418  NVSTGPEQREIPDVS  STGPEQREI        0.0676      24052.0                50.00     Sequence
   DRB1_0701  311  LPRQDLDDTDRDRSI  LDDTDRDRS        0.0675      24082.4                50.00     Sequence
   DRB1_0701  304  SGPRTDPLPRQDLDD  TDPLPRQDL        0.0665      24346.5                50.00     Sequence
   DRB1_0701  419  VSTGPEQREIPDVST  STGPEQREI        0.0648      24796.1                50.00     Sequence
   DRB1_0701  278  GEPPEAPKVLTDAER  GEPPEAPKV        0.0641      24993.2                50.00     Sequence
   DRB1_0701  355  ITRDVQVPDVRGQSS  TRDVQVPDV        0.0640      25006.8                50.00     Sequence
   DRB1_0701  585  MLDKGADVDAGGSQH  MLDKGADVD        0.0620      25565.7                50.00     Sequence
   DRB1_0701  312  PRQDLDDTDRDRSIG  LDDTDRDRS        0.0616      25669.6                50.00     Sequence
   DRB1_0701  444  TAAGFGRFKQANSPS  GRFKQANSP        0.0615      25701.6                50.00     Sequence
   DRB1_0701  305  GPRTDPLPRQDLDDT  TDPLPRQDL        0.0610      25841.6                50.00     Sequence
   DRB1_0701  313  RQDLDDTDRDRSIGS  LDDTDRDRS        0.0607      25920.2                50.00     Sequence
   DRB1_0701  314  QDLDDTDRDRSIGSV  LDDTDRDRS        0.0604      26020.0                50.00     Sequence
   DRB1_0701  310  PLPRQDLDDTDRDRS  LDDTDRDRS        0.0598      26167.9                50.00     Sequence
   DRB1_0701    7  SDRYELGEILGFGGM  YELGEILGF        0.0577      26772.5                50.00     Sequence
   DRB1_0701    8  DRYELGEILGFGGMS  YELGEILGF        0.0575      26843.6                50.00     Sequence
   DRB1_0701   71  VAVYDTGEAETPAGP  VYDTGEAET        0.0567      27083.7                50.00     Sequence
   DRB1_0701  356  TRDVQVPDVRGQSSA  TRDVQVPDV        0.0552      27512.8                50.00     Sequence
   DRB1_0701  307  RTDPLPRQDLDDTDR  RQDLDDTDR        0.0531      28141.8                50.00     Sequence
   DRB1_0701  308  TDPLPRQDLDDTDRD  RQDLDDTDR        0.0472      29996.2                50.00     Sequence
   DRB1_0701  306  PRTDPLPRQDLDDTD  TDPLPRQDL        0.0457      30489.6                50.00     Sequence
   DRB1_0701  489  SGPATKDIPDVAGQT  DIPDVAGQT        0.0422      31657.8                50.00     Sequence
   DRB1_0701  357  RDVQVPDVRGQSSAD  VPDVRGQSS        0.0422      31685.2                50.00     Sequence
   DRB1_0701  309  DPLPRQDLDDTDRDR  RQDLDDTDR        0.0418      31819.6                50.00     Sequence
-------------------------------------------------------------------------------------------------

Allele: DRB1_0701. Number of high binders 55. Number of weak binders 113. Number of peptides 612

-------------------------------------------------------------------------------------------------
-------------------------------------------------------------------------------------------------
      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
-------------------------------------------------------------------------------------------------
   DRB1_0802   50  SFYLRFRREAQNAAA  YLRFRREAQ        0.7226         20.1          SB     0.30     Sequence
   DRB1_0802   51  FYLRFRREAQNAAAL  FYLRFRREA        0.7187         21.0          SB     0.30     Sequence
   DRB1_0802   49  PSFYLRFRREAQNAA  YLRFRREAQ        0.7138         22.1          SB     0.30     Sequence
   DRB1_0802   48  DPSFYLRFRREAQNA  FYLRFRREA        0.6943         27.3          SB     0.40     Sequence
   DRB1_0802  379  RGFKIRTLQKPDSTI  RGFKIRTLQ        0.6914         28.2          SB     0.80     Sequence
   DRB1_0802  378  NRGFKIRTLQKPDST  RGFKIRTLQ        0.6769         33.0          SB     0.80     Sequence
   DRB1_0802  377  QNRGFKIRTLQKPDS  RGFKIRTLQ        0.6720         34.8          SB     0.80     Sequence
   DRB1_0802   47  RDPSFYLRFRREAQN  FYLRFRREA        0.6498         44.2          SB     1.00     Sequence
   DRB1_0802  380  GFKIRTLQKPDSTIP  FKIRTLQKP        0.6444         46.9          SB     2.00     Sequence
   DRB1_0802  323  RSIGSVGRWVAVVAV  SIGSVGRWV        0.6383         50.1          WB     2.00     Sequence
   DRB1_0802  376  LQNRGFKIRTLQKPD  RGFKIRTLQ        0.6215         60.1          WB     2.00     Sequence
   DRB1_0802  322  DRSIGSVGRWVAVVA  SIGSVGRWV        0.6190         61.7          WB     2.00     Sequence
   DRB1_0802  324  SIGSVGRWVAVVAVL  SIGSVGRWV        0.6187         61.9          WB     2.00     Sequence
   DRB1_0802  321  RDRSIGSVGRWVAVV  SIGSVGRWV        0.6135         65.5          WB     2.00     Sequence
   DRB1_0802   46  ARDPSFYLRFRREAQ  FYLRFRREA        0.6010         75.0          WB     4.00     Sequence
   DRB1_0802  320  DRDRSIGSVGRWVAV  SIGSVGRWV        0.5796         94.5          WB     4.00     Sequence
   DRB1_0802   52  YLRFRREAQNAAALN  YLRFRREAQ        0.5661        109.4          WB     4.00     Sequence
   DRB1_0802  375  TLQNRGFKIRTLQKP  RGFKIRTLQ        0.5641        111.7          WB     4.00     Sequence
   DRB1_0802  381  FKIRTLQKPDSTIPP  FKIRTLQKP        0.5604        116.3          WB     4.00     Sequence
   DRB1_0802  325  IGSVGRWVAVVAVLA  WVAVVAVLA        0.5543        124.2          WB     4.00     Sequence
   DRB1_0802  319  TDRDRSIGSVGRWVA  SIGSVGRWV        0.5452        137.2          WB     8.00     Sequence
```

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| DRB1_0802 | 446 | AGFGRFKQANSPSTP | GFGRFKQAN | 0.5348 | 153.4 | WB | 8.00 | Sequence |
| DRB1_0802 | 445 | AAGFGRFKQANSPST | GFGRFKQAN | 0.5335 | 155.6 | WB | 8.00 | Sequence |
| DRB1_0802 | 374 | ATLQNRGFKIRTLQK | RGFKIRTLQ | 0.5121 | 196.2 | WB | 8.00 | Sequence |
| DRB1_0802 | 434 | LTYAEAVKKLTAAGF | YAEAVKKLT | 0.5079 | 205.3 | WB | 8.00 | Sequence |
| DRB1_0802 | 435 | TYAEAVKKLTAAGFG | YAEAVKKLT | 0.4975 | 229.7 | WB | 8.00 | Sequence |
| DRB1_0802 | 433 | TLTYAEAVKKLTAAG | YAEAVKKLT | 0.4972 | 230.6 | WB | 8.00 | Sequence |
| DRB1_0802 | 447 | GFGRFKQANSPSTPE | GFGRFKQAN | 0.4969 | 231.2 | WB | 8.00 | Sequence |
| DRB1_0802 | 512 | NVYGFTKFSQASVDS | YGFTKFSQA | 0.4892 | 251.3 | WB | 8.00 | Sequence |
| DRB1_0802 | 513 | VYGFTKFSQASVDSP | YGFTKFSQA | 0.4775 | 285.2 | WB | 16.00 | Sequence |
| DRB1_0802 | 45 | LARDPSFYLRFRREA | FYLRFRREA | 0.4771 | 286.5 | WB | 16.00 | Sequence |
| DRB1_0802 | 436 | YAEAVKKLTAAGFGR | YAEAVKKLT | 0.4741 | 295.9 | WB | 16.00 | Sequence |
| DRB1_0802 | 444 | TAAGFGRFKQANSPS | GFGRFKQAN | 0.4712 | 305.3 | WB | 16.00 | Sequence |
| DRB1_0802 | 511 | LNVYGFTKFSQASVD | GFTKFSQAS | 0.4688 | 313.4 | WB | 16.00 | Sequence |
| DRB1_0802 | 514 | YGFTKFSQASVDSPR | GFTKFSQAS | 0.4665 | 321.4 | WB | 16.00 | Sequence |
| DRB1_0802 | 326 | GSVGRWVAVVAVLAV | WVAVVAVLA | 0.4647 | 327.5 | WB | 16.00 | Sequence |
| DRB1_0802 | 329 | GRWVAVVAVLAVLTV | WVAVVAVLA | 0.4637 | 331.2 | WB | 16.00 | Sequence |
| DRB1_0802 | 570 | WVDAEPRLRALGWTG | RLRALGWTG | 0.4598 | 345.3 | WB | 16.00 | Sequence |
| DRB1_0802 | 328 | VGRWVAVVAVLAVLT | WVAVVAVLA | 0.4549 | 364.2 | WB | 16.00 | Sequence |
| DRB1_0802 | 510 | NLNVYGFTKFSQASV | GFTKFSQAS | 0.4516 | 377.7 | WB | 16.00 | Sequence |
| DRB1_0802 | 327 | SVGRWVAVVAVLAVL | WVAVVAVLA | 0.4510 | 380.0 | WB | 16.00 | Sequence |
| DRB1_0802 | 33 | HRDVAVKVLRADLAR | RDVAVKVLR | 0.4488 | 389.1 | WB | 16.00 | Sequence |
| DRB1_0802 | 247 | DAVVLKALAKNPENR | VLKALAKNP | 0.4466 | 398.3 | WB | 16.00 | Sequence |
| DRB1_0802 | 598 | QHNRVVYQNPPAGTG | RVVYQNPPA | 0.4430 | 414.3 | WB | 16.00 | Sequence |
| DRB1_0802 | 432 | STLTYAEAVKKLTAA | YAEAVKKLT | 0.4427 | 415.5 | WB | 16.00 | Sequence |
| DRB1_0802 | 599 | HNRVVYQNPPAGTGV | RVVYQNPPA | 0.4427 | 415.8 | WB | 16.00 | Sequence |
| DRB1_0802 | 348 | AINTFGGITRDVQVP | INTFGGITR | 0.4423 | 417.3 | WB | 16.00 | Sequence |
| DRB1_0802 | 248 | AVVLKALAKNPENRY | VLKALAKNP | 0.4417 | 420.0 | WB | 16.00 | Sequence |
| DRB1_0802 | 34 | RDVAVKVLRADLARD | RDVAVKVLR | 0.4371 | 441.5 | WB | 16.00 | Sequence |
| DRB1_0802 | 600 | NRVVYQNPPAGTGVN | RVVYQNPPA | 0.4367 | 443.6 | WB | 16.00 | Sequence |
| DRB1_0802 | 246 | LDAVVLKALAKNPEN | VLKALAKNP | 0.4365 | 444.6 | WB | 16.00 | Sequence |
| DRB1_0802 | 448 | FGRFKQANSPSTPEL | RFKQANSPS | 0.4333 | 459.9 | WB | 16.00 | Sequence |
| DRB1_0802 | 431 | VSTLTYAEAVKKLTA | YAEAVKKLT | 0.4321 | 466.2 | WB | 16.00 | Sequence |
| DRB1_0802 | 258 | PENRYQTAAEMRADL | RYQTAAEMR | 0.4264 | 496.1 | WB | 16.00 | Sequence |
| DRB1_0802 | 573 | AEPRLRALGWTGMLD | RLRALGWTG | 0.4231 | 514.1 | | 16.00 | Sequence |
| DRB1_0802 | 571 | VDAEPRLRALGWTGM | RLRALGWTG | 0.4218 | 521.2 | | 16.00 | Sequence |
| DRB1_0802 | 572 | DAEPRLRALGWTGML | RLRALGWTG | 0.4217 | 521.5 | | 16.00 | Sequence |
| DRB1_0802 | 32 | LHRDVAVKVLRADLA | RDVAVKVLR | 0.4213 | 523.9 | | 16.00 | Sequence |
| DRB1_0802 | 601 | RVVYQNPPAGTGVNR | RVVYQNPPA | 0.4209 | 526.4 | | 16.00 | Sequence |
| DRB1_0802 | 330 | RWVAVVAVLAVLTVV | WVAVVAVLA | 0.4204 | 529.3 | | 16.00 | Sequence |
| DRB1_0802 | 256 | KNPENRYQTAAEMRA | RYQTAAEMR | 0.4166 | 551.3 | | 16.00 | Sequence |
| DRB1_0802 | 349 | INTFGGITRDVQVPD | TFGGITRDV | 0.4161 | 554.2 | | 16.00 | Sequence |
| DRB1_0802 | 249 | VVLKALAKNPENRYQ | VLKALAKNP | 0.4154 | 558.7 | | 16.00 | Sequence |
| DRB1_0802 | 245 | DLDAVVLKALAKNPE | VLKALAKNP | 0.4139 | 567.4 | | 16.00 | Sequence |
| DRB1_0802 | 515 | GFTKFSQASVDSPRP | GFTKFSQAS | 0.4129 | 573.7 | | 16.00 | Sequence |
| DRB1_0802 | 260 | NRYQTAAEMRADLVR | RYQTAAEMR | 0.4125 | 576.1 | | 16.00 | Sequence |
| DRB1_0802 | 597 | SQHNRVVYQNPPAGT | RVVYQNPPA | 0.4106 | 588.2 | | 16.00 | Sequence |
| DRB1_0802 | 257 | NPENRYQTAAEMRAD | RYQTAAEMR | 0.4102 | 590.9 | | 16.00 | Sequence |
| DRB1_0802 | 596 | GSQHNRVVYQNPPAG | RVVYQNPPA | 0.4102 | 591.1 | | 16.00 | Sequence |
| DRB1_0802 | 430 | DVSTLTYAEAVKKLT | YAEAVKKLT | 0.4099 | 592.4 | | 32.00 | Sequence |
| DRB1_0802 | 31 | RLHRDVAVKVLRADL | RDVAVKVLR | 0.4081 | 604.2 | | 32.00 | Sequence |
| DRB1_0802 | 331 | WVAVVAVLAVLTVVV | WVAVVAVLA | 0.4075 | 608.4 | | 32.00 | Sequence |
| DRB1_0802 | 373 | IATLQNRGFKIRTLQ | RGFKIRTLQ | 0.4060 | 618.2 | | 32.00 | Sequence |
| DRB1_0802 | 443 | LTAAGFGRFKQANSP | GFGRFKQAN | 0.4059 | 618.7 | | 32.00 | Sequence |
| DRB1_0802 | 568 | MFWVDAEPRLRALGW | WVDAEPRLR | 0.4035 | 635.1 | | 32.00 | Sequence |
| DRB1_0802 | 567 | GMFWVDAEPRLRALG | WVDAEPRLR | 0.4021 | 645.1 | | 32.00 | Sequence |
| DRB1_0802 | 259 | ENRYQTAAEMRADLV | RYQTAAEMR | 0.4009 | 653.6 | | 32.00 | Sequence |
| DRB1_0802 | 574 | EPRLRALGWTGMLDK | RLRALGWTG | 0.4001 | 658.9 | | 32.00 | Sequence |
| DRB1_0802 | 132 | GIIHRDVKPANIMIS | IIHRDVKPA | 0.4001 | 659.3 | | 32.00 | Sequence |
| DRB1_0802 | 575 | PRLRALGWTGMLDKG | RLRALGWTG | 0.3989 | 667.8 | | 32.00 | Sequence |
| DRB1_0802 | 449 | GRFKQANSPSTPELV | RFKQANSPS | 0.3985 | 670.4 | | 32.00 | Sequence |
| DRB1_0802 | 347 | IAINTFGGITRDVQV | INTFGGITR | 0.3970 | 681.6 | | 32.00 | Sequence |
| DRB1_0802 | 250 | VLKALAKNPENRYQT | VLKALAKNP | 0.3967 | 684.1 | | 32.00 | Sequence |
| DRB1_0802 | 382 | KIRTLQKPDSTIPPD | KIRTLQKPD | 0.3956 | 691.8 | | 32.00 | Sequence |
| DRB1_0802 | 350 | NTFGGITRDVQVPDV | TFGGITRDV | 0.3952 | 694.7 | | 32.00 | Sequence |
| DRB1_0802 | 569 | FWVDAEPRLRALGWT | WVDAEPRLR | 0.3943 | 701.4 | | 32.00 | Sequence |
| DRB1_0802 | 442 | KLTAAGFGRFKQANS | GFGRFKQAN | 0.3915 | 723.3 | | 32.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0802 | 261 | RYQTAAEMRADLVRV | RYQTAAEMR | 0.3893 | 740.7 | 32.00 | Sequence |
| DRB1_0802 | 351 | TFGGITRDVQVPDVR | TFGGITRDV | 0.3888 | 744.8 | 32.00 | Sequence |
| DRB1_0802 | 576 | RLRALGWTGMLDKGA | RLRALGWTG | 0.3863 | 765.0 | 32.00 | Sequence |
| DRB1_0802 | 165 | SGNSVTQTAAVIGTA | GNSVTQTAA | 0.3862 | 765.8 | 32.00 | Sequence |
| DRB1_0802 | 318 | DTDRDRSIGSVGRWV | SIGSVGRWV | 0.3800 | 819.5 | 32.00 | Sequence |
| DRB1_0802 | 292 | RTSLLSSAAGNLSGP | RTSLLSSAA | 0.3790 | 828.2 | 32.00 | Sequence |
| DRB1_0802 | 30 | LRLHRDVAVKVLRAD | RDVAVKVLR | 0.3778 | 838.6 | 32.00 | Sequence |
| DRB1_0802 | 595 | GGSQHNRVVYQNPPA | RVVYQNPPA | 0.3774 | 842.1 | 32.00 | Sequence |
| DRB1_0802 | 131 | NGIIHRDVKPANIMI | IIHRDVKPA | 0.3772 | 844.6 | 32.00 | Sequence |
| DRB1_0802 | 509 | KNLNVYGFTKFSQAS | GFTKFSQAS | 0.3753 | 862.1 | 32.00 | Sequence |
| DRB1_0802 | 220 | PVSVAYQHVREDPIP | VSVAYQHVR | 0.3726 | 887.7 | 32.00 | Sequence |
| DRB1_0802 | 244 | ADLDAVVLKALAKNP | VLKALAKNP | 0.3708 | 905.3 | 32.00 | Sequence |
| DRB1_0802 | 566 | SGMFWVDAEPRLRAL | WVDAEPRLR | 0.3700 | 912.8 | 32.00 | Sequence |
| DRB1_0802 | 346 | TIAINTFGGITRDVQ | INTFGGITR | 0.3682 | 930.7 | 32.00 | Sequence |
| DRB1_0802 | 29 | DLRLHRDVAVKVLRA | RDVAVKVLR | 0.3673 | 939.9 | 32.00 | Sequence |
| DRB1_0802 | 130 | QNGIIHRDVKPANIM | IIHRDVKPA | 0.3665 | 948.2 | 32.00 | Sequence |
| DRB1_0802 | 462 | LVGKVIGTNPPANQT | GKVIGTNPP | 0.3660 | 953.6 | 32.00 | Sequence |
| DRB1_0802 | 152 | KVMDFGIARAIADSG | DFGIARAIA | 0.3653 | 960.4 | 32.00 | Sequence |
| DRB1_0802 | 218 | DSPVSVAYQHVREDP | VSVAYQHVR | 0.3641 | 973.3 | 32.00 | Sequence |
| DRB1_0802 | 291 | ERTSLLSSAAGNLSG | RTSLLSSAA | 0.3613 | 1003.3 | 32.00 | Sequence |
| DRB1_0802 | 166 | GNSVTQTAAVIGTAQ | GNSVTQTAA | 0.3582 | 1036.9 | 32.00 | Sequence |
| DRB1_0802 | 133 | IIHRDVKPANIMISA | IIHRDVKPA | 0.3568 | 1052.8 | 32.00 | Sequence |
| DRB1_0802 | 23 | EVHLARDLRLHRDVA | HLARDLRLH | 0.3544 | 1080.6 | 32.00 | Sequence |
| DRB1_0802 | 22 | SEVHLARDLRLHRDV | HLARDLRLH | 0.3524 | 1104.8 | 32.00 | Sequence |
| DRB1_0802 | 439 | AVKKLTAAGFGRFKQ | AVKKLTAAG | 0.3500 | 1133.3 | 32.00 | Sequence |
| DRB1_0802 | 219 | SPVSVAYQHVREDPI | VSVAYQHVR | 0.3496 | 1138.7 | 32.00 | Sequence |
| DRB1_0802 | 255 | AKNPENRYQTAAEMR | RYQTAAEMR | 0.3493 | 1141.8 | 32.00 | Sequence |
| DRB1_0802 | 565 | LSGMFWVDAEPRLRA | WVDAEPRLR | 0.3486 | 1150.6 | 32.00 | Sequence |
| DRB1_0802 | 290 | AERTSLLSSAAGNLS | RTSLLSSAA | 0.3485 | 1152.3 | 32.00 | Sequence |
| DRB1_0802 | 441 | KKLTAAGFGRFKQAN | KKLTAAGFG | 0.3481 | 1157.2 | 32.00 | Sequence |
| DRB1_0802 | 151 | VKVMDFGIARAIADS | DFGIARAIA | 0.3474 | 1166.0 | 32.00 | Sequence |
| DRB1_0802 | 20 | GMSEVHLARDLRLHR | GMSEVHLAR | 0.3463 | 1180.1 | 32.00 | Sequence |
| DRB1_0802 | 450 | RFKQANSPSTPELVG | RFKQANSPS | 0.3438 | 1212.0 | 32.00 | Sequence |
| DRB1_0802 | 35 | DVAVKVLRADLARDP | AVKVLRADL | 0.3435 | 1215.8 | 32.00 | Sequence |
| DRB1_0802 | 28 | RDLRLHRDVAVKVLR | RDVAVKVLR | 0.3426 | 1227.8 | 32.00 | Sequence |
| DRB1_0802 | 164 | DSGNSVTQTAAVIGT | GNSVTQTAA | 0.3409 | 1249.9 | 32.00 | Sequence |
| DRB1_0802 | 460 | PELVGKVIGTNPPAN | LVGKVIGTN | 0.3404 | 1256.8 | 32.00 | Sequence |
| DRB1_0802 | 463 | VGKVIGTNPPANQTS | GKVIGTNPP | 0.3399 | 1264.3 | 32.00 | Sequence |
| DRB1_0802 | 96 | GVTLRDIVHTEGPMT | GVTLRDIVH | 0.3395 | 1269.8 | 32.00 | Sequence |
| DRB1_0802 | 127 | FSHQNGIIHRDVKPA | FSHQNGIIH | 0.3374 | 1298.6 | 32.00 | Sequence |
| DRB1_0802 | 217 | GDSPVSVAYQHVRED | VSVAYQHVR | 0.3368 | 1307.4 | 32.00 | Sequence |
| DRB1_0802 | 372 | AIATLQNRGFKIRTL | AIATLQNRG | 0.3337 | 1352.0 | 32.00 | Sequence |
| DRB1_0802 | 129 | HQNGIIHRDVKPANI | GIIHRDVKP | 0.3314 | 1385.7 | 32.00 | Sequence |
| DRB1_0802 | 107 | GPMTPKRAIEVIADA | GPMTPKRAI | 0.3303 | 1403.0 | 32.00 | Sequence |
| DRB1_0802 | 437 | AEAVKKLTAAGFGRF | AVKKLTAAG | 0.3299 | 1408.6 | 32.00 | Sequence |
| DRB1_0802 | 461 | ELVGKVIGTNPPANQ | GKVIGTNPP | 0.3296 | 1413.5 | 32.00 | Sequence |
| DRB1_0802 | 19 | GGMSEVHLARDLRLH | GMSEVHLAR | 0.3290 | 1421.7 | 32.00 | Sequence |
| DRB1_0802 | 93 | YVDGVTLRDIVHTEG | GVTLRDIVH | 0.3290 | 1422.6 | 32.00 | Sequence |
| DRB1_0802 | 438 | EAVKKLTAAGFGRFK | AVKKLTAAG | 0.3289 | 1424.7 | 32.00 | Sequence |
| DRB1_0802 | 53 | LRFRREAQNAAALNH | RFRREAQNA | 0.3288 | 1425.0 | 32.00 | Sequence |
| DRB1_0802 | 17 | GFGGMSEVHLARDLR | GMSEVHLAR | 0.3284 | 1431.8 | 32.00 | Sequence |
| DRB1_0802 | 142 | NIMISATNAVKVMDF | MISATNAVK | 0.3271 | 1451.2 | 32.00 | Sequence |
| DRB1_0802 | 24 | VHLARDLRLHRDVAV | HLARDLRLH | 0.3271 | 1452.5 | 32.00 | Sequence |
| DRB1_0802 | 345 | VTIAINTFGGITRDV | INTFGGITR | 0.3269 | 1454.5 | 32.00 | Sequence |
| DRB1_0802 | 149 | NAVKVMDFGIARAIA | VKVMDFGIA | 0.3269 | 1455.1 | 32.00 | Sequence |
| DRB1_0802 | 150 | AVKVMDFGIARAIAD | DFGIARAIA | 0.3266 | 1459.1 | 32.00 | Sequence |
| DRB1_0802 | 153 | VMDFGIARAIADSGN | DFGIARAIA | 0.3249 | 1486.3 | 32.00 | Sequence |
| DRB1_0802 | 144 | MISATNAVKVMDFGI | MISATNAVK | 0.3241 | 1499.8 | 32.00 | Sequence |
| DRB1_0802 | 221 | VSVAYQHVREDPIPP | VSVAYQHVR | 0.3238 | 1504.3 | 32.00 | Sequence |
| DRB1_0802 | 94 | VDGVTLRDIVHTEGP | GVTLRDIVH | 0.3217 | 1539.9 | 32.00 | Sequence |
| DRB1_0802 | 611 | TGVNRDGIITLRFGQ | GVNRDGIIT | 0.3201 | 1565.9 | 32.00 | Sequence |
| DRB1_0802 | 175 | VIGTAQYLSPEQARG | VIGTAQYLS | 0.3185 | 1593.2 | 50.00 | Sequence |
| DRB1_0802 | 163 | ADSGNSVTQTAAVIG | GNSVTQTAA | 0.3179 | 1603.5 | 50.00 | Sequence |
| DRB1_0802 | 95 | DGVTLRDIVHTEGPM | GVTLRDIVH | 0.3156 | 1644.6 | 50.00 | Sequence |
| DRB1_0802 | 459 | TPELVGKVIGTNPPA | GKVIGTNPP | 0.3152 | 1651.2 | 50.00 | Sequence |
| DRB1_0802 | 564 | DLSGMFWVDAEPRLR | WVDAEPRLR | 0.3151 | 1653.2 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0802 | 128 | SHQNGIIHRDVKPAN | GIIHRDVKP | 0.3148 | 1657.8 | 50.00 | Sequence |
| DRB1_0802 | 25 | HLARDLRLHRDVAVK | HLARDLRLH | 0.3148 | 1658.8 | 50.00 | Sequence |
| DRB1_0802 | 216 | TGDSPVSVAYQHVRE | VSVAYQHVR | 0.3147 | 1660.2 | 50.00 | Sequence |
| DRB1_0802 | 289 | DAERTSLLSSAAGNL | RTSLLSSAA | 0.3140 | 1673.3 | 50.00 | Sequence |
| DRB1_0802 | 21 | MSEVHLARDLRLHRD | HLARDLRLH | 0.3135 | 1681.4 | 50.00 | Sequence |
| DRB1_0802 | 106 | EGPMTPKRAIEVIAD | GPMTPKRAI | 0.3123 | 1704.5 | 50.00 | Sequence |
| DRB1_0802 | 352 | FGGITRDVQVPDVRG | GITRDVQVP | 0.3117 | 1714.9 | 50.00 | Sequence |
| DRB1_0802 | 140 | PANIMISATNAVKVM | MISATNAVK | 0.3104 | 1739.3 | 50.00 | Sequence |
| DRB1_0802 | 143 | IMISATNAVKVMDFG | MISATNAVK | 0.3091 | 1764.6 | 50.00 | Sequence |
| DRB1_0802 | 141 | ANIMISATNAVKVMD | MISATNAVK | 0.3091 | 1764.7 | 50.00 | Sequence |
| DRB1_0802 | 464 | GKVIGTNPPANQTSA | GKVIGTNPP | 0.3015 | 1915.6 | 50.00 | Sequence |
| DRB1_0802 | 215 | FTGDSPVSVAYQHVR | VSVAYQHVR | 0.3013 | 1918.6 | 50.00 | Sequence |
| DRB1_0802 | 154 | MDFGIARAIADSGNS | DFGIARAIA | 0.2998 | 1951.5 | 50.00 | Sequence |
| DRB1_0802 | 371 | DAIATLQNRGFKIRT | AIATLQNRG | 0.2991 | 1965.3 | 50.00 | Sequence |
| DRB1_0802 | 105 | TEGPMTPKRAIEVIA | GPMTPKRAI | 0.2975 | 1999.7 | 50.00 | Sequence |
| DRB1_0802 | 16 | LGFGGMSEVHLARDL | GMSEVHLAR | 0.2972 | 2006.4 | 50.00 | Sequence |
| DRB1_0802 | 36 | VAVKVLRADLARDPS | AVKVLRADL | 0.2950 | 2054.3 | 50.00 | Sequence |
| DRB1_0802 | 483 | VIIIVGSGPATKDIP | IIIVGSGPA | 0.2878 | 2222.5 | 50.00 | Sequence |
| DRB1_0802 | 18 | FGGMSEVHLARDLRL | GMSEVHLAR | 0.2876 | 2227.0 | 50.00 | Sequence |
| DRB1_0802 | 344 | VVTIAINTFGGITRD | AINTFGGIT | 0.2875 | 2229.0 | 50.00 | Sequence |
| DRB1_0802 | 429 | PDVSTLTYAEAVKKL | VSTLTYAEA | 0.2869 | 2242.9 | 50.00 | Sequence |
| DRB1_0802 | 484 | IIIVGSGPATKDIPD | IIIVGSGPA | 0.2867 | 2247.9 | 50.00 | Sequence |
| DRB1_0802 | 343 | VVVTIAINTFGGITR | VTIAINTFG | 0.2859 | 2267.9 | 50.00 | Sequence |
| DRB1_0802 | 126 | NFSHQNGIIHRDVKP | FSHQNGIIH | 0.2858 | 2269.9 | 50.00 | Sequence |
| DRB1_0802 | 139 | KPANIMISATNAVKV | MISATNAVK | 0.2853 | 2282.7 | 50.00 | Sequence |
| DRB1_0802 | 155 | DFGIARAIADSGNSV | DFGIARAIA | 0.2851 | 2288.1 | 50.00 | Sequence |
| DRB1_0802 | 594 | AGGSQHNRVVYQNPP | HNRVVYQNP | 0.2849 | 2293.3 | 50.00 | Sequence |
| DRB1_0802 | 482 | VVIIIVGSGPATKDI | IIIVGSGPA | 0.2848 | 2295.4 | 50.00 | Sequence |
| DRB1_0802 | 458 | STPELVGKVIGTNPP | PELVGKVIG | 0.2845 | 2302.4 | 50.00 | Sequence |
| DRB1_0802 | 548 | SVIELQVSKGNQFVM | VIELQVSKG | 0.2835 | 2325.9 | 50.00 | Sequence |
| DRB1_0802 | 44 | DLARDPSFYLRFRRE | SFYLRFRRE | 0.2829 | 2343.3 | 50.00 | Sequence |
| DRB1_0802 | 54 | RFRREAQNAAALNHP | RFRREAQNA | 0.2822 | 2360.1 | 50.00 | Sequence |
| DRB1_0802 | 92 | EYVDGVTLRDIVHTE | GVTLRDIVH | 0.2820 | 2365.8 | 50.00 | Sequence |
| DRB1_0802 | 174 | AVIGTAQYLSPEQAR | VIGTAQYLS | 0.2798 | 2423.2 | 50.00 | Sequence |
| DRB1_0802 | 480 | TNVVIIIVGSGPATK | IIIVGSGPA | 0.2776 | 2480.3 | 50.00 | Sequence |
| DRB1_0802 | 508 | QKNLNVYGFTKFSQA | VYGFTKFSQ | 0.2772 | 2490.0 | 50.00 | Sequence |
| DRB1_0802 | 15 | ILGFGGMSEVHLARD | GMSEVHLAR | 0.2761 | 2521.6 | 50.00 | Sequence |
| DRB1_0802 | 162 | IADSGNSVTQTAAVI | GNSVTQTAA | 0.2757 | 2532.8 | 50.00 | Sequence |
| DRB1_0802 | 138 | VKPANIMISATNAVK | MISATNAVK | 0.2739 | 2582.6 | 50.00 | Sequence |
| DRB1_0802 | 481 | NVVIIIVGSGPATKD | IIIVGSGPA | 0.2734 | 2594.8 | 50.00 | Sequence |
| DRB1_0802 | 610 | GTGVNRDGIITLRFG | GVNRDGIIT | 0.2734 | 2594.9 | 50.00 | Sequence |
| DRB1_0802 | 145 | ISATNAVKVMDFGIA | ISATNAVKV | 0.2733 | 2598.7 | 50.00 | Sequence |
| DRB1_0802 | 173 | AAVIGTAQYLSPEQA | VIGTAQYLS | 0.2706 | 2677.0 | 50.00 | Sequence |
| DRB1_0802 | 91 | MEYVDGVTLRDIVHT | GVTLRDIVH | 0.2702 | 2687.3 | 50.00 | Sequence |
| DRB1_0802 | 354 | GITRDVQVPDVRGQS | GITRDVQVP | 0.2689 | 2726.3 | 50.00 | Sequence |
| DRB1_0802 | 213 | PPFTGDSPVSVAYQH | PFTGDSPVS | 0.2681 | 2748.8 | 50.00 | Sequence |
| DRB1_0802 | 516 | FTKFSQASVDSPRPA | FTKFSQASV | 0.2675 | 2766.6 | 50.00 | Sequence |
| DRB1_0802 | 14 | EILGFGGMSEVHLAR | GMSEVHLAR | 0.2662 | 2806.9 | 50.00 | Sequence |
| DRB1_0802 | 479 | ITNVVIIIVGSGPAT | IIIVGSGPA | 0.2639 | 2875.3 | 50.00 | Sequence |
| DRB1_0802 | 288 | TDAERTSLLSSAAGN | RTSLLSSAA | 0.2633 | 2895.8 | 50.00 | Sequence |
| DRB1_0802 | 549 | VIELQVSKGNQFVMP | QVSKGNQFV | 0.2630 | 2905.5 | 50.00 | Sequence |
| DRB1_0802 | 552 | LQVSKGNQFVMPDLS | QVSKGNQFV | 0.2614 | 2955.0 | 50.00 | Sequence |
| DRB1_0802 | 27 | ARDLRLHRDVAVKVL | RDLRLHRDV | 0.2606 | 2980.9 | 50.00 | Sequence |
| DRB1_0802 | 370 | ADAIATLQNRGFKIR | AIATLQNRG | 0.2604 | 2986.7 | 50.00 | Sequence |
| DRB1_0802 | 171 | QTAAVIGTAQYLSPE | VIGTAQYLS | 0.2599 | 3004.9 | 50.00 | Sequence |
| DRB1_0802 | 205 | LYEVLTGEPPFTGDS | YEVLTGEPP | 0.2591 | 3028.8 | 50.00 | Sequence |
| DRB1_0802 | 169 | VTQTAAVIGTAQYLS | VIGTAQYLS | 0.2582 | 3059.3 | 50.00 | Sequence |
| DRB1_0802 | 547 | DSVIELQVSKGNQFV | QVSKGNQFV | 0.2580 | 3068.1 | 50.00 | Sequence |
| DRB1_0802 | 206 | YEVLTGEPPFTGDSP | YEVLTGEPP | 0.2573 | 3088.7 | 50.00 | Sequence |
| DRB1_0802 | 553 | QVSKGNQFVMPDLSG | QVSKGNQFV | 0.2571 | 3095.4 | 50.00 | Sequence |
| DRB1_0802 | 214 | PFTGDSPVSVAYQHV | PFTGDSPVS | 0.2557 | 3142.1 | 50.00 | Sequence |
| DRB1_0802 | 609 | AGTGVNRDGIITLRF | GVNRDGIIT | 0.2556 | 3146.4 | 50.00 | Sequence |
| DRB1_0802 | 353 | GGITRDVQVPDVRGQ | GITRDVQVP | 0.2545 | 3186.0 | 50.00 | Sequence |
| DRB1_0802 | 146 | SATNAVKVMDFGIAR | SATNAVKVM | 0.2541 | 3197.1 | 50.00 | Sequence |
| DRB1_0802 | 440 | VKKLTAAGFGRFKQA | KKLTAAGFG | 0.2540 | 3201.5 | 50.00 | Sequence |
| DRB1_0802 | 578 | RALGWTGMLDKGADV | WTGMLDKGA | 0.2518 | 3277.9 | 50.00 | Sequence |

```
DRB1_0802   37  AVKVLRADLARDPSF  AVKVLRADL        0.2517       3282.3                 50.00     Sequence
DRB1_0802  212  EPPFTGDSPVSVAYQ  PFTGDSPVS        0.2515       3289.7                 50.00     Sequence
DRB1_0802  551  ELQVSKGNQFVMPDL  QVSKGNQFV        0.2515       3290.3                 50.00     Sequence
DRB1_0802  243  SADLDAVVLKALAKN  DAVVLKALA        0.2505       3325.9                 50.00     Sequence
DRB1_0802  148  TNAVKVMDFGIARAI  VMDFGIARA        0.2501       3338.9                 50.00     Sequence
DRB1_0802  287  LTDAERTSLLSSAAG  RTSLLSSAA        0.2500       3342.6                 50.00     Sequence
DRB1_0802  104  HTEGPMTPKRAIEVI  GPMTPKRAI        0.2499       3347.6                 50.00     Sequence
DRB1_0802   97  VTLRDIVHTEGPMTP  VTLRDIVHT        0.2496       3356.6                 50.00     Sequence
DRB1_0802  136  RDVKPANIMISATNA  RDVKPANIM        0.2496       3357.7                 50.00     Sequence
DRB1_0802  134  IHRDVKPANIMISAT  IHRDVKPAN        0.2488       3386.5                 50.00     Sequence
DRB1_0802  577  LRALGWTGMLDKGAD  WTGMLDKGA        0.2488       3386.6                 50.00     Sequence
DRB1_0802  172  TAAVIGTAQYLSPEQ  VIGTAQYLS        0.2487       3391.9                 50.00     Sequence
DRB1_0802  176  IGTAQYLSPEQARGD  YLSPEQARG        0.2472       3445.1                 50.00     Sequence
DRB1_0802   26  LARDLRLHRDVAVKV  RDLRLHRDV        0.2472       3445.2                 50.00     Sequence
DRB1_0802  501  GQTVDVAQKNLNVYG  GQTVDVAQK        0.2471       3450.2                 50.00     Sequence
DRB1_0802  204  VLYEVLTGEPPFTGD  YEVLTGEPP        0.2464       3475.3                 50.00     Sequence
DRB1_0802  286  VLTDAERTSLLSSAA  RTSLLSSAA        0.2463       3480.8                 50.00     Sequence
DRB1_0802  108  PMTPKRAIEVIADAC  MTPKRAIEV        0.2449       3532.6                 50.00     Sequence
DRB1_0802  254  LAKNPENRYQTAAEM  KNPENRYQT        0.2449       3535.0                 50.00     Sequence
DRB1_0802  147  ATNAVKVMDFGIARA  ATNAVKVMD        0.2446       3545.2                 50.00     Sequence
DRB1_0802  167  NSVTQTAAVIGTAQY  VTQTAAVIG        0.2433       3595.8                 50.00     Sequence
DRB1_0802  223  VAYQHVREDPIPPSA  AYQHVREDP        0.2429       3612.6                 50.00     Sequence
DRB1_0802  170  TQTAAVIGTAQYLSP  VIGTAQYLS        0.2425       3626.7                 50.00     Sequence
DRB1_0802  202  GCVLYEVLTGEPPFT  YEVLTGEPP        0.2419       3649.6                 50.00     Sequence
DRB1_0802  581  GWTGMLDKGADVDAG  WTGMLDKGA        0.2413       3675.7                 50.00     Sequence
DRB1_0802  428  IPDVSTLTYAEAVKK  VSTLTYAEA        0.2411       3683.5                 50.00     Sequence
DRB1_0802  507  AQKNLNVYGFTKFSQ  VYGFTKFSQ        0.2410       3684.8                 50.00     Sequence
DRB1_0802  608  PAGTGVNRDGIITLR  GVNRDGIIT        0.2407       3696.3                 50.00     Sequence
DRB1_0802  178  TAQYLSPEQARGDSV  YLSPEQARG        0.2401       3720.9                 50.00     Sequence
DRB1_0802  593  DAGGSQHNRVVYQNP  GSQHNRVVY        0.2395       3745.5                 50.00     Sequence
DRB1_0802  203  CVLYEVLTGEPPFTG  YEVLTGEPP        0.2393       3752.9                 50.00     Sequence
DRB1_0802  262  YQTAAEMRADLVRVH  YQTAAEMRA        0.2388       3775.6                 50.00     Sequence
DRB1_0802  222  SVAYQHVREDPIPPS  AYQHVREDP        0.2376       3825.2                 50.00     Sequence
DRB1_0802  457  PSTPELVGKVIGTNP  PELVGKVIG        0.2362       3884.1                 50.00     Sequence
DRB1_0802  607  PPAGTGVNRDGIITL  GVNRDGIIT        0.2357       3902.8                 50.00     Sequence
DRB1_0802  177  GTAQYLSPEQARGDS  YLSPEQARG        0.2352       3925.2                 50.00     Sequence
DRB1_0802  383  IRTLQKPDSTIPPDH  IRTLQKPDS        0.2343       3963.8                 50.00     Sequence
DRB1_0802  125  LNFSHQNGIIHRDVK  FSHQNGIIH        0.2336       3993.9                 50.00     Sequence
DRB1_0802  550  IELQVSKGNQFVMPD  QVSKGNQFV        0.2330       4017.5                 50.00     Sequence
DRB1_0802  582  WTGMLDKGADVDAGG  WTGMLDKGA        0.2330       4018.7                 50.00     Sequence
DRB1_0802  580  LGWTGMLDKGADVDA  WTGMLDKGA        0.2321       4057.8                 50.00     Sequence
DRB1_0802  543  TVPVDSVIELQVSKG  PVDSVIELQ        0.2320       4061.8                 50.00     Sequence
DRB1_0802  369  SADAIATLQNRGFKI  AIATLQNRG        0.2311       4103.3                 50.00     Sequence
DRB1_0802  103  VHTEGPMTPKRAIEV  GPMTPKRAI        0.2308       4117.9                 50.00     Sequence
DRB1_0802  122  CQALNFSHQNGIIHR  FSHQNGIIH        0.2296       4171.2                 50.00     Sequence
DRB1_0802  334  VVAVLAVLTVVVTIA  VVAVLAVLT        0.2281       4237.3                 50.00     Sequence
DRB1_0802  544  VPVDSVIELQVSKGN  PVDSVIELQ        0.2278       4252.9                 50.00     Sequence
DRB1_0802  500  AGQTVDVAQKNLNVY  GQTVDVAQK        0.2277       4255.9                 50.00     Sequence
DRB1_0802  161  AIADSGNSVTQTAAV  GNSVTQTAA        0.2276       4259.9                 50.00     Sequence
DRB1_0802  556  KGNQFVMPDLSGMFW  GNQFVMPDL        0.2256       4355.9                 50.00     Sequence
DRB1_0802  137  DVKPANIMISATNAV  ANIMISATN        0.2248       4391.8                 50.00     Sequence
DRB1_0802  579  ALGWTGMLDKGADVD  WTGMLDKGA        0.2242       4420.8                 50.00     Sequence
DRB1_0802  606  NPPAGTGVNRDGIIT  GVNRDGIIT        0.2237       4442.3                 50.00     Sequence
DRB1_0802   90  VMEYVDGVTLRDIVH  GVTLRDIVH        0.2234       4460.7                 50.00     Sequence
DRB1_0802  200  SLGCVLYEVLTGEPP  YEVLTGEPP        0.2232       4467.1                 50.00     Sequence
DRB1_0802  521  QASVDSPRPAGEVTG  QASVDSPRP        0.2224       4508.3                 50.00     Sequence
DRB1_0802   38  VKVLRADLARDPSFY  VKVLRADLA        0.2220       4528.5                 50.00     Sequence
DRB1_0802  168  SVTQTAAVIGTAQYL  VTQTAAVIG        0.2218       4539.0                 50.00     Sequence
DRB1_0802  499  VAGQTVDVAQKNLNV  GQTVDVAQK        0.2209       4583.2                 50.00     Sequence
DRB1_0802  124  ALNFSHQNGIIHRDV  FSHQNGIIH        0.2208       4584.1                 50.00     Sequence
DRB1_0802  317  DDTDRDRSIGSVGRW  RDRSIGSVG        0.2208       4586.2                 50.00     Sequence
DRB1_0802  135  HRDVKPANIMISATN  RDVKPANIM        0.2206       4595.2                 50.00     Sequence
DRB1_0802  542  TTVPVDSVIELQVSK  PVDSVIELQ        0.2194       4656.0                 50.00     Sequence
DRB1_0802  109  MTPKRAIEVIADACQ  MTPKRAIEV        0.2187       4691.7                 50.00     Sequence
DRB1_0802  179  AQYLSPEQARGDSVD  YLSPEQARG        0.2184       4709.1                 50.00     Sequence
DRB1_0802  478  AITNVVIIIVGSGPA  IIIVGSGPA        0.2170       4779.7                 50.00     Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0802 | 121 | ACQALNFSHQNGIIH | FSHQNGIIH | 0.2168 | 4791.1 | 50.00 | Sequence |
| DRB1_0802 | 545 | PVDSVIELQVSKGNQ | PVDSVIELQ | 0.2165 | 4804.1 | 50.00 | Sequence |
| DRB1_0802 | 333 | AVVAVLAVLTVVVTI | VVAVLAVLT | 0.2160 | 4828.3 | 50.00 | Sequence |
| DRB1_0802 | 201 | LGCVLYEVLTGEPPF | YEVLTGEPP | 0.2159 | 4836.1 | 50.00 | Sequence |
| DRB1_0802 | 123 | QALNFSHQNGIIHRD | FSHQNGIIH | 0.2157 | 4845.9 | 50.00 | Sequence |
| DRB1_0802 | 102 | IVHTEGPMTPKRAIE | IVHTEGPMT | 0.2154 | 4862.6 | 50.00 | Sequence |
| DRB1_0802 | 475 | QTSAITNVVIIIVGS | QTSAITNVV | 0.2150 | 4882.6 | 50.00 | Sequence |
| DRB1_0802 | 518 | KFSQASVDSPRPAGE | QASVDSPRP | 0.2143 | 4917.6 | 50.00 | Sequence |
| DRB1_0802 | 520 | SQASVDSPRPAGEVT | QASVDSPRP | 0.2140 | 4934.5 | 50.00 | Sequence |
| DRB1_0802 | 13 | GEILGFGGMSEVHLA | GFGGMSEVH | 0.2138 | 4949.3 | 50.00 | Sequence |
| DRB1_0802 | 465 | KVIGTNPPANQTSAI | KVIGTNPPA | 0.2137 | 4952.4 | 50.00 | Sequence |
| DRB1_0802 | 557 | GNQFVMPDLSGMFWV | GNQFVMPDL | 0.2135 | 4961.7 | 50.00 | Sequence |
| DRB1_0802 | 342 | TVVVTIAINTFGGIT | VTIAINTFG | 0.2120 | 5044.2 | 50.00 | Sequence |
| DRB1_0802 | 592 | VDAGGSQHNRVVYQN | GSQHNRVVY | 0.2118 | 5055.4 | 50.00 | Sequence |
| DRB1_0802 | 332 | VAVVAVLAVLTVVVT | VVAVLAVLT | 0.2106 | 5122.9 | 50.00 | Sequence |
| DRB1_0802 | 88 | YIVMEYVDGVTLRDI | YIVMEYVDG | 0.2096 | 5174.9 | 50.00 | Sequence |
| DRB1_0802 | 224 | AYQHVREDPIPPSAR | AYQHVREDP | 0.2096 | 5176.2 | 50.00 | Sequence |
| DRB1_0802 | 211 | GEPPFTGDSPVSVAY | PFTGDSPVS | 0.2084 | 5243.2 | 50.00 | Sequence |
| DRB1_0802 | 498 | DVAGQTVDVAQKNLN | GQTVDVAQK | 0.2083 | 5252.9 | 50.00 | Sequence |
| DRB1_0802 | 267 | EMRADLVRVHNGEPP | MRADLVRVH | 0.2081 | 5261.4 | 50.00 | Sequence |
| DRB1_0802 | 61 | NAAALNHPAIVAVYD | AAALNHPAI | 0.2076 | 5288.6 | 50.00 | Sequence |
| DRB1_0802 | 55 | FRREAQNAAALNHPA | FRREAQNAA | 0.2073 | 5309.0 | 50.00 | Sequence |
| DRB1_0802 | 60 | QNAAALNHPAIVAVY | NAAALNHPA | 0.2069 | 5332.4 | 50.00 | Sequence |
| DRB1_0802 | 156 | FGIARAIADSGNSVT | FGIARAIAD | 0.2060 | 5381.8 | 50.00 | Sequence |
| DRB1_0802 | 242 | LSADLDAVVLKALAK | DAVVLKALA | 0.2060 | 5381.9 | 50.00 | Sequence |
| DRB1_0802 | 87 | PYIVMEYVDGVTLRD | YIVMEYVDG | 0.2059 | 5389.5 | 50.00 | Sequence |
| DRB1_0802 | 180 | QYLSPEQARGDSVDA | YLSPEQARG | 0.2057 | 5400.0 | 50.00 | Sequence |
| DRB1_0802 | 563 | PDLSGMFWVDAEPRL | MFWVDAEPR | 0.2052 | 5430.1 | 50.00 | Sequence |
| DRB1_0802 | 268 | MRADLVRVHNGEPPE | MRADLVRVH | 0.2052 | 5430.7 | 50.00 | Sequence |
| DRB1_0802 | 293 | TSLLSSAAGNLSGPR | TSLLSSAAG | 0.2034 | 5537.1 | 50.00 | Sequence |
| DRB1_0802 | 396 | DHVIGTDPAANTSVS | HVIGTDPAA | 0.2019 | 5624.1 | 50.00 | Sequence |
| DRB1_0802 | 555 | SKGNQFVMPDLSGMF | GNQFVMPDL | 0.2018 | 5635.5 | 50.00 | Sequence |
| DRB1_0802 | 554 | VSKGNQFVMPDLSGM | VSKGNQFVM | 0.2013 | 5665.5 | 50.00 | Sequence |
| DRB1_0802 | 541 | GTTVPVDSVIELQVS | PVDSVIELQ | 0.2008 | 5692.3 | 50.00 | Sequence |
| DRB1_0802 | 12 | LGEILGFGGMSEVHL | GFGGMSEVH | 0.2000 | 5745.2 | 50.00 | Sequence |
| DRB1_0802 | 181 | YLSPEQARGDSVDAR | YLSPEQARG | 0.1999 | 5748.7 | 50.00 | Sequence |
| DRB1_0802 | 269 | RADLVRVHNGEPPEA | LVRVHNGEP | 0.1999 | 5750.6 | 50.00 | Sequence |
| DRB1_0802 | 337 | VLAVLTVVVTIAINT | VLAVLTVVV | 0.1995 | 5775.8 | 50.00 | Sequence |
| DRB1_0802 | 519 | FSQASVDSPRPAGEV | QASVDSPRP | 0.1991 | 5797.1 | 50.00 | Sequence |
| DRB1_0802 | 602 | VVYQNPPAGTGVNRD | VVYQNPPAG | 0.1991 | 5802.8 | 50.00 | Sequence |
| DRB1_0802 | 517 | TKFSQASVDSPRPAG | QASVDSPRP | 0.1988 | 5817.8 | 50.00 | Sequence |
| DRB1_0802 | 43 | ADLARDPSFYLRFRR | PSFYLRFRR | 0.1983 | 5849.0 | 50.00 | Sequence |
| DRB1_0802 | 427 | EIPDVSTLTYAEAVK | VSTLTYAEA | 0.1983 | 5853.0 | 50.00 | Sequence |
| DRB1_0802 | 368 | SSADAIATLQNRGFK | AIATLQNRG | 0.1979 | 5876.4 | 50.00 | Sequence |
| DRB1_0802 | 251 | LKALAKNPENRYQTA | LKALAKNPE | 0.1977 | 5885.3 | 50.00 | Sequence |
| DRB1_0802 | 98 | TLRDIVHTEGPMTPK | IVHTEGPMT | 0.1974 | 5905.7 | 50.00 | Sequence |
| DRB1_0802 | 340 | VLTVVVTIAINTFGG | VLTVVVTIA | 0.1970 | 5930.0 | 50.00 | Sequence |
| DRB1_0802 | 474 | NQTSAITNVVIIIVG | QTSAITNVV | 0.1970 | 5932.0 | 50.00 | Sequence |
| DRB1_0802 | 59 | AQNAAALNHPAIVAV | NAAALNHPA | 0.1969 | 5937.7 | 50.00 | Sequence |
| DRB1_0802 | 456 | SPSTPELVGKVIGTN | PELVGKVIG | 0.1953 | 6040.0 | 50.00 | Sequence |
| DRB1_0802 | 39 | KVLRADLARDPSFYL | KVLRADLAR | 0.1946 | 6087.4 | 50.00 | Sequence |
| DRB1_0802 | 197 | DVYSLGCVLYEVLTG | VYSLGCVLY | 0.1942 | 6114.3 | 50.00 | Sequence |
| DRB1_0802 | 160 | RAIADSGNSVTQTAA | GNSVTQTAA | 0.1935 | 6161.2 | 50.00 | Sequence |
| DRB1_0802 | 546 | VDSVIELQVSKGNQF | VIELQVSKG | 0.1933 | 6178.2 | 50.00 | Sequence |
| DRB1_0802 | 503 | TVDVAQKNLNVYGFT | VDVAQKNLN | 0.1928 | 6211.6 | 50.00 | Sequence |
| DRB1_0802 | 295 | LLSSAAGNLSGPRTD | LLSSAAGNL | 0.1926 | 6225.5 | 50.00 | Sequence |
| DRB1_0802 | 86 | LPYIVMEYVDGVTLR | YIVMEYVDG | 0.1924 | 6234.4 | 50.00 | Sequence |
| DRB1_0802 | 395 | PDHVIGTDPAANTSV | HVIGTDPAA | 0.1921 | 6256.6 | 50.00 | Sequence |
| DRB1_0802 | 101 | DIVHTEGPMTPKRAI | GPMTPKRAI | 0.1908 | 6345.3 | 50.00 | Sequence |
| DRB1_0802 | 506 | VAQKNLNVYGFTKFS | NVYGFTKFS | 0.1902 | 6388.9 | 50.00 | Sequence |
| DRB1_0802 | 339 | AVLTVVVTIAINTFG | VLTVVVTIA | 0.1894 | 6444.1 | 50.00 | Sequence |
| DRB1_0802 | 502 | QTVDVAQKNLNVYGF | VDVAQKNLN | 0.1892 | 6456.5 | 50.00 | Sequence |
| DRB1_0802 | 531 | GEVTGTNPPAGTTVP | EVTGTNPPA | 0.1890 | 6466.1 | 50.00 | Sequence |
| DRB1_0802 | 266 | AEMRADLVRVHNGEP | MRADLVRVH | 0.1884 | 6509.8 | 50.00 | Sequence |
| DRB1_0802 | 253 | ALAKNPENRYQTAAE | KNPENRYQT | 0.1880 | 6543.3 | 50.00 | Sequence |
| DRB1_0802 | 530 | AGEVTGTNPPAGTTV | GEVTGTNPP | 0.1872 | 6594.7 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0802 | 335 | VAVLAVLTVVVTIAI | VLTVVVTIA | 0.1872 | 6599.2 | 50.00 | Sequence |
| DRB1_0802 | 11 | ELGEILGFGGMSEVH | GFGGMSEVH | 0.1867 | 6630.7 | 50.00 | Sequence |
| DRB1_0802 | 477 | SAITNVVIIIVGSGP | VIIIVGSGP | 0.1861 | 6678.6 | 50.00 | Sequence |
| DRB1_0802 | 336 | AVLAVLTVVVTIAIN | LAVLTVVVT | 0.1859 | 6690.4 | 50.00 | Sequence |
| DRB1_0802 | 294 | SLLSSAAGNLSGPRT | LSSAAGNLS | 0.1855 | 6716.3 | 50.00 | Sequence |
| DRB1_0802 | 485 | IIVGSGPATKDIPDV | IIVGSGPAT | 0.1854 | 6727.2 | 50.00 | Sequence |
| DRB1_0802 | 473 | ANQTSAITNVVIIIV | QTSAITNVV | 0.1846 | 6786.3 | 50.00 | Sequence |
| DRB1_0802 | 451 | FKQANSPSTPELVGK | FKQANSPST | 0.1845 | 6789.1 | 50.00 | Sequence |
| DRB1_0802 | 426 | REIPDVSTLTYAEAV | VSTLTYAEA | 0.1837 | 6853.7 | 50.00 | Sequence |
| DRB1_0802 | 198 | VYSLGCVLYEVLTGE | VYSLGCVLY | 0.1832 | 6889.5 | 50.00 | Sequence |
| DRB1_0802 | 362 | PDVRGQSSADAIATL | PDVRGQSSA | 0.1830 | 6901.4 | 50.00 | Sequence |
| DRB1_0802 | 397 | HVIGTDPAANTSVSA | HVIGTDPAA | 0.1828 | 6914.6 | 50.00 | Sequence |
| DRB1_0802 | 358 | DVQVPDVRGQSSADA | QVPDVRGQS | 0.1828 | 6914.8 | 50.00 | Sequence |
| DRB1_0802 | 338 | LAVLTVVVTIAINTF | VLTVVVTIA | 0.1826 | 6932.8 | 50.00 | Sequence |
| DRB1_0802 | 241 | GLSADLDAVVLKALA | DAVVLKALA | 0.1826 | 6935.7 | 50.00 | Sequence |
| DRB1_0802 | 196 | SDVYSLGCVLYEVLT | VYSLGCVLY | 0.1825 | 6943.9 | 50.00 | Sequence |
| DRB1_0802 | 210 | TGEPPFTGDSPVSVA | PFTGDSPVS | 0.1824 | 6951.1 | 50.00 | Sequence |
| DRB1_0802 | 85 | PLPYIVMEYVDGVTL | YIVMEYVDG | 0.1817 | 7001.6 | 50.00 | Sequence |
| DRB1_0802 | 361 | VPDVRGQSSADAIAT | PDVRGQSSA | 0.1811 | 7050.1 | 50.00 | Sequence |
| DRB1_0802 | 209 | LTGEPPFTGDSPVSV | PFTGDSPVS | 0.1805 | 7092.9 | 50.00 | Sequence |
| DRB1_0802 | 316 | LDDTDRDRSIGSVGR | RDRSIGSVG | 0.1787 | 7232.6 | 50.00 | Sequence |
| DRB1_0802 | 472 | PANQTSAITNVVIII | QTSAITNVV | 0.1784 | 7257.9 | 50.00 | Sequence |
| DRB1_0802 | 157 | GIARAIADSGNSVTQ | GIARAIADS | 0.1783 | 7265.9 | 50.00 | Sequence |
| DRB1_0802 | 360 | QVPDVRGQSSADAIA | QVPDVRGQS | 0.1780 | 7286.1 | 50.00 | Sequence |
| DRB1_0802 | 272 | LVRVHNGEPPEAPKV | LVRVHNGEP | 0.1779 | 7296.9 | 50.00 | Sequence |
| DRB1_0802 | 471 | PPANQTSAITNVVII | QTSAITNVV | 0.1779 | 7297.3 | 50.00 | Sequence |
| DRB1_0802 | 299 | AAGNLSGPRTDPLPR | AGNLSGPRT | 0.1774 | 7336.4 | 50.00 | Sequence |
| DRB1_0802 | 497 | PDVAGQTVDVAQKNL | GQTVDVAQK | 0.1772 | 7349.0 | 50.00 | Sequence |
| DRB1_0802 | 8 | DRYELGEILGFGGMS | RYELGEILG | 0.1766 | 7401.1 | 50.00 | Sequence |
| DRB1_0802 | 359 | VQVPDVRGQSSADAI | QVPDVRGQS | 0.1762 | 7431.1 | 50.00 | Sequence |
| DRB1_0802 | 58 | EAQNAAALNHPAIVA | AAALNHPAI | 0.1758 | 7460.1 | 50.00 | Sequence |
| DRB1_0802 | 540 | AGTTVPVDSVIELQV | PVDSVIELQ | 0.1758 | 7463.3 | 50.00 | Sequence |
| DRB1_0802 | 252 | KALAKNPENRYQTAA | KNPENRYQT | 0.1753 | 7505.4 | 50.00 | Sequence |
| DRB1_0802 | 394 | PPDHVIGTDPAANTS | HVIGTDPAA | 0.1751 | 7516.3 | 50.00 | Sequence |
| DRB1_0802 | 341 | LTVVVTIAINTFGGI | VTIAINTFG | 0.1749 | 7539.6 | 50.00 | Sequence |
| DRB1_0802 | 529 | PAGEVTGTNPPAGTT | GEVTGTNPP | 0.1746 | 7562.0 | 50.00 | Sequence |
| DRB1_0802 | 62 | AAALNHPAIVAVYDT | AAALNHPAI | 0.1745 | 7567.3 | 50.00 | Sequence |
| DRB1_0802 | 99 | LRDIVHTEGPMTPKR | IVHTEGPMT | 0.1723 | 7747.7 | 50.00 | Sequence |
| DRB1_0802 | 367 | QSSADAIATLQNRGF | AIATLQNRG | 0.1722 | 7757.6 | 50.00 | Sequence |
| DRB1_0802 | 199 | YSLGCVLYEVLTGEP | SLGCVLYEV | 0.1721 | 7765.6 | 50.00 | Sequence |
| DRB1_0802 | 4 | SHLSDRYELGEILGF | HLSDRYELG | 0.1715 | 7818.9 | 50.00 | Sequence |
| DRB1_0802 | 9 | RYELGEILGFGGMSE | RYELGEILG | 0.1714 | 7825.6 | 50.00 | Sequence |
| DRB1_0802 | 270 | ADLVRVHNGEPPEAP | LVRVHNGEP | 0.1711 | 7854.2 | 50.00 | Sequence |
| DRB1_0802 | 357 | RDVQVPDVRGQSSAD | QVPDVRGQS | 0.1707 | 7889.9 | 50.00 | Sequence |
| DRB1_0802 | 504 | VDVAQKNLNVYGFTK | VDVAQKNLN | 0.1701 | 7938.5 | 50.00 | Sequence |
| DRB1_0802 | 300 | AGNLSGPRTDPLPRQ | AGNLSGPRT | 0.1696 | 7980.9 | 50.00 | Sequence |
| DRB1_0802 | 5 | HLSDRYELGEILGFG | HLSDRYELG | 0.1694 | 7996.4 | 50.00 | Sequence |
| DRB1_0802 | 356 | TRDVQVPDVRGQSSA | RDVQVPDVR | 0.1680 | 8120.7 | 50.00 | Sequence |
| DRB1_0802 | 476 | TSAITNVVIIIVGSG | ITNVVIIIV | 0.1670 | 8209.0 | 50.00 | Sequence |
| DRB1_0802 | 591 | DVDAGGSQHNRVVYQ | GSQHNRVVY | 0.1666 | 8239.6 | 50.00 | Sequence |
| DRB1_0802 | 40 | VLRADLARDPSFYLR | RADLARDPS | 0.1665 | 8252.8 | 50.00 | Sequence |
| DRB1_0802 | 89 | IVMEYVDGVTLRDIV | YVDGVTLRD | 0.1654 | 8355.7 | 50.00 | Sequence |
| DRB1_0802 | 366 | GQSSADAIATLQNRG | AIATLQNRG | 0.1645 | 8432.7 | 50.00 | Sequence |
| DRB1_0802 | 285 | KVLTDAERTSLLSSA | VLTDAERTS | 0.1643 | 8449.3 | 50.00 | Sequence |
| DRB1_0802 | 392 | TIPPDHVIGTDPAAN | HVIGTDPAA | 0.1643 | 8454.9 | 50.00 | Sequence |
| DRB1_0802 | 265 | AAEMRADLVRVHNGE | MRADLVRVH | 0.1640 | 8476.6 | 50.00 | Sequence |
| DRB1_0802 | 3 | PSHLSDRYELGEILG | HLSDRYELG | 0.1639 | 8484.5 | 50.00 | Sequence |
| DRB1_0802 | 271 | DLVRVHNGEPPEAPK | LVRVHNGEP | 0.1629 | 8584.9 | 50.00 | Sequence |
| DRB1_0802 | 470 | NPPANQTSAITNVVI | QTSAITNVV | 0.1625 | 8618.6 | 50.00 | Sequence |
| DRB1_0802 | 355 | ITRDVQVPDVRGQSS | RDVQVPDVR | 0.1624 | 8627.9 | 50.00 | Sequence |
| DRB1_0802 | 393 | IPPDHVIGTDPAANT | HVIGTDPAA | 0.1622 | 8642.7 | 50.00 | Sequence |
| DRB1_0802 | 425 | QREIPDVSTLTYAEA | VSTLTYAEA | 0.1615 | 8708.4 | 50.00 | Sequence |
| DRB1_0802 | 558 | NQFVMPDLSGMFWVD | MPDLSGMFW | 0.1614 | 8723.1 | 50.00 | Sequence |
| DRB1_0802 | 232 | PIPPSARHEGLSADL | IPPSARHEG | 0.1608 | 8774.4 | 50.00 | Sequence |
| DRB1_0802 | 296 | LSSAAGNLSGPRTDP | LSSAAGNLS | 0.1607 | 8786.2 | 50.00 | Sequence |
| DRB1_0802 | 208 | VLTGEPPFTGDSPVS | PFTGDSPVS | 0.1605 | 8802.2 | 50.00 | Sequence |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| DRB1_0802 | 284 | PKVLTDAERTSLLSS | VLTDAERTS | 0.1599 | 8859.0 | 50.00 | Sequence |
| DRB1_0802 | 496 | IPDVAGQTVDVAQKN | GQTVDVAQK | 0.1599 | 8862.8 | 50.00 | Sequence |
| DRB1_0802 | 264 | TAAEMRADLVRVHNG | MRADLVRVH | 0.1597 | 8879.1 | 50.00 | Sequence |
| DRB1_0802 | 110 | TPKRAIEVIADACQA | PKRAIEVIA | 0.1590 | 8951.0 | 50.00 | Sequence |
| DRB1_0802 | 56 | RREAQNAAALNHPAI | RREAQNAAA | 0.1587 | 8979.8 | 50.00 | Sequence |
| DRB1_0802 | 263 | QTAAEMRADLVRVHN | MRADLVRVH | 0.1581 | 9041.7 | 50.00 | Sequence |
| DRB1_0802 | 231 | DPIPPSARHEGLSAD | IPPSARHEG | 0.1580 | 9043.2 | 50.00 | Sequence |
| DRB1_0802 | 301 | GNLSGPRTDPLPRQD | GNLSGPRTD | 0.1571 | 9132.5 | 50.00 | Sequence |
| DRB1_0802 | 559 | QFVMPDLSGMFWVDA | MPDLSGMFW | 0.1557 | 9271.9 | 50.00 | Sequence |
| DRB1_0802 | 7 | SDRYELGEILGFGGM | RYELGEILG | 0.1556 | 9285.1 | 50.00 | Sequence |
| DRB1_0802 | 315 | DLDDTDRDRSIGSVG | RDRSIGSVG | 0.1545 | 9397.3 | 50.00 | Sequence |
| DRB1_0802 | 455 | NSPSTPELVGKVIGT | PELVGKVIG | 0.1542 | 9427.3 | 50.00 | Sequence |
| DRB1_0802 | 225 | YQHVREDPIPPSARH | QHVREDPIP | 0.1540 | 9448.7 | 50.00 | Sequence |
| DRB1_0802 | 100 | RDIVHTEGPMTPKRA | IVHTEGPMT | 0.1536 | 9487.3 | 50.00 | Sequence |
| DRB1_0802 | 560 | FVMPDLSGMFWVDAE | MPDLSGMFW | 0.1534 | 9509.6 | 50.00 | Sequence |
| DRB1_0802 | 562 | MPDLSGMFWVDAEPR | MFWVDAEPR | 0.1532 | 9531.3 | 50.00 | Sequence |
| DRB1_0802 | 84 | GPLPYIVMEYVDGVT | YIVMEYVDG | 0.1530 | 9551.3 | 50.00 | Sequence |
| DRB1_0802 | 363 | DVRGQSSADAIATLQ | VRGQSSADA | 0.1527 | 9576.5 | 50.00 | Sequence |
| DRB1_0802 | 364 | VRGQSSADAIATLQN | VRGQSSADA | 0.1523 | 9620.9 | 50.00 | Sequence |
| DRB1_0802 | 522 | ASVDSPRPAGEVTGT | SVDSPRPAG | 0.1518 | 9677.9 | 50.00 | Sequence |
| DRB1_0802 | 469 | TNPPANQTSAITNVV | QTSAITNVV | 0.1502 | 9842.2 | 50.00 | Sequence |
| DRB1_0802 | 304 | SGPRTDPLPRQDLDD | GPRTDPLPR | 0.1500 | 9864.2 | 50.00 | Sequence |
| DRB1_0802 | 273 | VRVHNGEPPEAPKVL | VRVHNGEPP | 0.1498 | 9890.5 | 50.00 | Sequence |
| DRB1_0802 | 532 | EVTGTNPPAGTTVPV | EVTGTNPPA | 0.1495 | 9921.5 | 50.00 | Sequence |
| DRB1_0802 | 230 | EDPIPPSARHEGLSA | IPPSARHEG | 0.1490 | 9975.6 | 50.00 | Sequence |
| DRB1_0802 | 57 | REAQNAAALNHPAIV | NAAALNHPA | 0.1488 | 9989.6 | 50.00 | Sequence |
| DRB1_0802 | 111 | PKRAIEVIADACQAL | PKRAIEVIA | 0.1474 | 10142.7 | 50.00 | Sequence |
| DRB1_0802 | 41 | LRADLARDPSFYLRF | RADLARDPS | 0.1473 | 10161.0 | 50.00 | Sequence |
| DRB1_0802 | 82 | PAGPLPYIVMEYVDG | PAGPLPYIV | 0.1465 | 10247.4 | 50.00 | Sequence |
| DRB1_0802 | 64 | ALNHPAIVAVYDTGE | ALNHPAIVA | 0.1463 | 10264.8 | 50.00 | Sequence |
| DRB1_0802 | 528 | RPAGEVTGTNPPAGT | GEVTGTNPP | 0.1463 | 10269.7 | 50.00 | Sequence |
| DRB1_0802 | 590 | ADVDAGGSQHNRVVY | GSQHNRVVY | 0.1458 | 10320.5 | 50.00 | Sequence |
| DRB1_0802 | 495 | DIPDVAGQTVDVAQK | GQTVDVAQK | 0.1457 | 10330.6 | 50.00 | Sequence |
| DRB1_0802 | 233 | IPPSARHEGLSADLD | IPPSARHEG | 0.1437 | 10564.1 | 50.00 | Sequence |
| DRB1_0802 | 6 | LSDRYELGEILGFGG | RYELGEILG | 0.1436 | 10568.1 | 50.00 | Sequence |
| DRB1_0802 | 303 | LSGPRTDPLPRQDLD | GPRTDPLPR | 0.1435 | 10587.2 | 50.00 | Sequence |
| DRB1_0802 | 302 | NLSGPRTDPLPRQDL | GPRTDPLPR | 0.1426 | 10690.1 | 50.00 | Sequence |
| DRB1_0802 | 391 | STIPPDHVIGTDPAA | HVIGTDPAA | 0.1422 | 10731.0 | 50.00 | Sequence |
| DRB1_0802 | 604 | YQNPPAGTGVNRDGI | YQNPPAGTG | 0.1414 | 10832.1 | 50.00 | Sequence |
| DRB1_0802 | 297 | SSAAGNLSGPRTDPL | AGNLSGPRT | 0.1412 | 10856.8 | 50.00 | Sequence |
| DRB1_0802 | 414 | EITVNVSTGPEQREI | ITVNVSTGP | 0.1409 | 10883.6 | 50.00 | Sequence |
| DRB1_0802 | 298 | SAAGNLSGPRTDPLP | AGNLSGPRT | 0.1408 | 10896.7 | 50.00 | Sequence |
| DRB1_0802 | 527 | PRPAGEVTGTNPPAG | VTGTNPPAG | 0.1402 | 10966.5 | 50.00 | Sequence |
| DRB1_0802 | 415 | ITVNVSTGPEQREIP | ITVNVSTGP | 0.1396 | 11041.0 | 50.00 | Sequence |
| DRB1_0802 | 305 | GPRTDPLPRQDLDDT | GPRTDPLPR | 0.1393 | 11075.4 | 50.00 | Sequence |
| DRB1_0802 | 226 | QHVREDPIPPSARHE | QHVREDPIP | 0.1391 | 11095.7 | 50.00 | Sequence |
| DRB1_0802 | 454 | ANSPSTPELVGKVIG | PELVGKVIG | 0.1381 | 11224.3 | 50.00 | Sequence |
| DRB1_0802 | 42 | RADLARDPSFYLRFR | RADLARDPS | 0.1379 | 11245.3 | 50.00 | Sequence |
| DRB1_0802 | 283 | APKVLTDAERTSLLS | VLTDAERTS | 0.1375 | 11292.8 | 50.00 | Sequence |
| DRB1_0802 | 505 | DVAQKNLNVYGFTKF | NLNVYGFTK | 0.1375 | 11295.5 | 50.00 | Sequence |
| DRB1_0802 | 63 | AALNHPAIVAVYDTG | ALNHPAIVA | 0.1371 | 11338.9 | 50.00 | Sequence |
| DRB1_0802 | 195 | RSDVYSLGCVLYEVL | VYSLGCVLY | 0.1371 | 11345.2 | 50.00 | Sequence |
| DRB1_0802 | 412 | GDEITVNVSTGPEQR | ITVNVSTGP | 0.1364 | 11432.6 | 50.00 | Sequence |
| DRB1_0802 | 83 | AGPLPYIVMEYVDGV | YIVMEYVDG | 0.1363 | 11445.9 | 50.00 | Sequence |
| DRB1_0802 | 421 | TGPEQREIPDVSTLT | TGPEQREIP | 0.1357 | 11510.4 | 50.00 | Sequence |
| DRB1_0802 | 417 | VNVSTGPEQREIPDV | VNVSTGPEQ | 0.1351 | 11590.9 | 50.00 | Sequence |
| DRB1_0802 | 229 | REDPIPPSARHEGLS | IPPSARHEG | 0.1344 | 11685.1 | 50.00 | Sequence |
| DRB1_0802 | 0 | MTTPSHLSDRYELGE | HLSDRYELG | 0.1330 | 11862.0 | 50.00 | Sequence |
| DRB1_0802 | 2 | TPSHLSDRYELGEIL | HLSDRYELG | 0.1328 | 11883.7 | 50.00 | Sequence |
| DRB1_0802 | 10 | YELGEILGFGGMSEV | ELGEILGFG | 0.1317 | 12030.5 | 50.00 | Sequence |
| DRB1_0802 | 188 | RGDSVDARSDVYSLG | GDSVDARSD | 0.1315 | 12052.7 | 50.00 | Sequence |
| DRB1_0802 | 207 | EVLTGEPPFTGDSPV | VLTGEPPFT | 0.1296 | 12301.4 | 50.00 | Sequence |
| DRB1_0802 | 561 | VMPDLSGMFWVDAEP | GMFWVDAEP | 0.1291 | 12363.9 | 50.00 | Sequence |
| DRB1_0802 | 413 | DEITVNVSTGPEQRE | ITVNVSTGP | 0.1290 | 12388.8 | 50.00 | Sequence |
| DRB1_0802 | 120 | DACQALNFSHQNGII | CQALNFSHQ | 0.1289 | 12399.5 | 50.00 | Sequence |
| DRB1_0802 | 384 | RTLQKPDSTIPPDHV | LQKPDSTIP | 0.1284 | 12457.5 | 50.00 | Sequence |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| DRB1_0802 | 539 | PAGTTVPVDSVIELQ | TTVPVDSVI | 0.1280 | 12510.3 | 50.00 | Sequence |
| DRB1_0802 | 533 | VTGTNPPAGTTVPVD | VTGTNPPAG | 0.1278 | 12545.1 | 50.00 | Sequence |
| DRB1_0802 | 81 | TPAGPLPYIVMEYVD | PAGPLPYIV | 0.1278 | 12545.2 | 50.00 | Sequence |
| DRB1_0802 | 416 | TVNVSTGPEQREIPD | VNVSTGPEQ | 0.1277 | 12557.9 | 50.00 | Sequence |
| DRB1_0802 | 194 | ARSDVYSLGCVLYEV | VYSLGCVLY | 0.1250 | 12927.1 | 50.00 | Sequence |
| DRB1_0802 | 186 | QARGDSVDARSDVYS | GDSVDARSD | 0.1250 | 12927.9 | 50.00 | Sequence |
| DRB1_0802 | 227 | HVREDPIPPSARHEG | HVREDPIPP | 0.1250 | 12930.6 | 50.00 | Sequence |
| DRB1_0802 | 420 | STGPEQREIPDVSTL | TGPEQREIP | 0.1248 | 12955.9 | 50.00 | Sequence |
| DRB1_0802 | 80 | ETPAGPLPYIVMEYV | PAGPLPYIV | 0.1238 | 13104.8 | 50.00 | Sequence |
| DRB1_0802 | 189 | GDSVDARSDVYSLGC | GDSVDARSD | 0.1235 | 13136.9 | 50.00 | Sequence |
| DRB1_0802 | 603 | VYQNPPAGTGVNRDG | YQNPPAGTG | 0.1231 | 13205.3 | 50.00 | Sequence |
| DRB1_0802 | 69 | AIVAVYDTGEAETPA | AIVAVYDTG | 0.1230 | 13210.6 | 50.00 | Sequence |
| DRB1_0802 | 365 | RGQSSADAIATLQNR | GQSSADAIA | 0.1230 | 13212.0 | 50.00 | Sequence |
| DRB1_0802 | 187 | ARGDSVDARSDVYSL | RGDSVDARS | 0.1227 | 13260.1 | 50.00 | Sequence |
| DRB1_0802 | 411 | AGDEITVNVSTGPEQ | ITVNVSTGP | 0.1221 | 13341.4 | 50.00 | Sequence |
| DRB1_0802 | 68 | PAIVAVYDTGEAETP | AIVAVYDTG | 0.1213 | 13454.4 | 50.00 | Sequence |
| DRB1_0802 | 79 | AETPAGPLPYIVMEY | AETPAGPLP | 0.1211 | 13481.6 | 50.00 | Sequence |
| DRB1_0802 | 1 | TTPSHLSDRYELGEI | HLSDRYELG | 0.1207 | 13547.3 | 50.00 | Sequence |
| DRB1_0802 | 192 | VDARSDVYSLGCVLY | VYSLGCVLY | 0.1197 | 13693.1 | 50.00 | Sequence |
| DRB1_0802 | 74 | YDTGEAETPAGPLPY | YDTGEAETP | 0.1191 | 13776.7 | 50.00 | Sequence |
| DRB1_0802 | 73 | VYDTGEAETPAGPLP | YDTGEAETP | 0.1181 | 13926.4 | 50.00 | Sequence |
| DRB1_0802 | 385 | TLQKPDSTIPPDHVI | LQKPDSTIP | 0.1167 | 14142.2 | 50.00 | Sequence |
| DRB1_0802 | 386 | LQKPDSTIPPDHVIG | LQKPDSTIP | 0.1167 | 14145.2 | 50.00 | Sequence |
| DRB1_0802 | 228 | VREDPIPPSARHEGL | DPIPPSARH | 0.1156 | 14309.6 | 50.00 | Sequence |
| DRB1_0802 | 424 | EQREIPDVSTLTYAE | REIPDVSTL | 0.1154 | 14344.3 | 50.00 | Sequence |
| DRB1_0802 | 526 | SPRPAGEVTGTNPPA | GEVTGTNPP | 0.1154 | 14349.5 | 50.00 | Sequence |
| DRB1_0802 | 282 | EAPKVLTDAERTSLL | VLTDAERTS | 0.1148 | 14444.2 | 50.00 | Sequence |
| DRB1_0802 | 191 | SVDARSDVYSLGCVL | VDARSDVYS | 0.1145 | 14479.1 | 50.00 | Sequence |
| DRB1_0802 | 78 | EAETPAGPLPYIVME | AETPAGPLP | 0.1125 | 14806.5 | 50.00 | Sequence |
| DRB1_0802 | 466 | VIGTNPPANQTSAIT | VIGTNPPAN | 0.1123 | 14831.5 | 50.00 | Sequence |
| DRB1_0802 | 403 | PAANTSVSAGDEITV | AANTSVSAG | 0.1115 | 14962.7 | 50.00 | Sequence |
| DRB1_0802 | 419 | VSTGPEQREIPDVST | TGPEQREIP | 0.1106 | 15107.5 | 50.00 | Sequence |
| DRB1_0802 | 77 | GEAETPAGPLPYIVM | AETPAGPLP | 0.1104 | 15138.5 | 50.00 | Sequence |
| DRB1_0802 | 280 | PPEAPKVLTDAERTS | VLTDAERTS | 0.1096 | 15273.5 | 50.00 | Sequence |
| DRB1_0802 | 523 | SVDSPRPAGEVTGTN | SVDSPRPAG | 0.1094 | 15303.0 | 50.00 | Sequence |
| DRB1_0802 | 583 | TGMLDKGADVDAGGS | MLDKGADVD | 0.1090 | 15368.5 | 50.00 | Sequence |
| DRB1_0802 | 158 | IARAIADSGNSVTQT | IARAIADSG | 0.1079 | 15551.7 | 50.00 | Sequence |
| DRB1_0802 | 537 | NPPAGTTVPVDSVIE | NPPAGTTVP | 0.1073 | 15665.3 | 50.00 | Sequence |
| DRB1_0802 | 423 | PEQREIPDVSTLTYA | EIPDVSTLT | 0.1072 | 15680.6 | 50.00 | Sequence |
| DRB1_0802 | 468 | GTNPPANQTSAITNV | GTNPPANQT | 0.1071 | 15698.9 | 50.00 | Sequence |
| DRB1_0802 | 76 | TGEAETPAGPLPYIV | AETPAGPLP | 0.1069 | 15735.0 | 50.00 | Sequence |
| DRB1_0802 | 589 | GADVDAGGSQHNRVV | GGSQHNRVV | 0.1068 | 15746.7 | 50.00 | Sequence |
| DRB1_0802 | 240 | EGLSADLDAVVLKAL | LDAVVLKAL | 0.1067 | 15768.6 | 50.00 | Sequence |
| DRB1_0802 | 190 | DSVDARSDVYSLGCV | SVDARSDVY | 0.1066 | 15780.2 | 50.00 | Sequence |
| DRB1_0802 | 235 | PSARHEGLSADLDAV | PSARHEGLS | 0.1063 | 15827.0 | 50.00 | Sequence |
| DRB1_0802 | 422 | GPEQREIPDVSTLTY | PEQREIPDV | 0.1056 | 15957.7 | 50.00 | Sequence |
| DRB1_0802 | 193 | DARSDVYSLGCVLYE | VYSLGCVLY | 0.1048 | 16094.0 | 50.00 | Sequence |
| DRB1_0802 | 489 | SGPATKDIPDVAGQT | SGPATKDIP | 0.1045 | 16135.5 | 50.00 | Sequence |
| DRB1_0802 | 584 | GMLDKGADVDAGGSQ | MLDKGADVD | 0.1041 | 16212.5 | 50.00 | Sequence |
| DRB1_0802 | 486 | IVGSGPATKDIPDVA | IVGSGPATK | 0.1041 | 16214.8 | 50.00 | Sequence |
| DRB1_0802 | 234 | PPSARHEGLSADLDA | PSARHEGLS | 0.1039 | 16254.1 | 50.00 | Sequence |
| DRB1_0802 | 281 | PEAPKVLTDAERTSL | VLTDAERTS | 0.1026 | 16473.5 | 50.00 | Sequence |
| DRB1_0802 | 71 | VAVYDTGEAETPAGP | YDTGEAETP | 0.1011 | 16747.2 | 50.00 | Sequence |
| DRB1_0802 | 67 | HPAIVAVYDTGEAET | AIVAVYDTG | 0.1008 | 16796.5 | 50.00 | Sequence |
| DRB1_0802 | 467 | IGTNPPANQTSAITN | GTNPPANQT | 0.1005 | 16846.6 | 50.00 | Sequence |
| DRB1_0802 | 488 | GSGPATKDIPDVAGQ | SGPATKDIP | 0.1004 | 16868.5 | 50.00 | Sequence |
| DRB1_0802 | 117 | VIADACQALNFSHQN | VIADACQAL | 0.1000 | 16939.3 | 50.00 | Sequence |
| DRB1_0802 | 408 | SVSAGDEITVNVSTG | SVSAGDEIT | 0.0994 | 17047.4 | 50.00 | Sequence |
| DRB1_0802 | 418 | NVSTGPEQREIPDVS | TGPEQREIP | 0.0993 | 17078.2 | 50.00 | Sequence |
| DRB1_0802 | 410 | SAGDEITVNVSTGPE | GDEITVNVS | 0.0983 | 17261.8 | 50.00 | Sequence |
| DRB1_0802 | 535 | GTNPPAGTTVPVDSV | GTNPPAGTT | 0.0981 | 17303.8 | 50.00 | Sequence |
| DRB1_0802 | 116 | EVIADACQALNFSHQ | VIADACQAL | 0.0976 | 17383.8 | 50.00 | Sequence |
| DRB1_0802 | 536 | TNPPAGTTVPVDSVI | NPPAGTTVP | 0.0975 | 17410.7 | 50.00 | Sequence |
| DRB1_0802 | 75 | DTGEAETPAGPLPYI | AETPAGPLP | 0.0974 | 17438.2 | 50.00 | Sequence |
| DRB1_0802 | 490 | GPATKDIPDVAGQTV | PATKDIPDV | 0.0973 | 17449.7 | 50.00 | Sequence |
| DRB1_0802 | 119 | ADACQALNFSHQNGI | QALNFSHQN | 0.0972 | 17462.6 | 50.00 | Sequence |

```
   DRB1_0802  409  VSAGDEITVNVSTGP  GDEITVNVS        0.0970      17502.3                 50.00     Sequence
   DRB1_0802  605  QNPPAGTGVNRDGII  GTGVNRDGI        0.0961      17670.9                 50.00     Sequence
   DRB1_0802  538  PPAGTTVPVDSVIEL  TTVPVDSVI        0.0954      17810.2                 50.00     Sequence
   DRB1_0802  487  VGSGPATKDIPDVAG  PATKDIPDV        0.0953      17826.4                 50.00     Sequence
   DRB1_0802  274  RVHNGEPPEAPKVLT  RVHNGEPPE        0.0936      18160.7                 50.00     Sequence
   DRB1_0802   72  AVYDTGEAETPAGPL  YDTGEAETP        0.0927      18341.2                 50.00     Sequence
   DRB1_0802  185  EQARGDSVDARSDVY  GDSVDARSD        0.0926      18353.7                 50.00     Sequence
   DRB1_0802   70  IVAVYDTGEAETPAG  VAVYDTGEA        0.0925      18371.4                 50.00     Sequence
   DRB1_0802  407  TSVSAGDEITVNVST  SVSAGDEIT        0.0923      18427.1                 50.00     Sequence
   DRB1_0802  404  AANTSVSAGDEITVN  AANTSVSAG        0.0922      18434.7                 50.00     Sequence
   DRB1_0802  113  RAIEVIADACQALNF  RAIEVIADA        0.0922      18442.1                 50.00     Sequence
   DRB1_0802  525  DSPRPAGEVTGTNPP  GEVTGTNPP        0.0917      18538.5                 50.00     Sequence
   DRB1_0802  236  SARHEGLSADLDAVV  RHEGLSADL        0.0912      18640.1                 50.00     Sequence
   DRB1_0802  306  PRTDPLPRQDLDDTD  PRTDPLPRQ        0.0907      18748.1                 50.00     Sequence
   DRB1_0802  237  ARHEGLSADLDAVVL  RHEGLSADL        0.0901      18856.9                 50.00     Sequence
   DRB1_0802  279  EPPEAPKVLTDAERT  PKVLTDAER        0.0898      18933.6                 50.00     Sequence
   DRB1_0802  402  DPAANTSVSAGDEIT  DPAANTSVS        0.0894      19005.4                 50.00     Sequence
   DRB1_0802  115  IEVIADACQALNFSH  IEVIADACQ        0.0893      19032.4                 50.00     Sequence
   DRB1_0802  453  QANSPSTPELVGKVI  TPELVGKVI        0.0893      19033.0                 50.00     Sequence
   DRB1_0802   65  LNHPAIVAVYDTGEA  AIVAVYDTG        0.0885      19196.6                 50.00     Sequence
   DRB1_0802  534  TGTNPPAGTTVPVDS  GTNPPAGTT        0.0865      19608.0                 50.00     Sequence
   DRB1_0802  238  RHEGLSADLDAVVLK  RHEGLSADL        0.0862      19673.5                 50.00     Sequence
   DRB1_0802  112  KRAIEVIADACQALN  RAIEVIADA        0.0861      19692.7                 50.00     Sequence
   DRB1_0802  398  VIGTDPAANTSVSAG  VIGTDPAAN        0.0859      19739.8                 50.00     Sequence
   DRB1_0802  491  PATKDIPDVAGQTVD  IPDVAGQTV        0.0857      19771.2                 50.00     Sequence
   DRB1_0802  118  IADACQALNFSHQNG  QALNFSHQN        0.0853      19864.9                 50.00     Sequence
   DRB1_0802   66  NHPAIVAVYDTGEAE  AIVAVYDTG        0.0853      19865.8                 50.00     Sequence
   DRB1_0802  406  NTSVSAGDEITVNVS  SVSAGDEIT        0.0853      19867.9                 50.00     Sequence
   DRB1_0802  184  PEQARGDSVDARSDV  GDSVDARSD        0.0844      20068.9                 50.00     Sequence
   DRB1_0802  387  QKPDSTIPPDHVIGT  TIPPDHVIG        0.0838      20200.0                 50.00     Sequence
   DRB1_0802  390  DSTIPPDHVIGTDPA  TIPPDHVIG        0.0816      20690.0                 50.00     Sequence
   DRB1_0802  239  HEGLSADLDAVVLKA  GLSADLDAV        0.0810      20808.7                 50.00     Sequence
   DRB1_0802  114  AIEVIADACQALNFS  IEVIADACQ        0.0802      21004.6                 50.00     Sequence
   DRB1_0802  405  ANTSVSAGDEITVNV  SVSAGDEIT        0.0783      21438.1                 50.00     Sequence
   DRB1_0802  183  SPEQARGDSVDARSD  GDSVDARSD        0.0780      21511.1                 50.00     Sequence
   DRB1_0802  159  ARAIADSGNSVTQTA  SGNSVTQTA        0.0765      21847.6                 50.00     Sequence
   DRB1_0802  585  MLDKGADVDAGGSQH  MLDKGADVD        0.0733      22634.2                 50.00     Sequence
   DRB1_0802  452  KQANSPSTPELVGKV  KQANSPSTP        0.0730      22689.9                 50.00     Sequence
   DRB1_0802  314  QDLDDTDRDRSIGSV  LDDTDRDRS        0.0701      23416.4                 50.00     Sequence
   DRB1_0802  401  TDPAANTSVSAGDEI  AANTSVSAG        0.0688      23750.2                 50.00     Sequence
   DRB1_0802  400  GTDPAANTSVSAGDE  AANTSVSAG        0.0680      23966.5                 50.00     Sequence
   DRB1_0802  278  GEPPEAPKVLTDAER  PKVLTDAER        0.0675      24089.7                 50.00     Sequence
   DRB1_0802  494  KDIPDVAGQTVDVAQ  IPDVAGQTV        0.0671      24202.3                 50.00     Sequence
   DRB1_0802  388  KPDSTIPPDHVIGTD  TIPPDHVIG        0.0669      24247.1                 50.00     Sequence
   DRB1_0802  524  VDSPRPAGEVTGTNP  SPRPAGEVT        0.0668      24263.4                 50.00     Sequence
   DRB1_0802  493  TKDIPDVAGQTVDVA  IPDVAGQTV        0.0657      24565.1                 50.00     Sequence
   DRB1_0802  588  KGADVDAGGSQHNRV  VDAGGSQHN        0.0651      24716.5                 50.00     Sequence
   DRB1_0802  307  RTDPLPRQDLDDTDR  RTDPLPRQD        0.0641      24978.1                 50.00     Sequence
   DRB1_0802  399  IGTDPAANTSVSAGD  AANTSVSAG        0.0641      24996.2                 50.00     Sequence
   DRB1_0802  275  VHNGEPPEAPKVLTD  VHNGEPPEA        0.0639      25037.9                 50.00     Sequence
   DRB1_0802  389  PDSTIPPDHVIGTDP  TIPPDHVIG        0.0634      25190.9                 50.00     Sequence
   DRB1_0802  182  LSPEQARGDSVDARS  RGDSVDARS        0.0624      25452.8                 50.00     Sequence
   DRB1_0802  313  RQDLDDTDRDRSIGS  LDDTDRDRS        0.0583      26603.3                 50.00     Sequence
   DRB1_0802  276  HNGEPPEAPKVLTDA  HNGEPPEAP        0.0574      26876.1                 50.00     Sequence
   DRB1_0802  492  ATKDIPDVAGQTVDV  IPDVAGQTV        0.0560      27272.2                 50.00     Sequence
   DRB1_0802  277  NGEPPEAPKVLTDAE  PPEAPKVLT        0.0533      28086.4                 50.00     Sequence
   DRB1_0802  312  PRQDLDDTDRDRSIG  LDDTDRDRS        0.0525      28320.4                 50.00     Sequence
   DRB1_0802  586  LDKGADVDAGGSQHN  GADVDAGGS        0.0515      28626.7                 50.00     Sequence
   DRB1_0802  587  DKGADVDAGGSQHNR  VDAGGSQHN        0.0506      28906.2                 50.00     Sequence
   DRB1_0802  311  LPRQDLDDTDRDRSI  LDDTDRDRS        0.0409      32106.9                 50.00     Sequence
   DRB1_0802  310  PLPRQDLDDTDRDRS  LDDTDRDRS        0.0406      32223.2                 50.00     Sequence
   DRB1_0802  308  TDPLPRQDLDDTDRD  TDPLPRQDL        0.0294      36387.1                 50.00     Sequence
   DRB1_0802  309  DPLPRQDLDDTDRDR  LPRQDLDDT        0.0248      38236.5                 50.00     Sequence
-------------------------------------------------------------------------------------------

Allele: DRB1_0802. Number of high binders 9. Number of weak binders 45. Number of peptides 612
```

```
-------------------------------------------------------------------------------------------
-------------------------------------------------------------------------------------------
     Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
-------------------------------------------------------------------------------------------
   DRB1_0901  326  GSVGRWVAVVAVLAV  VGRWVAVVA         0.7296         18.6          SB     0.20     Sequence
   DRB1_0901  328  VGRWVAVVAVLAVLT  VGRWVAVVA         0.7278         19.0          SB     0.20     Sequence
   DRB1_0901  327  SVGRWVAVVAVLAVL  VGRWVAVVA         0.7262         19.4          SB     0.20     Sequence
   DRB1_0901  514  YGFTKFSQASVDSPR  FTKFSQASV         0.7213         20.4          SB     0.30     Sequence
   DRB1_0901  513  VYGFTKFSQASVDSP  FTKFSQASV         0.7088         23.3          SB     0.40     Sequence
   DRB1_0901  325  IGSVGRWVAVVAVLA  VGRWVAVVA         0.6993         25.9          SB     0.40     Sequence
   DRB1_0901  512  NVYGFTKFSQASVDS  FTKFSQASV         0.6945         27.3          SB     0.80     Sequence
   DRB1_0901  142  NIMISATNAVKVMDF  IMISATNAV         0.6934         27.6          SB     0.80     Sequence
   DRB1_0901  329  GRWVAVVAVLAVLTV  RWVAVVAVL         0.6815         31.4          SB     0.80     Sequence
   DRB1_0901  516  FTKFSQASVDSPRPA  FTKFSQASV         0.6798         32.0          SB     0.80     Sequence
   DRB1_0901  141  ANIMISATNAVKVMD  IMISATNAV         0.6789         32.3          SB     0.80     Sequence
   DRB1_0901  515  GFTKFSQASVDSPRP  FTKFSQASV         0.6762         33.2          SB     0.80     Sequence
   DRB1_0901  143  IMISATNAVKVMDFG  IMISATNAV         0.6620         38.8          SB     2.00     Sequence
   DRB1_0901  431  VSTLTYAEAVKKLTA  TLTYAEAVK         0.6573         40.8          SB     2.00     Sequence
   DRB1_0901  432  STLTYAEAVKKLTAA  TLTYAEAVK         0.6517         43.3          SB     2.00     Sequence
   DRB1_0901  433  TLTYAEAVKKLTAAG  TLTYAEAVK         0.6506         43.8          SB     2.00     Sequence
   DRB1_0901  511  LNVYGFTKFSQASVD  FTKFSQASV         0.6486         44.8          SB     2.00     Sequence
   DRB1_0901  330  RWVAVVAVLAVLTVV  RWVAVVAVL         0.6443         46.9          SB     2.00     Sequence
   DRB1_0901  430  DVSTLTYAEAVKKLT  TLTYAEAVK         0.6431         47.6          SB     2.00     Sequence
   DRB1_0901  260  NRYQTAAEMRADLVR  RYQTAAEMR         0.6429         47.6          SB     2.00     Sequence
   DRB1_0901   30  LRLHRDVAVKVLRAD  LRLHRDVAV         0.6367         50.9          WB     2.00     Sequence
   DRB1_0901  259  ENRYQTAAEMRADLV  RYQTAAEMR         0.6298         54.9          WB     4.00     Sequence
   DRB1_0901  324  SIGSVGRWVAVVAVL  RWVAVVAVL         0.6269         56.6          WB     4.00     Sequence
   DRB1_0901  261  RYQTAAEMRADLVRV  YQTAAEMRA         0.6232         59.0          WB     4.00     Sequence
   DRB1_0901  145  ISATNAVKVMDFGIA  ISATNAVKV         0.6163         63.5          WB     4.00     Sequence
   DRB1_0901   29  DLRLHRDVAVKVLRA  LRLHRDVAV         0.6123         66.3          WB     4.00     Sequence
   DRB1_0901  144  MISATNAVKVMDFGI  ISATNAVKV         0.6122         66.4          WB     4.00     Sequence
   DRB1_0901  140  PANIMISATNAVKVM  IMISATNAV         0.6058         71.1          WB     4.00     Sequence
   DRB1_0901  258  PENRYQTAAEMRADL  RYQTAAEMR         0.6027         73.6          WB     4.00     Sequence
   DRB1_0901   28  RDLRLHRDVAVKVLR  LRLHRDVAV         0.6012         74.8          WB     4.00     Sequence
   DRB1_0901  434  LTYAEAVKKLTAAGF  YAEAVKKLT         0.6009         75.0          WB     4.00     Sequence
   DRB1_0901  257  NPENRYQTAAEMRAD  RYQTAAEMR         0.5992         76.4          WB     4.00     Sequence
   DRB1_0901  151  VKVMDFGIARAIADS  VKVMDFGIA         0.5982         77.3          WB     4.00     Sequence
   DRB1_0901   27  ARDLRLHRDVAVKVL  LRLHRDVAV         0.5839         90.2          WB     8.00     Sequence
   DRB1_0901  429  PDVSTLTYAEAVKKL  TLTYAEAVK         0.5829         91.2          WB     8.00     Sequence
   DRB1_0901   31  RLHRDVAVKVLRADL  LHRDVAVKV         0.5824         91.6          WB     8.00     Sequence
   DRB1_0901   32  LHRDVAVKVLRADLA  LHRDVAVKV         0.5738        100.6          WB     8.00     Sequence
   DRB1_0901  150  AVKVMDFGIARAIAD  VKVMDFGIA         0.5696        105.3          WB     8.00     Sequence
   DRB1_0901  196  SDVYSLGCVLYEVLT  DVYSLGCVL         0.5679        107.3          WB     8.00     Sequence
   DRB1_0901  510  NLNVYGFTKFSQASV  FTKFSQASV         0.5666        108.8          WB     8.00     Sequence
   DRB1_0901  256  KNPENRYQTAAEMRA  RYQTAAEMR         0.5652        110.4          WB     8.00     Sequence
   DRB1_0901  139  KPANIMISATNAVKV  IMISATNAV         0.5606        116.0          WB     8.00     Sequence
   DRB1_0901   16  LGFGGMSEVHLARDL  FGGMSEVHL         0.5583        119.0          WB     8.00     Sequence
   DRB1_0901  153  VMDFGIARAIADSGN  FGIARAIAD         0.5558        122.2          WB     8.00     Sequence
   DRB1_0901  435  TYAEAVKKLTAAGFG  YAEAVKKLT         0.5520        127.4          WB     8.00     Sequence
   DRB1_0901  197  DVYSLGCVLYEVLTG  DVYSLGCVL         0.5517        127.8          WB     8.00     Sequence
   DRB1_0901  154  MDFGIARAIADSGNS  MDFGIARAI         0.5498        130.4          WB     8.00     Sequence
   DRB1_0901  448  FGRFKQANSPSTPEL  FGRFKQANS         0.5489        131.7          WB     8.00     Sequence
   DRB1_0901  293  TSLLSSAAGNLSGPR  LLSSAAGNL         0.5480        133.0          WB     8.00     Sequence
   DRB1_0901  137  DVKPANIMISATNAV  IMISATNAV         0.5475        133.8          WB    16.00     Sequence
   DRB1_0901  147  ATNAVKVMDFGIARA  VKVMDFGIA         0.5467        134.9          WB    16.00     Sequence
   DRB1_0901   15  ILGFGGMSEVHLARD  FGGMSEVHL         0.5431        140.3          WB    16.00     Sequence
   DRB1_0901  195  RSDVYSLGCVLYEVL  DVYSLGCVL         0.5412        143.2          WB    16.00     Sequence
   DRB1_0901  152  KVMDFGIARAIADSG  FGIARAIAD         0.5409        143.6          WB    16.00     Sequence
   DRB1_0901   26  LARDLRLHRDVAVKV  LRLHRDVAV         0.5375        149.0          WB    16.00     Sequence
   DRB1_0901  138  VKPANIMISATNAVK  IMISATNAV         0.5370        149.8          WB    16.00     Sequence
   DRB1_0901  292  RTSLLSSAAGNLSGP  LLSSAAGNL         0.5370        149.9          WB    16.00     Sequence
   DRB1_0901   90  VMEYVDGVTLRDIVH  YVDGVTLRD         0.5346        153.8          WB    16.00     Sequence
   DRB1_0901   89  IVMEYVDGVTLRDIV  YVDGVTLRD         0.5331        156.3          WB    16.00     Sequence
   DRB1_0901  236  SARHEGLSADLDAVV  RHEGLSADL         0.5321        158.0          WB    16.00     Sequence
   DRB1_0901  447  GFGRFKQANSPSTPE  FGRFKQANS         0.5320        158.1          WB    16.00     Sequence
```

```
DRB1_0901   14  EILGFGGMSEVHLAR  FGGMSEVHL         0.5317         158.7          WB    16.00      Sequence
DRB1_0901   13  GEILGFGGMSEVHLA  FGGMSEVHL         0.5315         159.1          WB    16.00      Sequence
DRB1_0901  331  WVAVVAVLAVLTVVV  WVAVVAVLA         0.5300         161.7          WB    16.00      Sequence
DRB1_0901  146  SATNAVKVMDFGIAR  VKVMDFGIA         0.5297         162.2          WB    16.00      Sequence
DRB1_0901  237  ARHEGLSADLDAVVL  RHEGLSADL         0.5270         166.9          WB    16.00      Sequence
DRB1_0901   18  FGGMSEVHLARDLRL  FGGMSEVHL         0.5260         168.7          WB    16.00      Sequence
DRB1_0901  323  RSIGSVGRWVAVVAV  VGRWVAVVA         0.5256         169.5          WB    16.00      Sequence
DRB1_0901  449  GRFKQANSPSTPELV  FKQANSPST         0.5242         172.2          WB    16.00      Sequence
DRB1_0901  156  FGIARAIADSGNSVT  FGIARAIAD         0.5226         175.0          WB    16.00      Sequence
DRB1_0901   35  DVAVKVLRADLARDP  VKVLRADLA         0.5218         176.5          WB    16.00      Sequence
DRB1_0901   34  RDVAVKVLRADLARD  VKVLRADLA         0.5174         185.3          WB    16.00      Sequence
DRB1_0901  235  PSARHEGLSADLDAV  RHEGLSADL         0.5173         185.5          WB    16.00      Sequence
DRB1_0901  291  ERTSLLSSAAGNLSG  LLSSAAGNL         0.5167         186.6          WB    16.00      Sequence
DRB1_0901  294  SLLSSAAGNLSGPRT  LLSSAAGNL         0.5163         187.4          WB    16.00      Sequence
DRB1_0901  446  AGFGRFKQANSPSTP  FGRFKQANS         0.5153         189.5          WB    16.00      Sequence
DRB1_0901  428  IPDVSTLTYAEAVKK  TLTYAEAVK         0.5152         189.8          WB    16.00      Sequence
DRB1_0901  568  MFWVDAEPRLRALGW  FWVDAEPRL         0.5100         200.6          WB    16.00      Sequence
DRB1_0901   88  YIVMEYVDGVTLRDI  YVDGVTLRD         0.5096         201.5          WB    16.00      Sequence
DRB1_0901  194  ARSDVYSLGCVLYEV  DVYSLGCVL         0.5055         210.7          WB    16.00      Sequence
DRB1_0901  566  SGMFWVDAEPRLRAL  FWVDAEPRL         0.5042         213.6          WB    16.00      Sequence
DRB1_0901  565  LSGMFWVDAEPRLRA  FWVDAEPRL         0.5029         216.7          WB    16.00      Sequence
DRB1_0901   63  AALNHPAIVAVYDTG  LNHPAIVAV         0.5013         220.4          WB    16.00      Sequence
DRB1_0901  167  NSVTQTAAVIGTAQY  SVTQTAAVI         0.5001         223.4          WB    16.00      Sequence
DRB1_0901   33  HRDVAVKVLRADLAR  HRDVAVKVL         0.5000         223.6          WB    16.00      Sequence
DRB1_0901  361  VPDVRGQSSADAIAT  RGQSSADAI         0.5000         223.7          WB    16.00      Sequence
DRB1_0901  155  DFGIARAIADSGNSV  FGIARAIAD         0.4979         228.7          WB    16.00      Sequence
DRB1_0901   17  GFGGMSEVHLARDLR  FGGMSEVHL         0.4972         230.6          WB    16.00      Sequence
DRB1_0901  567  GMFWVDAEPRLRALG  FWVDAEPRL         0.4965         232.2          WB    16.00      Sequence
DRB1_0901  517  TKFSQASVDSPRPAG  TKFSQASVD         0.4963         232.6          WB    16.00      Sequence
DRB1_0901  148  TNAVKVMDFGIARAI  VKVMDFGIA         0.4963         232.8          WB    16.00      Sequence
DRB1_0901  166  GNSVTQTAAVIGTAQ  SVTQTAAVI         0.4948         236.6          WB    16.00      Sequence
DRB1_0901  234  PPSARHEGLSADLDA  RHEGLSADL         0.4948         236.7          WB    16.00      Sequence
DRB1_0901   91  MEYVDGVTLRDIVHT  YVDGVTLRD         0.4947         236.7          WB    16.00      Sequence
DRB1_0901  359  VQVPDVRGQSSADAI  DVRGQSSAD         0.4936         239.7          WB    32.00      Sequence
DRB1_0901  569  FWVDAEPRLRALGWT  FWVDAEPRL         0.4921         243.6          WB    32.00      Sequence
DRB1_0901  125  LNFSHQNGIIHRDVK  LNFSHQNGI         0.4908         247.1          WB    32.00      Sequence
DRB1_0901  248  AVVLKALAKNPENRY  VVLKALAKN         0.4905         247.9          WB    32.00      Sequence
DRB1_0901   53  LRFRREAQNAAALNH  FRREAQNAA         0.4903         248.4          WB    32.00      Sequence
DRB1_0901   64  ALNHPAIVAVYDTGE  LNHPAIVAV         0.4898         249.8          WB    32.00      Sequence
DRB1_0901  249  VVLKALAKNPENRYQ  VVLKALAKN         0.4896         250.3          WB    32.00      Sequence
DRB1_0901  363  DVRGQSSADAIATLQ  RGQSSADAI         0.4894         250.9          WB    32.00      Sequence
DRB1_0901  290  AERTSLLSSAAGNLS  LLSSAAGNL         0.4889         252.1          WB    32.00      Sequence
DRB1_0901  445  AAGFGRFKQANSPST  FKQANSPST         0.4880         254.5          WB    32.00      Sequence
DRB1_0901  132  GIIHRDVKPANIMIS  DVKPANIMI         0.4877         255.3          WB    32.00      Sequence
DRB1_0901  436  YAEAVKKLTAAGFGR  YAEAVKKLT         0.4868         258.0          WB    32.00      Sequence
DRB1_0901  360  QVPDVRGQSSADAIA  RGQSSADAI         0.4851         262.7          WB    32.00      Sequence
DRB1_0901   52  YLRFRREAQNAAALN  FRREAQNAA         0.4851         262.8          WB    32.00      Sequence
DRB1_0901  193  DARSDVYSLGCVLYE  VYSLGCVLY         0.4850         262.9          WB    32.00      Sequence
DRB1_0901   36  VAVKVLRADLARDPS  VKVLRADLA         0.4849         263.3          WB    32.00      Sequence
DRB1_0901  165  SGNSVTQTAAVIGTA  SVTQTAAVI         0.4837         266.9          WB    32.00      Sequence
DRB1_0901   87  PYIVMEYVDGVTLRD  VMEYVDGVT         0.4825         270.3          WB    32.00      Sequence
DRB1_0901  232  PIPPSARHEGLSADL  RHEGLSADL         0.4821         271.5          WB    32.00      Sequence
DRB1_0901  362  PDVRGQSSADAIATL  RGQSSADAI         0.4800         277.7          WB    32.00      Sequence
DRB1_0901   62  AAALNHPAIVAVYDT  LNHPAIVAV         0.4781         283.4          WB    32.00      Sequence
DRB1_0901  101  DIVHTEGPMTPKRAI  IVHTEGPMT         0.4779         283.9          WB    32.00      Sequence
DRB1_0901  198  VYSLGCVLYEVLTGE  YSLGCVLYE         0.4774         285.5          WB    32.00      Sequence
DRB1_0901  564  DLSGMFWVDAEPRLR  FWVDAEPRL         0.4771         286.4          WB    32.00      Sequence
DRB1_0901   54  RFRREAQNAAALNHP  FRREAQNAA         0.4754         291.9          WB    32.00      Sequence
DRB1_0901  262  YQTAAEMRADLVRVH  YQTAAEMRA         0.4745         294.6          WB    32.00      Sequence
DRB1_0901  275  VHNGEPPEAPKVLTD  VHNGEPPEA         0.4713         305.1          WB    32.00      Sequence
DRB1_0901  273  VRVHNGEPPEAPKVL  VRVHNGEPP         0.4707         307.2          WB    32.00      Sequence
DRB1_0901  450  RFKQANSPSTPELVG  FKQANSPST         0.4701         309.2          WB    32.00      Sequence
DRB1_0901  168  SVTQTAAVIGTAQYL  SVTQTAAVI         0.4691         312.3          WB    32.00      Sequence
DRB1_0901  136  RDVKPANIMISATNA  VKPANIMIS         0.4688         313.6          WB    32.00      Sequence
DRB1_0901  133  IIHRDVKPANIMISA  RDVKPANIM         0.4676         317.6          WB    32.00      Sequence
DRB1_0901  233  IPPSARHEGLSADLD  RHEGLSADL         0.4675         317.8          WB    32.00      Sequence
```

```
DRB1_0901   37  AVKVLRADLARDPSF  VKVLRADLA         0.4674         318.1          WB    32.00      Sequence
DRB1_0901  247  DAVVLKALAKNPENR  LKALAKNPE         0.4661         322.7          WB    32.00      Sequence
DRB1_0901  124  ALNFSHQNGIIHRDV  NFSHQNGII         0.4660         323.1          WB    32.00      Sequence
DRB1_0901  149  NAVKVMDFGIARAIA  VKVMDFGIA         0.4656         324.5          WB    32.00      Sequence
DRB1_0901   12  LGEILGFGGMSEVHL  FGGMSEVHL         0.4640         330.0          WB    32.00      Sequence
DRB1_0901  134  IHRDVKPANIMISAT  RDVKPANIM         0.4633         332.6          WB    32.00      Sequence
DRB1_0901  135  HRDVKPANIMISATN  DVKPANIMI         0.4620         337.4          WB    32.00      Sequence
DRB1_0901  213  PPFTGDSPVSVAYQH  TGDSPVSVA         0.4619         337.8          WB    32.00      Sequence
DRB1_0901  176  IGTAQYLSPEQARGD  QYLSPEQAR         0.4618         338.1          WB    32.00      Sequence
DRB1_0901   50  SFYLRFRREAQNAAA  FRREAQNAA         0.4617         338.5          WB    32.00      Sequence
DRB1_0901   51  FYLRFRREAQNAAAL  FRREAQNAA         0.4615         339.2          WB    32.00      Sequence
DRB1_0901  164  DSGNSVTQTAAVIGT  SVTQTAAVI         0.4613         339.7          WB    32.00      Sequence
DRB1_0901  255  AKNPENRYQTAAEMR  RYQTAAEMR         0.4611         340.8          WB    32.00      Sequence
DRB1_0901  102  IVHTEGPMTPKRAIE  IVHTEGPMT         0.4609         341.5          WB    32.00      Sequence
DRB1_0901  554  VSKGNQFVMPDLSGM  QFVMPDLSG         0.4592         347.5          WB    32.00      Sequence
DRB1_0901  100  RDIVHTEGPMTPKRA  IVHTEGPMT         0.4588         349.1          WB    32.00      Sequence
DRB1_0901   97  VTLRDIVHTEGPMTP  IVHTEGPMT         0.4580         352.4          WB    32.00      Sequence
DRB1_0901  295  LLSSAAGNLSGPRTD  LLSSAAGNL         0.4574         354.7          WB    32.00      Sequence
DRB1_0901   21  MSEVHLARDLRLHRD  VHLARDLRL         0.4568         356.7          WB    32.00      Sequence
DRB1_0901  555  SKGNQFVMPDLSGMF  QFVMPDLSG         0.4551         363.5          WB    32.00      Sequence
DRB1_0901   38  VKVLRADLARDPSFY  VKVLRADLA         0.4544         366.4          WB    32.00      Sequence
DRB1_0901   19  GGMSEVHLARDLRLH  VHLARDLRL         0.4542         366.8          WB    32.00      Sequence
DRB1_0901  175  VIGTAQYLSPEQARG  QYLSPEQAR         0.4519         376.2          WB    32.00      Sequence
DRB1_0901  214  PFTGDSPVSVAYQHV  TGDSPVSVA         0.4503         382.8          WB    32.00      Sequence
DRB1_0901  322  DRSIGSVGRWVAVVA  VGRWVAVVA         0.4502         383.1          WB    32.00      Sequence
DRB1_0901  580  LGWTGMLDKGADVDA  MLDKGADVD         0.4498         385.1          WB    32.00      Sequence
DRB1_0901  246  LDAVVLKALAKNPEN  VVLKALAKN         0.4495         386.1          WB    32.00      Sequence
DRB1_0901  553  QVSKGNQFVMPDLSG  SKGNQFVMP         0.4489         388.8          WB    32.00      Sequence
DRB1_0901   55  FRREAQNAAALNHPA  FRREAQNAA         0.4476         394.3          WB    32.00      Sequence
DRB1_0901   92  EYVDGVTLRDIVHTE  YVDGVTLRD         0.4468         397.6          WB    32.00      Sequence
DRB1_0901  289  DAERTSLLSSAAGNL  LLSSAAGNL         0.4468         397.6          WB    32.00      Sequence
DRB1_0901   61  NAAALNHPAIVAVYD  ALNHPAIVA         0.4463         400.0          WB    32.00      Sequence
DRB1_0901  364  VRGQSSADAIATLQN  RGQSSADAI         0.4456         402.9          WB    32.00      Sequence
DRB1_0901  106  EGPMTPKRAIEVIAD  MTPKRAIEV         0.4455         403.5          WB    32.00      Sequence
DRB1_0901   65  LNHPAIVAVYDTGEA  LNHPAIVAV         0.4447         406.6          WB    32.00      Sequence
DRB1_0901  212  EPPFTGDSPVSVAYQ  TGDSPVSVA         0.4435         412.1          WB    32.00      Sequence
DRB1_0901   96  GVTLRDIVHTEGPMT  IVHTEGPMT         0.4426         416.2          WB    32.00      Sequence
DRB1_0901   20  GMSEVHLARDLRLHR  VHLARDLRL         0.4423         417.4          WB    32.00      Sequence
DRB1_0901  427  EIPDVSTLTYAEAVK  TLTYAEAVK         0.4412         422.5          WB    32.00      Sequence
DRB1_0901  274  RVHNGEPPEAPKVLT  VHNGEPPEA         0.4406         425.0          WB    32.00      Sequence
DRB1_0901   24  VHLARDLRLHRDVAV  VHLARDLRL         0.4393         431.1          WB    32.00      Sequence
DRB1_0901  579  ALGWTGMLDKGADVD  WTGMLDKGA         0.4390         432.6          WB    32.00      Sequence
DRB1_0901  210  TGEPPFTGDSPVSVA  TGDSPVSVA         0.4383         435.9          WB    32.00      Sequence
DRB1_0901  271  DLVRVHNGEPPEAPK  VHNGEPPEA         0.4376         439.1          WB    32.00      Sequence
DRB1_0901  131  NGIIHRDVKPANIMI  HRDVKPANI         0.4374         440.0          WB    32.00      Sequence
DRB1_0901   98  TLRDIVHTEGPMTPK  IVHTEGPMT         0.4366         443.9          WB    32.00      Sequence
DRB1_0901  105  TEGPMTPKRAIEVIA  PMTPKRAIE         0.4361         446.2          WB    32.00      Sequence
DRB1_0901  272  LVRVHNGEPPEAPKV  VRVHNGEPP         0.4353         450.4          WB    32.00      Sequence
DRB1_0901  238  RHEGLSADLDAVVLK  RHEGLSADL         0.4347         453.4          WB    32.00      Sequence
DRB1_0901  107  GPMTPKRAIEVIADA  MTPKRAIEV         0.4327         463.0          WB    32.00      Sequence
DRB1_0901   22  SEVHLARDLRLHRDV  VHLARDLRL         0.4323         465.3          WB    32.00      Sequence
DRB1_0901  179  AQYLSPEQARGDSVD  QYLSPEQAR         0.4314         469.8          WB    32.00      Sequence
DRB1_0901  123  QALNFSHQNGIIHRD  NFSHQNGII         0.4308         472.7          WB    32.00      Sequence
DRB1_0901  358  DVQVPDVRGQSSADA  VRGQSSADA         0.4305         474.1          WB    32.00      Sequence
DRB1_0901  484  IIIVGSGPATKDIPD  VGSGPATKD         0.4288         482.9          WB    32.00      Sequence
DRB1_0901  163  ADSGNSVTQTAAVIG  SVTQTAAVI         0.4280         487.3          WB    32.00      Sequence
DRB1_0901   49  PSFYLRFRREAQNAA  FRREAQNAA         0.4276         489.7          WB    32.00      Sequence
DRB1_0901  552  LQVSKGNQFVMPDLS  LQVSKGNQF         0.4270         492.8          WB    32.00      Sequence
DRB1_0901   83  AGPLPYIVMEYVDGV  GPLPYIVME         0.4265         495.4          WB    32.00      Sequence
DRB1_0901  126  NFSHQNGIIHRDVKP  NFSHQNGII         0.4263         496.5          WB    32.00      Sequence
DRB1_0901   25  HLARDLRLHRDVAVK  LRLHRDVAV         0.4258         499.1          WB    50.00      Sequence
DRB1_0901  177  GTAQYLSPEQARGDS  QYLSPEQAR         0.4256         500.0                50.00      Sequence
DRB1_0901  451  FKQANSPSTPELVGK  FKQANSPST         0.4252         502.3                50.00      Sequence
DRB1_0901  178  TAQYLSPEQARGDSV  QYLSPEQAR         0.4241         508.4                50.00      Sequence
DRB1_0901  332  VAVVAVLAVLTVVVT  VAVVAVLAV         0.4237         510.8                50.00      Sequence
DRB1_0901  211  GEPPFTGDSPVSVAY  TGDSPVSVA         0.4215         523.0                50.00      Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0901 | 215 | FTGDSPVSVAYQHVR | TGDSPVSVA | 0.4208 | 526.7 | 50.00 | Sequence |
| DRB1_0901 | 99 | LRDIVHTEGPMTPKR | IVHTEGPMT | 0.4176 | 545.4 | 50.00 | Sequence |
| DRB1_0901 | 86 | LPYIVMEYVDGVTLR | VMEYVDGVT | 0.4161 | 554.3 | 50.00 | Sequence |
| DRB1_0901 | 23 | EVHLARDLRLHRDVA | VHLARDLRL | 0.4150 | 560.8 | 50.00 | Sequence |
| DRB1_0901 | 104 | HTEGPMTPKRAIEVI | EGPMTPKRA | 0.4145 | 564.0 | 50.00 | Sequence |
| DRB1_0901 | 581 | GWTGMLDKGADVDAG | MLDKGADVD | 0.4142 | 566.0 | 50.00 | Sequence |
| DRB1_0901 | 222 | SVAYQHVREDPIPPS | YQHVREDPI | 0.4132 | 572.3 | 50.00 | Sequence |
| DRB1_0901 | 582 | WTGMLDKGADVDAGG | MLDKGADVD | 0.4129 | 574.0 | 50.00 | Sequence |
| DRB1_0901 | 483 | VIIIVGSGPATKDIP | VGSGPATKD | 0.4126 | 575.8 | 50.00 | Sequence |
| DRB1_0901 | 199 | YSLGCVLYEVLTGEP | LGCVLYEVL | 0.4117 | 581.6 | 50.00 | Sequence |
| DRB1_0901 | 550 | IELQVSKGNQFVMPD | LQVSKGNQF | 0.4116 | 581.9 | 50.00 | Sequence |
| DRB1_0901 | 570 | WVDAEPRLRALGWTG | WVDAEPRLR | 0.4097 | 594.2 | 50.00 | Sequence |
| DRB1_0901 | 509 | KNLNVYGFTKFSQAS | YGFTKFSQA | 0.4096 | 594.9 | 50.00 | Sequence |
| DRB1_0901 | 556 | KGNQFVMPDLSGMFW | QFVMPDLSG | 0.4091 | 598.0 | 50.00 | Sequence |
| DRB1_0901 | 563 | PDLSGMFWVDAEPRL | FWVDAEPRL | 0.4087 | 600.7 | 50.00 | Sequence |
| DRB1_0901 | 349 | INTFGGITRDVQVPD | GGITRDVQV | 0.4081 | 604.4 | 50.00 | Sequence |
| DRB1_0901 | 245 | DLDAVVLKALAKNPE | VVLKALAKN | 0.4071 | 610.8 | 50.00 | Sequence |
| DRB1_0901 | 130 | QNGIIHRDVKPANIM | IHRDVKPAN | 0.4067 | 613.4 | 50.00 | Sequence |
| DRB1_0901 | 60 | QNAAALNHPAIVAVY | ALNHPAIVA | 0.4067 | 613.9 | 50.00 | Sequence |
| DRB1_0901 | 103 | VHTEGPMTPKRAIEV | EGPMTPKRA | 0.4059 | 618.9 | 50.00 | Sequence |
| DRB1_0901 | 437 | AEAVKKLTAAGFGRF | KKLTAAGFG | 0.4056 | 620.9 | 50.00 | Sequence |
| DRB1_0901 | 403 | PAANTSVSAGDEITV | ANTSVSAGD | 0.4054 | 622.5 | 50.00 | Sequence |
| DRB1_0901 | 532 | EVTGTNPPAGTTVPV | TGTNPPAGT | 0.4053 | 622.8 | 50.00 | Sequence |
| DRB1_0901 | 485 | IIVGSGPATKDIPDV | VGSGPATKD | 0.4048 | 626.2 | 50.00 | Sequence |
| DRB1_0901 | 180 | QYLSPEQARGDSVDA | QYLSPEQAR | 0.4044 | 628.8 | 50.00 | Sequence |
| DRB1_0901 | 270 | ADLVRVHNGEPPEAP | VHNGEPPEA | 0.4029 | 639.4 | 50.00 | Sequence |
| DRB1_0901 | 486 | IVGSGPATKDIPDVA | VGSGPATKD | 0.4016 | 648.4 | 50.00 | Sequence |
| DRB1_0901 | 350 | NTFGGITRDVQVPDV | GGITRDVQV | 0.4014 | 649.5 | 50.00 | Sequence |
| DRB1_0901 | 84 | GPLPYIVMEYVDGVT | GPLPYIVME | 0.4010 | 652.6 | 50.00 | Sequence |
| DRB1_0901 | 192 | VDARSDVYSLGCVLY | VYSLGCVLY | 0.3997 | 661.9 | 50.00 | Sequence |
| DRB1_0901 | 531 | GEVTGTNPPAGTTVP | GTNPPAGTT | 0.3996 | 662.7 | 50.00 | Sequence |
| DRB1_0901 | 444 | TAAGFGRFKQANSPS | FGRFKQANS | 0.3995 | 663.4 | 50.00 | Sequence |
| DRB1_0901 | 157 | GIARAIADSGNSVTQ | IARAIADSG | 0.3991 | 666.2 | 50.00 | Sequence |
| DRB1_0901 | 549 | VIELQVSKGNQFVMP | VIELQVSKG | 0.3990 | 666.8 | 50.00 | Sequence |
| DRB1_0901 | 231 | DPIPPSARHEGLSAD | DPIPPSARH | 0.3971 | 680.5 | 50.00 | Sequence |
| DRB1_0901 | 380 | GFKIRTLQKPDSTIP | FKIRTLQKP | 0.3969 | 682.0 | 50.00 | Sequence |
| DRB1_0901 | 438 | EAVKKLTAAGFGRFK | KKLTAAGFG | 0.3966 | 684.1 | 50.00 | Sequence |
| DRB1_0901 | 376 | LQNRGFKIRTLQKPD | LQNRGFKIR | 0.3955 | 692.4 | 50.00 | Sequence |
| DRB1_0901 | 109 | MTPKRAIEVIADACQ | MTPKRAIEV | 0.3951 | 695.4 | 50.00 | Sequence |
| DRB1_0901 | 439 | AVKKLTAAGFGRFKQ | KKLTAAGFG | 0.3939 | 704.8 | 50.00 | Sequence |
| DRB1_0901 | 551 | ELQVSKGNQFVMPDL | LQVSKGNQF | 0.3935 | 707.7 | 50.00 | Sequence |
| DRB1_0901 | 78 | EAETPAGPLPYIVME | EAETPAGPL | 0.3923 | 717.3 | 50.00 | Sequence |
| DRB1_0901 | 440 | VKKLTAAGFGRFKQA | KKLTAAGFG | 0.3922 | 717.8 | 50.00 | Sequence |
| DRB1_0901 | 533 | VTGTNPPAGTTVPVD | TGTNPPAGT | 0.3918 | 720.6 | 50.00 | Sequence |
| DRB1_0901 | 174 | AVIGTAQYLSPEQAR | AQYLSPEQA | 0.3907 | 729.3 | 50.00 | Sequence |
| DRB1_0901 | 405 | ANTSVSAGDEITVNV | TSVSAGDEI | 0.3907 | 729.8 | 50.00 | Sequence |
| DRB1_0901 | 122 | CQALNFSHQNGIIHR | NFSHQNGII | 0.3906 | 730.5 | 50.00 | Sequence |
| DRB1_0901 | 353 | GGITRDVQVPDVRGQ | GGITRDVQV | 0.3893 | 740.5 | 50.00 | Sequence |
| DRB1_0901 | 381 | FKIRTLQKPDSTIPP | FKIRTLQKP | 0.3884 | 747.9 | 50.00 | Sequence |
| DRB1_0901 | 487 | VGSGPATKDIPDVAG | VGSGPATKD | 0.3880 | 751.1 | 50.00 | Sequence |
| DRB1_0901 | 404 | AANTSVSAGDEITVN | TSVSAGDEI | 0.3876 | 754.7 | 50.00 | Sequence |
| DRB1_0901 | 220 | PVSVAYQHVREDPIP | YQHVREDPI | 0.3871 | 758.7 | 50.00 | Sequence |
| DRB1_0901 | 351 | TFGGITRDVQVPDVR | TFGGITRDV | 0.3867 | 761.6 | 50.00 | Sequence |
| DRB1_0901 | 108 | PMTPKRAIEVIADAC | MTPKRAIEV | 0.3865 | 763.5 | 50.00 | Sequence |
| DRB1_0901 | 577 | LRALGWTGMLDKGAD | LGWTGMLDK | 0.3862 | 766.3 | 50.00 | Sequence |
| DRB1_0901 | 482 | VVIIIVGSGPATKDI | VGSGPATKD | 0.3860 | 767.8 | 50.00 | Sequence |
| DRB1_0901 | 347 | IAINTFGGITRDVQV | GGITRDVQV | 0.3850 | 775.9 | 50.00 | Sequence |
| DRB1_0901 | 375 | TLQNRGFKIRTLQKP | QNRGFKIRT | 0.3833 | 790.1 | 50.00 | Sequence |
| DRB1_0901 | 59 | AQNAAALNHPAIVAV | ALNHPAIVA | 0.3828 | 794.9 | 50.00 | Sequence |
| DRB1_0901 | 365 | RGQSSADAIATLQNR | RGQSSADAI | 0.3826 | 796.8 | 50.00 | Sequence |
| DRB1_0901 | 129 | HQNGIIHRDVKPANI | HQNGIIHRD | 0.3823 | 798.6 | 50.00 | Sequence |
| DRB1_0901 | 82 | PAGPLPYIVMEYVDG | GPLPYIVME | 0.3817 | 804.3 | 50.00 | Sequence |
| DRB1_0901 | 402 | DPAANTSVSAGDEIT | ANTSVSAGD | 0.3814 | 806.5 | 50.00 | Sequence |
| DRB1_0901 | 73 | VYDTGEAETPAGPLP | VYDTGEAET | 0.3814 | 806.6 | 50.00 | Sequence |
| DRB1_0901 | 348 | AINTFGGITRDVQVP | TFGGITRDV | 0.3811 | 809.1 | 50.00 | Sequence |
| DRB1_0901 | 453 | QANSPSTPELVGKVI | QANSPSTPE | 0.3810 | 810.7 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_0901 | 93 | YVDGVTLRDIVHTEG | YVDGVTLRD | 0.3807 | 812.6 | 50.00 | Sequence |
| DRB1_0901 | 72 | AVYDTGEAETPAGPL | VYDTGEAET | 0.3802 | 817.3 | 50.00 | Sequence |
| DRB1_0901 | 276 | HNGEPPEAPKVLTDA | EPPEAPKVL | 0.3799 | 820.1 | 50.00 | Sequence |
| DRB1_0901 | 578 | RALGWTGMLDKGADV | LGWTGMLDK | 0.3798 | 821.1 | 50.00 | Sequence |
| DRB1_0901 | 223 | VAYQHVREDPIPPSA | VAYQHVRED | 0.3792 | 826.4 | 50.00 | Sequence |
| DRB1_0901 | 221 | VSVAYQHVREDPIPP | YQHVREDPI | 0.3790 | 827.9 | 50.00 | Sequence |
| DRB1_0901 | 548 | SVIELQVSKGNQFVM | VIELQVSKG | 0.3781 | 836.1 | 50.00 | Sequence |
| DRB1_0901 | 530 | AGEVTGTNPPAGTTV | GTNPPAGTT | 0.3776 | 840.5 | 50.00 | Sequence |
| DRB1_0901 | 379 | RGFKIRTLQKPDSTI | FKIRTLQKP | 0.3775 | 842.0 | 50.00 | Sequence |
| DRB1_0901 | 374 | ATLQNRGFKIRTLQK | QNRGFKIRT | 0.3764 | 852.1 | 50.00 | Sequence |
| DRB1_0901 | 377 | QNRGFKIRTLQKPDS | QNRGFKIRT | 0.3755 | 859.8 | 50.00 | Sequence |
| DRB1_0901 | 508 | QKNLNVYGFTKFSQA | YGFTKFSQA | 0.3752 | 863.1 | 50.00 | Sequence |
| DRB1_0901 | 576 | RLRALGWTGMLDKGA | WTGMLDKGA | 0.3748 | 866.6 | 50.00 | Sequence |
| DRB1_0901 | 48 | DPSFYLRFRREAQNA | FYLRFRREA | 0.3741 | 873.3 | 50.00 | Sequence |
| DRB1_0901 | 128 | SHQNGIIHRDVKPAN | HQNGIIHRD | 0.3733 | 880.9 | 50.00 | Sequence |
| DRB1_0901 | 269 | RADLVRVHNGEPPEA | VHNGEPPEA | 0.3729 | 884.2 | 50.00 | Sequence |
| DRB1_0901 | 121 | ACQALNFSHQNGIIH | NFSHQNGII | 0.3729 | 885.0 | 50.00 | Sequence |
| DRB1_0901 | 474 | NQTSAITNVVIIIVG | QTSAITNVV | 0.3721 | 892.6 | 50.00 | Sequence |
| DRB1_0901 | 373 | IATLQNRGFKIRTLQ | QNRGFKIRT | 0.3715 | 898.1 | 50.00 | Sequence |
| DRB1_0901 | 557 | GNQFVMPDLSGMFWV | QFVMPDLSG | 0.3711 | 902.4 | 50.00 | Sequence |
| DRB1_0901 | 209 | LTGEPPFTGDSPVSV | FTGDSPVSV | 0.3710 | 902.8 | 50.00 | Sequence |
| DRB1_0901 | 598 | QHNRVVYQNPPAGTG | YQNPPAGTG | 0.3701 | 912.0 | 50.00 | Sequence |
| DRB1_0901 | 599 | HNRVVYQNPPAGTGV | YQNPPAGTG | 0.3695 | 917.8 | 50.00 | Sequence |
| DRB1_0901 | 81 | TPAGPLPYIVMEYVD | AGPLPYIVM | 0.3692 | 920.7 | 50.00 | Sequence |
| DRB1_0901 | 225 | YQHVREDPIPPSARH | YQHVREDPI | 0.3685 | 927.7 | 50.00 | Sequence |
| DRB1_0901 | 452 | KQANSPSTPELVGKV | QANSPSTPE | 0.3673 | 940.2 | 50.00 | Sequence |
| DRB1_0901 | 603 | VYQNPPAGTGVNRDG | YQNPPAGTG | 0.3665 | 947.5 | 50.00 | Sequence |
| DRB1_0901 | 277 | NGEPPEAPKVLTDAE | EPPEAPKVL | 0.3657 | 955.8 | 50.00 | Sequence |
| DRB1_0901 | 378 | NRGFKIRTLQKPDST | KIRTLQKPD | 0.3655 | 958.3 | 50.00 | Sequence |
| DRB1_0901 | 4 | SHLSDRYELGEILGF | RYELGEILG | 0.3654 | 959.6 | 50.00 | Sequence |
| DRB1_0901 | 169 | VTQTAAVIGTAQYLS | VTQTAAVIG | 0.3652 | 961.8 | 50.00 | Sequence |
| DRB1_0901 | 534 | TGTNPPAGTTVPVDS | TGTNPPAGT | 0.3649 | 964.0 | 50.00 | Sequence |
| DRB1_0901 | 443 | LTAAGFGRFKQANSP | FGRFKQANS | 0.3649 | 964.4 | 50.00 | Sequence |
| DRB1_0901 | 602 | VVYQNPPAGTGVNRD | YQNPPAGTG | 0.3648 | 966.0 | 50.00 | Sequence |
| DRB1_0901 | 47 | RDPSFYLRFRREAQN | FYLRFRREA | 0.3647 | 966.4 | 50.00 | Sequence |
| DRB1_0901 | 600 | NRVVYQNPPAGTGVN | YQNPPAGTG | 0.3646 | 967.2 | 50.00 | Sequence |
| DRB1_0901 | 558 | NQFVMPDLSGMFWVD | QFVMPDLSG | 0.3641 | 973.4 | 50.00 | Sequence |
| DRB1_0901 | 8 | DRYELGEILGFGGMS | DRYELGEIL | 0.3639 | 975.2 | 50.00 | Sequence |
| DRB1_0901 | 601 | RVVYQNPPAGTGVNR | YQNPPAGTG | 0.3634 | 980.3 | 50.00 | Sequence |
| DRB1_0901 | 127 | FSHQNGIIHRDVKPA | QNGIIHRDV | 0.3625 | 990.4 | 50.00 | Sequence |
| DRB1_0901 | 95 | DGVTLRDIVHTEGPM | DIVHTEGPM | 0.3622 | 993.3 | 50.00 | Sequence |
| DRB1_0901 | 472 | PANQTSAITNVVIII | QTSAITNVV | 0.3621 | 994.3 | 50.00 | Sequence |
| DRB1_0901 | 473 | ANQTSAITNVVIIIV | QTSAITNVV | 0.3611 | 1004.9 | 50.00 | Sequence |
| DRB1_0901 | 352 | FGGITRDVQVPDVRG | ITRDVQVPD | 0.3607 | 1009.2 | 50.00 | Sequence |
| DRB1_0901 | 471 | PPANQTSAITNVVII | QTSAITNVV | 0.3607 | 1009.6 | 50.00 | Sequence |
| DRB1_0901 | 250 | VLKALAKNPENRYQT | VLKALAKNP | 0.3599 | 1018.4 | 50.00 | Sequence |
| DRB1_0901 | 216 | TGDSPVSVAYQHVRE | TGDSPVSVA | 0.3582 | 1037.4 | 50.00 | Sequence |
| DRB1_0901 | 544 | VPVDSVIELQVSKGN | PVDSVIELQ | 0.3581 | 1038.4 | 50.00 | Sequence |
| DRB1_0901 | 80 | ETPAGPLPYIVMEYV | AGPLPYIVM | 0.3580 | 1038.8 | 50.00 | Sequence |
| DRB1_0901 | 11 | ELGEILGFGGMSEVH | LGFGGMSEV | 0.3579 | 1040.8 | 50.00 | Sequence |
| DRB1_0901 | 441 | KKLTAAGFGRFKQAN | KKLTAAGFG | 0.3564 | 1057.3 | 50.00 | Sequence |
| DRB1_0901 | 58 | EAQNAAALNHPAIVA | ALNHPAIVA | 0.3560 | 1062.0 | 50.00 | Sequence |
| DRB1_0901 | 39 | KVLRADLARDPSFYL | KVLRADLAR | 0.3554 | 1068.7 | 50.00 | Sequence |
| DRB1_0901 | 162 | IADSGNSVTQTAAVI | SVTQTAAVI | 0.3541 | 1084.1 | 50.00 | Sequence |
| DRB1_0901 | 286 | VLTDAERTSLLSSAA | LTDAERTSL | 0.3536 | 1090.4 | 50.00 | Sequence |
| DRB1_0901 | 547 | DSVIELQVSKGNQFV | LQVSKGNQF | 0.3535 | 1090.6 | 50.00 | Sequence |
| DRB1_0901 | 545 | PVDSVIELQVSKGNQ | PVDSVIELQ | 0.3534 | 1092.4 | 50.00 | Sequence |
| DRB1_0901 | 68 | PAIVAVYDTGEAETP | VYDTGEAET | 0.3532 | 1094.2 | 50.00 | Sequence |
| DRB1_0901 | 518 | KFSQASVDSPRPAGE | KFSQASVDS | 0.3532 | 1094.9 | 50.00 | Sequence |
| DRB1_0901 | 71 | VAVYDTGEAETPAGP | VYDTGEAET | 0.3531 | 1095.4 | 50.00 | Sequence |
| DRB1_0901 | 288 | TDAERTSLLSSAAGN | RTSLLSSAA | 0.3530 | 1097.5 | 50.00 | Sequence |
| DRB1_0901 | 583 | TGMLDKGADVDAGGS | MLDKGADVD | 0.3528 | 1098.9 | 50.00 | Sequence |
| DRB1_0901 | 333 | AVVAVLAVLTVVVTI | VAVLAVLTV | 0.3518 | 1111.4 | 50.00 | Sequence |
| DRB1_0901 | 442 | KLTAAGFGRFKQANS | FGRFKQANS | 0.3516 | 1114.4 | 50.00 | Sequence |
| DRB1_0901 | 406 | NTSVSAGDEITVNVS | TSVSAGDEI | 0.3512 | 1118.7 | 50.00 | Sequence |
| DRB1_0901 | 56 | RREAQNAAALNHPAI | RREAQNAAA | 0.3507 | 1124.4 | 50.00 | Sequence |

```
DRB1_0901  112  KRAIEVIADACQALN  IADACQALN         0.3507       1124.8                 50.00      Sequence
DRB1_0901  481  NVVIIIVGSGPATKD  IIIVGSGPA         0.3499       1134.3                 50.00      Sequence
DRB1_0901  454  ANSPSTPELVGKVIG  ANSPSTPEL         0.3494       1141.0                 50.00      Sequence
DRB1_0901  575  PRLRALGWTGMLDKG  PRLRALGWT         0.3491       1144.3                 50.00      Sequence
DRB1_0901  321  RDRSIGSVGRWVAVV  DRSIGSVGR         0.3477       1161.4                 50.00      Sequence
DRB1_0901   67  HPAIVAVYDTGEAET  VYDTGEAET         0.3469       1171.4                 50.00      Sequence
DRB1_0901  546  VDSVIELQVSKGNQF  VIELQVSKG         0.3465       1176.4                 50.00      Sequence
DRB1_0901  228  VREDPIPPSARHEGL  VREDPIPPS         0.3451       1194.5                 50.00      Sequence
DRB1_0901  354  GITRDVQVPDVRGQS  ITRDVQVPD         0.3450       1196.7                 50.00      Sequence
DRB1_0901   85  PLPYIVMEYVDGVTL  VMEYVDGVT         0.3450       1196.8                 50.00      Sequence
DRB1_0901  279  EPPEAPKVLTDAERT  EPPEAPKVL         0.3449       1198.2                 50.00      Sequence
DRB1_0901    3  PSHLSDRYELGEILG  RYELGEILG         0.3445       1202.2                 50.00      Sequence
DRB1_0901   79  AETPAGPLPYIVMEY  AGPLPYIVM         0.3433       1217.9                 50.00      Sequence
DRB1_0901   10  YELGEILGFGGMSEV  LGFGGMSEV         0.3427       1225.9                 50.00      Sequence
DRB1_0901  475  QTSAITNVVIIIVGS  QTSAITNVV         0.3426       1227.1                 50.00      Sequence
DRB1_0901  529  PAGEVTGTNPPAGTT  VTGTNPPAG         0.3425       1228.6                 50.00      Sequence
DRB1_0901  181  YLSPEQARGDSVDAR  YLSPEQARG         0.3419       1236.9                 50.00      Sequence
DRB1_0901   70  IVAVYDTGEAETPAG  VYDTGEAET         0.3418       1238.0                 50.00      Sequence
DRB1_0901   57  REAQNAAALNHPAIV  EAQNAAALN         0.3418       1238.8                 50.00      Sequence
DRB1_0901  407  TSVSAGDEITVNVST  TSVSAGDEI         0.3417       1240.2                 50.00      Sequence
DRB1_0901  120  DACQALNFSHQNGII  LNFSHQNGI         0.3415       1242.2                 50.00      Sequence
DRB1_0901  244  ADLDAVVLKALAKNP  DAVVLKALA         0.3415       1243.0                 50.00      Sequence
DRB1_0901  219  SPVSVAYQHVREDPI  YQHVREDPI         0.3413       1245.4                 50.00      Sequence
DRB1_0901  394  PPDHVIGTDPAANTS  DHVIGTDPA         0.3412       1246.7                 50.00      Sequence
DRB1_0901   77  GEAETPAGPLPYIVM  EAETPAGPL         0.3398       1265.0                 50.00      Sequence
DRB1_0901  239  HEGLSADLDAVVLKA  EGLSADLDA         0.3397       1267.4                 50.00      Sequence
DRB1_0901  464  GKVIGTNPPANQTSA  GTNPPANQT         0.3396       1267.9                 50.00      Sequence
DRB1_0901  227  HVREDPIPPSARHEG  VREDPIPPS         0.3393       1272.0                 50.00      Sequence
DRB1_0901    7  SDRYELGEILGFGGM  RYELGEILG         0.3392       1274.0                 50.00      Sequence
DRB1_0901  230  EDPIPPSARHEGLSA  DPIPPSARH         0.3384       1285.4                 50.00      Sequence
DRB1_0901  278  GEPPEAPKVLTDAER  EPPEAPKVL         0.3383       1286.2                 50.00      Sequence
DRB1_0901  110  TPKRAIEVIADACQA  PKRAIEVIA         0.3383       1286.3                 50.00      Sequence
DRB1_0901  396  DHVIGTDPAANTSVS  HVIGTDPAA         0.3374       1299.4                 50.00      Sequence
DRB1_0901  462  LVGKVIGTNPPANQT  IGTNPPANQ         0.3360       1318.0                 50.00      Sequence
DRB1_0901  240  EGLSADLDAVVLKAL  EGLSADLDA         0.3352       1329.7                 50.00      Sequence
DRB1_0901  254  LAKNPENRYQTAAEM  NRYQTAAEM         0.3351       1331.2                 50.00      Sequence
DRB1_0901  470  NPPANQTSAITNVVI  QTSAITNVV         0.3349       1334.7                 50.00      Sequence
DRB1_0901  399  IGTDPAANTSVSAGD  IGTDPAANT         0.3338       1349.8                 50.00      Sequence
DRB1_0901  395  PDHVIGTDPAANTSV  DHVIGTDPA         0.3336       1353.1                 50.00      Sequence
DRB1_0901  426  REIPDVSTLTYAEAV  VSTLTYAEA         0.3331       1360.3                 50.00      Sequence
DRB1_0901  543  TVPVDSVIELQVSKG  PVDSVIELQ         0.3331       1360.4                 50.00      Sequence
DRB1_0901  346  TIAINTFGGITRDVQ  TFGGITRDV         0.3327       1366.4                 50.00      Sequence
DRB1_0901  341  LTVVVTIAINTFGGI  LTVVVTIAI         0.3313       1387.0                 50.00      Sequence
DRB1_0901  574  EPRLRALGWTGMLDK  PRLRALGWT         0.3313       1387.9                 50.00      Sequence
DRB1_0901  320  DRDRSIGSVGRWVAV  DRDRSIGSV         0.3312       1389.4                 50.00      Sequence
DRB1_0901  296  LSSAAGNLSGPRTDP  LSSAAGNLS         0.3310       1392.1                 50.00      Sequence
DRB1_0901  597  SQHNRVVYQNPPAGT  VYQNPPAGT         0.3305       1399.3                 50.00      Sequence
DRB1_0901  463  VGKVIGTNPPANQTS  KVIGTNPPA         0.3302       1404.0                 50.00      Sequence
DRB1_0901  224  AYQHVREDPIPPSAR  YQHVREDPI         0.3299       1409.3                 50.00      Sequence
DRB1_0901  584  GMLDKGADVDAGGSQ  MLDKGADVD         0.3295       1415.1                 50.00      Sequence
DRB1_0901  340  VLTVVVTIAINTFGG  LTVVVTIAI         0.3292       1419.0                 50.00      Sequence
DRB1_0901  585  MLDKGADVDAGGSQH  MLDKGADVD         0.3282       1434.9                 50.00      Sequence
DRB1_0901  542  TTVPVDSVIELQVSK  PVDSVIELQ         0.3270       1453.5                 50.00      Sequence
DRB1_0901  372  AIATLQNRGFKIRTL  QNRGFKIRT         0.3265       1461.3                 50.00      Sequence
DRB1_0901   75  DTGEAETPAGPLPYI  EAETPAGPL         0.3265       1461.4                 50.00      Sequence
DRB1_0901  111  PKRAIEVIADACQAL  PKRAIEVIA         0.3262       1466.6                 50.00      Sequence
DRB1_0901    5  HLSDRYELGEILGFG  RYELGEILG         0.3245       1493.7                 50.00      Sequence
DRB1_0901  465  KVIGTNPPANQTSAI  IGTNPPANQ         0.3229       1518.7                 50.00      Sequence
DRB1_0901  467  IGTNPPANQTSAITN  IGTNPPANQ         0.3228       1520.6                 50.00      Sequence
DRB1_0901   74  YDTGEAETPAGPLPY  EAETPAGPL         0.3225       1526.6                 50.00      Sequence
DRB1_0901  201  LGCVLYEVLTGEPPF  LGCVLYEVL         0.3222       1530.3                 50.00      Sequence
DRB1_0901  338  LAVLTVVVTIAINTF  LTVVVTIAI         0.3220       1533.8                 50.00      Sequence
DRB1_0901  339  AVLTVVVTIAINTFG  LTVVVTIAI         0.3215       1542.8                 50.00      Sequence
DRB1_0901   46  ARDPSFYLRFRREAQ  FYLRFRREA         0.3214       1544.9                 50.00      Sequence
DRB1_0901  226  QHVREDPIPPSARHE  VREDPIPPS         0.3213       1546.1                 50.00      Sequence
DRB1_0901  397  HVIGTDPAANTSVSA  IGTDPAANT         0.3212       1547.6                 50.00      Sequence
```

```
DRB1_0901    6  LSDRYELGEILGFGG  RYELGEILG         0.3209       1552.2               50.00     Sequence
DRB1_0901  559  QFVMPDLSGMFWVDA  QFVMPDLSG         0.3204       1561.7               50.00     Sequence
DRB1_0901  355  ITRDVQVPDVRGQSS  ITRDVQVPD         0.3203       1562.7               50.00     Sequence
DRB1_0901  287  LTDAERTSLLSSAAG  LTDAERTSL         0.3202       1565.1               50.00     Sequence
DRB1_0901  382  KIRTLQKPDSTIPPD  KIRTLQKPD         0.3199       1570.0               50.00     Sequence
DRB1_0901  466  VIGTNPPANQTSAIT  IGTNPPANQ         0.3198       1571.5               50.00     Sequence
DRB1_0901   76  TGEAETPAGPLPYIV  EAETPAGPL         0.3197       1572.5               50.00     Sequence
DRB1_0901   69  AIVAVYDTGEAETPA  VYDTGEAET         0.3192       1580.8               50.00     Sequence
DRB1_0901  114  AIEVIADACQALNFS  EVIADACQA         0.3184       1595.7               50.00     Sequence
DRB1_0901  469  TNPPANQTSAITNVV  QTSAITNVV         0.3181       1600.8               50.00     Sequence
DRB1_0901  345  VTIAINTFGGITRDV  TFGGITRDV         0.3168       1623.5               50.00     Sequence
DRB1_0901  337  VLAVLTVVVTIAINT  LTVVVTIAI         0.3167       1625.2               50.00     Sequence
DRB1_0901   66  NHPAIVAVYDTGEAE  NHPAIVAVY         0.3166       1625.9               50.00     Sequence
DRB1_0901  541  GTTVPVDSVIELQVS  PVDSVIELQ         0.3148       1659.3               50.00     Sequence
DRB1_0901  303  LSGPRTDPLPRQDLD  LSGPRTDPL         0.3146       1662.2               50.00     Sequence
DRB1_0901  357  RDVQVPDVRGQSSAD  DVQVPDVRG         0.3144       1665.7               50.00     Sequence
DRB1_0901   40  VLRADLARDPSFYLR  VLRADLARD         0.3143       1667.2               50.00     Sequence
DRB1_0901  535  GTNPPAGTTVPVDSV  GTNPPAGTT         0.3138       1676.5               50.00     Sequence
DRB1_0901  539  PAGTTVPVDSVIELQ  AGTTVPVDS         0.3137       1678.3               50.00     Sequence
DRB1_0901  158  IARAIADSGNSVTQT  IARAIADSG         0.3136       1680.1               50.00     Sequence
DRB1_0901  301  GNLSGPRTDPLPRQD  GNLSGPRTD         0.3128       1694.7               50.00     Sequence
DRB1_0901  229  REDPIPPSARHEGLS  DPIPPSARH         0.3117       1715.4               50.00     Sequence
DRB1_0901  371  DAIATLQNRGFKIRT  LQNRGFKIR         0.3116       1717.5               50.00     Sequence
DRB1_0901  200  SLGCVLYEVLTGEPP  LGCVLYEVL         0.3113       1722.2               50.00     Sequence
DRB1_0901  401  TDPAANTSVSAGDEI  DPAANTSVS         0.3106       1735.6               50.00     Sequence
DRB1_0901  113  RAIEVIADACQALNF  IADACQALN         0.3097       1751.8               50.00     Sequence
DRB1_0901  540  AGTTVPVDSVIELQV  AGTTVPVDS         0.3096       1755.3               50.00     Sequence
DRB1_0901  191  SVDARSDVYSLGCVL  DVYSLGCVL         0.3088       1770.5               50.00     Sequence
DRB1_0901  285  KVLTDAERTSLLSSA  LTDAERTSL         0.3083       1780.2               50.00     Sequence
DRB1_0901  604  YQNPPAGTGVNRDGI  YQNPPAGTG         0.3079       1786.2               50.00     Sequence
DRB1_0901  398  VIGTDPAANTSVSAG  IGTDPAANT         0.3078       1789.7               50.00     Sequence
DRB1_0901    9  RYELGEILGFGGMSE  RYELGEILG         0.3075       1795.7               50.00     Sequence
DRB1_0901  334  VVAVLAVLTVVVTIA  VAVLAVLTV         0.3071       1802.9               50.00     Sequence
DRB1_0901  208  VLTGEPPFTGDSPVS  VLTGEPPFT         0.3069       1807.2               50.00     Sequence
DRB1_0901  573  AEPRLRALGWTGMLD  PRLRALGWT         0.3065       1813.8               50.00     Sequence
DRB1_0901  173  AAVIGTAQYLSPEQA  AQYLSPEQA         0.3064       1816.0               50.00     Sequence
DRB1_0901  267  EMRADLVRVHNGEPP  EMRADLVRV         0.3062       1819.8               50.00     Sequence
DRB1_0901  299  AAGNLSGPRTDPLPR  LSGPRTDPL         0.3058       1828.5               50.00     Sequence
DRB1_0901  115  IEVIADACQALNFSH  IADACQALN         0.3052       1839.7               50.00     Sequence
DRB1_0901  205  LYEVLTGEPPFTGDS  YEVLTGEPP         0.3049       1846.3               50.00     Sequence
DRB1_0901  280  PPEAPKVLTDAERTS  PPEAPKVLT         0.3043       1858.2               50.00     Sequence
DRB1_0901  461  ELVGKVIGTNPPANQ  IGTNPPANQ         0.3041       1861.8               50.00     Sequence
DRB1_0901   45  LARDPSFYLRFRREA  FYLRFRREA         0.3038       1868.7               50.00     Sequence
DRB1_0901  298  SAAGNLSGPRTDPLP  GNLSGPRTD         0.3030       1884.9               50.00     Sequence
DRB1_0901  204  VLYEVLTGEPPFTGD  LYEVLTGEP         0.3028       1887.6               50.00     Sequence
DRB1_0901  300  AGNLSGPRTDPLPRQ  LSGPRTDPL         0.3028       1889.4               50.00     Sequence
DRB1_0901  243  SADLDAVVLKALAKN  LDAVVLKAL         0.3016       1912.5               50.00     Sequence
DRB1_0901  425  QREIPDVSTLTYAEA  VSTLTYAEA         0.3008       1930.3               50.00     Sequence
DRB1_0901  117  VIADACQALNFSHQN  IADACQALN         0.3001       1943.6               50.00     Sequence
DRB1_0901  319  TDRDRSIGSVGRWVA  DRDRSIGSV         0.2998       1950.5               50.00     Sequence
DRB1_0901  335  VAVLAVLTVVVTIAI  VAVLAVLTV         0.2988       1971.4               50.00     Sequence
DRB1_0901  455  NSPSTPELVGKVIGT  NSPSTPELV         0.2979       1991.6               50.00     Sequence
DRB1_0901  116  EVIADACQALNFSHQ  IADACQALN         0.2973       2005.3               50.00     Sequence
DRB1_0901  393  IPPDHVIGTDPAANT  DHVIGTDPA         0.2970       2011.4               50.00     Sequence
DRB1_0901  572  DAEPRLRALGWTGML  PRLRALGWT         0.2949       2057.7               50.00     Sequence
DRB1_0901  416  TVNVSTGPEQREIPD  VNVSTGPEQ         0.2923       2116.0               50.00     Sequence
DRB1_0901  522  ASVDSPRPAGEVTGT  DSPRPAGEV         0.2912       2140.4               50.00     Sequence
DRB1_0901  400  GTDPAANTSVSAGDE  DPAANTSVS         0.2908       2150.9               50.00     Sequence
DRB1_0901  284  PKVLTDAERTSLLSS  LTDAERTSL         0.2906       2154.5               50.00     Sequence
DRB1_0901  571  VDAEPRLRALGWTGM  PRLRALGWT         0.2905       2156.5               50.00     Sequence
DRB1_0901  265  AAEMRADLVRVHNGE  EMRADLVRV         0.2896       2178.7               50.00     Sequence
DRB1_0901  488  GSGPATKDIPDVAGQ  GSGPATKDI         0.2889       2194.6               50.00     Sequence
DRB1_0901  242  LSADLDAVVLKALAK  LSADLDAVV         0.2885       2204.5               50.00     Sequence
DRB1_0901  336  AVLAVLTVVVTIAIN  LTVVVTIAI         0.2877       2222.7               50.00     Sequence
DRB1_0901  536  TNPPAGTTVPVDSVI  TNPPAGTTV         0.2870       2239.6               50.00     Sequence
DRB1_0901  493  TKDIPDVAGQTVDVA  DVAGQTVDV         0.2869       2243.4               50.00     Sequence
```

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| DRB1_0901 | 408 | SVSAGDEITVNVSTG | SVSAGDEIT | 0.2869 | 2243.5 | | 50.00 | Sequence |
| DRB1_0901 | 523 | SVDSPRPAGEVTGTN | DSPRPAGEV | 0.2865 | 2252.4 | | 50.00 | Sequence |
| DRB1_0901 | 492 | ATKDIPDVAGQTVDV | IPDVAGQTV | 0.2859 | 2266.9 | | 50.00 | Sequence |
| DRB1_0901 | 202 | GCVLYEVLTGEPPFT | VLYEVLTGE | 0.2859 | 2268.5 | | 50.00 | Sequence |
| DRB1_0901 | 366 | GQSSADAIATLQNRG | GQSSADAIA | 0.2855 | 2276.6 | | 50.00 | Sequence |
| DRB1_0901 | 251 | LKALAKNPENRYQTA | LKALAKNPE | 0.2845 | 2302.1 | | 50.00 | Sequence |
| DRB1_0901 | 562 | MPDLSGMFWVDAEPR | MFWVDAEPR | 0.2834 | 2330.8 | | 50.00 | Sequence |
| DRB1_0901 | 118 | IADACQALNFSHQNG | IADACQALN | 0.2833 | 2331.9 | | 50.00 | Sequence |
| DRB1_0901 | 525 | DSPRPAGEVTGTNPP | DSPRPAGEV | 0.2833 | 2332.5 | | 50.00 | Sequence |
| DRB1_0901 | 183 | SPEQARGDSVDARSD | RGDSVDARS | 0.2824 | 2355.8 | | 50.00 | Sequence |
| DRB1_0901 | 203 | CVLYEVLTGEPPFTG | VLTGEPPFT | 0.2821 | 2363.3 | | 50.00 | Sequence |
| DRB1_0901 | 538 | PPAGTTVPVDSVIEL | PAGTTVPVD | 0.2812 | 2386.7 | | 50.00 | Sequence |
| DRB1_0901 | 611 | TGVNRDGIITLRFGQ | TGVNRDGII | 0.2811 | 2387.1 | | 50.00 | Sequence |
| DRB1_0901 | 521 | QASVDSPRPAGEVTG | DSPRPAGEV | 0.2808 | 2394.8 | | 50.00 | Sequence |
| DRB1_0901 | 170 | TQTAAVIGTAQYLSP | TQTAAVIGT | 0.2808 | 2395.8 | | 50.00 | Sequence |
| DRB1_0901 | 182 | LSPEQARGDSVDARS | RGDSVDARS | 0.2800 | 2417.0 | | 50.00 | Sequence |
| DRB1_0901 | 595 | GGSQHNRVVYQNPPA | GSQHNRVVY | 0.2800 | 2417.6 | | 50.00 | Sequence |
| DRB1_0901 | 415 | ITVNVSTGPEQREIP | TVNVSTGPE | 0.2797 | 2425.3 | | 50.00 | Sequence |
| DRB1_0901 | 494 | KDIPDVAGQTVDVAQ | IPDVAGQTV | 0.2796 | 2427.4 | | 50.00 | Sequence |
| DRB1_0901 | 524 | VDSPRPAGEVTGTNP | DSPRPAGEV | 0.2792 | 2437.7 | | 50.00 | Sequence |
| DRB1_0901 | 385 | TLQKPDSTIPPDHVI | STIPPDHVI | 0.2788 | 2449.1 | | 50.00 | Sequence |
| DRB1_0901 | 302 | NLSGPRTDPLPRQDL | SGPRTDPLP | 0.2786 | 2452.7 | | 50.00 | Sequence |
| DRB1_0901 | 206 | YEVLTGEPPFTGDSP | YEVLTGEPP | 0.2785 | 2456.9 | | 50.00 | Sequence |
| DRB1_0901 | 241 | GLSADLDAVVLKALA | LSADLDAVV | 0.2780 | 2469.8 | | 50.00 | Sequence |
| DRB1_0901 | 528 | RPAGEVTGTNPPAGT | VTGTNPPAG | 0.2774 | 2486.7 | | 50.00 | Sequence |
| DRB1_0901 | 594 | AGGSQHNRVVYQNPP | GSQHNRVVY | 0.2760 | 2522.5 | | 50.00 | Sequence |
| DRB1_0901 | 391 | STIPPDHVIGTDPAA | DHVIGTDPA | 0.2759 | 2526.3 | | 50.00 | Sequence |
| DRB1_0901 | 94 | VDGVTLRDIVHTEGP | DGVTLRDIV | 0.2754 | 2540.4 | | 50.00 | Sequence |
| DRB1_0901 | 188 | RGDSVDARSDVYSLG | RGDSVDARS | 0.2739 | 2582.8 | | 50.00 | Sequence |
| DRB1_0901 | 190 | DSVDARSDVYSLGCV | DSVDARSDV | 0.2726 | 2617.0 | | 50.00 | Sequence |
| DRB1_0901 | 185 | EQARGDSVDARSDVY | RGDSVDARS | 0.2723 | 2626.0 | | 50.00 | Sequence |
| DRB1_0901 | 264 | TAAEMRADLVRVHNG | AAEMRADLV | 0.2718 | 2642.4 | | 50.00 | Sequence |
| DRB1_0901 | 266 | AEMRADLVRVHNGEP | EMRADLVRV | 0.2715 | 2651.1 | | 50.00 | Sequence |
| DRB1_0901 | 392 | TIPPDHVIGTDPAAN | DHVIGTDPA | 0.2706 | 2675.9 | | 50.00 | Sequence |
| DRB1_0901 | 263 | QTAAEMRADLVRVHN | AAEMRADLV | 0.2702 | 2688.1 | | 50.00 | Sequence |
| DRB1_0901 | 490 | GPATKDIPDVAGQTV | ATKDIPDVA | 0.2689 | 2724.8 | | 50.00 | Sequence |
| DRB1_0901 | 414 | EITVNVSTGPEQREI | VNVSTGPEQ | 0.2681 | 2749.6 | | 50.00 | Sequence |
| DRB1_0901 | 370 | ADAIATLQNRGFKIR | LQNRGFKIR | 0.2677 | 2761.4 | | 50.00 | Sequence |
| DRB1_0901 | 207 | EVLTGEPPFTGDSPV | VLTGEPPFT | 0.2677 | 2762.2 | | 50.00 | Sequence |
| DRB1_0901 | 537 | NPPAGTTVPVDSVIE | PAGTTVPVD | 0.2673 | 2773.8 | | 50.00 | Sequence |
| DRB1_0901 | 417 | VNVSTGPEQREIPDV | VNVSTGPEQ | 0.2670 | 2782.2 | | 50.00 | Sequence |
| DRB1_0901 | 186 | QARGDSVDARSDVYS | RGDSVDARS | 0.2670 | 2783.4 | | 50.00 | Sequence |
| DRB1_0901 | 383 | IRTLQKPDSTIPPDH | TLQKPDSTI | 0.2659 | 2815.1 | | 50.00 | Sequence |
| DRB1_0901 | 596 | GSQHNRVVYQNPPAG | GSQHNRVVY | 0.2655 | 2828.5 | | 50.00 | Sequence |
| DRB1_0901 | 606 | NPPAGTGVNRDGIIT | TGVNRDGII | 0.2649 | 2846.7 | | 50.00 | Sequence |
| DRB1_0901 | 184 | PEQARGDSVDARSDV | RGDSVDARS | 0.2649 | 2847.1 | | 50.00 | Sequence |
| DRB1_0901 | 495 | DIPDVAGQTVDVAQK | IPDVAGQTV | 0.2643 | 2863.7 | | 50.00 | Sequence |
| DRB1_0901 | 560 | FVMPDLSGMFWVDAE | VMPDLSGMF | 0.2633 | 2897.0 | | 50.00 | Sequence |
| DRB1_0901 | 304 | SGPRTDPLPRQDLDD | RTDPLPRQD | 0.2632 | 2898.0 | | 50.00 | Sequence |
| DRB1_0901 | 390 | DSTIPPDHVIGTDPA | DHVIGTDPA | 0.2631 | 2901.0 | | 50.00 | Sequence |
| DRB1_0901 | 561 | VMPDLSGMFWVDAEP | VMPDLSGMF | 0.2628 | 2911.4 | | 50.00 | Sequence |
| DRB1_0901 | 283 | APKVLTDAERTSLLS | LTDAERTSL | 0.2627 | 2914.5 | | 50.00 | Sequence |
| DRB1_0901 | 610 | GTGVNRDGIITLRFG | TGVNRDGII | 0.2625 | 2920.0 | | 50.00 | Sequence |
| DRB1_0901 | 480 | TNVVIIIVGSGPATK | IIIVGSGPA | 0.2624 | 2925.2 | | 50.00 | Sequence |
| DRB1_0901 | 419 | VSTGPEQREIPDVST | VSTGPEQRE | 0.2618 | 2942.4 | | 50.00 | Sequence |
| DRB1_0901 | 0 | MTTPSHLSDRYELGE | MTTPSHLSD | 0.2605 | 2984.2 | | 50.00 | Sequence |
| DRB1_0901 | 344 | VVTIAINTFGGITRD | VVTIAINTF | 0.2594 | 3019.6 | | 50.00 | Sequence |
| DRB1_0901 | 496 | IPDVAGQTVDVAQKN | IPDVAGQTV | 0.2593 | 3023.2 | | 50.00 | Sequence |
| DRB1_0901 | 422 | GPEQREIPDVSTLTY | EQREIPDVS | 0.2588 | 3039.1 | | 50.00 | Sequence |
| DRB1_0901 | 489 | SGPATKDIPDVAGQT | ATKDIPDVA | 0.2587 | 3044.3 | | 50.00 | Sequence |
| DRB1_0901 | 342 | TVVVTIAINTFGGIT | TVVVTIAIN | 0.2578 | 3071.6 | | 50.00 | Sequence |
| DRB1_0901 | 268 | MRADLVRVHNGEPPE | VRVHNGEPP | 0.2577 | 3076.4 | | 50.00 | Sequence |
| DRB1_0901 | 605 | QNPPAGTGVNRDGII | QNPPAGTGV | 0.2547 | 3178.4 | | 50.00 | Sequence |
| DRB1_0901 | 519 | FSQASVDSPRPAGEV | FSQASVDSP | 0.2542 | 3195.2 | | 50.00 | Sequence |
| DRB1_0901 | 520 | SQASVDSPRPAGEVT | DSPRPAGEV | 0.2537 | 3211.5 | | 50.00 | Sequence |
| DRB1_0901 | 297 | SSAAGNLSGPRTDPL | LSGPRTDPL | 0.2535 | 3219.6 | | 50.00 | Sequence |

```
DRB1_0901  305  GPRTDPLPRQDLDDT  RTDPLPRQD         0.2532        3230.6                 50.00     Sequence
DRB1_0901  318  DTDRDRSIGSVGRWV  DRDRSIGSV         0.2531        3232.5                 50.00     Sequence
DRB1_0901  386  LQKPDSTIPPDHVIG  KPDSTIPPD         0.2529        3240.4                 50.00     Sequence
DRB1_0901  161  AIADSGNSVTQTAAV  NSVTQTAAV         0.2527        3248.1                 50.00     Sequence
DRB1_0901  424  EQREIPDVSTLTYAE  QREIPDVST         0.2525        3253.7                 50.00     Sequence
DRB1_0901  421  TGPEQREIPDVSTLT  QREIPDVST         0.2519        3274.6                 50.00     Sequence
DRB1_0901    2  TPSHLSDRYELGEIL  SHLSDRYEL         0.2519        3275.5                 50.00     Sequence
DRB1_0901  418  NVSTGPEQREIPDVS  VSTGPEQRE         0.2519        3276.7                 50.00     Sequence
DRB1_0901  119  ADACQALNFSHQNGI  LNFSHQNGI         0.2514        3292.8                 50.00     Sequence
DRB1_0901  459  TPELVGKVIGTNPPA  TPELVGKVI         0.2514        3294.4                 50.00     Sequence
DRB1_0901  356  TRDVQVPDVRGQSSA  TRDVQVPDV         0.2509        3312.1                 50.00     Sequence
DRB1_0901  593  DAGGSQHNRVVYQNP  GGSQHNRVV         0.2506        3322.8                 50.00     Sequence
DRB1_0901  479  ITNVVIIIVGSGPAT  IIVGSGPAT         0.2498        3349.6                 50.00     Sequence
DRB1_0901  423  PEQREIPDVSTLTYA  EQREIPDVS         0.2494        3365.2                 50.00     Sequence
DRB1_0901  218  DSPVSVAYQHVREDP  VAYQHVRED         0.2464        3476.7                 50.00     Sequence
DRB1_0901  476  TSAITNVVIIIVGSG  ITNVVIIIV         0.2460        3492.2                 50.00     Sequence
DRB1_0901  413  DEITVNVSTGPEQRE  VNVSTGPEQ         0.2460        3492.3                 50.00     Sequence
DRB1_0901  498  DVAGQTVDVAQKNLN  DVAGQTVDV         0.2458        3497.5                 50.00     Sequence
DRB1_0901  592  VDAGGSQHNRVVYQN  GGSQHNRVV         0.2453        3519.9                 50.00     Sequence
DRB1_0901  388  KPDSTIPPDHVIGTD  DSTIPPDHV         0.2452        3521.4                 50.00     Sequence
DRB1_0901  172  TAAVIGTAQYLSPEQ  AVIGTAQYL         0.2436        3582.2                 50.00     Sequence
DRB1_0901  497  PDVAGQTVDVAQKNL  DVAGQTVDV         0.2436        3582.5                 50.00     Sequence
DRB1_0901  187  ARGDSVDARSDVYSL  RGDSVDARS         0.2436        3583.7                 50.00     Sequence
DRB1_0901  456  SPSTPELVGKVIGTN  TPELVGKVI         0.2432        3600.1                 50.00     Sequence
DRB1_0901  281  PEAPKVLTDAERTSL  LTDAERTSL         0.2427        3619.1                 50.00     Sequence
DRB1_0901  458  STPELVGKVIGTNPP  ELVGKVIGT         0.2424        3629.7                 50.00     Sequence
DRB1_0901  607  PPAGTGVNRDGIITL  TGVNRDGII         0.2421        3641.3                 50.00     Sequence
DRB1_0901  171  QTAAVIGTAQYLSPE  VIGTAQYLS         0.2414        3668.3                 50.00     Sequence
DRB1_0901  460  PELVGKVIGTNPPAN  KVIGTNPPA         0.2405        3705.3                 50.00     Sequence
DRB1_0901  306  PRTDPLPRQDLDDTD  RTDPLPRQD         0.2402        3717.9                 50.00     Sequence
DRB1_0901  468  GTNPPANQTSAITNV  GTNPPANQT         0.2402        3718.6                 50.00     Sequence
DRB1_0901  507  AQKNLNVYGFTKFSQ  LNVYGFTKF         0.2400        3724.0                 50.00     Sequence
DRB1_0901  608  PAGTGVNRDGIITLR  TGVNRDGII         0.2400        3725.7                 50.00     Sequence
DRB1_0901  420  STGPEQREIPDVSTL  QREIPDVST         0.2398        3735.4                 50.00     Sequence
DRB1_0901  253  ALAKNPENRYQTAAE  LAKNPENRY         0.2386        3784.7                 50.00     Sequence
DRB1_0901  217  GDSPVSVAYQHVRED  VSVAYQHVR         0.2369        3852.0                 50.00     Sequence
DRB1_0901  384  RTLQKPDSTIPPDHV  TLQKPDSTI         0.2369        3853.7                 50.00     Sequence
DRB1_0901  491  PATKDIPDVAGQTVD  IPDVAGQTV         0.2364        3874.1                 50.00     Sequence
DRB1_0901  368  SSADAIATLQNRGFK  SSADAIATL         0.2362        3881.4                 50.00     Sequence
DRB1_0901  609  AGTGVNRDGIITLRF  TGVNRDGII         0.2347        3944.1                 50.00     Sequence
DRB1_0901  387  QKPDSTIPPDHVIGT  STIPPDHVI         0.2334        4003.1                 50.00     Sequence
DRB1_0901  343  VVVTIAINTFGGITR  VVVTIAINT         0.2329        4021.3                 50.00     Sequence
DRB1_0901  591  DVDAGGSQHNRVVYQ  AGGSQHNRV         0.2321        4056.3                 50.00     Sequence
DRB1_0901  189  GDSVDARSDVYSLGC  VDARSDVYS         0.2297        4164.2                 50.00     Sequence
DRB1_0901   41  LRADLARDPSFYLRF  LARDPSFYL         0.2297        4165.4                 50.00     Sequence
DRB1_0901   44  DLARDPSFYLRFRRE  LARDPSFYL         0.2296        4169.7                 50.00     Sequence
DRB1_0901  369  SADAIATLQNRGFKI  SADAIATLQ         0.2281        4237.8                 50.00     Sequence
DRB1_0901  477  SAITNVVIIIVGSGP  SAITNVVII         0.2274        4271.7                 50.00     Sequence
DRB1_0901    1  TTPSHLSDRYELGEI  PSHLSDRYE         0.2273        4276.4                 50.00     Sequence
DRB1_0901  282  EAPKVLTDAERTSLL  LTDAERTSL         0.2267        4304.5                 50.00     Sequence
DRB1_0901  159  ARAIADSGNSVTQTA  IADSGNSVT         0.2256        4352.9                 50.00     Sequence
DRB1_0901  409  VSAGDEITVNVSTGP  VSAGDEITV         0.2248        4392.1                 50.00     Sequence
DRB1_0901  457  PSTPELVGKVIGTNP  TPELVGKVI         0.2247        4394.4                 50.00     Sequence
DRB1_0901  367  QSSADAIATLQNRGF  QSSADAIAT         0.2247        4394.6                 50.00     Sequence
DRB1_0901  317  DDTDRDRSIGSVGRW  DRDRSIGSV         0.2242        4422.6                 50.00     Sequence
DRB1_0901  389  PDSTIPPDHVIGTDP  DSTIPPDHV         0.2241        4425.0                 50.00     Sequence
DRB1_0901  412  GDEITVNVSTGPEQR  VNVSTGPEQ         0.2235        4451.7                 50.00     Sequence
DRB1_0901  252  KALAKNPENRYQTAA  LAKNPENRY         0.2232        4466.2                 50.00     Sequence
DRB1_0901  307  RTDPLPRQDLDDTDR  RTDPLPRQD         0.2214        4558.6                 50.00     Sequence
DRB1_0901  478  AITNVVIIIVGSGPA  ITNVVIIIV         0.2194        4657.0                 50.00     Sequence
DRB1_0901  527  PRPAGEVTGTNPPAG  VTGTNPPAG         0.2192        4664.7                 50.00     Sequence
DRB1_0901  160  RAIADSGNSVTQTAA  IADSGNSVT         0.2169        4782.3                 50.00     Sequence
DRB1_0901  506  VAQKNLNVYGFTKFS  LNVYGFTKF         0.2134        4970.3                 50.00     Sequence
DRB1_0901   42  RADLARDPSFYLRFR  LARDPSFYL         0.2092        5200.3                 50.00     Sequence
DRB1_0901  526  SPRPAGEVTGTNPPA  EVTGTNPPA         0.2084        5242.5                 50.00     Sequence
DRB1_0901   43  ADLARDPSFYLRFRR  LARDPSFYL         0.2083        5248.1                 50.00     Sequence
```

```
   DRB1_0901  590  ADVDAGGSQHNRVVY  AGGSQHNRV        0.2062       5369.3                  50.00     Sequence
   DRB1_0901  411  AGDEITVNVSTGPEQ  VNVSTGPEQ        0.1905       6366.7                  50.00     Sequence
   DRB1_0901  499  VAGQTVDVAQKNLNV  VAGQTVDVA        0.1903       6380.6                  50.00     Sequence
   DRB1_0901  589  GADVDAGGSQHNRVV  AGGSQHNRV        0.1863       6664.4                  50.00     Sequence
   DRB1_0901  586  LDKGADVDAGGSQHN  LDKGADVDA        0.1831       6892.7                  50.00     Sequence
   DRB1_0901  505  DVAQKNLNVYGFTKF  LNVYGFTKF        0.1754       7498.8                  50.00     Sequence
   DRB1_0901  308  TDPLPRQDLDDTDRD  TDPLPRQDL        0.1717       7797.0                  50.00     Sequence
   DRB1_0901  500  AGQTVDVAQKNLNVY  TVDVAQKNL        0.1693       8009.9                  50.00     Sequence
   DRB1_0901  316  LDDTDRDRSIGSVGR  DRDRSIGSV        0.1691       8021.0                  50.00     Sequence
   DRB1_0901  501  GQTVDVAQKNLNVYG  TVDVAQKNL        0.1622       8647.3                  50.00     Sequence
   DRB1_0901  503  TVDVAQKNLNVYGFT  TVDVAQKNL        0.1602       8832.2                  50.00     Sequence
   DRB1_0901  502  QTVDVAQKNLNVYGF  TVDVAQKNL        0.1601       8845.3                  50.00     Sequence
   DRB1_0901  410  SAGDEITVNVSTGPE  AGDEITVNV        0.1473      10161.0                  50.00     Sequence
   DRB1_0901  309  DPLPRQDLDDTDRDR  LPRQDLDDT        0.1378      11254.8                  50.00     Sequence
   DRB1_0901  588  KGADVDAGGSQHNRV  AGGSQHNRV        0.1351      11594.2                  50.00     Sequence
   DRB1_0901  315  DLDDTDRDRSIGSVG  DRDRSIGSV        0.1330      11861.1                  50.00     Sequence
   DRB1_0901  504  VDVAQKNLNVYGFTK  KNLNVYGFT        0.1277      12563.9                  50.00     Sequence
   DRB1_0901  310  PLPRQDLDDTDRDRS  LPRQDLDDT        0.1048      16095.2                  50.00     Sequence
   DRB1_0901  587  DKGADVDAGGSQHNR  DKGADVDAG        0.0965      17594.2                  50.00     Sequence
   DRB1_0901  311  LPRQDLDDTDRDRSI  LPRQDLDDT        0.0946      17956.5                  50.00     Sequence
   DRB1_0901  314  QDLDDTDRDRSIGSV  DRDRSIGSV        0.0931      18264.1                  50.00     Sequence
   DRB1_0901  312  PRQDLDDTDRDRSIG  PRQDLDDTD        0.0671      24192.1                  50.00     Sequence
   DRB1_0901  313  RQDLDDTDRDRSIGS  QDLDDTDRD        0.0583      26610.2                  50.00     Sequence
------------------------------------------------------------------------------------------------

Allele: DRB1_0901. Number of high binders 20. Number of weak binders 168. Number of peptides 612

------------------------------------------------------------------------------------------------
------------------------------------------------------------------------------------------------
      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
------------------------------------------------------------------------------------------------
   DRB1_1101  380  GFKIRTLQKPDSTIP  IRTLQKPDS        0.7327         18.0         SB     2.00     Sequence
   DRB1_1101  379  RGFKIRTLQKPDSTI  KIRTLQKPD        0.7139         22.1         SB     2.00     Sequence
   DRB1_1101   50  SFYLRFRREAQNAAA  YLRFRREAQ        0.6731         34.4         SB     4.00     Sequence
   DRB1_1101  378  NRGFKIRTLQKPDST  KIRTLQKPD        0.6724         34.6         SB     4.00     Sequence
   DRB1_1101  381  FKIRTLQKPDSTIPP  IRTLQKPDS        0.6674         36.6         SB     4.00     Sequence
   DRB1_1101   49  PSFYLRFRREAQNAA  YLRFRREAQ        0.6646         37.7         SB     4.00     Sequence
   DRB1_1101   51  FYLRFRREAQNAAAL  YLRFRREAQ        0.6630         38.3         SB     4.00     Sequence
   DRB1_1101  377  QNRGFKIRTLQKPDS  FKIRTLQKP        0.6511         43.6         SB     4.00     Sequence
   DRB1_1101  247  DAVVLKALAKNPENR  VLKALAKNP        0.6377         50.4         WB     8.00     Sequence
   DRB1_1101  248  AVVLKALAKNPENRY  VLKALAKNP        0.6276         56.2         WB     8.00     Sequence
   DRB1_1101   48  DPSFYLRFRREAQNA  FYLRFRREA        0.6220         59.7         WB     8.00     Sequence
   DRB1_1101  246  LDAVVLKALAKNPEN  AVVLKALAK        0.6161         63.6         WB     8.00     Sequence
   DRB1_1101  151  VKVMDFGIARAIADS  MDFGIARAI        0.5964         78.8         WB     8.00     Sequence
   DRB1_1101  150  AVKVMDFGIARAIAD  FGIARAIAD        0.5963         78.9         WB     8.00     Sequence
   DRB1_1101  376  LQNRGFKIRTLQKPD  FKIRTLQKP        0.5948         80.2         WB     8.00     Sequence
   DRB1_1101  245  DLDAVVLKALAKNPE  AVVLKALAK        0.5933         81.5         WB     8.00     Sequence
   DRB1_1101  152  KVMDFGIARAIADSG  FGIARAIAD        0.5878         86.5         WB     8.00     Sequence
   DRB1_1101  153  VMDFGIARAIADSGN  FGIARAIAD        0.5854         88.7         WB     8.00     Sequence
   DRB1_1101   52  YLRFRREAQNAAALN  YLRFRREAQ        0.5789         95.2         WB     8.00     Sequence
   DRB1_1101  512  NVYGFTKFSQASVDS  VYGFTKFSQ        0.5641        111.8         WB    16.00     Sequence
   DRB1_1101   35  DVAVKVLRADLARDP  AVKVLRADL        0.5631        113.0         WB    16.00     Sequence
   DRB1_1101  511  LNVYGFTKFSQASVD  NVYGFTKFS        0.5618        114.5         WB    16.00     Sequence
   DRB1_1101  510  NLNVYGFTKFSQASV  VYGFTKFSQ        0.5540        124.6         WB    16.00     Sequence
   DRB1_1101   34  RDVAVKVLRADLARD  AVKVLRADL        0.5500        130.1         WB    16.00     Sequence
   DRB1_1101  244  ADLDAVVLKALAKNP  AVVLKALAK        0.5476        133.7         WB    16.00     Sequence
   DRB1_1101   47  RDPSFYLRFRREAQN  YLRFRREAQ        0.5433        139.9         WB    16.00     Sequence
   DRB1_1101  154  MDFGIARAIADSGNS  FGIARAIAD        0.5431        140.2         WB    16.00     Sequence
   DRB1_1101  375  TLQNRGFKIRTLQKP  QNRGFKIRT        0.5428        140.8         WB    16.00     Sequence
   DRB1_1101   36  VAVKVLRADLARDPS  VKVLRADLA        0.5422        141.7         WB    16.00     Sequence
   DRB1_1101  249  VVLKALAKNPENRYQ  VLKALAKNP        0.5287        163.9         WB    16.00     Sequence
   DRB1_1101  149  NAVKVMDFGIARAIA  VKVMDFGIA        0.5258        169.1         WB    16.00     Sequence
   DRB1_1101  434  LTYAEAVKKLTAAGF  YAEAVKKLT        0.5253        170.1         WB    16.00     Sequence
   DRB1_1101   33  HRDVAVKVLRADLAR  AVKVLRADL        0.5210        178.2         WB    16.00     Sequence
   DRB1_1101  576  RLRALGWTGMLDKGA  LGWTGMLDK        0.5123        195.7         WB    16.00     Sequence
   DRB1_1101  433  TLTYAEAVKKLTAAG  YAEAVKKLT        0.5093        202.2         WB    16.00     Sequence
```

```
DRB1_1101  382  KIRTLQKPDSTIPPD  IRTLQKPDS         0.5081         204.8          WB    16.00      Sequence
DRB1_1101   37  AVKVLRADLARDPSF  VKVLRADLA         0.5016         219.8          WB    16.00      Sequence
DRB1_1101  509  KNLNVYGFTKFSQAS  VYGFTKFSQ         0.4980         228.5          WB    16.00      Sequence
DRB1_1101  513  VYGFTKFSQASVDSP  FTKFSQASV         0.4949         236.2          WB    16.00      Sequence
DRB1_1101  148  TNAVKVMDFGIARAI  AVKVMDFGI         0.4915         245.2          WB    16.00      Sequence
DRB1_1101  575  PRLRALGWTGMLDKG  RLRALGWTG         0.4911         246.2          WB    16.00      Sequence
DRB1_1101  574  EPRLRALGWTGMLDK  RLRALGWTG         0.4868         257.9          WB    16.00      Sequence
DRB1_1101  573  AEPRLRALGWTGMLD  RLRALGWTG         0.4861         260.0          WB    16.00      Sequence
DRB1_1101  435  TYAEAVKKLTAAGFG  YAEAVKKLT         0.4840         265.8          WB    16.00      Sequence
DRB1_1101  372  AIATLQNRGFKIRTL  AIATLQNRG         0.4840         266.0          WB    16.00      Sequence
DRB1_1101  371  DAIATLQNRGFKIRT  AIATLQNRG         0.4793         279.8          WB    16.00      Sequence
DRB1_1101  436  YAEAVKKLTAAGFGR  YAEAVKKLT         0.4773         285.9          WB    16.00      Sequence
DRB1_1101   32  LHRDVAVKVLRADLA  AVKVLRADL         0.4742         295.8          WB    16.00      Sequence
DRB1_1101  141  ANIMISATNAVKVMD  ANIMISATN         0.4707         307.0          WB    32.00      Sequence
DRB1_1101  140  PANIMISATNAVKVM  ANIMISATN         0.4692         312.1          WB    32.00      Sequence
DRB1_1101  432  STLTYAEAVKKLTAA  YAEAVKKLT         0.4681         315.8          WB    32.00      Sequence
DRB1_1101  572  DAEPRLRALGWTGML  RLRALGWTG         0.4653         325.6          WB    32.00      Sequence
DRB1_1101  431  VSTLTYAEAVKKLTA  YAEAVKKLT         0.4647         327.7          WB    32.00      Sequence
DRB1_1101  290  AERTSLLSSAAGNLS  TSLLSSAAG         0.4620         337.3          WB    32.00      Sequence
DRB1_1101  571  VDAEPRLRALGWTGM  RLRALGWTG         0.4612         340.3          WB    32.00      Sequence
DRB1_1101  370  ADAIATLQNRGFKIR  AIATLQNRG         0.4612         340.4          WB    32.00      Sequence
DRB1_1101  139  KPANIMISATNAVKV  ANIMISATN         0.4580         352.4          WB    32.00      Sequence
DRB1_1101  250  VLKALAKNPENRYQT  VLKALAKNP         0.4500         384.2          WB    32.00      Sequence
DRB1_1101  291  ERTSLLSSAAGNLSG  TSLLSSAAG         0.4495         386.0          WB    32.00      Sequence
DRB1_1101  374  ATLQNRGFKIRTLQK  QNRGFKIRT         0.4470         396.8          WB    32.00      Sequence
DRB1_1101  124  ALNFSHQNGIIHRDV  FSHQNGIIH         0.4458         402.1          WB    32.00      Sequence
DRB1_1101  446  AGFGRFKQANSPSTP  FGRFKQANS         0.4425         416.4          WB    32.00      Sequence
DRB1_1101   46  ARDPSFYLRFRREAQ  YLRFRREAQ         0.4420         418.9          WB    32.00      Sequence
DRB1_1101  138  VKPANIMISATNAVK  ANIMISATN         0.4409         424.0          WB    32.00      Sequence
DRB1_1101  445  AAGFGRFKQANSPST  FGRFKQANS         0.4377         438.9          WB    32.00      Sequence
DRB1_1101  508  QKNLNVYGFTKFSQA  VYGFTKFSQ         0.4375         439.9          WB    32.00      Sequence
DRB1_1101  243  SADLDAVVLKALAKN  AVVLKALAK         0.4367         443.4          WB    32.00      Sequence
DRB1_1101   22  SEVHLARDLRLHRDV  VHLARDLRL         0.4342         455.8          WB    32.00      Sequence
DRB1_1101   21  MSEVHLARDLRLHRD  VHLARDLRL         0.4297         478.3          WB    32.00      Sequence
DRB1_1101  373  IATLQNRGFKIRTLQ  QNRGFKIRT         0.4280         487.5          WB    32.00      Sequence
DRB1_1101  289  DAERTSLLSSAAGNL  RTSLLSSAA         0.4277         488.8          WB    32.00      Sequence
DRB1_1101  147  ATNAVKVMDFGIARA  AVKVMDFGI         0.4247         505.0                32.00      Sequence
DRB1_1101   23  EVHLARDLRLHRDVA  VHLARDLRL         0.4240         508.8                32.00      Sequence
DRB1_1101  570  WVDAEPRLRALGWTG  RLRALGWTG         0.4239         509.2                32.00      Sequence
DRB1_1101  578  RALGWTGMLDKGADV  LGWTGMLDK         0.4239         509.6                32.00      Sequence
DRB1_1101  577  LRALGWTGMLDKGAD  LGWTGMLDK         0.4231         514.1                32.00      Sequence
DRB1_1101  447  GFGRFKQANSPSTPE  FGRFKQANS         0.4226         516.8                32.00      Sequence
DRB1_1101  195  RSDVYSLGCVLYEVL  VYSLGCVLY         0.4224         517.6                32.00      Sequence
DRB1_1101  292  RTSLLSSAAGNLSGP  TSLLSSAAG         0.4209         526.5                32.00      Sequence
DRB1_1101  123  QALNFSHQNGIIHRD  FSHQNGIIH         0.4201         530.9                32.00      Sequence
DRB1_1101  125  LNFSHQNGIIHRDVK  FSHQNGIIH         0.4190         537.3                32.00      Sequence
DRB1_1101  579  ALGWTGMLDKGADVD  LGWTGMLDK         0.4180         543.0                32.00      Sequence
DRB1_1101  430  DVSTLTYAEAVKKLT  YAEAVKKLT         0.4176         545.3                32.00      Sequence
DRB1_1101  437  AEAVKKLTAAGFGRF  AVKKLTAAG         0.4140         567.3                32.00      Sequence
DRB1_1101   24  VHLARDLRLHRDVAV  VHLARDLRL         0.4129         573.6                32.00      Sequence
DRB1_1101  369  SADAIATLQNRGFKI  AIATLQNRG         0.4076         607.5                32.00      Sequence
DRB1_1101   13  GEILGFGGMSEVHLA  LGFGGMSEV         0.4059         619.0                32.00      Sequence
DRB1_1101  332  VAVVAVLAVLTVVVT  VAVLAVLTV         0.4038         633.4                32.00      Sequence
DRB1_1101  155  DFGIARAIADSGNSV  FGIARAIAD         0.4017         647.9                32.00      Sequence
DRB1_1101  331  WVAVVAVLAVLTVVV  VVAVLAVLT         0.4016         648.7                32.00      Sequence
DRB1_1101   14  EILGFGGMSEVHLAR  ILGFGGMSE         0.4015         649.2                32.00      Sequence
DRB1_1101   20  GMSEVHLARDLRLHR  VHLARDLRL         0.4011         652.1                32.00      Sequence
DRB1_1101  565  LSGMFWVDAEPRLRA  MFWVDAEPR         0.4007         654.8                32.00      Sequence
DRB1_1101   31  RLHRDVAVKVLRADL  AVKVLRADL         0.4006         655.2                32.00      Sequence
DRB1_1101  196  SDVYSLGCVLYEVLT  VYSLGCVLY         0.4006         655.3                32.00      Sequence
DRB1_1101  514  YGFTKFSQASVDSPR  FTKFSQASV         0.3991         666.1                32.00      Sequence
DRB1_1101  448  FGRFKQANSPSTPEL  FKQANSPST         0.3981         673.3                32.00      Sequence
DRB1_1101  194  ARSDVYSLGCVLYEV  VYSLGCVLY         0.3980         674.5                32.00      Sequence
DRB1_1101   12  LGEILGFGGMSEVHL  ILGFGGMSE         0.3978         675.9                32.00      Sequence
DRB1_1101  482  VVIIIVGSGPATKDI  IIIVGSGPA         0.3921         718.5                32.00      Sequence
DRB1_1101  333  AVVAVLAVLTVVVTI  VAVLAVLTV         0.3899         736.0                32.00      Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_1101 | 122 | CQALNFSHQNGIIHR | FSHQNGIIH | 0.3894 | 739.6 | 32.00 | Sequence |
| DRB1_1101 | 328 | VGRWVAVVAVLAVLT | VAVVAVLAV | 0.3872 | 757.8 | 32.00 | Sequence |
| DRB1_1101 | 330 | RWVAVVAVLAVLTVV | VVAVLAVLT | 0.3859 | 768.4 | 32.00 | Sequence |
| DRB1_1101 | 197 | DVYSLGCVLYEVLTG | VYSLGCVLY | 0.3814 | 806.6 | 32.00 | Sequence |
| DRB1_1101 | 137 | DVKPANIMISATNAV | ANIMISATN | 0.3806 | 814.2 | 32.00 | Sequence |
| DRB1_1101 | 444 | TAAGFGRFKQANSPS | FGRFKQANS | 0.3804 | 815.2 | 32.00 | Sequence |
| DRB1_1101 | 53 | LRFRREAQNAAALNH | LRFRREAQN | 0.3775 | 841.4 | 32.00 | Sequence |
| DRB1_1101 | 438 | EAVKKLTAAGFGRFK | AVKKLTAAG | 0.3768 | 847.7 | 32.00 | Sequence |
| DRB1_1101 | 481 | NVVIIIVGSGPATKD | IIIVGSGPA | 0.3766 | 849.5 | 32.00 | Sequence |
| DRB1_1101 | 329 | GRWVAVVAVLAVLTV | VAVVAVLAV | 0.3766 | 849.7 | 32.00 | Sequence |
| DRB1_1101 | 126 | NFSHQNGIIHRDVKP | FSHQNGIIH | 0.3760 | 855.5 | 32.00 | Sequence |
| DRB1_1101 | 25 | HLARDLRLHRDVAVK | LRLHRDVAV | 0.3755 | 859.6 | 32.00 | Sequence |
| DRB1_1101 | 580 | LGWTGMLDKGADVDA | WTGMLDKGA | 0.3747 | 867.4 | 32.00 | Sequence |
| DRB1_1101 | 334 | VVAVLAVLTVVVTIA | VVAVLAVLT | 0.3744 | 870.6 | 32.00 | Sequence |
| DRB1_1101 | 439 | AVKKLTAAGFGRFKQ | AVKKLTAAG | 0.3741 | 872.8 | 32.00 | Sequence |
| DRB1_1101 | 26 | LARDLRLHRDVAVKV | DLRLHRDVA | 0.3721 | 892.6 | 32.00 | Sequence |
| DRB1_1101 | 564 | DLSGMFWVDAEPRLR | MFWVDAEPR | 0.3719 | 893.7 | 32.00 | Sequence |
| DRB1_1101 | 323 | RSIGSVGRWVAVVAV | IGSVGRWVA | 0.3717 | 896.4 | 32.00 | Sequence |
| DRB1_1101 | 322 | DRSIGSVGRWVAVVA | IGSVGRWVA | 0.3707 | 906.0 | 32.00 | Sequence |
| DRB1_1101 | 27 | ARDLRLHRDVAVKVL | LRLHRDVAV | 0.3684 | 928.2 | 32.00 | Sequence |
| DRB1_1101 | 146 | SATNAVKVMDFGIAR | AVKVMDFGI | 0.3653 | 960.7 | 32.00 | Sequence |
| DRB1_1101 | 121 | ACQALNFSHQNGIIH | FSHQNGIIH | 0.3634 | 980.0 | 32.00 | Sequence |
| DRB1_1101 | 15 | ILGFGGMSEVHLARD | GFGGMSEVH | 0.3612 | 1003.4 | 32.00 | Sequence |
| DRB1_1101 | 38 | VKVLRADLARDPSFY | VKVLRADLA | 0.3573 | 1047.3 | 32.00 | Sequence |
| DRB1_1101 | 259 | ENRYQTAAEMRADLV | YQTAAEMRA | 0.3564 | 1057.2 | 32.00 | Sequence |
| DRB1_1101 | 321 | RDRSIGSVGRWVAVV | IGSVGRWVA | 0.3548 | 1075.8 | 32.00 | Sequence |
| DRB1_1101 | 28 | RDLRLHRDVAVKVLR | LRLHRDVAV | 0.3531 | 1096.0 | 50.00 | Sequence |
| DRB1_1101 | 193 | DARSDVYSLGCVLYE | VYSLGCVLY | 0.3530 | 1097.4 | 50.00 | Sequence |
| DRB1_1101 | 11 | ELGEILGFGGMSEVH | ILGFGGMSE | 0.3514 | 1116.1 | 50.00 | Sequence |
| DRB1_1101 | 343 | VVVTIAINTFGGITR | VTIAINTFG | 0.3498 | 1135.7 | 50.00 | Sequence |
| DRB1_1101 | 293 | TSLLSSAAGNLSGPR | TSLLSSAAG | 0.3481 | 1157.3 | 50.00 | Sequence |
| DRB1_1101 | 345 | VTIAINTFGGITRDV | VTIAINTFG | 0.3478 | 1161.1 | 50.00 | Sequence |
| DRB1_1101 | 172 | TAAVIGTAQYLSPEQ | AAVIGTAQY | 0.3471 | 1169.2 | 50.00 | Sequence |
| DRB1_1101 | 173 | AAVIGTAQYLSPEQA | AVIGTAQYL | 0.3462 | 1181.1 | 50.00 | Sequence |
| DRB1_1101 | 483 | VIIIVGSGPATKDIP | IIIVGSGPA | 0.3401 | 1261.5 | 50.00 | Sequence |
| DRB1_1101 | 338 | LAVLTVVVTIAINTF | LTVVVTIAI | 0.3397 | 1266.5 | 50.00 | Sequence |
| DRB1_1101 | 568 | MFWVDAEPRLRALGW | MFWVDAEPR | 0.3388 | 1278.9 | 50.00 | Sequence |
| DRB1_1101 | 340 | VLTVVVTIAINTFGG | VVVTIAINT | 0.3383 | 1286.0 | 50.00 | Sequence |
| DRB1_1101 | 242 | LSADLDAVVLKALAK | AVVLKALAK | 0.3382 | 1287.1 | 50.00 | Sequence |
| DRB1_1101 | 142 | NIMISATNAVKVMDF | ISATNAVKV | 0.3381 | 1289.3 | 50.00 | Sequence |
| DRB1_1101 | 127 | FSHQNGIIHRDVKPA | FSHQNGIIH | 0.3380 | 1290.3 | 50.00 | Sequence |
| DRB1_1101 | 260 | NRYQTAAEMRADLVR | YQTAAEMRA | 0.3377 | 1294.0 | 50.00 | Sequence |
| DRB1_1101 | 342 | TVVVTIAINTFGGIT | VTIAINTFG | 0.3375 | 1297.9 | 50.00 | Sequence |
| DRB1_1101 | 335 | VAVLAVLTVVVTIAI | LTVVVTIAI | 0.3373 | 1300.4 | 50.00 | Sequence |
| DRB1_1101 | 339 | AVLTVVVTIAINTFG | LTVVVTIAI | 0.3365 | 1311.7 | 50.00 | Sequence |
| DRB1_1101 | 327 | SVGRWVAVVAVLAVL | WVAVVAVLA | 0.3364 | 1312.4 | 50.00 | Sequence |
| DRB1_1101 | 288 | TDAERTSLLSSAAGN | RTSLLSSAA | 0.3361 | 1317.0 | 50.00 | Sequence |
| DRB1_1101 | 563 | PDLSGMFWVDAEPRL | MFWVDAEPR | 0.3355 | 1325.2 | 50.00 | Sequence |
| DRB1_1101 | 566 | SGMFWVDAEPRLRAL | MFWVDAEPR | 0.3349 | 1333.9 | 50.00 | Sequence |
| DRB1_1101 | 567 | GMFWVDAEPRLRALG | MFWVDAEPR | 0.3346 | 1338.9 | 50.00 | Sequence |
| DRB1_1101 | 507 | AQKNLNVYGFTKFSQ | VYGFTKFSQ | 0.3339 | 1349.2 | 50.00 | Sequence |
| DRB1_1101 | 324 | SIGSVGRWVAVVAVL | IGSVGRWVA | 0.3336 | 1353.4 | 50.00 | Sequence |
| DRB1_1101 | 515 | GFTKFSQASVDSPRP | FTKFSQASV | 0.3324 | 1370.9 | 50.00 | Sequence |
| DRB1_1101 | 341 | LTVVVTIAINTFGGI | VVVTIAINT | 0.3319 | 1378.2 | 50.00 | Sequence |
| DRB1_1101 | 449 | GRFKQANSPSTPELV | FKQANSPST | 0.3306 | 1397.9 | 50.00 | Sequence |
| DRB1_1101 | 136 | RDVKPANIMISATNA | VKPANIMIS | 0.3303 | 1402.4 | 50.00 | Sequence |
| DRB1_1101 | 344 | VVTIAINTFGGITRD | VTIAINTFG | 0.3291 | 1420.3 | 50.00 | Sequence |
| DRB1_1101 | 171 | QTAAVIGTAQYLSPE | AAVIGTAQY | 0.3287 | 1427.3 | 50.00 | Sequence |
| DRB1_1101 | 326 | GSVGRWVAVVAVLAV | WVAVVAVLA | 0.3283 | 1433.1 | 50.00 | Sequence |
| DRB1_1101 | 480 | TNVVIIIVGSGPATK | IIIVGSGPA | 0.3277 | 1441.9 | 50.00 | Sequence |
| DRB1_1101 | 348 | AINTFGGITRDVQVP | INTFGGITR | 0.3262 | 1466.7 | 50.00 | Sequence |
| DRB1_1101 | 258 | PENRYQTAAEMRADL | YQTAAEMRA | 0.3249 | 1486.6 | 50.00 | Sequence |
| DRB1_1101 | 337 | VLAVLTVVVTIAINT | LTVVVTIAI | 0.3248 | 1488.0 | 50.00 | Sequence |
| DRB1_1101 | 347 | IAINTFGGITRDVQV | INTFGGITR | 0.3248 | 1488.2 | 50.00 | Sequence |
| DRB1_1101 | 368 | SSADAIATLQNRGFK | AIATLQNRG | 0.3223 | 1530.0 | 50.00 | Sequence |
| DRB1_1101 | 19 | GGMSEVHLARDLRLH | VHLARDLRL | 0.3222 | 1531.1 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_1101 | 9 | RYELGEILGFGGMSE | RYELGEILG | 0.3222 | 1531.6 | 50.00 | Sequence |
| DRB1_1101 | 29 | DLRLHRDVAVKVLRA | LRLHRDVAV | 0.3221 | 1533.0 | 50.00 | Sequence |
| DRB1_1101 | 320 | DRDRSIGSVGRWVAV | IGSVGRWVA | 0.3215 | 1542.5 | 50.00 | Sequence |
| DRB1_1101 | 336 | AVLAVLTVVVTIAIN | LAVLTVVVT | 0.3209 | 1552.0 | 50.00 | Sequence |
| DRB1_1101 | 325 | IGSVGRWVAVVAVLA | WVAVVAVLA | 0.3204 | 1561.4 | 50.00 | Sequence |
| DRB1_1101 | 6 | LSDRYELGEILGFGG | RYELGEILG | 0.3191 | 1584.0 | 50.00 | Sequence |
| DRB1_1101 | 156 | FGIARAIADSGNSVT | FGIARAIAD | 0.3184 | 1595.2 | 50.00 | Sequence |
| DRB1_1101 | 346 | TIAINTFGGITRDVQ | INTFGGITR | 0.3182 | 1598.7 | 50.00 | Sequence |
| DRB1_1101 | 145 | ISATNAVKVMDFGIA | VKVMDFGIA | 0.3173 | 1614.0 | 50.00 | Sequence |
| DRB1_1101 | 443 | LTAAGFGRFKQANSP | FGRFKQANS | 0.3167 | 1624.3 | 50.00 | Sequence |
| DRB1_1101 | 130 | QNGIIHRDVKPANIM | IIHRDVKPA | 0.3153 | 1649.9 | 50.00 | Sequence |
| DRB1_1101 | 442 | KLTAAGFGRFKQANS | AAGFGRFKQ | 0.3143 | 1667.0 | 50.00 | Sequence |
| DRB1_1101 | 7 | SDRYELGEILGFGGM | RYELGEILG | 0.3138 | 1676.4 | 50.00 | Sequence |
| DRB1_1101 | 440 | VKKLTAAGFGRFKQA | VKKLTAAGF | 0.3128 | 1695.5 | 50.00 | Sequence |
| DRB1_1101 | 261 | RYQTAAEMRADLVRV | YQTAAEMRA | 0.3122 | 1705.8 | 50.00 | Sequence |
| DRB1_1101 | 569 | FWVDAEPRLRALGWT | VDAEPRLRA | 0.3117 | 1715.2 | 50.00 | Sequence |
| DRB1_1101 | 198 | VYSLGCVLYEVLTGE | VYSLGCVLY | 0.3116 | 1717.8 | 50.00 | Sequence |
| DRB1_1101 | 30 | LRLHRDVAVKVLRAD | LRLHRDVAV | 0.3095 | 1755.6 | 50.00 | Sequence |
| DRB1_1101 | 484 | IIIVGSGPATKDIPD | IIIVGSGPA | 0.3093 | 1759.7 | 50.00 | Sequence |
| DRB1_1101 | 16 | LGFGGMSEVHLARDL | GFGGMSEVH | 0.3081 | 1783.9 | 50.00 | Sequence |
| DRB1_1101 | 131 | NGIIHRDVKPANIMI | IIHRDVKPA | 0.3077 | 1790.5 | 50.00 | Sequence |
| DRB1_1101 | 562 | MPDLSGMFWVDAEPR | MFWVDAEPR | 0.3072 | 1800.3 | 50.00 | Sequence |
| DRB1_1101 | 8 | DRYELGEILGFGGMS | RYELGEILG | 0.3066 | 1811.8 | 50.00 | Sequence |
| DRB1_1101 | 192 | VDARSDVYSLGCVLY | VYSLGCVLY | 0.3047 | 1850.1 | 50.00 | Sequence |
| DRB1_1101 | 266 | AEMRADLVRVHNGEP | RADLVRVHN | 0.3031 | 1883.2 | 50.00 | Sequence |
| DRB1_1101 | 429 | PDVSTLTYAEAVKKL | VSTLTYAEA | 0.3021 | 1903.7 | 50.00 | Sequence |
| DRB1_1101 | 170 | TQTAAVIGTAQYLSP | AAVIGTAQY | 0.3008 | 1930.1 | 50.00 | Sequence |
| DRB1_1101 | 174 | AVIGTAQYLSPEQAR | VIGTAQYLS | 0.3007 | 1931.8 | 50.00 | Sequence |
| DRB1_1101 | 5 | HLSDRYELGEILGFG | RYELGEILG | 0.2995 | 1957.3 | 50.00 | Sequence |
| DRB1_1101 | 428 | IPDVSTLTYAEAVKK | VSTLTYAEA | 0.2993 | 1962.0 | 50.00 | Sequence |
| DRB1_1101 | 267 | EMRADLVRVHNGEPP | RADLVRVHN | 0.2985 | 1978.3 | 50.00 | Sequence |
| DRB1_1101 | 128 | SHQNGIIHRDVKPAN | NGIIHRDVK | 0.2977 | 1996.3 | 50.00 | Sequence |
| DRB1_1101 | 349 | INTFGGITRDVQVPD | INTFGGITR | 0.2951 | 2053.5 | 50.00 | Sequence |
| DRB1_1101 | 129 | HQNGIIHRDVKPANI | IIHRDVKPA | 0.2937 | 2084.1 | 50.00 | Sequence |
| DRB1_1101 | 132 | GIIHRDVKPANIMIS | IIHRDVKPA | 0.2905 | 2157.1 | 50.00 | Sequence |
| DRB1_1101 | 135 | HRDVKPANIMISATN | VKPANIMIS | 0.2900 | 2168.2 | 50.00 | Sequence |
| DRB1_1101 | 450 | RFKQANSPSTPELVG | FKQANSPST | 0.2893 | 2185.7 | 50.00 | Sequence |
| DRB1_1101 | 96 | GVTLRDIVHTEGPMT | VTLRDIVHT | 0.2866 | 2251.3 | 50.00 | Sequence |
| DRB1_1101 | 319 | TDRDRSIGSVGRWVA | IGSVGRWVA | 0.2858 | 2271.1 | 50.00 | Sequence |
| DRB1_1101 | 383 | IRTLQKPDSTIPPDH | IRTLQKPDS | 0.2837 | 2320.9 | 50.00 | Sequence |
| DRB1_1101 | 10 | YELGEILGFGGMSEV | EILGFGGMS | 0.2824 | 2356.2 | 50.00 | Sequence |
| DRB1_1101 | 45 | LARDPSFYLRFRREA | FYLRFRREA | 0.2810 | 2391.6 | 50.00 | Sequence |
| DRB1_1101 | 257 | NPENRYQTAAEMRAD | YQTAAEMRA | 0.2806 | 2401.9 | 50.00 | Sequence |
| DRB1_1101 | 133 | IIHRDVKPANIMISA | IIHRDVKPA | 0.2797 | 2425.7 | 50.00 | Sequence |
| DRB1_1101 | 581 | GWTGMLDKGADVDAG | WTGMLDKGA | 0.2790 | 2443.9 | 50.00 | Sequence |
| DRB1_1101 | 479 | ITNVVIIIVGSGPAT | VVIIIVGSG | 0.2747 | 2558.5 | 50.00 | Sequence |
| DRB1_1101 | 265 | AAEMRADLVRVHNGE | RADLVRVHN | 0.2745 | 2565.5 | 50.00 | Sequence |
| DRB1_1101 | 144 | MISATNAVKVMDFGI | TNAVKVMDF | 0.2718 | 2640.8 | 50.00 | Sequence |
| DRB1_1101 | 143 | IMISATNAVKVMDFG | IMISATNAV | 0.2702 | 2686.9 | 50.00 | Sequence |
| DRB1_1101 | 93 | YVDGVTLRDIVHTEG | VTLRDIVHT | 0.2688 | 2727.5 | 50.00 | Sequence |
| DRB1_1101 | 557 | GNQFVMPDLSGMFWV | QFVMPDLSG | 0.2663 | 2802.8 | 50.00 | Sequence |
| DRB1_1101 | 558 | NQFVMPDLSGMFWVD | QFVMPDLSG | 0.2655 | 2826.6 | 50.00 | Sequence |
| DRB1_1101 | 268 | MRADLVRVHNGEPPE | RADLVRVHN | 0.2647 | 2852.0 | 50.00 | Sequence |
| DRB1_1101 | 88 | YIVMEYVDGVTLRDI | YIVMEYVDG | 0.2642 | 2868.6 | 50.00 | Sequence |
| DRB1_1101 | 251 | LKALAKNPENRYQTA | KALAKNPEN | 0.2640 | 2874.6 | 50.00 | Sequence |
| DRB1_1101 | 134 | IHRDVKPANIMISAT | VKPANIMIS | 0.2636 | 2887.0 | 50.00 | Sequence |
| DRB1_1101 | 87 | PYIVMEYVDGVTLRD | YIVMEYVDG | 0.2625 | 2919.6 | 50.00 | Sequence |
| DRB1_1101 | 95 | DGVTLRDIVHTEGPM | VTLRDIVHT | 0.2616 | 2948.8 | 50.00 | Sequence |
| DRB1_1101 | 86 | LPYIVMEYVDGVTLR | YIVMEYVDG | 0.2615 | 2951.6 | 50.00 | Sequence |
| DRB1_1101 | 287 | LTDAERTSLLSSAAG | RTSLLSSAA | 0.2606 | 2981.8 | 50.00 | Sequence |
| DRB1_1101 | 556 | KGNQFVMPDLSGMFW | QFVMPDLSG | 0.2599 | 3004.1 | 50.00 | Sequence |
| DRB1_1101 | 516 | FTKFSQASVDSPRPA | FTKFSQASV | 0.2580 | 3066.0 | 50.00 | Sequence |
| DRB1_1101 | 4 | SHLSDRYELGEILGF | RYELGEILG | 0.2580 | 3067.7 | 50.00 | Sequence |
| DRB1_1101 | 97 | VTLRDIVHTEGPMTP | LRDIVHTEG | 0.2546 | 3181.6 | 50.00 | Sequence |
| DRB1_1101 | 94 | VDGVTLRDIVHTEGP | VTLRDIVHT | 0.2540 | 3201.2 | 50.00 | Sequence |
| DRB1_1101 | 441 | KKLTAAGFGRFKQAN | LTAAGFGRF | 0.2537 | 3212.8 | 50.00 | Sequence |

```
DRB1_1101  559  QFVMPDLSGMFWVDA  QFVMPDLSG         0.2510        3309.4                 50.00     Sequence
DRB1_1101   17  GFGGMSEVHLARDLR  GFGGMSEVH         0.2505        3324.7                 50.00     Sequence
DRB1_1101  478  AITNVVIIIVGSGPA  VVIIIVGSG         0.2484        3400.7                 50.00     Sequence
DRB1_1101  427  EIPDVSTLTYAEAVK  IPDVSTLTY         0.2484        3403.2                 50.00     Sequence
DRB1_1101  425  QREIPDVSTLTYAEA  IPDVSTLTY         0.2480        3417.5                 50.00     Sequence
DRB1_1101  549  VIELQVSKGNQFVMP  VIELQVSKG         0.2474        3438.1                 50.00     Sequence
DRB1_1101  169  VTQTAAVIGTAQYLS  AAVIGTAQY         0.2469        3458.9                 50.00     Sequence
DRB1_1101  548  SVIELQVSKGNQFVM  VIELQVSKG         0.2456        3508.3                 50.00     Sequence
DRB1_1101   91  MEYVDGVTLRDIVHT  YVDGVTLRD         0.2438        3574.3                 50.00     Sequence
DRB1_1101  256  KNPENRYQTAAEMRA  YQTAAEMRA         0.2436        3585.3                 50.00     Sequence
DRB1_1101  426  REIPDVSTLTYAEAV  IPDVSTLTY         0.2432        3598.5                 50.00     Sequence
DRB1_1101  262  YQTAAEMRADLVRVH  YQTAAEMRA         0.2425        3625.9                 50.00     Sequence
DRB1_1101  367  QSSADAIATLQNRGF  AIATLQNRG         0.2398        3734.9                 50.00     Sequence
DRB1_1101   18  FGGMSEVHLARDLRL  VHLARDLRL         0.2387        3777.8                 50.00     Sequence
DRB1_1101   99  LRDIVHTEGPMTPKR  IVHTEGPMT         0.2379        3812.5                 50.00     Sequence
DRB1_1101   85  PLPYIVMEYVDGVTL  YIVMEYVDG         0.2362        3882.8                 50.00     Sequence
DRB1_1101  264  TAAEMRADLVRVHNG  RADLVRVHN         0.2358        3898.9                 50.00     Sequence
DRB1_1101   92  EYVDGVTLRDIVHTE  VTLRDIVHT         0.2352        3924.9                 50.00     Sequence
DRB1_1101  547  DSVIELQVSKGNQFV  VIELQVSKG         0.2335        3997.1                 50.00     Sequence
DRB1_1101  269  RADLVRVHNGEPPEA  RADLVRVHN         0.2305        4129.0                 50.00     Sequence
DRB1_1101  350  NTFGGITRDVQVPDV  FGGITRDVQ         0.2294        4177.9                 50.00     Sequence
DRB1_1101  561  VMPDLSGMFWVDAEP  LSGMFWVDA         0.2280        4241.6                 50.00     Sequence
DRB1_1101  555  SKGNQFVMPDLSGMF  QFVMPDLSG         0.2267        4303.0                 50.00     Sequence
DRB1_1101  504  VDVAQKNLNVYGFTK  AQKNLNVYG         0.2265        4311.5                 50.00     Sequence
DRB1_1101  506  VAQKNLNVYGFTKFS  AQKNLNVYG         0.2257        4350.9                 50.00     Sequence
DRB1_1101   54  RFRREAQNAAALNHP  FRREAQNAA         0.2249        4384.8                 50.00     Sequence
DRB1_1101  175  VIGTAQYLSPEQARG  VIGTAQYLS         0.2236        4449.5                 50.00     Sequence
DRB1_1101   98  TLRDIVHTEGPMTPK  LRDIVHTEG         0.2222        4518.4                 50.00     Sequence
DRB1_1101  599  HNRVVYQNPPAGTGV  VYQNPPAGT         0.2215        4553.5                 50.00     Sequence
DRB1_1101  598  QHNRVVYQNPPAGTG  HNRVVYQNP         0.2212        4566.4                 50.00     Sequence
DRB1_1101  205  LYEVLTGEPPFTGDS  YEVLTGEPP         0.2211        4571.3                 50.00     Sequence
DRB1_1101  611  TGVNRDGIITLRFGQ  RDGIITLRF         0.2211        4573.4                 50.00     Sequence
DRB1_1101  546  VDSVIELQVSKGNQF  VIELQVSKG         0.2202        4615.5                 50.00     Sequence
DRB1_1101  204  VLYEVLTGEPPFTGD  YEVLTGEPP         0.2182        4717.0                 50.00     Sequence
DRB1_1101  477  SAITNVVIIIVGSGP  AITNVVIII         0.2133        4972.8                 50.00     Sequence
DRB1_1101  597  SQHNRVVYQNPPAGT  HNRVVYQNP         0.2133        4972.9                 50.00     Sequence
DRB1_1101  560  FVMPDLSGMFWVDAE  LSGMFWVDA         0.2116        5063.6                 50.00     Sequence
DRB1_1101  203  CVLYEVLTGEPPFTG  LYEVLTGEP         0.2107        5115.6                 50.00     Sequence
DRB1_1101  318  DTDRDRSIGSVGRWV  DRSIGSVGR         0.2105        5124.1                 50.00     Sequence
DRB1_1101  600  NRVVYQNPPAGTGVN  VYQNPPAGT         0.2103        5136.3                 50.00     Sequence
DRB1_1101  503  TVDVAQKNLNVYGFT  VDVAQKNLN         0.2098        5165.8                 50.00     Sequence
DRB1_1101  118  IADACQALNFSHQNG  ACQALNFSH         0.2084        5246.2                 50.00     Sequence
DRB1_1101  462  LVGKVIGTNPPANQT  KVIGTNPPA         0.2076        5291.6                 50.00     Sequence
DRB1_1101  596  GSQHNRVVYQNPPAG  HNRVVYQNP         0.2063        5365.8                 50.00     Sequence
DRB1_1101  120  DACQALNFSHQNGII  ACQALNFSH         0.2062        5368.4                 50.00     Sequence
DRB1_1101  582  WTGMLDKGADVDAGG  WTGMLDKGA         0.2053        5423.9                 50.00     Sequence
DRB1_1101    3  PSHLSDRYELGEILG  RYELGEILG         0.2051        5436.0                 50.00     Sequence
DRB1_1101  202  GCVLYEVLTGEPPFT  LYEVLTGEP         0.2045        5467.9                 50.00     Sequence
DRB1_1101  294  SLLSSAAGNLSGPRT  SSAAGNLSG         0.2043        5480.4                 50.00     Sequence
DRB1_1101  476  TSAITNVVIIIVGSG  AITNVVIII         0.2043        5484.6                 50.00     Sequence
DRB1_1101  610  GTGVNRDGIITLRFG  GVNRDGIIT         0.2041        5496.5                 50.00     Sequence
DRB1_1101   90  VMEYVDGVTLRDIVH  MEYVDGVTL         0.2037        5515.6                 50.00     Sequence
DRB1_1101  463  VGKVIGTNPPANQTS  KVIGTNPPA         0.2029        5566.9                 50.00     Sequence
DRB1_1101   60  QNAAALNHPAIVAVY  ALNHPAIVA         0.2029        5568.7                 50.00     Sequence
DRB1_1101  609  AGTGVNRDGIITLRF  GVNRDGIIT         0.2023        5605.4                 50.00     Sequence
DRB1_1101  550  IELQVSKGNQFVMPD  LQVSKGNQF         0.2020        5620.4                 50.00     Sequence
DRB1_1101  168  SVTQTAAVIGTAQYL  VTQTAAVIG         0.2017        5640.8                 50.00     Sequence
DRB1_1101  102  IVHTEGPMTPKRAIE  IVHTEGPMT         0.2009        5686.5                 50.00     Sequence
DRB1_1101  106  EGPMTPKRAIEVIAD  MTPKRAIEV         0.1984        5843.2                 50.00     Sequence
DRB1_1101  100  RDIVHTEGPMTPKRA  IVHTEGPMT         0.1981        5864.2                 50.00     Sequence
DRB1_1101  505  DVAQKNLNVYGFTKF  AQKNLNVYG         0.1979        5873.2                 50.00     Sequence
DRB1_1101  601  RVVYQNPPAGTGVNR  VYQNPPAGT         0.1977        5889.5                 50.00     Sequence
DRB1_1101  105  TEGPMTPKRAIEVIA  GPMTPKRAI         0.1969        5941.0                 50.00     Sequence
DRB1_1101  101  DIVHTEGPMTPKRAI  IVHTEGPMT         0.1968        5943.6                 50.00     Sequence
DRB1_1101   59  AQNAAALNHPAIVAV  AAALNHPAI         0.1962        5984.5                 50.00     Sequence
DRB1_1101  119  ADACQALNFSHQNGI  ACQALNFSH         0.1961        5990.7                 50.00     Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_1101 | 351 | TFGGITRDVQVPDVR | FGGITRDVQ | 0.1951 | 6055.5 | 50.00 | Sequence |
| DRB1_1101 | 89 | IVMEYVDGVTLRDIV | MEYVDGVTL | 0.1938 | 6140.3 | 50.00 | Sequence |
| DRB1_1101 | 502 | QTVDVAQKNLNVYGF | VDVAQKNLN | 0.1936 | 6155.4 | 50.00 | Sequence |
| DRB1_1101 | 595 | GGSQHNRVVYQNPPA | HNRVVYQNP | 0.1921 | 6258.4 | 50.00 | Sequence |
| DRB1_1101 | 475 | QTSAITNVVIIIVGS | ITNVVIIIV | 0.1899 | 6407.1 | 50.00 | Sequence |
| DRB1_1101 | 84 | GPLPYIVMEYVDGVT | YIVMEYVDG | 0.1892 | 6456.8 | 50.00 | Sequence |
| DRB1_1101 | 461 | ELVGKVIGTNPPANQ | KVIGTNPPA | 0.1890 | 6471.7 | 50.00 | Sequence |
| DRB1_1101 | 295 | LLSSAAGNLSGPRTD | SSAAGNLSG | 0.1870 | 6613.5 | 50.00 | Sequence |
| DRB1_1101 | 473 | ANQTSAITNVVIIIV | TSAITNVVI | 0.1867 | 6629.1 | 50.00 | Sequence |
| DRB1_1101 | 424 | EQREIPDVSTLTYAE | IPDVSTLTY | 0.1865 | 6645.3 | 50.00 | Sequence |
| DRB1_1101 | 107 | GPMTPKRAIEVIADA | GPMTPKRAI | 0.1863 | 6664.0 | 50.00 | Sequence |
| DRB1_1101 | 263 | QTAAEMRADLVRVHN | RADLVRVHN | 0.1855 | 6721.7 | 50.00 | Sequence |
| DRB1_1101 | 39 | KVLRADLARDPSFYL | VLRADLARD | 0.1849 | 6761.5 | 50.00 | Sequence |
| DRB1_1101 | 61 | NAAALNHPAIVAVYD | ALNHPAIVA | 0.1847 | 6778.4 | 50.00 | Sequence |
| DRB1_1101 | 545 | PVDSVIELQVSKGNQ | VIELQVSKG | 0.1842 | 6812.7 | 50.00 | Sequence |
| DRB1_1101 | 167 | NSVTQTAAVIGTAQY | VTQTAAVIG | 0.1839 | 6837.5 | 50.00 | Sequence |
| DRB1_1101 | 474 | NQTSAITNVVIIIVG | TSAITNVVI | 0.1804 | 7103.3 | 50.00 | Sequence |
| DRB1_1101 | 296 | LSSAAGNLSGPRTDP | SSAAGNLSG | 0.1797 | 7150.6 | 50.00 | Sequence |
| DRB1_1101 | 117 | VIADACQALNFSHQN | ACQALNFSH | 0.1797 | 7151.1 | 50.00 | Sequence |
| DRB1_1101 | 176 | IGTAQYLSPEQARGD | AQYLSPEQA | 0.1797 | 7155.7 | 50.00 | Sequence |
| DRB1_1101 | 501 | GQTVDVAQKNLNVYG | VDVAQKNLN | 0.1797 | 7157.4 | 50.00 | Sequence |
| DRB1_1101 | 206 | YEVLTGEPPFTGDSP | YEVLTGEPP | 0.1777 | 7314.0 | 50.00 | Sequence |
| DRB1_1101 | 286 | VLTDAERTSLLSSAA | RTSLLSSAA | 0.1768 | 7378.7 | 50.00 | Sequence |
| DRB1_1101 | 283 | APKVLTDAERTSLLS | VLTDAERTS | 0.1767 | 7389.3 | 50.00 | Sequence |
| DRB1_1101 | 252 | KALAKNPENRYQTAA | KALAKNPEN | 0.1762 | 7427.1 | 50.00 | Sequence |
| DRB1_1101 | 284 | PKVLTDAERTSLLSS | VLTDAERTS | 0.1761 | 7436.3 | 50.00 | Sequence |
| DRB1_1101 | 199 | YSLGCVLYEVLTGEP | YSLGCVLYE | 0.1761 | 7439.0 | 50.00 | Sequence |
| DRB1_1101 | 460 | PELVGKVIGTNPPAN | PELVGKVIG | 0.1757 | 7470.0 | 50.00 | Sequence |
| DRB1_1101 | 554 | VSKGNQFVMPDLSGM | QFVMPDLSG | 0.1757 | 7472.1 | 50.00 | Sequence |
| DRB1_1101 | 201 | LGCVLYEVLTGEPPF | LYEVLTGEP | 0.1754 | 7491.1 | 50.00 | Sequence |
| DRB1_1101 | 464 | GKVIGTNPPANQTSA | KVIGTNPPA | 0.1730 | 7694.9 | 50.00 | Sequence |
| DRB1_1101 | 44 | DLARDPSFYLRFRRE | SFYLRFRRE | 0.1720 | 7774.7 | 50.00 | Sequence |
| DRB1_1101 | 58 | EAQNAAALNHPAIVA | AAALNHPAI | 0.1719 | 7781.5 | 50.00 | Sequence |
| DRB1_1101 | 103 | VHTEGPMTPKRAIEV | GPMTPKRAI | 0.1714 | 7828.1 | 50.00 | Sequence |
| DRB1_1101 | 285 | KVLTDAERTSLLSSA | VLTDAERTS | 0.1710 | 7863.4 | 50.00 | Sequence |
| DRB1_1101 | 459 | TPELVGKVIGTNPPA | PELVGKVIG | 0.1689 | 8036.8 | 50.00 | Sequence |
| DRB1_1101 | 485 | IIVGSGPATKDIPDV | IIVGSGPAT | 0.1685 | 8076.6 | 50.00 | Sequence |
| DRB1_1101 | 317 | DDTDRDRSIGSVGRW | RDRSIGSVG | 0.1678 | 8136.0 | 50.00 | Sequence |
| DRB1_1101 | 297 | SSAAGNLSGPRTDPL | AGNLSGPRT | 0.1677 | 8146.4 | 50.00 | Sequence |
| DRB1_1101 | 104 | HTEGPMTPKRAIEVI | GPMTPKRAI | 0.1677 | 8148.4 | 50.00 | Sequence |
| DRB1_1101 | 552 | LQVSKGNQFVMPDLS | LQVSKGNQF | 0.1676 | 8159.2 | 50.00 | Sequence |
| DRB1_1101 | 551 | ELQVSKGNQFVMPDL | LQVSKGNQF | 0.1669 | 8218.4 | 50.00 | Sequence |
| DRB1_1101 | 220 | PVSVAYQHVREDPIP | VSVAYQHVR | 0.1639 | 8486.9 | 50.00 | Sequence |
| DRB1_1101 | 219 | SPVSVAYQHVREDPI | VSVAYQHVR | 0.1639 | 8489.5 | 50.00 | Sequence |
| DRB1_1101 | 451 | FKQANSPSTPELVGK | FKQANSPST | 0.1634 | 8531.0 | 50.00 | Sequence |
| DRB1_1101 | 594 | AGGSQHNRVVYQNPP | SQHNRVVYQ | 0.1633 | 8543.6 | 50.00 | Sequence |
| DRB1_1101 | 544 | VPVDSVIELQVSKGN | VDSVIELQV | 0.1627 | 8597.4 | 50.00 | Sequence |
| DRB1_1101 | 472 | PANQTSAITNVVIII | TSAITNVVI | 0.1625 | 8616.2 | 50.00 | Sequence |
| DRB1_1101 | 108 | PMTPKRAIEVIADAC | PKRAIEVIA | 0.1623 | 8633.0 | 50.00 | Sequence |
| DRB1_1101 | 166 | GNSVTQTAAVIGTAQ | VTQTAAVIG | 0.1618 | 8684.3 | 50.00 | Sequence |
| DRB1_1101 | 62 | AAALNHPAIVAVYDT | ALNHPAIVA | 0.1604 | 8818.1 | 50.00 | Sequence |
| DRB1_1101 | 83 | AGPLPYIVMEYVDGV | YIVMEYVDG | 0.1592 | 8933.5 | 50.00 | Sequence |
| DRB1_1101 | 116 | EVIADACQALNFSHQ | IADACQALN | 0.1561 | 9238.3 | 50.00 | Sequence |
| DRB1_1101 | 423 | PEQREIPDVSTLTYA | IPDVSTLTY | 0.1554 | 9305.2 | 50.00 | Sequence |
| DRB1_1101 | 241 | GLSADLDAVVLKALA | DAVVLKALA | 0.1538 | 9469.0 | 50.00 | Sequence |
| DRB1_1101 | 109 | MTPKRAIEVIADACQ | PKRAIEVIA | 0.1538 | 9470.6 | 50.00 | Sequence |
| DRB1_1101 | 465 | KVIGTNPPANQTSAI | KVIGTNPPA | 0.1526 | 9594.2 | 50.00 | Sequence |
| DRB1_1101 | 115 | IEVIADACQALNFSH | IADACQALN | 0.1523 | 9622.6 | 50.00 | Sequence |
| DRB1_1101 | 458 | STPELVGKVIGTNPP | PELVGKVIG | 0.1518 | 9676.7 | 50.00 | Sequence |
| DRB1_1101 | 212 | EPPFTGDSPVSVAYQ | FTGDSPVSV | 0.1514 | 9713.6 | 50.00 | Sequence |
| DRB1_1101 | 200 | SLGCVLYEVLTGEPP | CVLYEVLTG | 0.1499 | 9880.6 | 50.00 | Sequence |
| DRB1_1101 | 414 | EITVNVSTGPEQREI | ITVNVSTGP | 0.1493 | 9936.1 | 50.00 | Sequence |
| DRB1_1101 | 282 | EAPKVLTDAERTSLL | KVLTDAERT | 0.1493 | 9941.7 | 50.00 | Sequence |
| DRB1_1101 | 165 | SGNSVTQTAAVIGTA | VTQTAAVIG | 0.1490 | 9976.2 | 50.00 | Sequence |
| DRB1_1101 | 113 | RAIEVIADACQALNF | AIEVIADAC | 0.1490 | 9976.7 | 50.00 | Sequence |
| DRB1_1101 | 366 | GQSSADAIATLQNRG | AIATLQNRG | 0.1488 | 9990.2 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_1101 | 178 | TAQYLSPEQARGDSV | QYLSPEQAR | 0.1479 | 10090.1 | 50.00 | Sequence |
| DRB1_1101 | 352 | FGGITRDVQVPDVRG | FGGITRDVQ | 0.1477 | 10119.2 | 50.00 | Sequence |
| DRB1_1101 | 177 | GTAQYLSPEQARGDS | QYLSPEQAR | 0.1475 | 10137.1 | 50.00 | Sequence |
| DRB1_1101 | 553 | QVSKGNQFVMPDLSG | QFVMPDLSG | 0.1472 | 10167.4 | 50.00 | Sequence |
| DRB1_1101 | 608 | PAGTGVNRDGIITLR | GVNRDGIIT | 0.1471 | 10177.8 | 50.00 | Sequence |
| DRB1_1101 | 114 | AIEVIADACQALNFS | IEVIADACQ | 0.1461 | 10292.8 | 50.00 | Sequence |
| DRB1_1101 | 211 | GEPPFTGDSPVSVAY | FTGDSPVSV | 0.1459 | 10309.3 | 50.00 | Sequence |
| DRB1_1101 | 221 | VSVAYQHVREDPIPP | VSVAYQHVR | 0.1449 | 10419.9 | 50.00 | Sequence |
| DRB1_1101 | 55 | FRREAQNAAALNHPA | FRREAQNAA | 0.1447 | 10452.5 | 50.00 | Sequence |
| DRB1_1101 | 40 | VLRADLARDPSFYLR | VLRADLARD | 0.1437 | 10559.6 | 50.00 | Sequence |
| DRB1_1101 | 543 | TVPVDSVIELQVSKG | VDSVIELQV | 0.1436 | 10569.7 | 50.00 | Sequence |
| DRB1_1101 | 602 | VVYQNPPAGTGVNRD | VYQNPPAGT | 0.1434 | 10594.3 | 50.00 | Sequence |
| DRB1_1101 | 593 | DAGGSQHNRVVYQNP | GSQHNRVVY | 0.1427 | 10681.3 | 50.00 | Sequence |
| DRB1_1101 | 157 | GIARAIADSGNSVTQ | IARAIADSG | 0.1424 | 10713.8 | 50.00 | Sequence |
| DRB1_1101 | 222 | SVAYQHVREDPIPPS | YQHVREDPI | 0.1411 | 10860.9 | 50.00 | Sequence |
| DRB1_1101 | 270 | ADLVRVHNGEPPEAP | LVRVHNGEP | 0.1410 | 10872.4 | 50.00 | Sequence |
| DRB1_1101 | 413 | DEITVNVSTGPEQRE | ITVNVSTGP | 0.1407 | 10908.9 | 50.00 | Sequence |
| DRB1_1101 | 112 | KRAIEVIADACQALN | RAIEVIADA | 0.1392 | 11094.2 | 50.00 | Sequence |
| DRB1_1101 | 218 | DSPVSVAYQHVREDP | VSVAYQHVR | 0.1388 | 11134.7 | 50.00 | Sequence |
| DRB1_1101 | 191 | SVDARSDVYSLGCVL | RSDVYSLGC | 0.1380 | 11229.3 | 50.00 | Sequence |
| DRB1_1101 | 500 | AGQTVDVAQKNLNVY | VDVAQKNLN | 0.1379 | 11251.2 | 50.00 | Sequence |
| DRB1_1101 | 213 | PPFTGDSPVSVAYQH | FTGDSPVSV | 0.1373 | 11318.0 | 50.00 | Sequence |
| DRB1_1101 | 179 | AQYLSPEQARGDSVD | QYLSPEQAR | 0.1370 | 11351.0 | 50.00 | Sequence |
| DRB1_1101 | 471 | PPANQTSAITNVVII | TSAITNVVI | 0.1369 | 11365.6 | 50.00 | Sequence |
| DRB1_1101 | 111 | PKRAIEVIADACQAL | PKRAIEVIA | 0.1366 | 11409.6 | 50.00 | Sequence |
| DRB1_1101 | 415 | ITVNVSTGPEQREIP | ITVNVSTGP | 0.1365 | 11421.9 | 50.00 | Sequence |
| DRB1_1101 | 63 | AALNHPAIVAVYDTG | ALNHPAIVA | 0.1361 | 11471.7 | 50.00 | Sequence |
| DRB1_1101 | 412 | GDEITVNVSTGPEQR | ITVNVSTGP | 0.1360 | 11476.7 | 50.00 | Sequence |
| DRB1_1101 | 158 | IARAIADSGNSVTQT | IARAIADSG | 0.1348 | 11629.7 | 50.00 | Sequence |
| DRB1_1101 | 298 | SAAGNLSGPRTDPLP | AGNLSGPRT | 0.1338 | 11751.1 | 50.00 | Sequence |
| DRB1_1101 | 457 | PSTPELVGKVIGTNP | PELVGKVIG | 0.1330 | 11855.1 | 50.00 | Sequence |
| DRB1_1101 | 223 | VAYQHVREDPIPPSA | YQHVREDPI | 0.1307 | 12153.5 | 50.00 | Sequence |
| DRB1_1101 | 224 | AYQHVREDPIPPSAR | YQHVREDPI | 0.1300 | 12254.9 | 50.00 | Sequence |
| DRB1_1101 | 164 | DSGNSVTQTAAVIGT | NSVTQTAAV | 0.1289 | 12401.3 | 50.00 | Sequence |
| DRB1_1101 | 82 | PAGPLPYIVMEYVDG | LPYIVMEYV | 0.1273 | 12618.1 | 50.00 | Sequence |
| DRB1_1101 | 542 | TTVPVDSVIELQVSK | VDSVIELQV | 0.1249 | 12941.8 | 50.00 | Sequence |
| DRB1_1101 | 361 | VPDVRGQSSADAIAT | VRGQSSADA | 0.1246 | 12992.3 | 50.00 | Sequence |
| DRB1_1101 | 422 | GPEQREIPDVSTLTY | IPDVSTLTY | 0.1234 | 13162.3 | 50.00 | Sequence |
| DRB1_1101 | 64 | ALNHPAIVAVYDTGE | ALNHPAIVA | 0.1232 | 13180.2 | 50.00 | Sequence |
| DRB1_1101 | 41 | LRADLARDPSFYLRF | RADLARDPS | 0.1230 | 13211.0 | 50.00 | Sequence |
| DRB1_1101 | 607 | PPAGTGVNRDGIITL | GVNRDGIIT | 0.1228 | 13236.0 | 50.00 | Sequence |
| DRB1_1101 | 57 | REAQNAAALNHPAIV | AAALNHPAI | 0.1227 | 13254.0 | 50.00 | Sequence |
| DRB1_1101 | 255 | AKNPENRYQTAAEMR | RYQTAAEMR | 0.1227 | 13255.1 | 50.00 | Sequence |
| DRB1_1101 | 110 | TPKRAIEVIADACQA | PKRAIEVIA | 0.1223 | 13309.4 | 50.00 | Sequence |
| DRB1_1101 | 214 | PFTGDSPVSVAYQHV | FTGDSPVSV | 0.1222 | 13324.1 | 50.00 | Sequence |
| DRB1_1101 | 299 | AAGNLSGPRTDPLPR | AGNLSGPRT | 0.1214 | 13444.5 | 50.00 | Sequence |
| DRB1_1101 | 603 | VYQNPPAGTGVNRDG | VYQNPPAGT | 0.1213 | 13452.9 | 50.00 | Sequence |
| DRB1_1101 | 271 | DLVRVHNGEPPEAPK | LVRVHNGEP | 0.1206 | 13557.2 | 50.00 | Sequence |
| DRB1_1101 | 396 | DHVIGTDPAANTSVS | HVIGTDPAA | 0.1205 | 13572.0 | 50.00 | Sequence |
| DRB1_1101 | 360 | QVPDVRGQSSADAIA | VPDVRGQSS | 0.1204 | 13594.2 | 50.00 | Sequence |
| DRB1_1101 | 210 | TGEPPFTGDSPVSVA | FTGDSPVSV | 0.1203 | 13611.8 | 50.00 | Sequence |
| DRB1_1101 | 217 | GDSPVSVAYQHVRED | VSVAYQHVR | 0.1201 | 13628.4 | 50.00 | Sequence |
| DRB1_1101 | 470 | NPPANQTSAITNVVI | TSAITNVVI | 0.1177 | 13989.8 | 50.00 | Sequence |
| DRB1_1101 | 395 | PDHVIGTDPAANTSV | HVIGTDPAA | 0.1174 | 14032.4 | 50.00 | Sequence |
| DRB1_1101 | 281 | PEAPKVLTDAERTSL | VLTDAERTS | 0.1169 | 14110.1 | 50.00 | Sequence |
| DRB1_1101 | 592 | VDAGGSQHNRVVYQN | SQHNRVVYQ | 0.1159 | 14268.6 | 50.00 | Sequence |
| DRB1_1101 | 272 | LVRVHNGEPPEAPKV | LVRVHNGEP | 0.1156 | 14320.5 | 50.00 | Sequence |
| DRB1_1101 | 56 | RREAQNAAALNHPAI | RREAQNAAA | 0.1152 | 14381.0 | 50.00 | Sequence |
| DRB1_1101 | 358 | DVQVPDVRGQSSADA | VPDVRGQSS | 0.1148 | 14440.3 | 50.00 | Sequence |
| DRB1_1101 | 359 | VQVPDVRGQSSADAI | VPDVRGQSS | 0.1127 | 14772.8 | 50.00 | Sequence |
| DRB1_1101 | 42 | RADLARDPSFYLRFR | LARDPSFYL | 0.1121 | 14860.1 | 50.00 | Sequence |
| DRB1_1101 | 215 | FTGDSPVSVAYQHVR | FTGDSPVSV | 0.1119 | 14893.8 | 50.00 | Sequence |
| DRB1_1101 | 2 | TPSHLSDRYELGEIL | HLSDRYELG | 0.1118 | 14915.4 | 50.00 | Sequence |
| DRB1_1101 | 180 | QYLSPEQARGDSVDA | QYLSPEQAR | 0.1118 | 14922.7 | 50.00 | Sequence |
| DRB1_1101 | 397 | HVIGTDPAANTSVSA | HVIGTDPAA | 0.1106 | 15102.5 | 50.00 | Sequence |
| DRB1_1101 | 235 | PSARHEGLSADLDAV | RHEGLSADL | 0.1093 | 15320.7 | 50.00 | Sequence |

```
DRB1_1101   69  AIVAVYDTGEAETPA  VAVYDTGEA        0.1086      15441.2            50.00     Sequence
DRB1_1101  236  SARHEGLSADLDAVV  RHEGLSADL        0.1076      15606.5            50.00     Sequence
DRB1_1101   68  PAIVAVYDTGEAETP  VAVYDTGEA        0.1075      15632.1            50.00     Sequence
DRB1_1101  254  LAKNPENRYQTAAEM  LAKNPENRY        0.1071      15697.7            50.00     Sequence
DRB1_1101  316  LDDTDRDRSIGSVGR  RDRSIGSVG        0.1064      15811.3            50.00     Sequence
DRB1_1101  456  SPSTPELVGKVIGTN  PELVGKVIG        0.1054      15986.6            50.00     Sequence
DRB1_1101    1  TTPSHLSDRYELGEI  HLSDRYELG        0.1051      16040.4            50.00     Sequence
DRB1_1101   43  ADLARDPSFYLRFRR  PSFYLRFRR        0.1050      16061.3            50.00     Sequence
DRB1_1101  300  AGNLSGPRTDPLPRQ  AGNLSGPRT        0.1046      16121.5            50.00     Sequence
DRB1_1101  411  AGDEITVNVSTGPEQ  ITVNVSTGP        0.1044      16156.8            50.00     Sequence
DRB1_1101  499  VAGQTVDVAQKNLNV  VDVAQKNLN        0.1027      16457.8            50.00     Sequence
DRB1_1101  362  PDVRGQSSADAIATL  VRGQSSADA        0.1024      16511.1            50.00     Sequence
DRB1_1101  517  TKFSQASVDSPRPAG  KFSQASVDS        0.1023      16527.0            50.00     Sequence
DRB1_1101  394  PPDHVIGTDPAANTS  HVIGTDPAA        0.1016      16663.5            50.00     Sequence
DRB1_1101  591  DVDAGGSQHNRVVYQ  GSQHNRVVY        0.1001      16928.5            50.00     Sequence
DRB1_1101    0  MTTPSHLSDRYELGE  MTTPSHLSD        0.0993      17077.8            50.00     Sequence
DRB1_1101   67  HPAIVAVYDTGEAET  AIVAVYDTG        0.0990      17130.4            50.00     Sequence
DRB1_1101  353  GGITRDVQVPDVRGQ  ITRDVQVPD        0.0989      17155.1            50.00     Sequence
DRB1_1101  163  ADSGNSVTQTAAVIG  NSVTQTAAV        0.0987      17192.0            50.00     Sequence
DRB1_1101  209  LTGEPPFTGDSPVSV  FTGDSPVSV        0.0982      17281.2            50.00     Sequence
DRB1_1101  541  GTTVPVDSVIELQVS  VDSVIELQV        0.0968      17550.3            50.00     Sequence
DRB1_1101   81  TPAGPLPYIVMEYVD  LPYIVMEYV        0.0966      17590.0            50.00     Sequence
DRB1_1101  216  TGDSPVSVAYQHVRE  VSVAYQHVR        0.0957      17762.9            50.00     Sequence
DRB1_1101  606  NPPAGTGVNRDGIIT  AGTGVNRDG        0.0956      17765.0            50.00     Sequence
DRB1_1101  159  ARAIADSGNSVTQTA  RAIADSGNS        0.0956      17768.5            50.00     Sequence
DRB1_1101  225  YQHVREDPIPPSARH  YQHVREDPI        0.0954      17802.3            50.00     Sequence
DRB1_1101  518  KFSQASVDSPRPAGE  KFSQASVDS        0.0948      17925.1            50.00     Sequence
DRB1_1101  234  PPSARHEGLSADLDA  SARHEGLSA        0.0942      18041.6            50.00     Sequence
DRB1_1101  363  DVRGQSSADAIATLQ  VRGQSSADA        0.0941      18066.2            50.00     Sequence
DRB1_1101  233  IPPSARHEGLSADLD  SARHEGLSA        0.0936      18154.4            50.00     Sequence
DRB1_1101   80  ETPAGPLPYIVMEYV  LPYIVMEYV        0.0921      18455.8            50.00     Sequence
DRB1_1101  253  ALAKNPENRYQTAAE  LAKNPENRY        0.0917      18546.7            50.00     Sequence
DRB1_1101  207  EVLTGEPPFTGDSPV  LTGEPPFTG        0.0906      18758.0            50.00     Sequence
DRB1_1101   70  IVAVYDTGEAETPAG  VYDTGEAET        0.0901      18870.0            50.00     Sequence
DRB1_1101  280  PPEAPKVLTDAERTS  KVLTDAERT        0.0899      18901.9            50.00     Sequence
DRB1_1101   66  NHPAIVAVYDTGEAE  AIVAVYDTG        0.0875      19407.9            50.00     Sequence
DRB1_1101   71  VAVYDTGEAETPAGP  VYDTGEAET        0.0862      19680.3            50.00     Sequence
DRB1_1101  357  RDVQVPDVRGQSSAD  VPDVRGQSS        0.0854      19841.1            50.00     Sequence
DRB1_1101   65  LNHPAIVAVYDTGEA  AIVAVYDTG        0.0842      20095.4            50.00     Sequence
DRB1_1101  416  TVNVSTGPEQREIPD  VNVSTGPEQ        0.0840      20152.2            50.00     Sequence
DRB1_1101  354  GITRDVQVPDVRGQS  ITRDVQVPD        0.0836      20240.7            50.00     Sequence
DRB1_1101  583  TGMLDKGADVDAGGS  TGMLDKGAD        0.0822      20549.4            50.00     Sequence
DRB1_1101  160  RAIADSGNSVTQTAA  RAIADSGNS        0.0800      21047.6            50.00     Sequence
DRB1_1101  405  ANTSVSAGDEITVNV  VSAGDEITV        0.0800      21048.8            50.00     Sequence
DRB1_1101  406  NTSVSAGDEITVNVS  VSAGDEITV        0.0798      21080.2            50.00     Sequence
DRB1_1101  540  AGTTVPVDSVIELQV  TVPVDSVIE        0.0789      21303.5            50.00     Sequence
DRB1_1101  208  VLTGEPPFTGDSPVS  LTGEPPFTG        0.0784      21407.7            50.00     Sequence
DRB1_1101  530  AGEVTGTNPPAGTTV  VTGTNPPAG        0.0779      21527.6            50.00     Sequence
DRB1_1101  393  IPPDHVIGTDPAANT  HVIGTDPAA        0.0773      21668.7            50.00     Sequence
DRB1_1101  232  PIPPSARHEGLSADL  SARHEGLSA        0.0770      21738.0            50.00     Sequence
DRB1_1101  356  TRDVQVPDVRGQSSA  VPDVRGQSS        0.0767      21804.0            50.00     Sequence
DRB1_1101  355  ITRDVQVPDVRGQSS  ITRDVQVPD        0.0765      21843.6            50.00     Sequence
DRB1_1101  417  VNVSTGPEQREIPDV  VSTGPEQRE        0.0762      21932.4            50.00     Sequence
DRB1_1101  531  GEVTGTNPPAGTTVP  VTGTNPPAG        0.0753      22135.8            50.00     Sequence
DRB1_1101  410  SAGDEITVNVSTGPE  ITVNVSTGP        0.0751      22189.8            50.00     Sequence
DRB1_1101  237  ARHEGLSADLDAVVL  RHEGLSADL        0.0741      22439.4            50.00     Sequence
DRB1_1101  364  VRGQSSADAIATLQN  VRGQSSADA        0.0737      22520.2            50.00     Sequence
DRB1_1101  407  TSVSAGDEITVNVST  VSAGDEITV        0.0734      22603.4            50.00     Sequence
DRB1_1101  238  RHEGLSADLDAVVLK  RHEGLSADL        0.0733      22620.5            50.00     Sequence
DRB1_1101  409  VSAGDEITVNVSTGP  VSAGDEITV        0.0724      22842.4            50.00     Sequence
DRB1_1101  181  YLSPEQARGDSVDAR  YLSPEQARG        0.0715      23069.4            50.00     Sequence
DRB1_1101  455  NSPSTPELVGKVIGT  PELVGKVIG        0.0715      23073.6            50.00     Sequence
DRB1_1101  469  TNPPANQTSAITNVV  ANQTSAITN        0.0708      23248.3            50.00     Sequence
DRB1_1101  315  DLDDTDRDRSIGSVG  DTDRDRSIG        0.0708      23254.6            50.00     Sequence
DRB1_1101  403  PAANTSVSAGDEITV  VSAGDEITV        0.0702      23388.8            50.00     Sequence
DRB1_1101  404  AANTSVSAGDEITVN  VSAGDEITV        0.0702      23402.7            50.00     Sequence
```

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| DRB1_1101 | 498 | DVAGQTVDVAQKNLN | VDVAQKNLN | 0.0698 | 23499.9 | 50.00 | Sequence |
| DRB1_1101 | 190 | DSVDARSDVYSLGCV | RSDVYSLGC | 0.0696 | 23537.8 | 50.00 | Sequence |
| DRB1_1101 | 72 | AVYDTGEAETPAGPL | VYDTGEAET | 0.0688 | 23757.1 | 50.00 | Sequence |
| DRB1_1101 | 466 | VIGTNPPANQTSAIT | VIGTNPPAN | 0.0685 | 23819.9 | 50.00 | Sequence |
| DRB1_1101 | 162 | IADSGNSVTQTAAVI | NSVTQTAAV | 0.0683 | 23873.3 | 50.00 | Sequence |
| DRB1_1101 | 408 | SVSAGDEITVNVSTG | VSAGDEITV | 0.0673 | 24136.4 | 50.00 | Sequence |
| DRB1_1101 | 188 | RGDSVDARSDVYSLG | SVDARSDVY | 0.0659 | 24503.0 | 50.00 | Sequence |
| DRB1_1101 | 529 | PAGEVTGTNPPAGTT | EVTGTNPPA | 0.0651 | 24729.9 | 50.00 | Sequence |
| DRB1_1101 | 279 | EPPEAPKVLTDAERT | KVLTDAERT | 0.0649 | 24770.6 | 50.00 | Sequence |
| DRB1_1101 | 398 | VIGTDPAANTSVSAG | VIGTDPAAN | 0.0646 | 24846.3 | 50.00 | Sequence |
| DRB1_1101 | 189 | GDSVDARSDVYSLGC | SVDARSDVY | 0.0646 | 24858.1 | 50.00 | Sequence |
| DRB1_1101 | 519 | FSQASVDSPRPAGEV | FSQASVDSP | 0.0642 | 24960.0 | 50.00 | Sequence |
| DRB1_1101 | 161 | AIADSGNSVTQTAAV | AIADSGNSV | 0.0641 | 24997.8 | 50.00 | Sequence |
| DRB1_1101 | 79 | AETPAGPLPYIVMEY | PAGPLPYIV | 0.0637 | 25097.0 | 50.00 | Sequence |
| DRB1_1101 | 226 | QHVREDPIPPSARHE | HVREDPIPP | 0.0632 | 25231.8 | 50.00 | Sequence |
| DRB1_1101 | 532 | EVTGTNPPAGTTVPV | EVTGTNPPA | 0.0632 | 25236.7 | 50.00 | Sequence |
| DRB1_1101 | 240 | EGLSADLDAVVLKAL | DLDAVVLKA | 0.0630 | 25295.5 | 50.00 | Sequence |
| DRB1_1101 | 227 | HVREDPIPPSARHEG | HVREDPIPP | 0.0608 | 25896.1 | 50.00 | Sequence |
| DRB1_1101 | 231 | DPIPPSARHEGLSAD | SARHEGLSA | 0.0600 | 26115.9 | 50.00 | Sequence |
| DRB1_1101 | 365 | RGQSSADAIATLQNR | DAIATLQNR | 0.0595 | 26259.8 | 50.00 | Sequence |
| DRB1_1101 | 73 | VYDTGEAETPAGPLP | VYDTGEAET | 0.0593 | 26320.1 | 50.00 | Sequence |
| DRB1_1101 | 239 | HEGLSADLDAVVLKA | LSADLDAVV | 0.0587 | 26487.3 | 50.00 | Sequence |
| DRB1_1101 | 78 | EAETPAGPLPYIVME | ETPAGPLPY | 0.0581 | 26661.2 | 50.00 | Sequence |
| DRB1_1101 | 77 | GEAETPAGPLPYIVM | ETPAGPLPY | 0.0581 | 26675.4 | 50.00 | Sequence |
| DRB1_1101 | 590 | ADVDAGGSQHNRVVY | GSQHNRVVY | 0.0581 | 26677.4 | 50.00 | Sequence |
| DRB1_1101 | 539 | PAGTTVPVDSVIELQ | TVPVDSVIE | 0.0571 | 26961.2 | 50.00 | Sequence |
| DRB1_1101 | 584 | GMLDKGADVDAGGSQ | GMLDKGADV | 0.0560 | 27276.9 | 50.00 | Sequence |
| DRB1_1101 | 402 | DPAANTSVSAGDEIT | ANTSVSAGD | 0.0556 | 27390.2 | 50.00 | Sequence |
| DRB1_1101 | 392 | TIPPDHVIGTDPAAN | DHVIGTDPA | 0.0555 | 27440.3 | 50.00 | Sequence |
| DRB1_1101 | 384 | RTLQKPDSTIPPDHV | RTLQKPDST | 0.0546 | 27695.3 | 50.00 | Sequence |
| DRB1_1101 | 187 | ARGDSVDARSDVYSL | SVDARSDVY | 0.0544 | 27745.7 | 50.00 | Sequence |
| DRB1_1101 | 605 | QNPPAGTGVNRDGII | AGTGVNRDG | 0.0531 | 28137.8 | 50.00 | Sequence |
| DRB1_1101 | 586 | LDKGADVDAGGSQHN | LDKGADVDA | 0.0530 | 28185.7 | 50.00 | Sequence |
| DRB1_1101 | 230 | EDPIPPSARHEGLSA | IPPSARHEG | 0.0524 | 28368.0 | 50.00 | Sequence |
| DRB1_1101 | 520 | SQASVDSPRPAGEVT | SVDSPRPAG | 0.0522 | 28420.2 | 50.00 | Sequence |
| DRB1_1101 | 486 | IVGSGPATKDIPDVA | IVGSGPATK | 0.0520 | 28471.9 | 50.00 | Sequence |
| DRB1_1101 | 186 | QARGDSVDARSDVYS | QARGDSVDA | 0.0512 | 28730.3 | 50.00 | Sequence |
| DRB1_1101 | 528 | RPAGEVTGTNPPAGT | VTGTNPPAG | 0.0510 | 28783.5 | 50.00 | Sequence |
| DRB1_1101 | 521 | QASVDSPRPAGEVTG | SVDSPRPAG | 0.0492 | 29377.6 | 50.00 | Sequence |
| DRB1_1101 | 585 | MLDKGADVDAGGSQH | LDKGADVDA | 0.0488 | 29503.1 | 50.00 | Sequence |
| DRB1_1101 | 604 | YQNPPAGTGVNRDGI | YQNPPAGTG | 0.0486 | 29541.7 | 50.00 | Sequence |
| DRB1_1101 | 314 | QDLDDTDRDRSIGSV | LDDTDRDRS | 0.0464 | 30250.7 | 50.00 | Sequence |
| DRB1_1101 | 401 | TDPAANTSVSAGDEI | PAANTSVSA | 0.0463 | 30313.6 | 50.00 | Sequence |
| DRB1_1101 | 454 | ANSPSTPELVGKVIG | PELVGKVIG | 0.0460 | 30383.6 | 50.00 | Sequence |
| DRB1_1101 | 183 | SPEQARGDSVDARSD | QARGDSVDA | 0.0435 | 31241.3 | 50.00 | Sequence |
| DRB1_1101 | 301 | GNLSGPRTDPLPRQD | NLSGPRTDP | 0.0432 | 31338.5 | 50.00 | Sequence |
| DRB1_1101 | 527 | PRPAGEVTGTNPPAG | EVTGTNPPA | 0.0430 | 31405.0 | 50.00 | Sequence |
| DRB1_1101 | 522 | ASVDSPRPAGEVTGT | SVDSPRPAG | 0.0423 | 31628.7 | 50.00 | Sequence |
| DRB1_1101 | 302 | NLSGPRTDPLPRQDL | NLSGPRTDP | 0.0420 | 31734.6 | 50.00 | Sequence |
| DRB1_1101 | 468 | GTNPPANQTSAITNV | ANQTSAITN | 0.0417 | 31835.4 | 50.00 | Sequence |
| DRB1_1101 | 533 | VTGTNPPAGTTVPVD | VTGTNPPAG | 0.0415 | 31925.4 | 50.00 | Sequence |
| DRB1_1101 | 182 | LSPEQARGDSVDARS | QARGDSVDA | 0.0413 | 31980.0 | 50.00 | Sequence |
| DRB1_1101 | 497 | PDVAGQTVDVAQKNL | QTVDVAQKN | 0.0413 | 31989.4 | 50.00 | Sequence |
| DRB1_1101 | 184 | PEQARGDSVDARSDV | QARGDSVDA | 0.0408 | 32167.4 | 50.00 | Sequence |
| DRB1_1101 | 418 | NVSTGPEQREIPDVS | VSTGPEQRE | 0.0403 | 32325.8 | 50.00 | Sequence |
| DRB1_1101 | 589 | GADVDAGGSQHNRVV | VDAGGSQHN | 0.0401 | 32395.9 | 50.00 | Sequence |
| DRB1_1101 | 273 | VRVHNGEPPEAPKVL | RVHNGEPPE | 0.0401 | 32400.8 | 50.00 | Sequence |
| DRB1_1101 | 391 | STIPPDHVIGTDPAA | DHVIGTDPA | 0.0400 | 32418.3 | 50.00 | Sequence |
| DRB1_1101 | 185 | EQARGDSVDARSDVY | QARGDSVDA | 0.0399 | 32453.1 | 50.00 | Sequence |
| DRB1_1101 | 400 | GTDPAANTSVSAGDE | PAANTSVSA | 0.0396 | 32568.4 | 50.00 | Sequence |
| DRB1_1101 | 399 | IGTDPAANTSVSAGD | IGTDPAANT | 0.0386 | 32942.7 | 50.00 | Sequence |
| DRB1_1101 | 74 | YDTGEAETPAGPLPY | YDTGEAETP | 0.0384 | 32989.4 | 50.00 | Sequence |
| DRB1_1101 | 228 | VREDPIPPSARHEGL | VREDPIPPS | 0.0383 | 33054.4 | 50.00 | Sequence |
| DRB1_1101 | 313 | RQDLDDTDRDRSIGS | LDDTDRDRS | 0.0367 | 33616.7 | 50.00 | Sequence |
| DRB1_1101 | 305 | GPRTDPLPRQDLDDT | TDPLPRQDL | 0.0364 | 33711.1 | 50.00 | Sequence |
| DRB1_1101 | 490 | GPATKDIPDVAGQTV | TKDIPDVAG | 0.0361 | 33846.3 | 50.00 | Sequence |

```
   DRB1_1101  523  SVDSPRPAGEVTGTN  SVDSPRPAG         0.0360      33880.4                 50.00     Sequence
   DRB1_1101  304  SGPRTDPLPRQDLDD  TDPLPRQDL         0.0355      34049.8                 50.00     Sequence
   DRB1_1101  588  KGADVDAGGSQHNRV  VDAGGSQHN         0.0352      34171.9                 50.00     Sequence
   DRB1_1101  526  SPRPAGEVTGTNPPA  EVTGTNPPA         0.0350      34250.4                 50.00     Sequence
   DRB1_1101   76  TGEAETPAGPLPYIV  ETPAGPLPY         0.0349      34291.6                 50.00     Sequence
   DRB1_1101  538  PPAGTTVPVDSVIEL  AGTTVPVDS         0.0345      34423.9                 50.00     Sequence
   DRB1_1101  385  TLQKPDSTIPPDHVI  TLQKPDSTI         0.0344      34467.1                 50.00     Sequence
   DRB1_1101  467  IGTNPPANQTSAITN  IGTNPPANQ         0.0342      34549.3                 50.00     Sequence
   DRB1_1101  274  RVHNGEPPEAPKVLT  RVHNGEPPE         0.0337      34722.4                 50.00     Sequence
   DRB1_1101  491  PATKDIPDVAGQTVD  ATKDIPDVA         0.0337      34739.0                 50.00     Sequence
   DRB1_1101  492  ATKDIPDVAGQTVDV  ATKDIPDVA         0.0329      35039.8                 50.00     Sequence
   DRB1_1101  303  LSGPRTDPLPRQDLD  RTDPLPRQD         0.0327      35110.0                 50.00     Sequence
   DRB1_1101  229  REDPIPPSARHEGLS  IPPSARHEG         0.0326      35147.6                 50.00     Sequence
   DRB1_1101  496  IPDVAGQTVDVAQKN  IPDVAGQTV         0.0322      35305.1                 50.00     Sequence
   DRB1_1101  278  GEPPEAPKVLTDAER  PPEAPKVLT         0.0316      35540.0                 50.00     Sequence
   DRB1_1101  419  VSTGPEQREIPDVST  VSTGPEQRE         0.0312      35679.5                 50.00     Sequence
   DRB1_1101  390  DSTIPPDHVIGTDPA  TIPPDHVIG         0.0304      35979.1                 50.00     Sequence
   DRB1_1101  489  SGPATKDIPDVAGQT  TKDIPDVAG         0.0300      36155.5                 50.00     Sequence
   DRB1_1101  493  TKDIPDVAGQTVDVA  IPDVAGQTV         0.0297      36249.1                 50.00     Sequence
   DRB1_1101  306  PRTDPLPRQDLDDTD  TDPLPRQDL         0.0294      36381.6                 50.00     Sequence
   DRB1_1101  525  DSPRPAGEVTGTNPP  PRPAGEVTG         0.0292      36452.9                 50.00     Sequence
   DRB1_1101  537  NPPAGTTVPVDSVIE  AGTTVPVDS         0.0283      36823.1                 50.00     Sequence
   DRB1_1101   75  DTGEAETPAGPLPYI  ETPAGPLPY         0.0276      37081.4                 50.00     Sequence
   DRB1_1101  453  QANSPSTPELVGKVI  SPSTPELVG         0.0275      37151.3                 50.00     Sequence
   DRB1_1101  587  DKGADVDAGGSQHNR  VDAGGSQHN         0.0270      37342.7                 50.00     Sequence
   DRB1_1101  487  VGSGPATKDIPDVAG  TKDIPDVAG         0.0253      38016.2                 50.00     Sequence
   DRB1_1101  524  VDSPRPAGEVTGTNP  PRPAGEVTG         0.0252      38083.7                 50.00     Sequence
   DRB1_1101  495  DIPDVAGQTVDVAQK  IPDVAGQTV         0.0249      38175.7                 50.00     Sequence
   DRB1_1101  452  KQANSPSTPELVGKV  SPSTPELVG         0.0243      38431.8                 50.00     Sequence
   DRB1_1101  277  NGEPPEAPKVLTDAE  PPEAPKVLT         0.0242      38489.7                 50.00     Sequence
   DRB1_1101  389  PDSTIPPDHVIGTDP  DSTIPPDHV         0.0241      38503.0                 50.00     Sequence
   DRB1_1101  307  RTDPLPRQDLDDTDR  TDPLPRQDL         0.0239      38622.3                 50.00     Sequence
   DRB1_1101  494  KDIPDVAGQTVDVAQ  IPDVAGQTV         0.0239      38623.6                 50.00     Sequence
   DRB1_1101  421  TGPEQREIPDVSTLT  QREIPDVST         0.0234      38796.6                 50.00     Sequence
   DRB1_1101  488  GSGPATKDIPDVAGQ  TKDIPDVAG         0.0233      38877.7                 50.00     Sequence
   DRB1_1101  275  VHNGEPPEAPKVLTD  VHNGEPPEA         0.0225      39216.1                 50.00     Sequence
   DRB1_1101  276  HNGEPPEAPKVLTDA  PPEAPKVLT         0.0222      39305.7                 50.00     Sequence
   DRB1_1101  386  LQKPDSTIPPDHVIG  DSTIPPDHV         0.0215      39602.0                 50.00     Sequence
   DRB1_1101  388  KPDSTIPPDHVIGTD  DSTIPPDHV         0.0213      39713.1                 50.00     Sequence
   DRB1_1101  420  STGPEQREIPDVSTL  QREIPDVST         0.0207      39956.2                 50.00     Sequence
   DRB1_1101  387  QKPDSTIPPDHVIGT  DSTIPPDHV         0.0207      39986.0                 50.00     Sequence
   DRB1_1101  312  PRQDLDDTDRDRSIG  LDDTDRDRS         0.0201      40246.4                 50.00     Sequence
   DRB1_1101  536  TNPPAGTTVPVDSVI  AGTTVPVDS         0.0181      41119.3                 50.00     Sequence
   DRB1_1101  311  LPRQDLDDTDRDRSI  LDDTDRDRS         0.0180      41173.1                 50.00     Sequence
   DRB1_1101  534  TGTNPPAGTTVPVDS  TGTNPPAGT         0.0174      41439.1                 50.00     Sequence
   DRB1_1101  310  PLPRQDLDDTDRDRS  RQDLDDTDR         0.0162      41973.8                 50.00     Sequence
   DRB1_1101  535  GTNPPAGTTVPVDSV  AGTTVPVDS         0.0158      42142.6                 50.00     Sequence
   DRB1_1101  308  TDPLPRQDLDDTDRD  TDPLPRQDL         0.0143      42814.6                 50.00     Sequence
   DRB1_1101  309  DPLPRQDLDDTDRDR  RQDLDDTDR         0.0119      43980.4                 50.00     Sequence
--------------------------------------------------------------------------------------------------

Allele: DRB1_1101. Number of high binders 8. Number of weak binders 63. Number of peptides 612

--------------------------------------------------------------------------------------------------
--------------------------------------------------------------------------------------------------
      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
--------------------------------------------------------------------------------------------------
   DRB1_1302  140  PANIMISATNAVKVM  ISATNAVKV         0.8508          5.0          SB      0.05     Sequence
   DRB1_1302  139  KPANIMISATNAVKV  IMISATNAV         0.8468          5.2          SB      0.05     Sequence
   DRB1_1302  141  ANIMISATNAVKVMD  ISATNAVKV         0.8446          5.4          SB      0.05     Sequence
   DRB1_1302  142  NIMISATNAVKVMDF  ISATNAVKV         0.8373          5.8          SB      0.05     Sequence
   DRB1_1302  143  IMISATNAVKVMDFG  ISATNAVKV         0.8273          6.5          SB      0.05     Sequence
   DRB1_1302  138  VKPANIMISATNAVK  IMISATNAV         0.7740         11.5          SB      0.30     Sequence
   DRB1_1302  338  LAVLTVVVTIAINTF  LTVVVTIAI         0.7690         12.2          SB      0.30     Sequence
   DRB1_1302  339  AVLTVVVTIAINTFG  LTVVVTIAI         0.7544         14.3          SB      0.40     Sequence
   DRB1_1302  137  DVKPANIMISATNAV  IMISATNAV         0.7394         16.8          SB      0.80     Sequence
```

```
DRB1_1302  340  VLTVVVTIAINTFGG  LTVVVTIAI         0.7394          16.8            SB      0.80       Sequence
DRB1_1302  335  VAVLAVLTVVVTIAI  LTVVVTIAI         0.7280          19.0            SB      0.80       Sequence
DRB1_1302  144  MISATNAVKVMDFGI  ISATNAVKV         0.7264          19.3            SB      0.80       Sequence
DRB1_1302  341  LTVVVTIAINTFGGI  LTVVVTIAI         0.7247          19.7            SB      0.80       Sequence
DRB1_1302  337  VLAVLTVVVTIAINT  LTVVVTIAI         0.7184          21.1            SB      1.00       Sequence
DRB1_1302  336  AVLAVLTVVVTIAIN  LTVVVTIAI         0.7182          21.1            SB      1.00       Sequence
DRB1_1302  548  SVIELQVSKGNQFVM  LQVSKGNQF         0.6954          27.0            SB      2.00       Sequence
DRB1_1302  549  VIELQVSKGNQFVMP  LQVSKGNQF         0.6775          32.8            SB      2.00       Sequence
DRB1_1302  145  ISATNAVKVMDFGIA  ISATNAVKV         0.6757          33.4            SB      2.00       Sequence
DRB1_1302  550  IELQVSKGNQFVMPD  LQVSKGNQF         0.6543          42.1            SB      4.00       Sequence
DRB1_1302  331  WVAVVAVLAVLTVVV  VLAVLTVVV         0.6412          48.6            SB      4.00       Sequence
DRB1_1302  551  ELQVSKGNQFVMPDL  LQVSKGNQF         0.6388          49.8            SB      4.00       Sequence
DRB1_1302  328  VGRWVAVVAVLAVLT  VAVVAVLAV         0.6382          50.1            WB      4.00       Sequence
DRB1_1302  329  GRWVAVVAVLAVLTV  VAVVAVLAV         0.6218          59.9            WB      4.00       Sequence
DRB1_1302  332  VAVVAVLAVLTVVVT  VLAVLTVVV         0.6190          61.7            WB      4.00       Sequence
DRB1_1302  552  LQVSKGNQFVMPDLS  LQVSKGNQF         0.6135          65.5            WB      4.00       Sequence
DRB1_1302  547  DSVIELQVSKGNQFV  LQVSKGNQF         0.6134          65.5            WB      4.00       Sequence
DRB1_1302  473  ANQTSAITNVVIIIV  TSAITNVVI         0.6120          66.6            WB      4.00       Sequence
DRB1_1302  327  SVGRWVAVVAVLAVL  VAVVAVLAV         0.6113          67.1            WB      4.00       Sequence
DRB1_1302  471  PPANQTSAITNVVII  QTSAITNVV         0.6059          71.1            WB      8.00       Sequence
DRB1_1302   27  ARDLRLHRDVAVKVL  LHRDVAVKV         0.6055          71.4            WB      8.00       Sequence
DRB1_1302  472  PANQTSAITNVVIII  QTSAITNVV         0.6022          74.0            WB      8.00       Sequence
DRB1_1302  474  NQTSAITNVVIIIVG  TSAITNVVI         0.5979          77.5            WB      8.00       Sequence
DRB1_1302   29  DLRLHRDVAVKVLRA  LHRDVAVKV         0.5962          78.9            WB      8.00       Sequence
DRB1_1302  326  GSVGRWVAVVAVLAV  VAVVAVLAV         0.5962          78.9            WB      8.00       Sequence
DRB1_1302   28  RDLRLHRDVAVKVLR  LHRDVAVKV         0.5942          80.7            WB      8.00       Sequence
DRB1_1302  330  RWVAVVAVLAVLTVV  VAVVAVLAV         0.5912          83.4            WB      8.00       Sequence
DRB1_1302   26  LARDLRLHRDVAVKV  LHRDVAVKV         0.5839          90.2            WB      8.00       Sequence
DRB1_1302   30  LRLHRDVAVKVLRAD  LHRDVAVKV         0.5819          92.2            WB      8.00       Sequence
DRB1_1302  470  NPPANQTSAITNVVI  QTSAITNVV         0.5771          97.1            WB      8.00       Sequence
DRB1_1302  167  NSVTQTAAVIGTAQY  SVTQTAAVI         0.5646         111.2            WB      8.00       Sequence
DRB1_1302   53  LRFRREAQNAAALNH  REAQNAAAL         0.5626         113.6            WB      8.00       Sequence
DRB1_1302  333  AVVAVLAVLTVVVTI  VLAVLTVVV         0.5614         115.1            WB      8.00       Sequence
DRB1_1302  546  VDSVIELQVSKGNQF  LQVSKGNQF         0.5613         115.2            WB      8.00       Sequence
DRB1_1302  475  QTSAITNVVIIIVGS  TSAITNVVI         0.5589         118.2            WB      8.00       Sequence
DRB1_1302   52  YLRFRREAQNAAALN  REAQNAAAL         0.5534         125.5            WB      8.00       Sequence
DRB1_1302  164  DSGNSVTQTAAVIGT  SVTQTAAVI         0.5531         125.9            WB      8.00       Sequence
DRB1_1302  163  ADSGNSVTQTAAVIG  SVTQTAAVI         0.5527         126.4            WB      8.00       Sequence
DRB1_1302  168  SVTQTAAVIGTAQYL  SVTQTAAVI         0.5506         129.3            WB      8.00       Sequence
DRB1_1302   54  RFRREAQNAAALNHP  REAQNAAAL         0.5488         131.9            WB      8.00       Sequence
DRB1_1302  162  IADSGNSVTQTAAVI  SVTQTAAVI         0.5466         135.0            WB      8.00       Sequence
DRB1_1302  165  SGNSVTQTAAVIGTA  SVTQTAAVI         0.5421         141.8            WB      8.00       Sequence
DRB1_1302   55  FRREAQNAAALNHPA  REAQNAAAL         0.5353         152.6            WB      8.00       Sequence
DRB1_1302   60  QNAAALNHPAIVAVY  LNHPAIVAV         0.5350         153.0            WB      8.00       Sequence
DRB1_1302  166  GNSVTQTAAVIGTAQ  SVTQTAAVI         0.5345         154.0            WB     16.00       Sequence
DRB1_1302  334  VVAVLAVLTVVVTIA  VLAVLTVVV         0.5341         154.6            WB     16.00       Sequence
DRB1_1302   59  AQNAAALNHPAIVAV  LNHPAIVAV         0.5314         159.3            WB     16.00       Sequence
DRB1_1302  342  TVVVTIAINTFGGIT  VVTIAINTF         0.5303         161.1            WB     16.00       Sequence
DRB1_1302   51  FYLRFRREAQNAAAL  REAQNAAAL         0.5300         161.6            WB     16.00       Sequence
DRB1_1302   32  LHRDVAVKVLRADLA  LHRDVAVKV         0.5226         175.0            WB     16.00       Sequence
DRB1_1302   56  RREAQNAAALNHPAI  REAQNAAAL         0.5205         179.2            WB     16.00       Sequence
DRB1_1302  478  AITNVVIIIVGSGPA  IIIVGSGPA         0.5199         180.4            WB     16.00       Sequence
DRB1_1302   61  NAAALNHPAIVAVYD  LNHPAIVAV         0.5171         185.9            WB     16.00       Sequence
DRB1_1302  479  ITNVVIIIVGSGPAT  IIIVGSGPA         0.5100         200.7            WB     16.00       Sequence
DRB1_1302  343  VVVTIAINTFGGITR  VVTIAINTF         0.5088         203.3            WB     16.00       Sequence
DRB1_1302  476  TSAITNVVIIIVGSG  TSAITNVVI         0.5069         207.4            WB     16.00       Sequence
DRB1_1302   31  RLHRDVAVKVLRADL  LHRDVAVKV         0.5063         208.8            WB     16.00       Sequence
DRB1_1302  469  TNPPANQTSAITNVV  QTSAITNVV         0.5058         210.0            WB     16.00       Sequence
DRB1_1302   62  AAALNHPAIVAVYDT  LNHPAIVAV         0.5025         217.8            WB     16.00       Sequence
DRB1_1302   57  REAQNAAALNHPAIV  REAQNAAAL         0.5009         221.3            WB     16.00       Sequence
DRB1_1302  480  TNVVIIIVGSGPATK  IIIVGSGPA         0.4877         255.6            WB     16.00       Sequence
DRB1_1302  325  IGSVGRWVAVVAVLA  GRWVAVVAV         0.4847         263.9            WB     16.00       Sequence
DRB1_1302  136  RDVKPANIMISATNA  VKPANIMIS         0.4818         272.2            WB     16.00       Sequence
DRB1_1302   63  AALNHPAIVAVYDTG  LNHPAIVAV         0.4818         272.2            WB     16.00       Sequence
DRB1_1302  122  CQALNFSHQNGIIHR  FSHQNGIIH         0.4775         285.2            WB     16.00       Sequence
DRB1_1302  481  NVVIIIVGSGPATKD  IIIVGSGPA         0.4772         286.0            WB     16.00       Sequence
```

```
DRB1_1302  133  IIHRDVKPANIMISA  VKPANIMIS        0.4734        298.3         WB    16.00      Sequence
DRB1_1302  132  GIIHRDVKPANIMIS  VKPANIMIS        0.4713        305.1         WB    16.00      Sequence
DRB1_1302  123  QALNFSHQNGIIHRD  FSHQNGIIH        0.4659        323.4         WB    16.00      Sequence
DRB1_1302  556  KGNQFVMPDLSGMFW  VMPDLSGMF        0.4653        325.6         WB    16.00      Sequence
DRB1_1302  135  HRDVKPANIMISATN  VKPANIMIS        0.4653        325.7         WB    16.00      Sequence
DRB1_1302  482  VVIIIVGSGPATKDI  IIIVGSGPA        0.4650        326.7         WB    16.00      Sequence
DRB1_1302  134  IHRDVKPANIMISAT  VKPANIMIS        0.4644        328.8         WB    16.00      Sequence
DRB1_1302  169  VTQTAAVIGTAQYLS  AAVIGTAQY        0.4634        332.4         WB    16.00      Sequence
DRB1_1302  121  ACQALNFSHQNGIIH  FSHQNGIIH        0.4625        335.6         WB    16.00      Sequence
DRB1_1302  557  GNQFVMPDLSGMFWV  VMPDLSGMF        0.4571        355.6         WB    16.00      Sequence
DRB1_1302  170  TQTAAVIGTAQYLSP  AAVIGTAQY        0.4552        363.0         WB    16.00      Sequence
DRB1_1302  344  VVTIAINTFGGITRD  VVTIAINTF        0.4542        366.9         WB    16.00      Sequence
DRB1_1302  372  AIATLQNRGFKIRTL  TLQNRGFKI        0.4526        373.3         WB    16.00      Sequence
DRB1_1302  124  ALNFSHQNGIIHRDV  FSHQNGIIH        0.4500        384.3         WB    16.00      Sequence
DRB1_1302  483  VIIIVGSGPATKDIP  IIIVGSGPA        0.4488        389.3         WB    16.00      Sequence
DRB1_1302  324  SIGSVGRWVAVVAVL  RWVAVVAVL        0.4487        389.6         WB    16.00      Sequence
DRB1_1302  477  SAITNVVIIIVGSGP  SAITNVVII        0.4477        393.7         WB    16.00      Sequence
DRB1_1302  437  AEAVKKLTAAGFGRF  VKKLTAAGF        0.4464        399.2         WB    16.00      Sequence
DRB1_1302   64  ALNHPAIVAVYDTGE  LNHPAIVAV        0.4457        402.5         WB    16.00      Sequence
DRB1_1302  290  AERTSLLSSAAGNLS  LLSSAAGNL        0.4409        423.7         WB    32.00      Sequence
DRB1_1302  435  TYAEAVKKLTAAGFG  VKKLTAAGF        0.4367        443.4         WB    32.00      Sequence
DRB1_1302  434  LTYAEAVKKLTAAGF  VKKLTAAGF        0.4356        448.8         WB    32.00      Sequence
DRB1_1302  558  NQFVMPDLSGMFWVD  VMPDLSGMF        0.4346        453.6         WB    32.00      Sequence
DRB1_1302  505  DVAQKNLNVYGFTKF  VAQKNLNVY        0.4346        454.0         WB    32.00      Sequence
DRB1_1302  436  YAEAVKKLTAAGFGR  VKKLTAAGF        0.4331        461.0         WB    32.00      Sequence
DRB1_1302  103  VHTEGPMTPKRAIEV  MTPKRAIEV        0.4328        462.5         WB    32.00      Sequence
DRB1_1302  171  QTAAVIGTAQYLSPE  AAVIGTAQY        0.4320        466.8         WB    32.00      Sequence
DRB1_1302  125  LNFSHQNGIIHRDVK  FSHQNGIIH        0.4309        472.1         WB    32.00      Sequence
DRB1_1302  291  ERTSLLSSAAGNLSG  LLSSAAGNL        0.4308        472.8         WB    32.00      Sequence
DRB1_1302  161  AIADSGNSVTQTAAV  NSVTQTAAV        0.4299        477.5         WB    32.00      Sequence
DRB1_1302  371  DAIATLQNRGFKIRT  TLQNRGFKI        0.4294        480.2         WB    32.00      Sequence
DRB1_1302  373  IATLQNRGFKIRTLQ  TLQNRGFKI        0.4286        484.2         WB    32.00      Sequence
DRB1_1302   65  LNHPAIVAVYDTGEA  LNHPAIVAV        0.4248        504.4               32.00      Sequence
DRB1_1302  502  QTVDVAQKNLNVYGF  VAQKNLNVY        0.4219        520.8               32.00      Sequence
DRB1_1302   86  LPYIVMEYVDGVTLR  MEYVDGVTL        0.4214        523.3               32.00      Sequence
DRB1_1302   85  PLPYIVMEYVDGVTL  MEYVDGVTL        0.4213        523.9               32.00      Sequence
DRB1_1302  374  ATLQNRGFKIRTLQK  TLQNRGFKI        0.4177        544.6               32.00      Sequence
DRB1_1302  500  AGQTVDVAQKNLNVY  VAQKNLNVY        0.4170        549.1               32.00      Sequence
DRB1_1302  438  EAVKKLTAAGFGRFK  VKKLTAAGF        0.4167        550.6               32.00      Sequence
DRB1_1302  370  ADAIATLQNRGFKIR  TLQNRGFKI        0.4166        551.3               32.00      Sequence
DRB1_1302  503  TVDVAQKNLNVYGFT  VAQKNLNVY        0.4149        561.6               32.00      Sequence
DRB1_1302  104  HTEGPMTPKRAIEVI  MTPKRAIEV        0.4147        562.6               32.00      Sequence
DRB1_1302  323  RSIGSVGRWVAVVAV  GRWVAVVAV        0.4136        569.3               32.00      Sequence
DRB1_1302  559  QFVMPDLSGMFWVDA  VMPDLSGMF        0.4134        570.7               32.00      Sequence
DRB1_1302  555  SKGNQFVMPDLSGMF  VMPDLSGMF        0.4115        582.7               32.00      Sequence
DRB1_1302   87  PYIVMEYVDGVTLRD  MEYVDGVTL        0.4103        590.1               32.00      Sequence
DRB1_1302  501  GQTVDVAQKNLNVYG  VAQKNLNVY        0.4089        599.1               32.00      Sequence
DRB1_1302  292  RTSLLSSAAGNLSGP  LLSSAAGNL        0.4075        608.6               32.00      Sequence
DRB1_1302   88  YIVMEYVDGVTLRDI  MEYVDGVTL        0.4062        617.0               32.00      Sequence
DRB1_1302  267  EMRADLVRVHNGEPP  LVRVHNGEP        0.4060        618.1               32.00      Sequence
DRB1_1302  484  IIIVGSGPATKDIPD  IIIVGSGPA        0.4055        621.5               32.00      Sequence
DRB1_1302  131  NGIIHRDVKPANIMI  DVKPANIMI        0.4053        623.1               32.00      Sequence
DRB1_1302  369  SADAIATLQNRGFKI  TLQNRGFKI        0.4030        638.6               32.00      Sequence
DRB1_1302  289  DAERTSLLSSAAGNL  LLSSAAGNL        0.4021        645.1               32.00      Sequence
DRB1_1302  504  VDVAQKNLNVYGFTK  VAQKNLNVY        0.4008        653.9               32.00      Sequence
DRB1_1302  422  GPEQREIPDVSTLTY  IPDVSTLTY        0.4007        654.5               32.00      Sequence
DRB1_1302  248  AVVLKALAKNPENRY  LAKNPENRY        0.4005        656.2               32.00      Sequence
DRB1_1302  172  TAAVIGTAQYLSPEQ  AVIGTAQYL        0.3991        666.3               32.00      Sequence
DRB1_1302  266  AEMRADLVRVHNGEP  LVRVHNGEP        0.3937        706.5               32.00      Sequence
DRB1_1302  105  TEGPMTPKRAIEVIA  MTPKRAIEV        0.3934        708.2               32.00      Sequence
DRB1_1302  423  PEQREIPDVSTLTYA  IPDVSTLTY        0.3930        711.3               32.00      Sequence
DRB1_1302  538  PPAGTTVPVDSVIEL  VPVDSVIEL        0.3927        713.7               32.00      Sequence
DRB1_1302   24  VHLARDLRLHRDVAV  VHLARDLRL        0.3925        715.4               32.00      Sequence
DRB1_1302  439  AVKKLTAAGFGRFKQ  VKKLTAAGF        0.3888        745.0               32.00      Sequence
DRB1_1302  375  TLQNRGFKIRTLQKP  TLQNRGFKI        0.3880        751.5               32.00      Sequence
DRB1_1302  426  REIPDVSTLTYAEAV  IPDVSTLTY        0.3848        778.1               32.00      Sequence
```

| | | | | | | |
|---|---|---|---|---|---|---|
| DRB1_1302 | 126 | NFSHQNGIIHRDVKP | FSHQNGIIH | 0.3838 | 786.6 | 32.00 | Sequence |
| DRB1_1302 | 320 | DRDRSIGSVGRWVAV | GSVGRWVAV | 0.3824 | 797.7 | 32.00 | Sequence |
| DRB1_1302 | 425 | QREIPDVSTLTYAEA | IPDVSTLTY | 0.3809 | 811.6 | 32.00 | Sequence |
| DRB1_1302 | 540 | AGTTVPVDSVIELQV | VPVDSVIEL | 0.3781 | 835.7 | 32.00 | Sequence |
| DRB1_1302 | 424 | EQREIPDVSTLTYAE | IPDVSTLTY | 0.3780 | 837.3 | 32.00 | Sequence |
| DRB1_1302 | 293 | TSLLSSAAGNLSGPR | LLSSAAGNL | 0.3775 | 841.6 | 32.00 | Sequence |
| DRB1_1302 | 461 | ELVGKVIGTNPPANQ | KVIGTNPPA | 0.3772 | 844.3 | 32.00 | Sequence |
| DRB1_1302 | 268 | MRADLVRVHNGEPPE | LVRVHNGEP | 0.3747 | 867.4 | 32.00 | Sequence |
| DRB1_1302 | 89 | IVMEYVDGVTLRDIV | MEYVDGVTL | 0.3734 | 879.6 | 32.00 | Sequence |
| DRB1_1302 | 112 | KRAIEVIADACQALN | VIADACQAL | 0.3729 | 884.9 | 32.00 | Sequence |
| DRB1_1302 | 539 | PAGTTVPVDSVIELQ | VPVDSVIEL | 0.3717 | 896.0 | 32.00 | Sequence |
| DRB1_1302 | 173 | AAVIGTAQYLSPEQA | AAVIGTAQY | 0.3714 | 898.8 | 32.00 | Sequence |
| DRB1_1302 | 560 | FVMPDLSGMFWVDAE | VMPDLSGMF | 0.3701 | 912.1 | 32.00 | Sequence |
| DRB1_1302 | 440 | VKKLTAAGFGRFKQA | VKKLTAAGF | 0.3701 | 912.1 | 32.00 | Sequence |
| DRB1_1302 | 428 | IPDVSTLTYAEAVKK | IPDVSTLTY | 0.3670 | 943.3 | 32.00 | Sequence |
| DRB1_1302 | 506 | VAQKNLNVYGFTKFS | VAQKNLNVY | 0.3660 | 952.8 | 32.00 | Sequence |
| DRB1_1302 | 106 | EGPMTPKRAIEVIAD | MTPKRAIEV | 0.3657 | 956.3 | 32.00 | Sequence |
| DRB1_1302 | 462 | LVGKVIGTNPPANQT | KVIGTNPPA | 0.3623 | 992.0 | 32.00 | Sequence |
| DRB1_1302 | 553 | QVSKGNQFVMPDLSG | VSKGNQFVM | 0.3621 | 994.4 | 32.00 | Sequence |
| DRB1_1302 | 294 | SLLSSAAGNLSGPRT | LLSSAAGNL | 0.3591 | 1026.7 | 32.00 | Sequence |
| DRB1_1302 | 541 | GTTVPVDSVIELQVS | VPVDSVIEL | 0.3558 | 1064.8 | 32.00 | Sequence |
| DRB1_1302 | 269 | RADLVRVHNGEPPEA | LVRVHNGEP | 0.3548 | 1075.7 | 32.00 | Sequence |
| DRB1_1302 | 460 | PELVGKVIGTNPPAN | KVIGTNPPA | 0.3546 | 1078.6 | 32.00 | Sequence |
| DRB1_1302 | 609 | AGTGVNRDGIITLRF | VNRDGIITL | 0.3538 | 1087.4 | 32.00 | Sequence |
| DRB1_1302 | 113 | RAIEVIADACQALNF | VIADACQAL | 0.3527 | 1100.7 | 32.00 | Sequence |
| DRB1_1302 | 111 | PKRAIEVIADACQAL | VIADACQAL | 0.3512 | 1118.9 | 32.00 | Sequence |
| DRB1_1302 | 321 | RDRSIGSVGRWVAVV | GSVGRWVAV | 0.3489 | 1146.5 | 32.00 | Sequence |
| DRB1_1302 | 20 | GMSEVHLARDLRLHR | VHLARDLRL | 0.3488 | 1147.9 | 32.00 | Sequence |
| DRB1_1302 | 39 | KVLRADLARDPSFYL | LARDPSFYL | 0.3481 | 1157.0 | 32.00 | Sequence |
| DRB1_1302 | 107 | GPMTPKRAIEVIADA | MTPKRAIEV | 0.3476 | 1162.5 | 32.00 | Sequence |
| DRB1_1302 | 465 | KVIGTNPPANQTSAI | PPANQTSAI | 0.3473 | 1167.0 | 32.00 | Sequence |
| DRB1_1302 | 572 | DAEPRLRALGWTGML | RALGWTGML | 0.3465 | 1177.0 | 32.00 | Sequence |
| DRB1_1302 | 40 | VLRADLARDPSFYLR | LARDPSFYL | 0.3450 | 1195.8 | 32.00 | Sequence |
| DRB1_1302 | 543 | TVPVDSVIELQVSKG | VPVDSVIEL | 0.3439 | 1210.5 | 32.00 | Sequence |
| DRB1_1302 | 591 | DVDAGGSQHNRVVYQ | GSQHNRVVY | 0.3429 | 1224.0 | 32.00 | Sequence |
| DRB1_1302 | 468 | GTNPPANQTSAITNV | NQTSAITNV | 0.3425 | 1229.6 | 32.00 | Sequence |
| DRB1_1302 | 295 | LLSSAAGNLSGPRTD | LLSSAAGNL | 0.3419 | 1237.3 | 32.00 | Sequence |
| DRB1_1302 | 607 | PPAGTGVNRDGIITL | VNRDGIITL | 0.3414 | 1243.7 | 32.00 | Sequence |
| DRB1_1302 | 463 | VGKVIGTNPPANQTS | KVIGTNPPA | 0.3406 | 1255.2 | 32.00 | Sequence |
| DRB1_1302 | 554 | VSKGNQFVMPDLSGM | VSKGNQFVM | 0.3400 | 1262.4 | 32.00 | Sequence |
| DRB1_1302 | 610 | GTGVNRDGIITLRFG | VNRDGIITL | 0.3398 | 1265.5 | 32.00 | Sequence |
| DRB1_1302 | 578 | RALGWTGMLDKGADV | GMLDKGADV | 0.3393 | 1272.2 | 32.00 | Sequence |
| DRB1_1302 | 83 | AGPLPYIVMEYVDGV | IVMEYVDGV | 0.3391 | 1275.6 | 32.00 | Sequence |
| DRB1_1302 | 18 | FGGMSEVHLARDLRL | VHLARDLRL | 0.3381 | 1289.5 | 32.00 | Sequence |
| DRB1_1302 | 595 | GGSQHNRVVYQNPPA | RVVYQNPPA | 0.3380 | 1290.0 | 32.00 | Sequence |
| DRB1_1302 | 50 | SFYLRFRREAQNAAA | RREAQNAAA | 0.3378 | 1293.3 | 32.00 | Sequence |
| DRB1_1302 | 270 | ADLVRVHNGEPPEAP | LVRVHNGEP | 0.3377 | 1294.0 | 32.00 | Sequence |
| DRB1_1302 | 427 | EIPDVSTLTYAEAVK | IPDVSTLTY | 0.3373 | 1300.1 | 32.00 | Sequence |
| DRB1_1302 | 19 | GGMSEVHLARDLRLH | VHLARDLRL | 0.3369 | 1306.5 | 32.00 | Sequence |
| DRB1_1302 | 249 | VVLKALAKNPENRYQ | LAKNPENRY | 0.3352 | 1329.4 | 32.00 | Sequence |
| DRB1_1302 | 459 | TPELVGKVIGTNPPA | KVIGTNPPA | 0.3346 | 1339.0 | 32.00 | Sequence |
| DRB1_1302 | 41 | LRADLARDPSFYLRF | LARDPSFYL | 0.3342 | 1344.0 | 32.00 | Sequence |
| DRB1_1302 | 592 | VDAGGSQHNRVVYQN | GSQHNRVVY | 0.3341 | 1346.6 | 32.00 | Sequence |
| DRB1_1302 | 21 | MSEVHLARDLRLHRD | VHLARDLRL | 0.3337 | 1351.4 | 32.00 | Sequence |
| DRB1_1302 | 608 | PAGTGVNRDGIITLR | VNRDGIITL | 0.3329 | 1363.7 | 32.00 | Sequence |
| DRB1_1302 | 599 | HNRVVYQNPPAGTGV | VYQNPPAGT | 0.3325 | 1370.2 | 32.00 | Sequence |
| DRB1_1302 | 322 | DRSIGSVGRWVAVVA | GSVGRWVAV | 0.3317 | 1381.4 | 32.00 | Sequence |
| DRB1_1302 | 90 | VMEYVDGVTLRDIVH | MEYVDGVTL | 0.3307 | 1396.2 | 32.00 | Sequence |
| DRB1_1302 | 84 | GPLPYIVMEYVDGVT | IVMEYVDGV | 0.3304 | 1401.0 | 32.00 | Sequence |
| DRB1_1302 | 245 | DLDAVVLKALAKNPE | VLKALAKNP | 0.3301 | 1405.2 | 32.00 | Sequence |
| DRB1_1302 | 91 | MEYVDGVTLRDIVHT | MEYVDGVTL | 0.3286 | 1428.2 | 50.00 | Sequence |
| DRB1_1302 | 600 | NRVVYQNPPAGTGVN | VYQNPPAGT | 0.3267 | 1457.6 | 50.00 | Sequence |
| DRB1_1302 | 573 | AEPRLRALGWTGMLD | RALGWTGML | 0.3255 | 1476.6 | 50.00 | Sequence |
| DRB1_1302 | 574 | EPRLRALGWTGMLDK | RALGWTGML | 0.3244 | 1495.7 | 50.00 | Sequence |
| DRB1_1302 | 561 | VMPDLSGMFWVDAEP | VMPDLSGMF | 0.3238 | 1505.4 | 50.00 | Sequence |
| DRB1_1302 | 114 | AIEVIADACQALNFS | VIADACQAL | 0.3232 | 1513.7 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_1302 | 156 | FGIARAIADSGNSVT | AIADSGNSV | 0.3231 | 1516.9 | 50.00 | Sequence |
| DRB1_1302 | 271 | DLVRVHNGEPPEAPK | LVRVHNGEP | 0.3220 | 1534.1 | 50.00 | Sequence |
| DRB1_1302 | 120 | DACQALNFSHQNGII | NFSHQNGII | 0.3210 | 1550.3 | 50.00 | Sequence |
| DRB1_1302 | 597 | SQHNRVVYQNPPAGT | VYQNPPAGT | 0.3210 | 1551.3 | 50.00 | Sequence |
| DRB1_1302 | 246 | LDAVVLKALAKNPEN | VLKALAKNP | 0.3209 | 1552.2 | 50.00 | Sequence |
| DRB1_1302 | 42 | RADLARDPSFYLRFR | LARDPSFYL | 0.3201 | 1566.8 | 50.00 | Sequence |
| DRB1_1302 | 542 | TTVPVDSVIELQVSK | VPVDSVIEL | 0.3199 | 1570.3 | 50.00 | Sequence |
| DRB1_1302 | 22 | SEVHLARDLRLHRDV | VHLARDLRL | 0.3188 | 1588.2 | 50.00 | Sequence |
| DRB1_1302 | 272 | LVRVHNGEPPEAPKV | LVRVHNGEP | 0.3182 | 1599.3 | 50.00 | Sequence |
| DRB1_1302 | 25 | HLARDLRLHRDVAVK | LRLHRDVAV | 0.3176 | 1609.7 | 50.00 | Sequence |
| DRB1_1302 | 250 | VLKALAKNPENRYQT | LAKNPENRY | 0.3169 | 1622.2 | 50.00 | Sequence |
| DRB1_1302 | 244 | ADLDAVVLKALAKNP | AVVLKALAK | 0.3165 | 1627.7 | 50.00 | Sequence |
| DRB1_1302 | 362 | PDVRGQSSADAIATL | RGQSSADAI | 0.3165 | 1628.3 | 50.00 | Sequence |
| DRB1_1302 | 243 | SADLDAVVLKALAKN | AVVLKALAK | 0.3152 | 1651.6 | 50.00 | Sequence |
| DRB1_1302 | 593 | DAGGSQHNRVVYQNP | GSQHNRVVY | 0.3147 | 1661.1 | 50.00 | Sequence |
| DRB1_1302 | 575 | PRLRALGWTGMLDKG | RALGWTGML | 0.3145 | 1663.9 | 50.00 | Sequence |
| DRB1_1302 | 242 | LSADLDAVVLKALAK | AVVLKALAK | 0.3113 | 1723.4 | 50.00 | Sequence |
| DRB1_1302 | 157 | GIARAIADSGNSVTQ | AIADSGNSV | 0.3106 | 1735.2 | 50.00 | Sequence |
| DRB1_1302 | 127 | FSHQNGIIHRDVKPA | FSHQNGIIH | 0.3101 | 1745.0 | 50.00 | Sequence |
| DRB1_1302 | 611 | TGVNRDGIITLRFGQ | VNRDGIITL | 0.3099 | 1749.3 | 50.00 | Sequence |
| DRB1_1302 | 130 | QNGIIHRDVKPANIM | RDVKPANIM | 0.3083 | 1778.5 | 50.00 | Sequence |
| DRB1_1302 | 594 | AGGSQHNRVVYQNPP | GSQHNRVVY | 0.3073 | 1799.5 | 50.00 | Sequence |
| DRB1_1302 | 241 | GLSADLDAVVLKALA | DAVVLKALA | 0.3070 | 1805.5 | 50.00 | Sequence |
| DRB1_1302 | 544 | VPVDSVIELQVSKGN | VPVDSVIEL | 0.3059 | 1825.3 | 50.00 | Sequence |
| DRB1_1302 | 601 | RVVYQNPPAGTGVNR | VYQNPPAGT | 0.3055 | 1833.4 | 50.00 | Sequence |
| DRB1_1302 | 23 | EVHLARDLRLHRDVA | VHLARDLRL | 0.3050 | 1844.1 | 50.00 | Sequence |
| DRB1_1302 | 58 | EAQNAAALNHPAIVA | AALNHPAIV | 0.3031 | 1882.2 | 50.00 | Sequence |
| DRB1_1302 | 33 | HRDVAVKVLRADLAR | VKVLRADLA | 0.3031 | 1883.2 | 50.00 | Sequence |
| DRB1_1302 | 347 | IAINTFGGITRDVQV | GGITRDVQV | 0.3024 | 1895.9 | 50.00 | Sequence |
| DRB1_1302 | 598 | QHNRVVYQNPPAGTG | VYQNPPAGT | 0.3012 | 1922.0 | 50.00 | Sequence |
| DRB1_1302 | 43 | ADLARDPSFYLRFRR | LARDPSFYL | 0.3010 | 1926.5 | 50.00 | Sequence |
| DRB1_1302 | 363 | DVRGQSSADAIATLQ | RGQSSADAI | 0.3003 | 1939.8 | 50.00 | Sequence |
| DRB1_1302 | 361 | VPDVRGQSSADAIAT | RGQSSADAI | 0.3002 | 1942.4 | 50.00 | Sequence |
| DRB1_1302 | 108 | PMTPKRAIEVIADAC | MTPKRAIEV | 0.2992 | 1963.1 | 50.00 | Sequence |
| DRB1_1302 | 262 | YQTAAEMRADLVRVH | EMRADLVRV | 0.2990 | 1967.0 | 50.00 | Sequence |
| DRB1_1302 | 34 | RDVAVKVLRADLARD | VKVLRADLA | 0.2988 | 1972.4 | 50.00 | Sequence |
| DRB1_1302 | 254 | LAKNPENRYQTAAEM | LAKNPENRY | 0.2976 | 1997.9 | 50.00 | Sequence |
| DRB1_1302 | 115 | IEVIADACQALNFSH | VIADACQAL | 0.2975 | 2000.6 | 50.00 | Sequence |
| DRB1_1302 | 596 | GSQHNRVVYQNPPAG | VVYQNPPAG | 0.2971 | 2009.2 | 50.00 | Sequence |
| DRB1_1302 | 148 | TNAVKVMDFGIARAI | KVMDFGIAR | 0.2962 | 2027.9 | 50.00 | Sequence |
| DRB1_1302 | 364 | VRGQSSADAIATLQN | RGQSSADAI | 0.2937 | 2083.7 | 50.00 | Sequence |
| DRB1_1302 | 467 | IGTNPPANQTSAITN | PPANQTSAI | 0.2936 | 2085.5 | 50.00 | Sequence |
| DRB1_1302 | 466 | VIGTNPPANQTSAIT | PPANQTSAI | 0.2930 | 2100.5 | 50.00 | Sequence |
| DRB1_1302 | 464 | GKVIGTNPPANQTSA | KVIGTNPPA | 0.2928 | 2103.5 | 50.00 | Sequence |
| DRB1_1302 | 432 | STLTYAEAVKKLTAA | LTYAEAVKK | 0.2927 | 2106.9 | 50.00 | Sequence |
| DRB1_1302 | 360 | QVPDVRGQSSADAIA | RGQSSADAI | 0.2914 | 2135.8 | 50.00 | Sequence |
| DRB1_1302 | 359 | VQVPDVRGQSSADAI | RGQSSADAI | 0.2908 | 2149.3 | 50.00 | Sequence |
| DRB1_1302 | 158 | IARAIADSGNSVTQT | AIADSGNSV | 0.2908 | 2151.3 | 50.00 | Sequence |
| DRB1_1302 | 101 | DIVHTEGPMTPKRAI | IVHTEGPMT | 0.2907 | 2153.4 | 50.00 | Sequence |
| DRB1_1302 | 576 | RLRALGWTGMLDKGA | RALGWTGML | 0.2890 | 2192.6 | 50.00 | Sequence |
| DRB1_1302 | 109 | MTPKRAIEVIADACQ | MTPKRAIEV | 0.2882 | 2210.9 | 50.00 | Sequence |
| DRB1_1302 | 409 | VSAGDEITVNVSTGP | ITVNVSTGP | 0.2874 | 2230.1 | 50.00 | Sequence |
| DRB1_1302 | 146 | SATNAVKVMDFGIAR | AVKVMDFGI | 0.2869 | 2243.7 | 50.00 | Sequence |
| DRB1_1302 | 431 | VSTLTYAEAVKKLTA | LTYAEAVKK | 0.2867 | 2248.2 | 50.00 | Sequence |
| DRB1_1302 | 236 | SARHEGLSADLDAVV | LSADLDAVV | 0.2862 | 2260.8 | 50.00 | Sequence |
| DRB1_1302 | 590 | ADVDAGGSQHNRVVY | GSQHNRVVY | 0.2860 | 2264.3 | 50.00 | Sequence |
| DRB1_1302 | 263 | QTAAEMRADLVRVHN | EMRADLVRV | 0.2834 | 2329.7 | 50.00 | Sequence |
| DRB1_1302 | 44 | DLARDPSFYLRFRRE | LARDPSFYL | 0.2832 | 2335.1 | 50.00 | Sequence |
| DRB1_1302 | 116 | EVIADACQALNFSHQ | VIADACQAL | 0.2832 | 2335.6 | 50.00 | Sequence |
| DRB1_1302 | 429 | PDVSTLTYAEAVKKL | LTYAEAVKK | 0.2826 | 2349.4 | 50.00 | Sequence |
| DRB1_1302 | 319 | TDRDRSIGSVGRWVA | RSIGSVGRW | 0.2825 | 2351.2 | 50.00 | Sequence |
| DRB1_1302 | 507 | AQKNLNVYGFTKFSQ | QKNLNVYGF | 0.2803 | 2410.0 | 50.00 | Sequence |
| DRB1_1302 | 159 | ARAIADSGNSVTQTA | AIADSGNSV | 0.2790 | 2442.6 | 50.00 | Sequence |
| DRB1_1302 | 430 | DVSTLTYAEAVKKLT | LTYAEAVKK | 0.2787 | 2452.3 | 50.00 | Sequence |
| DRB1_1302 | 237 | ARHEGLSADLDAVVL | LSADLDAVV | 0.2785 | 2455.3 | 50.00 | Sequence |
| DRB1_1302 | 421 | TGPEQREIPDVSTLT | REIPDVSTL | 0.2783 | 2463.0 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_1302 | 247 | DAVVLKALAKNPENR | VLKALAKNP | 0.2782 | 2463.3 | 50.00 | Sequence |
| DRB1_1302 | 499 | VAGQTVDVAQKNLNV | DVAQKNLNV | 0.2769 | 2500.5 | 50.00 | Sequence |
| DRB1_1302 | 240 | EGLSADLDAVVLKAL | LSADLDAVV | 0.2762 | 2517.2 | 50.00 | Sequence |
| DRB1_1302 | 117 | VIADACQALNFSHQN | VIADACQAL | 0.2750 | 2549.9 | 50.00 | Sequence |
| DRB1_1302 | 160 | RAIADSGNSVTQTAA | AIADSGNSV | 0.2748 | 2555.6 | 50.00 | Sequence |
| DRB1_1302 | 35 | DVAVKVLRADLARDP | VKVLRADLA | 0.2746 | 2563.1 | 50.00 | Sequence |
| DRB1_1302 | 264 | TAAEMRADLVRVHNG | EMRADLVRV | 0.2744 | 2567.0 | 50.00 | Sequence |
| DRB1_1302 | 251 | LKALAKNPENRYQTA | LAKNPENRY | 0.2732 | 2601.9 | 50.00 | Sequence |
| DRB1_1302 | 155 | DFGIARAIADSGNSV | AIADSGNSV | 0.2728 | 2614.0 | 50.00 | Sequence |
| DRB1_1302 | 348 | AINTFGGITRDVQVP | GGITRDVQV | 0.2725 | 2620.4 | 50.00 | Sequence |
| DRB1_1302 | 577 | LRALGWTGMLDKGAD | RALGWTGML | 0.2711 | 2659.9 | 50.00 | Sequence |
| DRB1_1302 | 97 | VTLRDIVHTEGPMTP | IVHTEGPMT | 0.2710 | 2665.5 | 50.00 | Sequence |
| DRB1_1302 | 96 | GVTLRDIVHTEGPMT | IVHTEGPMT | 0.2705 | 2677.6 | 50.00 | Sequence |
| DRB1_1302 | 410 | SAGDEITVNVSTGPE | ITVNVSTGP | 0.2703 | 2684.1 | 50.00 | Sequence |
| DRB1_1302 | 445 | AAGFGRFKQANSPST | FKQANSPST | 0.2692 | 2717.5 | 50.00 | Sequence |
| DRB1_1302 | 318 | DTDRDRSIGSVGRWV | RSIGSVGRW | 0.2677 | 2760.8 | 50.00 | Sequence |
| DRB1_1302 | 150 | AVKVMDFGIARAIAD | MDFGIARAI | 0.2672 | 2774.6 | 50.00 | Sequence |
| DRB1_1302 | 238 | RHEGLSADLDAVVLK | LSADLDAVV | 0.2670 | 2781.0 | 50.00 | Sequence |
| DRB1_1302 | 446 | AGFGRFKQANSPSTP | FKQANSPST | 0.2669 | 2785.4 | 50.00 | Sequence |
| DRB1_1302 | 147 | ATNAVKVMDFGIARA | KVMDFGIAR | 0.2668 | 2788.8 | 50.00 | Sequence |
| DRB1_1302 | 367 | QSSADAIATLQNRGF | IATLQNRGF | 0.2649 | 2846.0 | 50.00 | Sequence |
| DRB1_1302 | 485 | IIVGSGPATKDIPDV | IIVGSGPAT | 0.2646 | 2856.4 | 50.00 | Sequence |
| DRB1_1302 | 447 | GFGRFKQANSPSTPE | FKQANSPST | 0.2635 | 2889.9 | 50.00 | Sequence |
| DRB1_1302 | 45 | LARDPSFYLRFRREA | LARDPSFYL | 0.2630 | 2904.5 | 50.00 | Sequence |
| DRB1_1302 | 602 | VVYQNPPAGTGVNRD | VYQNPPAGT | 0.2622 | 2931.8 | 50.00 | Sequence |
| DRB1_1302 | 368 | SSADAIATLQNRGFK | IATLQNRGF | 0.2608 | 2975.3 | 50.00 | Sequence |
| DRB1_1302 | 317 | DDTDRDRSIGSVGRW | RSIGSVGRW | 0.2606 | 2979.8 | 50.00 | Sequence |
| DRB1_1302 | 102 | IVHTEGPMTPKRAIE | IVHTEGPMT | 0.2605 | 2983.8 | 50.00 | Sequence |
| DRB1_1302 | 98 | TLRDIVHTEGPMTPK | IVHTEGPMT | 0.2602 | 2995.6 | 50.00 | Sequence |
| DRB1_1302 | 149 | NAVKVMDFGIARAIA | KVMDFGIAR | 0.2597 | 3009.1 | 50.00 | Sequence |
| DRB1_1302 | 215 | FTGDSPVSVAYQHVR | VSVAYQHVR | 0.2596 | 3015.1 | 50.00 | Sequence |
| DRB1_1302 | 261 | RYQTAAEMRADLVRV | EMRADLVRV | 0.2595 | 3017.5 | 50.00 | Sequence |
| DRB1_1302 | 219 | SPVSVAYQHVREDPI | YQHVREDPI | 0.2582 | 3060.4 | 50.00 | Sequence |
| DRB1_1302 | 265 | AAEMRADLVRVHNGE | EMRADLVRV | 0.2570 | 3101.0 | 50.00 | Sequence |
| DRB1_1302 | 411 | AGDEITVNVSTGPEQ | ITVNVSTGP | 0.2566 | 3114.4 | 50.00 | Sequence |
| DRB1_1302 | 508 | QKNLNVYGFTKFSQA | QKNLNVYGF | 0.2566 | 3114.4 | 50.00 | Sequence |
| DRB1_1302 | 259 | ENRYQTAAEMRADLV | AAEMRADLV | 0.2551 | 3163.3 | 50.00 | Sequence |
| DRB1_1302 | 12 | LGEILGFGGMSEVHL | LGFGGMSEV | 0.2536 | 3215.8 | 50.00 | Sequence |
| DRB1_1302 | 151 | VKVMDFGIARAIADS | KVMDFGIAR | 0.2534 | 3222.3 | 50.00 | Sequence |
| DRB1_1302 | 13 | GEILGFGGMSEVHLA | LGFGGMSEV | 0.2521 | 3270.2 | 50.00 | Sequence |
| DRB1_1302 | 571 | VDAEPRLRALGWTGM | LRALGWTGM | 0.2515 | 3290.7 | 50.00 | Sequence |
| DRB1_1302 | 345 | VTIAINTFGGITRDV | IAINTFGGI | 0.2511 | 3303.6 | 50.00 | Sequence |
| DRB1_1302 | 433 | TLTYAEAVKKLTAAG | LTYAEAVKK | 0.2511 | 3305.3 | 50.00 | Sequence |
| DRB1_1302 | 252 | KALAKNPENRYQTAA | LAKNPENRY | 0.2504 | 3330.9 | 50.00 | Sequence |
| DRB1_1302 | 99 | LRDIVHTEGPMTPKR | IVHTEGPMT | 0.2500 | 3344.5 | 50.00 | Sequence |
| DRB1_1302 | 129 | HQNGIIHRDVKPANI | HRDVKPANI | 0.2496 | 3359.8 | 50.00 | Sequence |
| DRB1_1302 | 580 | LGWTGMLDKGADVDA | GMLDKGADV | 0.2488 | 3385.8 | 50.00 | Sequence |
| DRB1_1302 | 10 | YELGEILGFGGMSEV | LGFGGMSEV | 0.2486 | 3393.9 | 50.00 | Sequence |
| DRB1_1302 | 579 | ALGWTGMLDKGADVD | GMLDKGADV | 0.2486 | 3394.3 | 50.00 | Sequence |
| DRB1_1302 | 448 | FGRFKQANSPSTPEL | FKQANSPST | 0.2486 | 3394.3 | 50.00 | Sequence |
| DRB1_1302 | 376 | LQNRGFKIRTLQKPD | GFKIRTLQK | 0.2475 | 3436.1 | 50.00 | Sequence |
| DRB1_1302 | 260 | NRYQTAAEMRADLVR | AAEMRADLV | 0.2464 | 3477.3 | 50.00 | Sequence |
| DRB1_1302 | 174 | AVIGTAQYLSPEQAR | AVIGTAQYL | 0.2448 | 3535.4 | 50.00 | Sequence |
| DRB1_1302 | 365 | RGQSSADAIATLQNR | RGQSSADAI | 0.2437 | 3578.6 | 50.00 | Sequence |
| DRB1_1302 | 100 | RDIVHTEGPMTPKRA | IVHTEGPMT | 0.2429 | 3611.6 | 50.00 | Sequence |
| DRB1_1302 | 581 | GWTGMLDKGADVDAG | GMLDKGADV | 0.2428 | 3613.2 | 50.00 | Sequence |
| DRB1_1302 | 15 | ILGFGGMSEVHLARD | LGFGGMSEV | 0.2413 | 3672.2 | 50.00 | Sequence |
| DRB1_1302 | 412 | GDEITVNVSTGPEQR | ITVNVSTGP | 0.2411 | 3681.7 | 50.00 | Sequence |
| DRB1_1302 | 377 | QNRGFKIRTLQKPDS | GFKIRTLQK | 0.2395 | 3747.5 | 50.00 | Sequence |
| DRB1_1302 | 458 | STPELVGKVIGTNPP | GKVIGTNPP | 0.2392 | 3757.6 | 50.00 | Sequence |
| DRB1_1302 | 349 | INTFGGITRDVQVPD | GGITRDVQV | 0.2390 | 3767.8 | 50.00 | Sequence |
| DRB1_1302 | 449 | GRFKQANSPSTPELV | FKQANSPST | 0.2381 | 3804.5 | 50.00 | Sequence |
| DRB1_1302 | 152 | KVMDFGIARAIADSG | KVMDFGIAR | 0.2370 | 3848.7 | 50.00 | Sequence |
| DRB1_1302 | 216 | TGDSPVSVAYQHVRE | VSVAYQHVR | 0.2362 | 3883.8 | 50.00 | Sequence |
| DRB1_1302 | 220 | PVSVAYQHVREDPIP | YQHVREDPI | 0.2359 | 3895.3 | 50.00 | Sequence |
| DRB1_1302 | 11 | ELGEILGFGGMSEVH | LGFGGMSEV | 0.2338 | 3984.3 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_1302 | 253 | ALAKNPENRYQTAAE | LAKNPENRY | 0.2324 | 4045.0 | 50.00 | Sequence |
| DRB1_1302 | 408 | SVSAGDEITVNVSTG | EITVNVSTG | 0.2304 | 4134.8 | 50.00 | Sequence |
| DRB1_1302 | 217 | GDSPVSVAYQHVRED | VSVAYQHVR | 0.2294 | 4176.4 | 50.00 | Sequence |
| DRB1_1302 | 350 | NTFGGITRDVQVPDV | GGITRDVQV | 0.2291 | 4194.4 | 50.00 | Sequence |
| DRB1_1302 | 36 | VAVKVLRADLARDPS | VKVLRADLA | 0.2269 | 4292.0 | 50.00 | Sequence |
| DRB1_1302 | 492 | ATKDIPDVAGQTVDV | DVAGQTVDV | 0.2265 | 4312.4 | 50.00 | Sequence |
| DRB1_1302 | 380 | GFKIRTLQKPDSTIP | LQKPDSTIP | 0.2260 | 4333.2 | 50.00 | Sequence |
| DRB1_1302 | 496 | IPDVAGQTVDVAQKN | DVAGQTVDV | 0.2260 | 4337.4 | 50.00 | Sequence |
| DRB1_1302 | 495 | DIPDVAGQTVDVAQK | IPDVAGQTV | 0.2252 | 4372.7 | 50.00 | Sequence |
| DRB1_1302 | 239 | HEGLSADLDAVVLKA | LSADLDAVV | 0.2250 | 4384.6 | 50.00 | Sequence |
| DRB1_1302 | 582 | WTGMLDKGADVDAGG | GMLDKGADV | 0.2249 | 4387.5 | 50.00 | Sequence |
| DRB1_1302 | 346 | TIAINTFGGITRDVQ | IAINTFGGI | 0.2242 | 4421.4 | 50.00 | Sequence |
| DRB1_1302 | 16 | LGFGGMSEVHLARDL | LGFGGMSEV | 0.2238 | 4441.5 | 50.00 | Sequence |
| DRB1_1302 | 413 | DEITVNVSTGPEQRE | ITVNVSTGP | 0.2219 | 4532.9 | 50.00 | Sequence |
| DRB1_1302 | 536 | TNPPAGTTVPVDSVI | GTTVPVDSV | 0.2218 | 4535.2 | 50.00 | Sequence |
| DRB1_1302 | 192 | VDARSDVYSLGCVLY | VYSLGCVLY | 0.2208 | 4585.0 | 50.00 | Sequence |
| DRB1_1302 | 493 | TKDIPDVAGQTVDVA | DVAGQTVDV | 0.2196 | 4645.5 | 50.00 | Sequence |
| DRB1_1302 | 537 | NPPAGTTVPVDSVIE | TVPVDSVIE | 0.2188 | 4687.2 | 50.00 | Sequence |
| DRB1_1302 | 351 | TFGGITRDVQVPDVR | GGITRDVQV | 0.2161 | 4826.8 | 50.00 | Sequence |
| DRB1_1302 | 393 | IPPDHVIGTDPAANT | IGTDPAANT | 0.2160 | 4829.5 | 50.00 | Sequence |
| DRB1_1302 | 14 | EILGFGGMSEVHLAR | LGFGGMSEV | 0.2157 | 4844.1 | 50.00 | Sequence |
| DRB1_1302 | 605 | QNPPAGTGVNRDGII | TGVNRDGII | 0.2156 | 4850.4 | 50.00 | Sequence |
| DRB1_1302 | 450 | RFKQANSPSTPELVG | FKQANSPST | 0.2148 | 4892.3 | 50.00 | Sequence |
| DRB1_1302 | 37 | AVKVLRADLARDPSF | VKVLRADLA | 0.2144 | 4915.6 | 50.00 | Sequence |
| DRB1_1302 | 195 | RSDVYSLGCVLYEVL | VYSLGCVLY | 0.2136 | 4955.4 | 50.00 | Sequence |
| DRB1_1302 | 396 | DHVIGTDPAANTSVS | IGTDPAANT | 0.2135 | 4960.6 | 50.00 | Sequence |
| DRB1_1302 | 193 | DARSDVYSLGCVLYE | VYSLGCVLY | 0.2132 | 4978.9 | 50.00 | Sequence |
| DRB1_1302 | 583 | TGMLDKGADVDAGGS | GMLDKGADV | 0.2108 | 5109.7 | 50.00 | Sequence |
| DRB1_1302 | 414 | EITVNVSTGPEQREI | ITVNVSTGP | 0.2107 | 5114.1 | 50.00 | Sequence |
| DRB1_1302 | 352 | FGGITRDVQVPDVRG | GGITRDVQV | 0.2102 | 5146.0 | 50.00 | Sequence |
| DRB1_1302 | 494 | KDIPDVAGQTVDVAQ | IPDVAGQTV | 0.2096 | 5175.9 | 50.00 | Sequence |
| DRB1_1302 | 397 | HVIGTDPAANTSVSA | IGTDPAANT | 0.2091 | 5205.9 | 50.00 | Sequence |
| DRB1_1302 | 498 | DVAGQTVDVAQKNLN | TVDVAQKNL | 0.2090 | 5211.6 | 50.00 | Sequence |
| DRB1_1302 | 584 | GMLDKGADVDAGGSQ | GMLDKGADV | 0.2090 | 5213.2 | 50.00 | Sequence |
| DRB1_1302 | 603 | VYQNPPAGTGVNRDG | VYQNPPAGT | 0.2071 | 5316.6 | 50.00 | Sequence |
| DRB1_1302 | 381 | FKIRTLQKPDSTIPP | LQKPDSTIP | 0.2061 | 5379.4 | 50.00 | Sequence |
| DRB1_1302 | 535 | GTNPPAGTTVPVDSV | GTTVPVDSV | 0.2059 | 5387.7 | 50.00 | Sequence |
| DRB1_1302 | 398 | VIGTDPAANTSVSAG | IGTDPAANT | 0.2050 | 5442.9 | 50.00 | Sequence |
| DRB1_1302 | 395 | PDHVIGTDPAANTSV | IGTDPAANT | 0.2038 | 5511.1 | 50.00 | Sequence |
| DRB1_1302 | 403 | PAANTSVSAGDEITV | VSAGDEITV | 0.2038 | 5511.7 | 50.00 | Sequence |
| DRB1_1302 | 457 | PSTPELVGKVIGTNP | ELVGKVIGT | 0.2037 | 5519.2 | 50.00 | Sequence |
| DRB1_1302 | 353 | GGITRDVQVPDVRGQ | GGITRDVQV | 0.2007 | 5698.7 | 50.00 | Sequence |
| DRB1_1302 | 256 | KNPENRYQTAAEMRA | NRYQTAAEM | 0.2002 | 5729.3 | 50.00 | Sequence |
| DRB1_1302 | 194 | ARSDVYSLGCVLYEV | VYSLGCVLY | 0.1979 | 5877.5 | 50.00 | Sequence |
| DRB1_1302 | 235 | PSARHEGLSADLDAV | RHEGLSADL | 0.1975 | 5898.0 | 50.00 | Sequence |
| DRB1_1302 | 532 | EVTGTNPPAGTTVPV | PPAGTTVPV | 0.1974 | 5908.7 | 50.00 | Sequence |
| DRB1_1302 | 218 | DSPVSVAYQHVREDP | VSVAYQHVR | 0.1972 | 5921.5 | 50.00 | Sequence |
| DRB1_1302 | 530 | AGEVTGTNPPAGTTV | TNPPAGTTV | 0.1969 | 5937.7 | 50.00 | Sequence |
| DRB1_1302 | 119 | ADACQALNFSHQNGI | LNFSHQNGI | 0.1968 | 5948.0 | 50.00 | Sequence |
| DRB1_1302 | 221 | VSVAYQHVREDPIPP | YQHVREDPI | 0.1966 | 5957.3 | 50.00 | Sequence |
| DRB1_1302 | 404 | AANTSVSAGDEITVN | VSAGDEITV | 0.1966 | 5959.2 | 50.00 | Sequence |
| DRB1_1302 | 288 | TDAERTSLLSSAAGN | RTSLLSSAA | 0.1949 | 6067.3 | 50.00 | Sequence |
| DRB1_1302 | 382 | KIRTLQKPDSTIPPD | LQKPDSTIP | 0.1942 | 6112.9 | 50.00 | Sequence |
| DRB1_1302 | 420 | STGPEQREIPDVSTL | REIPDVSTL | 0.1941 | 6125.3 | 50.00 | Sequence |
| DRB1_1302 | 255 | AKNPENRYQTAAEMR | NRYQTAAEM | 0.1930 | 6197.9 | 50.00 | Sequence |
| DRB1_1302 | 287 | LTDAERTSLLSSAAG | RTSLLSSAA | 0.1928 | 6209.4 | 50.00 | Sequence |
| DRB1_1302 | 191 | SVDARSDVYSLGCVL | DVYSLGCVL | 0.1928 | 6210.8 | 50.00 | Sequence |
| DRB1_1302 | 394 | PPDHVIGTDPAANTS | IGTDPAANT | 0.1924 | 6237.8 | 50.00 | Sequence |
| DRB1_1302 | 497 | PDVAGQTVDVAQKNL | TVDVAQKNL | 0.1922 | 6249.5 | 50.00 | Sequence |
| DRB1_1302 | 66 | NHPAIVAVYDTGEAE | VAVYDTGEA | 0.1911 | 6326.7 | 50.00 | Sequence |
| DRB1_1302 | 257 | NPENRYQTAAEMRAD | NRYQTAAEM | 0.1908 | 6345.1 | 50.00 | Sequence |
| DRB1_1302 | 197 | DVYSLGCVLYEVLTG | VYSLGCVLY | 0.1902 | 6383.1 | 50.00 | Sequence |
| DRB1_1302 | 405 | ANTSVSAGDEITVNV | VSAGDEITV | 0.1901 | 6391.8 | 50.00 | Sequence |
| DRB1_1302 | 384 | RTLQKPDSTIPPDHV | LQKPDSTIP | 0.1894 | 6443.6 | 50.00 | Sequence |
| DRB1_1302 | 379 | RGFKIRTLQKPDSTI | TLQKPDSTI | 0.1878 | 6553.9 | 50.00 | Sequence |
| DRB1_1302 | 38 | VKVLRADLARDPSFY | VKVLRADLA | 0.1873 | 6592.0 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_1302 | 399 | IGTDPAANTSVSAGD | TDPAANTSV | 0.1856 | 6710.6 | 50.00 | Sequence |
| DRB1_1302 | 378 | NRGFKIRTLQKPDST | GFKIRTLQK | 0.1841 | 6820.8 | 50.00 | Sequence |
| DRB1_1302 | 383 | IRTLQKPDSTIPPDH | LQKPDSTIP | 0.1841 | 6821.3 | 50.00 | Sequence |
| DRB1_1302 | 606 | NPPAGTGVNRDGIIT | TGVNRDGII | 0.1837 | 6852.7 | 50.00 | Sequence |
| DRB1_1302 | 490 | GPATKDIPDVAGQTV | IPDVAGQTV | 0.1835 | 6865.9 | 50.00 | Sequence |
| DRB1_1302 | 385 | TLQKPDSTIPPDHVI | LQKPDSTIP | 0.1823 | 6955.6 | 50.00 | Sequence |
| DRB1_1302 | 286 | VLTDAERTSLLSSAA | RTSLLSSAA | 0.1822 | 6965.7 | 50.00 | Sequence |
| DRB1_1302 | 153 | VMDFGIARAIADSGN | FGIARAIAD | 0.1818 | 6990.2 | 50.00 | Sequence |
| DRB1_1302 | 510 | NLNVYGFTKFSQASV | FTKFSQASV | 0.1814 | 7026.8 | 50.00 | Sequence |
| DRB1_1302 | 196 | SDVYSLGCVLYEVLT | VYSLGCVLY | 0.1807 | 7074.0 | 50.00 | Sequence |
| DRB1_1302 | 545 | PVDSVIELQVSKGNQ | VIELQVSKG | 0.1805 | 7091.5 | 50.00 | Sequence |
| DRB1_1302 | 570 | WVDAEPRLRALGWTG | RLRALGWTG | 0.1800 | 7127.4 | 50.00 | Sequence |
| DRB1_1302 | 533 | VTGTNPPAGTTVPVD | PPAGTTVPV | 0.1800 | 7132.0 | 50.00 | Sequence |
| DRB1_1302 | 528 | RPAGEVTGTNPPAGT | EVTGTNPPA | 0.1799 | 7135.3 | 50.00 | Sequence |
| DRB1_1302 | 589 | GADVDAGGSQHNRVV | GGSQHNRVV | 0.1795 | 7167.8 | 50.00 | Sequence |
| DRB1_1302 | 531 | GEVTGTNPPAGTTVP | TNPPAGTTV | 0.1782 | 7267.4 | 50.00 | Sequence |
| DRB1_1302 | 128 | SHQNGIIHRDVKPAN | IIHRDVKPA | 0.1782 | 7268.0 | 50.00 | Sequence |
| DRB1_1302 | 406 | NTSVSAGDEITVNVS | VSAGDEITV | 0.1781 | 7280.5 | 50.00 | Sequence |
| DRB1_1302 | 387 | QKPDSTIPPDHVIGT | IPPDHVIGT | 0.1770 | 7366.9 | 50.00 | Sequence |
| DRB1_1302 | 190 | DSVDARSDVYSLGCV | SVDARSDVY | 0.1768 | 7382.8 | 50.00 | Sequence |
| DRB1_1302 | 80 | ETPAGPLPYIVMEYV | LPYIVMEYV | 0.1764 | 7417.5 | 50.00 | Sequence |
| DRB1_1302 | 569 | FWVDAEPRLRALGWT | FWVDAEPRL | 0.1762 | 7428.0 | 50.00 | Sequence |
| DRB1_1302 | 491 | PATKDIPDVAGQTVD | IPDVAGQTV | 0.1740 | 7612.3 | 50.00 | Sequence |
| DRB1_1302 | 407 | TSVSAGDEITVNVST | VSAGDEITV | 0.1719 | 7787.0 | 50.00 | Sequence |
| DRB1_1302 | 214 | PFTGDSPVSVAYQHV | FTGDSPVSV | 0.1717 | 7797.7 | 50.00 | Sequence |
| DRB1_1302 | 258 | PENRYQTAAEMRADL | NRYQTAAEM | 0.1717 | 7801.9 | 50.00 | Sequence |
| DRB1_1302 | 358 | DVQVPDVRGQSSADA | VRGQSSADA | 0.1711 | 7849.0 | 50.00 | Sequence |
| DRB1_1302 | 189 | GDSVDARSDVYSLGC | SVDARSDVY | 0.1710 | 7862.7 | 50.00 | Sequence |
| DRB1_1302 | 529 | PAGEVTGTNPPAGTT | EVTGTNPPA | 0.1701 | 7935.0 | 50.00 | Sequence |
| DRB1_1302 | 198 | VYSLGCVLYEVLTGE | VYSLGCVLY | 0.1701 | 7935.6 | 50.00 | Sequence |
| DRB1_1302 | 564 | DLSGMFWVDAEPRLR | FWVDAEPRL | 0.1684 | 8083.8 | 50.00 | Sequence |
| DRB1_1302 | 451 | FKQANSPSTPELVGK | FKQANSPST | 0.1682 | 8104.2 | 50.00 | Sequence |
| DRB1_1302 | 509 | KNLNVYGFTKFSQAS | LNVYGFTKF | 0.1682 | 8106.0 | 50.00 | Sequence |
| DRB1_1302 | 566 | SGMFWVDAEPRLRAL | FWVDAEPRL | 0.1674 | 8177.0 | 50.00 | Sequence |
| DRB1_1302 | 199 | YSLGCVLYEVLTGEP | LYEVLTGEP | 0.1671 | 8201.4 | 50.00 | Sequence |
| DRB1_1302 | 281 | PEAPKVLTDAERTSL | KVLTDAERT | 0.1666 | 8244.2 | 50.00 | Sequence |
| DRB1_1302 | 565 | LSGMFWVDAEPRLRA | FWVDAEPRL | 0.1649 | 8394.6 | 50.00 | Sequence |
| DRB1_1302 | 534 | TGTNPPAGTTVPVDS | TNPPAGTTV | 0.1633 | 8543.2 | 50.00 | Sequence |
| DRB1_1302 | 77 | GEAETPAGPLPYIVM | EAETPAGPL | 0.1619 | 8674.5 | 50.00 | Sequence |
| DRB1_1302 | 568 | MFWVDAEPRLRALGW | FWVDAEPRL | 0.1613 | 8733.1 | 50.00 | Sequence |
| DRB1_1302 | 154 | MDFGIARAIADSGNS | MDFGIARAI | 0.1612 | 8740.8 | 50.00 | Sequence |
| DRB1_1302 | 388 | KPDSTIPPDHVIGTD | IPPDHVIGT | 0.1601 | 8844.1 | 50.00 | Sequence |
| DRB1_1302 | 201 | LGCVLYEVLTGEPPF | LYEVLTGEP | 0.1598 | 8871.4 | 50.00 | Sequence |
| DRB1_1302 | 297 | SSAAGNLSGPRTDPL | LSGPRTDPL | 0.1594 | 8912.9 | 50.00 | Sequence |
| DRB1_1302 | 456 | SPSTPELVGKVIGTN | ELVGKVIGT | 0.1593 | 8925.7 | 50.00 | Sequence |
| DRB1_1302 | 282 | EAPKVLTDAERTSLL | KVLTDAERT | 0.1592 | 8929.1 | 50.00 | Sequence |
| DRB1_1302 | 511 | LNVYGFTKFSQASVD | FTKFSQASV | 0.1558 | 9265.3 | 50.00 | Sequence |
| DRB1_1302 | 604 | YQNPPAGTGVNRDGI | QNPPAGTGV | 0.1556 | 9289.0 | 50.00 | Sequence |
| DRB1_1302 | 567 | GMFWVDAEPRLRALG | FWVDAEPRL | 0.1550 | 9349.6 | 50.00 | Sequence |
| DRB1_1302 | 386 | LQKPDSTIPPDHVIG | LQKPDSTIP | 0.1542 | 9425.4 | 50.00 | Sequence |
| DRB1_1302 | 78 | EAETPAGPLPYIVME | EAETPAGPL | 0.1533 | 9523.5 | 50.00 | Sequence |
| DRB1_1302 | 202 | GCVLYEVLTGEPPFT | VLTGEPPFT | 0.1529 | 9562.7 | 50.00 | Sequence |
| DRB1_1302 | 200 | SLGCVLYEVLTGEPP | LGCVLYEVL | 0.1519 | 9664.6 | 50.00 | Sequence |
| DRB1_1302 | 280 | PPEAPKVLTDAERTS | KVLTDAERT | 0.1517 | 9689.9 | 50.00 | Sequence |
| DRB1_1302 | 562 | MPDLSGMFWVDAEPR | MPDLSGMFW | 0.1516 | 9700.4 | 50.00 | Sequence |
| DRB1_1302 | 279 | EPPEAPKVLTDAERT | KVLTDAERT | 0.1512 | 9733.2 | 50.00 | Sequence |
| DRB1_1302 | 81 | TPAGPLPYIVMEYVD | LPYIVMEYV | 0.1509 | 9774.5 | 50.00 | Sequence |
| DRB1_1302 | 390 | DSTIPPDHVIGTDPA | DSTIPPDHV | 0.1503 | 9828.8 | 50.00 | Sequence |
| DRB1_1302 | 296 | LSSAAGNLSGPRTDP | LSSAAGNLS | 0.1502 | 9840.2 | 50.00 | Sequence |
| DRB1_1302 | 299 | AAGNLSGPRTDPLPR | LSGPRTDPL | 0.1498 | 9885.1 | 50.00 | Sequence |
| DRB1_1302 | 17 | GFGGMSEVHLARDLR | MSEVHLARD | 0.1492 | 9955.2 | 50.00 | Sequence |
| DRB1_1302 | 67 | HPAIVAVYDTGEAET | VAVYDTGEA | 0.1490 | 9976.8 | 50.00 | Sequence |
| DRB1_1302 | 283 | APKVLTDAERTSLLS | KVLTDAERT | 0.1481 | 10074.2 | 50.00 | Sequence |
| DRB1_1302 | 298 | SAAGNLSGPRTDPLP | LSGPRTDPL | 0.1479 | 10092.7 | 50.00 | Sequence |
| DRB1_1302 | 444 | TAAGFGRFKQANSPS | RFKQANSPS | 0.1477 | 10112.5 | 50.00 | Sequence |
| DRB1_1302 | 366 | GQSSADAIATLQNRG | QSSADAIAT | 0.1476 | 10123.4 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_1302 | 389 | PDSTIPPDHVIGTDP | IPPDHVIGT | 0.1456 | 10347.2 | 50.00 | Sequence |
| DRB1_1302 | 401 | TDPAANTSVSAGDEI | TSVSAGDEI | 0.1448 | 10439.0 | 50.00 | Sequence |
| DRB1_1302 | 95 | DGVTLRDIVHTEGPM | DIVHTEGPM | 0.1445 | 10475.9 | 50.00 | Sequence |
| DRB1_1302 | 400 | GTDPAANTSVSAGDE | TDPAANTSV | 0.1439 | 10539.5 | 50.00 | Sequence |
| DRB1_1302 | 211 | GEPPFTGDSPVSVAY | FTGDSPVSV | 0.1437 | 10562.9 | 50.00 | Sequence |
| DRB1_1302 | 82 | PAGPLPYIVMEYVDG | LPYIVMEYV | 0.1419 | 10765.3 | 50.00 | Sequence |
| DRB1_1302 | 284 | PKVLTDAERTSLLSS | KVLTDAERT | 0.1410 | 10876.5 | 50.00 | Sequence |
| DRB1_1302 | 455 | NSPSTPELVGKVIGT | ELVGKVIGT | 0.1407 | 10914.8 | 50.00 | Sequence |
| DRB1_1302 | 213 | PPFTGDSPVSVAYQH | FTGDSPVSV | 0.1402 | 10968.8 | 50.00 | Sequence |
| DRB1_1302 | 441 | KKLTAAGFGRFKQAN | LTAAGFGRF | 0.1391 | 11098.1 | 50.00 | Sequence |
| DRB1_1302 | 212 | EPPFTGDSPVSVAYQ | FTGDSPVSV | 0.1388 | 11138.7 | 50.00 | Sequence |
| DRB1_1302 | 300 | AGNLSGPRTDPLPRQ | LSGPRTDPL | 0.1386 | 11162.5 | 50.00 | Sequence |
| DRB1_1302 | 203 | CVLYEVLTGEPPFTG | VLTGEPPFT | 0.1381 | 11217.0 | 50.00 | Sequence |
| DRB1_1302 | 527 | PRPAGEVTGTNPPAG | EVTGTNPPA | 0.1380 | 11233.3 | 50.00 | Sequence |
| DRB1_1302 | 222 | SVAYQHVREDPIPPS | YQHVREDPI | 0.1379 | 11241.2 | 50.00 | Sequence |
| DRB1_1302 | 526 | SPRPAGEVTGTNPPA | EVTGTNPPA | 0.1370 | 11356.6 | 50.00 | Sequence |
| DRB1_1302 | 75 | DTGEAETPAGPLPYI | EAETPAGPL | 0.1370 | 11359.6 | 50.00 | Sequence |
| DRB1_1302 | 415 | ITVNVSTGPEQREIP | ITVNVSTGP | 0.1342 | 11700.1 | 50.00 | Sequence |
| DRB1_1302 | 187 | ARGDSVDARSDVYSL | SVDARSDVY | 0.1336 | 11775.0 | 50.00 | Sequence |
| DRB1_1302 | 285 | KVLTDAERTSLLSSA | KVLTDAERT | 0.1334 | 11805.3 | 50.00 | Sequence |
| DRB1_1302 | 232 | PIPPSARHEGLSADL | RHEGLSADL | 0.1331 | 11848.6 | 50.00 | Sequence |
| DRB1_1302 | 68 | PAIVAVYDTGEAETP | VAVYDTGEA | 0.1327 | 11895.5 | 50.00 | Sequence |
| DRB1_1302 | 392 | TIPPDHVIGTDPAAN | VIGTDPAAN | 0.1325 | 11918.5 | 50.00 | Sequence |
| DRB1_1302 | 185 | EQARGDSVDARSDVY | SVDARSDVY | 0.1321 | 11980.1 | 50.00 | Sequence |
| DRB1_1302 | 76 | TGEAETPAGPLPYIV | EAETPAGPL | 0.1320 | 11983.6 | 50.00 | Sequence |
| DRB1_1302 | 110 | TPKRAIEVIADACQA | EVIADACQA | 0.1314 | 12063.5 | 50.00 | Sequence |
| DRB1_1302 | 79 | AETPAGPLPYIVMEY | AGPLPYIVM | 0.1303 | 12214.7 | 50.00 | Sequence |
| DRB1_1302 | 74 | YDTGEAETPAGPLPY | EAETPAGPL | 0.1301 | 12231.2 | 50.00 | Sequence |
| DRB1_1302 | 180 | QYLSPEQARGDSVDA | QARGDSVDA | 0.1297 | 12286.4 | 50.00 | Sequence |
| DRB1_1302 | 188 | RGDSVDARSDVYSLG | SVDARSDVY | 0.1287 | 12416.0 | 50.00 | Sequence |
| DRB1_1302 | 391 | STIPPDHVIGTDPAA | IPPDHVIGT | 0.1286 | 12442.0 | 50.00 | Sequence |
| DRB1_1302 | 223 | VAYQHVREDPIPPSA | YQHVREDPI | 0.1284 | 12468.1 | 50.00 | Sequence |
| DRB1_1302 | 184 | PEQARGDSVDARSDV | QARGDSVDA | 0.1277 | 12562.0 | 50.00 | Sequence |
| DRB1_1302 | 354 | GITRDVQVPDVRGQS | DVQVPDVRG | 0.1276 | 12569.7 | 50.00 | Sequence |
| DRB1_1302 | 563 | PDLSGMFWVDAEPRL | FWVDAEPRL | 0.1274 | 12598.3 | 50.00 | Sequence |
| DRB1_1302 | 92 | EYVDGVTLRDIVHTE | GVTLRDIVH | 0.1262 | 12762.1 | 50.00 | Sequence |
| DRB1_1302 | 233 | IPPSARHEGLSADLD | RHEGLSADL | 0.1250 | 12932.9 | 50.00 | Sequence |
| DRB1_1302 | 225 | YQHVREDPIPPSARH | YQHVREDPI | 0.1250 | 12935.9 | 50.00 | Sequence |
| DRB1_1302 | 186 | QARGDSVDARSDVYS | QARGDSVDA | 0.1247 | 12977.4 | 50.00 | Sequence |
| DRB1_1302 | 224 | AYQHVREDPIPPSAR | YQHVREDPI | 0.1245 | 12994.0 | 50.00 | Sequence |
| DRB1_1302 | 301 | GNLSGPRTDPLPRQD | LSGPRTDPL | 0.1244 | 13015.2 | 50.00 | Sequence |
| DRB1_1302 | 452 | KQANSPSTPELVGKV | STPELVGKV | 0.1241 | 13059.8 | 50.00 | Sequence |
| DRB1_1302 | 273 | VRVHNGEPPEAPKVL | GEPPEAPKV | 0.1237 | 13108.1 | 50.00 | Sequence |
| DRB1_1302 | 49 | PSFYLRFRREAQNAA | FRREAQNAA | 0.1235 | 13145.1 | 50.00 | Sequence |
| DRB1_1302 | 181 | YLSPEQARGDSVDAR | QARGDSVDA | 0.1206 | 13560.0 | 50.00 | Sequence |
| DRB1_1302 | 8 | DRYELGEILGFGGMS | GEILGFGGM | 0.1206 | 13560.9 | 50.00 | Sequence |
| DRB1_1302 | 118 | IADACQALNFSHQNG | QALNFSHQN | 0.1193 | 13757.3 | 50.00 | Sequence |
| DRB1_1302 | 355 | ITRDVQVPDVRGQSS | DVQVPDVRG | 0.1186 | 13856.5 | 50.00 | Sequence |
| DRB1_1302 | 357 | RDVQVPDVRGQSSAD | DVRGQSSAD | 0.1182 | 13921.1 | 50.00 | Sequence |
| DRB1_1302 | 234 | PPSARHEGLSADLDA | RHEGLSADL | 0.1181 | 13925.0 | 50.00 | Sequence |
| DRB1_1302 | 402 | DPAANTSVSAGDEIT | TSVSAGDEI | 0.1162 | 14217.0 | 50.00 | Sequence |
| DRB1_1302 | 69 | AIVAVYDTGEAETPA | VAVYDTGEA | 0.1161 | 14234.6 | 50.00 | Sequence |
| DRB1_1302 | 316 | LDDTDRDRSIGSVGR | DRSIGSVGR | 0.1149 | 14422.8 | 50.00 | Sequence |
| DRB1_1302 | 9 | RYELGEILGFGGMSE | EILGFGGMS | 0.1144 | 14494.9 | 50.00 | Sequence |
| DRB1_1302 | 204 | VLYEVLTGEPPFTGD | VLTGEPPFT | 0.1137 | 14604.0 | 50.00 | Sequence |
| DRB1_1302 | 302 | NLSGPRTDPLPRQDL | LSGPRTDPL | 0.1133 | 14675.1 | 50.00 | Sequence |
| DRB1_1302 | 7 | SDRYELGEILGFGGM | LGEILGFGG | 0.1129 | 14734.0 | 50.00 | Sequence |
| DRB1_1302 | 183 | SPEQARGDSVDARSD | QARGDSVDA | 0.1110 | 15040.5 | 50.00 | Sequence |
| DRB1_1302 | 442 | KLTAAGFGRFKQANS | LTAAGFGRF | 0.1106 | 15108.8 | 50.00 | Sequence |
| DRB1_1302 | 182 | LSPEQARGDSVDARS | QARGDSVDA | 0.1105 | 15132.4 | 50.00 | Sequence |
| DRB1_1302 | 453 | QANSPSTPELVGKVI | STPELVGKV | 0.1087 | 15425.3 | 50.00 | Sequence |
| DRB1_1302 | 275 | VHNGEPPEAPKVLTD | GEPPEAPKV | 0.1072 | 15680.6 | 50.00 | Sequence |
| DRB1_1302 | 210 | TGEPPFTGDSPVSVA | FTGDSPVSV | 0.1068 | 15750.3 | 50.00 | Sequence |
| DRB1_1302 | 303 | LSGPRTDPLPRQDLD | LSGPRTDPL | 0.1062 | 15851.4 | 50.00 | Sequence |
| DRB1_1302 | 93 | YVDGVTLRDIVHTEG | GVTLRDIVH | 0.1056 | 15955.6 | 50.00 | Sequence |
| DRB1_1302 | 205 | LYEVLTGEPPFTGDS | VLTGEPPFT | 0.1051 | 16045.0 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_1302 | 356 | TRDVQVPDVRGQSSA | DVQVPDVRG | 0.1041 | 16210.5 | 50.00 | Sequence |
| DRB1_1302 | 512 | NVYGFTKFSQASVDS | FTKFSQASV | 0.1023 | 16522.2 | 50.00 | Sequence |
| DRB1_1302 | 175 | VIGTAQYLSPEQARG | IGTAQYLSP | 0.1011 | 16742.3 | 50.00 | Sequence |
| DRB1_1302 | 443 | LTAAGFGRFKQANSP | LTAAGFGRF | 0.1009 | 16789.5 | 50.00 | Sequence |
| DRB1_1302 | 94 | VDGVTLRDIVHTEGP | GVTLRDIVH | 0.0999 | 16973.0 | 50.00 | Sequence |
| DRB1_1302 | 515 | GFTKFSQASVDSPRP | FTKFSQASV | 0.0996 | 17014.4 | 50.00 | Sequence |
| DRB1_1302 | 516 | FTKFSQASVDSPRPA | QASVDSPRP | 0.0995 | 17039.8 | 50.00 | Sequence |
| DRB1_1302 | 274 | RVHNGEPPEAPKVLT | GEPPEAPKV | 0.0988 | 17162.7 | 50.00 | Sequence |
| DRB1_1302 | 6 | LSDRYELGEILGFGG | YELGEILGF | 0.0985 | 17232.3 | 50.00 | Sequence |
| DRB1_1302 | 278 | GEPPEAPKVLTDAER | GEPPEAPKV | 0.0981 | 17290.0 | 50.00 | Sequence |
| DRB1_1302 | 70 | IVAVYDTGEAETPAG | VAVYDTGEA | 0.0981 | 17307.2 | 50.00 | Sequence |
| DRB1_1302 | 72 | AVYDTGEAETPAGPL | EAETPAGPL | 0.0980 | 17325.6 | 50.00 | Sequence |
| DRB1_1302 | 276 | HNGEPPEAPKVLTDA | GEPPEAPKV | 0.0978 | 17359.3 | 50.00 | Sequence |
| DRB1_1302 | 178 | TAQYLSPEQARGDSV | PEQARGDSV | 0.0966 | 17582.4 | 50.00 | Sequence |
| DRB1_1302 | 179 | AQYLSPEQARGDSVD | PEQARGDSV | 0.0962 | 17657.7 | 50.00 | Sequence |
| DRB1_1302 | 209 | LTGEPPFTGDSPVSV | FTGDSPVSV | 0.0961 | 17677.2 | 50.00 | Sequence |
| DRB1_1302 | 513 | VYGFTKFSQASVDSP | FTKFSQASV | 0.0955 | 17793.7 | 50.00 | Sequence |
| DRB1_1302 | 277 | NGEPPEAPKVLTDAE | GEPPEAPKV | 0.0953 | 17831.6 | 50.00 | Sequence |
| DRB1_1302 | 315 | DLDDTDRDRSIGSVG | DRDRSIGSV | 0.0940 | 18074.0 | 50.00 | Sequence |
| DRB1_1302 | 2 | TPSHLSDRYELGEIL | DRYELGEIL | 0.0930 | 18276.6 | 50.00 | Sequence |
| DRB1_1302 | 454 | ANSPSTPELVGKVIG | STPELVGKV | 0.0926 | 18365.6 | 50.00 | Sequence |
| DRB1_1302 | 73 | VYDTGEAETPAGPLP | EAETPAGPL | 0.0921 | 18451.8 | 50.00 | Sequence |
| DRB1_1302 | 176 | IGTAQYLSPEQARGD | IGTAQYLSP | 0.0911 | 18651.4 | 50.00 | Sequence |
| DRB1_1302 | 314 | QDLDDTDRDRSIGSV | DRDRSIGSV | 0.0880 | 19285.5 | 50.00 | Sequence |
| DRB1_1302 | 514 | YGFTKFSQASVDSPR | FTKFSQASV | 0.0875 | 19402.1 | 50.00 | Sequence |
| DRB1_1302 | 486 | IVGSGPATKDIPDVA | IVGSGPATK | 0.0875 | 19405.0 | 50.00 | Sequence |
| DRB1_1302 | 525 | DSPRPAGEVTGTNPP | GEVTGTNPP | 0.0874 | 19426.2 | 50.00 | Sequence |
| DRB1_1302 | 4 | SHLSDRYELGEILGF | DRYELGEIL | 0.0872 | 19457.6 | 50.00 | Sequence |
| DRB1_1302 | 517 | TKFSQASVDSPRPAG | ASVDSPRPA | 0.0858 | 19759.0 | 50.00 | Sequence |
| DRB1_1302 | 518 | KFSQASVDSPRPAGE | ASVDSPRPA | 0.0800 | 21033.0 | 50.00 | Sequence |
| DRB1_1302 | 5 | HLSDRYELGEILGFG | DRYELGEIL | 0.0793 | 21200.7 | 50.00 | Sequence |
| DRB1_1302 | 416 | TVNVSTGPEQREIPD | TVNVSTGPE | 0.0781 | 21477.6 | 50.00 | Sequence |
| DRB1_1302 | 588 | KGADVDAGGSQHNRV | AGGSQHNRV | 0.0763 | 21898.8 | 50.00 | Sequence |
| DRB1_1302 | 586 | LDKGADVDAGGSQHN | DVDAGGSQH | 0.0730 | 22683.5 | 50.00 | Sequence |
| DRB1_1302 | 3 | PSHLSDRYELGEILG | DRYELGEIL | 0.0720 | 22942.4 | 50.00 | Sequence |
| DRB1_1302 | 489 | SGPATKDIPDVAGQT | DIPDVAGQT | 0.0704 | 23349.4 | 50.00 | Sequence |
| DRB1_1302 | 585 | MLDKGADVDAGGSQH | DVDAGGSQH | 0.0692 | 23637.9 | 50.00 | Sequence |
| DRB1_1302 | 519 | FSQASVDSPRPAGEV | QASVDSPRP | 0.0691 | 23672.4 | 50.00 | Sequence |
| DRB1_1302 | 587 | DKGADVDAGGSQHNR | DVDAGGSQH | 0.0689 | 23731.2 | 50.00 | Sequence |
| DRB1_1302 | 419 | VSTGPEQREIPDVST | QREIPDVST | 0.0676 | 24052.2 | 50.00 | Sequence |
| DRB1_1302 | 520 | SQASVDSPRPAGEVT | QASVDSPRP | 0.0657 | 24560.6 | 50.00 | Sequence |
| DRB1_1302 | 206 | YEVLTGEPPFTGDSP | VLTGEPPFT | 0.0649 | 24773.5 | 50.00 | Sequence |
| DRB1_1302 | 521 | QASVDSPRPAGEVTG | QASVDSPRP | 0.0645 | 24887.4 | 50.00 | Sequence |
| DRB1_1302 | 46 | ARDPSFYLRFRREAQ | RDPSFYLRF | 0.0637 | 25089.7 | 50.00 | Sequence |
| DRB1_1302 | 524 | VDSPRPAGEVTGTNP | DSPRPAGEV | 0.0619 | 25604.7 | 50.00 | Sequence |
| DRB1_1302 | 227 | HVREDPIPPSARHEG | DPIPPSARH | 0.0616 | 25682.4 | 50.00 | Sequence |
| DRB1_1302 | 177 | GTAQYLSPEQARGDS | AQYLSPEQA | 0.0607 | 25923.6 | 50.00 | Sequence |
| DRB1_1302 | 48 | DPSFYLRFRREAQNA | RFRREAQNA | 0.0605 | 25988.2 | 50.00 | Sequence |
| DRB1_1302 | 522 | ASVDSPRPAGEVTGT | ASVDSPRPA | 0.0596 | 26244.8 | 50.00 | Sequence |
| DRB1_1302 | 207 | EVLTGEPPFTGDSPV | VLTGEPPFT | 0.0594 | 26303.9 | 50.00 | Sequence |
| DRB1_1302 | 71 | VAVYDTGEAETPAGP | VAVYDTGEA | 0.0592 | 26350.1 | 50.00 | Sequence |
| DRB1_1302 | 228 | VREDPIPPSARHEGL | DPIPPSARH | 0.0585 | 26550.7 | 50.00 | Sequence |
| DRB1_1302 | 1 | TTPSHLSDRYELGEI | TPSHLSDRY | 0.0584 | 26586.0 | 50.00 | Sequence |
| DRB1_1302 | 230 | EDPIPPSARHEGLSA | DPIPPSARH | 0.0542 | 27807.3 | 50.00 | Sequence |
| DRB1_1302 | 226 | QHVREDPIPPSARHE | DPIPPSARH | 0.0542 | 27813.6 | 50.00 | Sequence |
| DRB1_1302 | 487 | VGSGPATKDIPDVAG | VGSGPATKD | 0.0539 | 27917.6 | 50.00 | Sequence |
| DRB1_1302 | 229 | REDPIPPSARHEGLS | DPIPPSARH | 0.0536 | 28005.7 | 50.00 | Sequence |
| DRB1_1302 | 0 | MTTPSHLSDRYELGE | TPSHLSDRY | 0.0535 | 28032.7 | 50.00 | Sequence |
| DRB1_1302 | 231 | DPIPPSARHEGLSAD | DPIPPSARH | 0.0521 | 28455.0 | 50.00 | Sequence |
| DRB1_1302 | 47 | RDPSFYLRFRREAQN | RDPSFYLRF | 0.0481 | 29702.9 | 50.00 | Sequence |
| DRB1_1302 | 208 | VLTGEPPFTGDSPVS | VLTGEPPFT | 0.0463 | 30287.7 | 50.00 | Sequence |
| DRB1_1302 | 523 | SVDSPRPAGEVTGTN | DSPRPAGEV | 0.0426 | 31537.5 | 50.00 | Sequence |
| DRB1_1302 | 488 | GSGPATKDIPDVAGQ | GSGPATKDI | 0.0424 | 31598.6 | 50.00 | Sequence |
| DRB1_1302 | 417 | VNVSTGPEQREIPDV | VNVSTGPEQ | 0.0388 | 32853.0 | 50.00 | Sequence |
| DRB1_1302 | 313 | RQDLDDTDRDRSIGS | TDRDRSIGS | 0.0375 | 33316.5 | 50.00 | Sequence |
| DRB1_1302 | 418 | NVSTGPEQREIPDVS | VSTGPEQRE | 0.0302 | 36063.3 | 50.00 | Sequence |

```
   DRB1_1302  304  SGPRTDPLPRQDLDD  PRTDPLPRQ        0.0291      36513.3                50.00     Sequence
   DRB1_1302  305  GPRTDPLPRQDLDDT  PRTDPLPRQ        0.0287      36645.1                50.00     Sequence
   DRB1_1302  311  LPRQDLDDTDRDRSI  DDTDRDRSI        0.0270      37337.9                50.00     Sequence
   DRB1_1302  312  PRQDLDDTDRDRSIG  DDTDRDRSI        0.0235      38769.3                50.00     Sequence
   DRB1_1302  307  RTDPLPRQDLDDTDR  LPRQDLDDT        0.0223      39267.4                50.00     Sequence
   DRB1_1302  306  PRTDPLPRQDLDDTD  PRTDPLPRQ        0.0219      39433.5                50.00     Sequence
   DRB1_1302  308  TDPLPRQDLDDTDRD  QDLDDTDRD        0.0182      41070.8                50.00     Sequence
   DRB1_1302  310  PLPRQDLDDTDRDRS  QDLDDTDRD        0.0150      42530.6                50.00     Sequence
   DRB1_1302  309  DPLPRQDLDDTDRDR  QDLDDTDRD        0.0147      42640.7                50.00     Sequence
-----------------------------------------------------------------------------------------------

Allele: DRB1_1302. Number of high binders 21. Number of weak binders 86. Number of peptides 612

-----------------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------------
      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
-----------------------------------------------------------------------------------------------
   DRB1_1501  370  ADAIATLQNRGFKIR  AIATLQNRG        0.6929         27.7          SB     2.00     Sequence
   DRB1_1501  371  DAIATLQNRGFKIRT  AIATLQNRG        0.6871         29.5          SB     2.00     Sequence
   DRB1_1501  369  SADAIATLQNRGFKI  AIATLQNRG        0.6836         30.7          SB     2.00     Sequence
   DRB1_1501   12  LGEILGFGGMSEVHL  EILGFGGMS        0.6510         43.7          SB     4.00     Sequence
   DRB1_1501   11  ELGEILGFGGMSEVH  EILGFGGMS        0.6483         45.0          SB     4.00     Sequence
   DRB1_1501  372  AIATLQNRGFKIRTL  AIATLQNRG        0.6412         48.5          SB     4.00     Sequence
   DRB1_1501   13  GEILGFGGMSEVHLA  EILGFGGMS        0.6348         52.0          WB     4.00     Sequence
   DRB1_1501   27  ARDLRLHRDVAVKVL  RLHRDVAVK        0.6265         56.9          WB     8.00     Sequence
   DRB1_1501   26  LARDLRLHRDVAVKV  RLHRDVAVK        0.6235         58.7          WB     8.00     Sequence
   DRB1_1501   28  RDLRLHRDVAVKVLR  RLHRDVAVK        0.6197         61.3          WB     8.00     Sequence
   DRB1_1501  437  AEAVKKLTAAGFGRF  AVKKLTAAG        0.6110         67.3          WB     8.00     Sequence
   DRB1_1501  368  SSADAIATLQNRGFK  AIATLQNRG        0.6082         69.4          WB     8.00     Sequence
   DRB1_1501   14  EILGFGGMSEVHLAR  EILGFGGMS        0.6066         70.5          WB     8.00     Sequence
   DRB1_1501   25  HLARDLRLHRDVAVK  RLHRDVAVK        0.6018         74.3          WB     8.00     Sequence
   DRB1_1501  436  YAEAVKKLTAAGFGR  AVKKLTAAG        0.6014         74.6          WB     8.00     Sequence
   DRB1_1501  149  NAVKVMDFGIARAIA  KVMDFGIAR        0.6007         75.2          WB     8.00     Sequence
   DRB1_1501  481  NVVIIIVGSGPATKD  IIIVGSGPA        0.5993         76.4          WB     8.00     Sequence
   DRB1_1501   10  YELGEILGFGGMSEV  EILGFGGMS        0.5962         79.0          WB     8.00     Sequence
   DRB1_1501  438  EAVKKLTAAGFGRFK  AVKKLTAAG        0.5944         80.5          WB     8.00     Sequence
   DRB1_1501  148  TNAVKVMDFGIARAI  KVMDFGIAR        0.5880         86.3          WB     8.00     Sequence
   DRB1_1501  482  VVIIIVGSGPATKDI  IIIVGSGPA        0.5863         87.9          WB     8.00     Sequence
   DRB1_1501   29  DLRLHRDVAVKVLRA  RLHRDVAVK        0.5858         88.4          WB     8.00     Sequence
   DRB1_1501   30  LRLHRDVAVKVLRAD  RLHRDVAVK        0.5856         88.6          WB     8.00     Sequence
   DRB1_1501  480  TNVVIIIVGSGPATK  IIIVGSGPA        0.5835         90.6          WB     8.00     Sequence
   DRB1_1501    9  RYELGEILGFGGMSE  EILGFGGMS        0.5810         93.1          WB     8.00     Sequence
   DRB1_1501  150  AVKVMDFGIARAIAD  KVMDFGIAR        0.5809         93.2          WB     8.00     Sequence
   DRB1_1501   35  DVAVKVLRADLARDP  AVKVLRADL        0.5795         94.6          WB     8.00     Sequence
   DRB1_1501   34  RDVAVKVLRADLARD  AVKVLRADL        0.5761         98.2          WB     8.00     Sequence
   DRB1_1501   36  VAVKVLRADLARDPS  AVKVLRADL        0.5724        102.2          WB     8.00     Sequence
   DRB1_1501  435  TYAEAVKKLTAAGFG  AVKKLTAAG        0.5720        102.6          WB     8.00     Sequence
   DRB1_1501  147  ATNAVKVMDFGIARA  KVMDFGIAR        0.5671        108.2          WB    16.00     Sequence
   DRB1_1501  244  ADLDAVVLKALAKNP  VVLKALAKN        0.5635        112.5          WB    16.00     Sequence
   DRB1_1501  573  AEPRLRALGWTGMLD  RLRALGWTG        0.5608        115.8          WB    16.00     Sequence
   DRB1_1501  483  VIIIVGSGPATKDIP  IIIVGSGPA        0.5581        119.2          WB    16.00     Sequence
   DRB1_1501  439  AVKKLTAAGFGRFKQ  AVKKLTAAG        0.5571        120.5          WB    16.00     Sequence
   DRB1_1501   33  HRDVAVKVLRADLAR  AVKVLRADL        0.5557        122.3          WB    16.00     Sequence
   DRB1_1501  367  QSSADAIATLQNRGF  AIATLQNRG        0.5557        122.4          WB    16.00     Sequence
   DRB1_1501  245  DLDAVVLKALAKNPE  VVLKALAKN        0.5544        124.2          WB    16.00     Sequence
   DRB1_1501   24  VHLARDLRLHRDVAV  HLARDLRLH        0.5496        130.7          WB    16.00     Sequence
   DRB1_1501   37  AVKVLRADLARDPSF  AVKVLRADL        0.5453        136.9          WB    16.00     Sequence
   DRB1_1501   31  RLHRDVAVKVLRADL  RLHRDVAVK        0.5453        137.0          WB    16.00     Sequence
   DRB1_1501  434  LTYAEAVKKLTAAGF  AVKKLTAAG        0.5448        137.7          WB    16.00     Sequence
   DRB1_1501  479  ITNVVIIIVGSGPAT  IIIVGSGPA        0.5426        141.0          WB    16.00     Sequence
   DRB1_1501  246  LDAVVLKALAKNPEN  VVLKALAKN        0.5412        143.2          WB    16.00     Sequence
   DRB1_1501  151  VKVMDFGIARAIADS  KVMDFGIAR        0.5389        146.7          WB    16.00     Sequence
   DRB1_1501  574  EPRLRALGWTGMLDK  RLRALGWTG        0.5331        156.4          WB    16.00     Sequence
   DRB1_1501  247  DAVVLKALAKNPENR  VVLKALAKN        0.5304        160.9          WB    16.00     Sequence
   DRB1_1501  373  IATLQNRGFKIRTLQ  TLQNRGFKI        0.5292        163.0          WB    16.00     Sequence
   DRB1_1501  324  SIGSVGRWVAVVAVL  SVGRWVAVV        0.5268        167.3          WB    16.00     Sequence
```

```
DRB1_1501  243  SADLDAVVLKALAKN  VVLKALAKN        0.5250        170.6        WB    16.00      Sequence
DRB1_1501  575  PRLRALGWTGMLDKG  RLRALGWTG        0.5240        172.5        WB    16.00      Sequence
DRB1_1501  146  SATNAVKVMDFGIAR  KVMDFGIAR        0.5158        188.5        WB    16.00      Sequence
DRB1_1501  323  RSIGSVGRWVAVVAV  SVGRWVAVV        0.5143        191.5        WB    16.00      Sequence
DRB1_1501  576  RLRALGWTGMLDKGA  RLRALGWTG        0.5140        192.2        WB    16.00      Sequence
DRB1_1501  572  DAEPRLRALGWTGML  RLRALGWTG        0.5104        199.8        WB    16.00      Sequence
DRB1_1501  322  DRSIGSVGRWVAVVA  SVGRWVAVV        0.5050        211.9        WB    16.00      Sequence
DRB1_1501   47  RDPSFYLRFRREAQN  FYLRFRREA        0.5037        214.8        WB    16.00      Sequence
DRB1_1501   23  EVHLARDLRLHRDVA  HLARDLRLH        0.4993        225.4        WB    16.00      Sequence
DRB1_1501  374  ATLQNRGFKIRTLQK  TLQNRGFKI        0.4979        228.8        WB    16.00      Sequence
DRB1_1501  484  IIIVGSGPATKDIPD  IIIVGSGPA        0.4964        232.5        WB    16.00      Sequence
DRB1_1501  445  AAGFGRFKQANSPST  GFGRFKQAN        0.4904        248.0        WB    16.00      Sequence
DRB1_1501   32  LHRDVAVKVLRADLA  AVKVLRADL        0.4894        250.8        WB    32.00      Sequence
DRB1_1501    8  DRYELGEILGFGGMS  EILGFGGMS        0.4889        252.1        WB    32.00      Sequence
DRB1_1501  444  TAAGFGRFKQANSPS  GFGRFKQAN        0.4876        255.7        WB    32.00      Sequence
DRB1_1501  325  IGSVGRWVAVVAVLA  SVGRWVAVV        0.4867        258.3        WB    32.00      Sequence
DRB1_1501  510  NLNVYGFTKFSQASV  GFTKFSQAS        0.4830        268.7        WB    32.00      Sequence
DRB1_1501  321  RDRSIGSVGRWVAVV  SIGSVGRWV        0.4785        282.3        WB    32.00      Sequence
DRB1_1501  248  AVVLKALAKNPENRY  VVLKALAKN        0.4776        284.8        WB    32.00      Sequence
DRB1_1501  326  GSVGRWVAVVAVLAV  SVGRWVAVV        0.4773        285.8        WB    32.00      Sequence
DRB1_1501  571  VDAEPRLRALGWTGM  RLRALGWTG        0.4773        286.0        WB    32.00      Sequence
DRB1_1501  152  KVMDFGIARAIADSG  KVMDFGIAR        0.4772        286.3        WB    32.00      Sequence
DRB1_1501  442  KLTAAGFGRFKQANS  GFGRFKQAN        0.4769        287.0        WB    32.00      Sequence
DRB1_1501  375  TLQNRGFKIRTLQKP  TLQNRGFKI        0.4744        294.9        WB    32.00      Sequence
DRB1_1501  509  KNLNVYGFTKFSQAS  GFTKFSQAS        0.4736        297.4        WB    32.00      Sequence
DRB1_1501   46  ARDPSFYLRFRREAQ  FYLRFRREA        0.4720        302.8        WB    32.00      Sequence
DRB1_1501   49  PSFYLRFRREAQNAA  FYLRFRREA        0.4715        304.4        WB    32.00      Sequence
DRB1_1501  478  AITNVVIIIVGSGPA  IIIVGSGPA        0.4704        308.0        WB    32.00      Sequence
DRB1_1501  443  LTAAGFGRFKQANSP  GFGRFKQAN        0.4692        312.0        WB    32.00      Sequence
DRB1_1501   15  ILGFGGMSEVHLARD  GFGGMSEVH        0.4681        315.6        WB    32.00      Sequence
DRB1_1501  433  TLTYAEAVKKLTAAG  AVKKLTAAG        0.4677        317.1        WB    32.00      Sequence
DRB1_1501  290  AERTSLLSSAAGNLS  RTSLLSSAA        0.4670        319.7        WB    32.00      Sequence
DRB1_1501   22  SEVHLARDLRLHRDV  HLARDLRLH        0.4638        331.0        WB    32.00      Sequence
DRB1_1501   48  DPSFYLRFRREAQNA  FYLRFRREA        0.4606        342.6        WB    32.00      Sequence
DRB1_1501  121  ACQALNFSHQNGIIH  ACQALNFSH        0.4579        352.7        WB    32.00      Sequence
DRB1_1501   20  GMSEVHLARDLRLHR  HLARDLRLH        0.4566        357.8        WB    32.00      Sequence
DRB1_1501  289  DAERTSLLSSAAGNL  RTSLLSSAA        0.4542        367.1        WB    32.00      Sequence
DRB1_1501  511  LNVYGFTKFSQASVD  GFTKFSQAS        0.4521        375.6        WB    32.00      Sequence
DRB1_1501  611  TGVNRDGIITLRFGQ  GIITLRFGQ        0.4514        378.3        WB    32.00      Sequence
DRB1_1501  140  PANIMISATNAVKVM  MISATNAVK        0.4514        378.5        WB    32.00      Sequence
DRB1_1501  446  AGFGRFKQANSPSTP  GFGRFKQAN        0.4509        380.5        WB    32.00      Sequence
DRB1_1501  570  WVDAEPRLRALGWTG  RLRALGWTG        0.4506        381.6        WB    32.00      Sequence
DRB1_1501  291  ERTSLLSSAAGNLSG  RTSLLSSAA        0.4493        387.1        WB    32.00      Sequence
DRB1_1501  139  KPANIMISATNAVKV  MISATNAVK        0.4483        391.2        WB    32.00      Sequence
DRB1_1501   21  MSEVHLARDLRLHRD  HLARDLRLH        0.4434        412.7        WB    32.00      Sequence
DRB1_1501  120  DACQALNFSHQNGII  ACQALNFSH        0.4432        413.3        WB    32.00      Sequence
DRB1_1501  441  KKLTAAGFGRFKQAN  GFGRFKQAN        0.4360        447.1        WB    32.00      Sequence
DRB1_1501  507  AQKNLNVYGFTKFSQ  AQKNLNVYG        0.4354        450.0        WB    32.00      Sequence
DRB1_1501  327  SVGRWVAVVAVLAVL  SVGRWVAVV        0.4352        450.8        WB    32.00      Sequence
DRB1_1501  141  ANIMISATNAVKVMD  MISATNAVK        0.4302        475.9        WB    32.00      Sequence
DRB1_1501  292  RTSLLSSAAGNLSGP  SLLSSAAGN        0.4289        482.8        WB    32.00      Sequence
DRB1_1501  508  QKNLNVYGFTKFSQA  NVYGFTKFS        0.4254        501.1              32.00      Sequence
DRB1_1501  123  QALNFSHQNGIIHRD  LNFSHQNGI        0.4217        521.9              32.00      Sequence
DRB1_1501   45  LARDPSFYLRFRREA  PSFYLRFRR        0.4172        547.5              32.00      Sequence
DRB1_1501  119  ADACQALNFSHQNGI  ACQALNFSH        0.4163        553.3              32.00      Sequence
DRB1_1501  506  VAQKNLNVYGFTKFS  VAQKNLNVY        0.4160        555.1              32.00      Sequence
DRB1_1501   50  SFYLRFRREAQNAAA  FYLRFRREA        0.4142        566.0              32.00      Sequence
DRB1_1501  376  LQNRGFKIRTLQKPD  KIRTLQKPD        0.4135        569.8              32.00      Sequence
DRB1_1501  548  SVIELQVSKGNQFVM  VIELQVSKG        0.4108        587.0              32.00      Sequence
DRB1_1501  138  VKPANIMISATNAVK  ANIMISATN        0.4106        588.3              32.00      Sequence
DRB1_1501  100  RDIVHTEGPMTPKRA  IVHTEGPMT        0.4092        597.3              32.00      Sequence
DRB1_1501   38  VKVLRADLARDPSFY  KVLRADLAR        0.4056        620.7              32.00      Sequence
DRB1_1501  122  CQALNFSHQNGIIHR  NFSHQNGII        0.4045        628.5              32.00      Sequence
DRB1_1501  320  DRDRSIGSVGRWVAV  SIGSVGRWV        0.4031        637.8              32.00      Sequence
DRB1_1501  512  NVYGFTKFSQASVDS  GFTKFSQAS        0.4000        659.8              32.00      Sequence
DRB1_1501  118  IADACQALNFSHQNG  ACQALNFSH        0.3975        677.6              32.00      Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_1501 | 366 | GQSSADAIATLQNRG | AIATLQNRG | 0.3971 | 680.7 | 32.00 | Sequence |
| DRB1_1501 | 99 | LRDIVHTEGPMTPKR | IVHTEGPMT | 0.3960 | 688.7 | 32.00 | Sequence |
| DRB1_1501 | 242 | LSADLDAVVLKALAK | AVVLKALAK | 0.3957 | 690.9 | 32.00 | Sequence |
| DRB1_1501 | 377 | QNRGFKIRTLQKPDS | KIRTLQKPD | 0.3939 | 704.5 | 32.00 | Sequence |
| DRB1_1501 | 51 | FYLRFRREAQNAAAL | FYLRFRREA | 0.3936 | 706.9 | 32.00 | Sequence |
| DRB1_1501 | 288 | TDAERTSLLSSAAGN | RTSLLSSAA | 0.3910 | 727.4 | 32.00 | Sequence |
| DRB1_1501 | 19 | GGMSEVHLARDLRLH | HLARDLRLH | 0.3894 | 740.0 | 32.00 | Sequence |
| DRB1_1501 | 249 | VVLKALAKNPENRYQ | VVLKALAKN | 0.3881 | 750.4 | 32.00 | Sequence |
| DRB1_1501 | 461 | ELVGKVIGTNPPANQ | LVGKVIGTN | 0.3874 | 756.1 | 32.00 | Sequence |
| DRB1_1501 | 333 | AVVAVLAVLTVVVTI | AVLTVVVTI | 0.3819 | 802.3 | 50.00 | Sequence |
| DRB1_1501 | 460 | PELVGKVIGTNPPAN | LVGKVIGTN | 0.3791 | 827.3 | 50.00 | Sequence |
| DRB1_1501 | 142 | NIMISATNAVKVMDF | MISATNAVK | 0.3788 | 830.1 | 50.00 | Sequence |
| DRB1_1501 | 610 | GTGVNRDGIITLRFG | RDGIITLRF | 0.3772 | 844.4 | 50.00 | Sequence |
| DRB1_1501 | 597 | SQHNRVVYQNPPAGT | RVVYQNPPA | 0.3769 | 847.3 | 50.00 | Sequence |
| DRB1_1501 | 505 | DVAQKNLNVYGFTKF | AQKNLNVYG | 0.3754 | 861.1 | 50.00 | Sequence |
| DRB1_1501 | 596 | GSQHNRVVYQNPPAG | NRVVYQNPP | 0.3741 | 873.5 | 50.00 | Sequence |
| DRB1_1501 | 101 | DIVHTEGPMTPKRAI | IVHTEGPMT | 0.3736 | 878.3 | 50.00 | Sequence |
| DRB1_1501 | 343 | VVVTIAINTFGGITR | VVTIAINTF | 0.3732 | 881.9 | 50.00 | Sequence |
| DRB1_1501 | 447 | GFGRFKQANSPSTPE | GFGRFKQAN | 0.3727 | 886.9 | 50.00 | Sequence |
| DRB1_1501 | 65 | LNHPAIVAVYDTGEA | AIVAVYDTG | 0.3723 | 890.4 | 50.00 | Sequence |
| DRB1_1501 | 16 | LGFGGMSEVHLARDL | GFGGMSEVH | 0.3720 | 893.7 | 50.00 | Sequence |
| DRB1_1501 | 344 | VVTIAINTFGGITRD | VTIAINTFG | 0.3718 | 895.4 | 50.00 | Sequence |
| DRB1_1501 | 131 | NGIIHRDVKPANIMI | IIHRDVKPA | 0.3717 | 895.7 | 50.00 | Sequence |
| DRB1_1501 | 193 | DARSDVYSLGCVLYE | DVYSLGCVL | 0.3709 | 904.0 | 50.00 | Sequence |
| DRB1_1501 | 98 | TLRDIVHTEGPMTPK | IVHTEGPMT | 0.3708 | 904.4 | 50.00 | Sequence |
| DRB1_1501 | 334 | VVAVLAVLTVVVTIA | VAVLAVLTV | 0.3704 | 909.2 | 50.00 | Sequence |
| DRB1_1501 | 598 | QHNRVVYQNPPAGTG | RVVYQNPPA | 0.3702 | 910.3 | 50.00 | Sequence |
| DRB1_1501 | 201 | LGCVLYEVLTGEPPF | VLYEVLTGE | 0.3698 | 914.4 | 50.00 | Sequence |
| DRB1_1501 | 63 | AALNHPAIVAVYDTG | AIVAVYDTG | 0.3698 | 914.6 | 50.00 | Sequence |
| DRB1_1501 | 577 | LRALGWTGMLDKGAD | RALGWTGML | 0.3696 | 916.3 | 50.00 | Sequence |
| DRB1_1501 | 337 | VLAVLTVVVTIAINT | VLAVLTVVV | 0.3695 | 917.3 | 50.00 | Sequence |
| DRB1_1501 | 192 | VDARSDVYSLGCVLY | DVYSLGCVL | 0.3690 | 923.1 | 50.00 | Sequence |
| DRB1_1501 | 89 | IVMEYVDGVTLRDIV | EYVDGVTLR | 0.3688 | 924.4 | 50.00 | Sequence |
| DRB1_1501 | 599 | HNRVVYQNPPAGTGV | RVVYQNPPA | 0.3651 | 962.3 | 50.00 | Sequence |
| DRB1_1501 | 504 | VDVAQKNLNVYGFTK | VAQKNLNVY | 0.3634 | 979.8 | 50.00 | Sequence |
| DRB1_1501 | 378 | NRGFKIRTLQKPDST | RGFKIRTLQ | 0.3631 | 983.9 | 50.00 | Sequence |
| DRB1_1501 | 547 | DSVIELQVSKGNQFV | VIELQVSKG | 0.3620 | 995.5 | 50.00 | Sequence |
| DRB1_1501 | 319 | TDRDRSIGSVGRWVA | SIGSVGRWV | 0.3618 | 997.3 | 50.00 | Sequence |
| DRB1_1501 | 117 | VIADACQALNFSHQN | ACQALNFSH | 0.3589 | 1029.6 | 50.00 | Sequence |
| DRB1_1501 | 88 | YIVMEYVDGVTLRDI | EYVDGVTLR | 0.3580 | 1039.5 | 50.00 | Sequence |
| DRB1_1501 | 345 | VTIAINTFGGITRDV | AINTFGGIT | 0.3573 | 1047.3 | 50.00 | Sequence |
| DRB1_1501 | 339 | AVLTVVVTIAINTFG | VVVTIAINT | 0.3570 | 1050.9 | 50.00 | Sequence |
| DRB1_1501 | 130 | QNGIIHRDVKPANIM | IIHRDVKPA | 0.3564 | 1057.7 | 50.00 | Sequence |
| DRB1_1501 | 90 | VMEYVDGVTLRDIVH | EYVDGVTLR | 0.3561 | 1060.5 | 50.00 | Sequence |
| DRB1_1501 | 459 | TPELVGKVIGTNPPA | LVGKVIGTN | 0.3561 | 1060.8 | 50.00 | Sequence |
| DRB1_1501 | 202 | GCVLYEVLTGEPPFT | EVLTGEPPF | 0.3553 | 1069.7 | 50.00 | Sequence |
| DRB1_1501 | 66 | NHPAIVAVYDTGEAE | AIVAVYDTG | 0.3553 | 1069.7 | 50.00 | Sequence |
| DRB1_1501 | 124 | ALNFSHQNGIIHRDV | LNFSHQNGI | 0.3547 | 1077.4 | 50.00 | Sequence |
| DRB1_1501 | 332 | VAVVAVLAVLTVVVT | AVLAVLTVV | 0.3546 | 1078.3 | 50.00 | Sequence |
| DRB1_1501 | 97 | VTLRDIVHTEGPMTP | IVHTEGPMT | 0.3540 | 1085.1 | 50.00 | Sequence |
| DRB1_1501 | 335 | VAVLAVLTVVVTIAI | VLAVLTVVV | 0.3534 | 1092.3 | 50.00 | Sequence |
| DRB1_1501 | 132 | GIIHRDVKPANIMIS | IIHRDVKPA | 0.3522 | 1106.2 | 50.00 | Sequence |
| DRB1_1501 | 331 | WVAVVAVLAVLTVVV | VVAVLAVLT | 0.3522 | 1107.0 | 50.00 | Sequence |
| DRB1_1501 | 336 | AVLAVLTVVVTIAIN | VLAVLTVVV | 0.3519 | 1110.5 | 50.00 | Sequence |
| DRB1_1501 | 513 | VYGFTKFSQASVDSP | GFTKFSQAS | 0.3519 | 1110.6 | 50.00 | Sequence |
| DRB1_1501 | 440 | VKKLTAAGFGRFKQA | KLTAAGFGR | 0.3508 | 1123.5 | 50.00 | Sequence |
| DRB1_1501 | 44 | DLARDPSFYLRFRRE | PSFYLRFRR | 0.3485 | 1151.7 | 50.00 | Sequence |
| DRB1_1501 | 137 | DVKPANIMISATNAV | ANIMISATN | 0.3483 | 1154.5 | 50.00 | Sequence |
| DRB1_1501 | 64 | ALNHPAIVAVYDTGE | AIVAVYDTG | 0.3483 | 1154.5 | 50.00 | Sequence |
| DRB1_1501 | 191 | SVDARSDVYSLGCVL | DVYSLGCVL | 0.3480 | 1158.3 | 50.00 | Sequence |
| DRB1_1501 | 197 | DVYSLGCVLYEVLTG | DVYSLGCVL | 0.3473 | 1166.9 | 50.00 | Sequence |
| DRB1_1501 | 379 | RGFKIRTLQKPDSTI | KIRTLQKPD | 0.3446 | 1200.9 | 50.00 | Sequence |
| DRB1_1501 | 173 | AAVIGTAQYLSPEQA | VIGTAQYLS | 0.3446 | 1201.4 | 50.00 | Sequence |
| DRB1_1501 | 609 | AGTGVNRDGIITLRF | GVNRDGIIT | 0.3427 | 1226.3 | 50.00 | Sequence |
| DRB1_1501 | 341 | LTVVVTIAINTFGGI | LTVVVTIAI | 0.3424 | 1231.0 | 50.00 | Sequence |
| DRB1_1501 | 503 | TVDVAQKNLNVYGFT | AQKNLNVYG | 0.3414 | 1244.4 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_1501 | 91 | MEYVDGVTLRDIVHT | EYVDGVTLR | 0.3413 | 1244.6 | 50.00 | Sequence |
| DRB1_1501 | 458 | STPELVGKVIGTNPP | LVGKVIGTN | 0.3409 | 1251.1 | 50.00 | Sequence |
| DRB1_1501 | 462 | LVGKVIGTNPPANQT | LVGKVIGTN | 0.3408 | 1251.2 | 50.00 | Sequence |
| DRB1_1501 | 338 | LAVLTVVVTIAINTF | LTVVVTIAI | 0.3403 | 1258.3 | 50.00 | Sequence |
| DRB1_1501 | 546 | VDSVIELQVSKGNQF | VIELQVSKG | 0.3402 | 1260.7 | 50.00 | Sequence |
| DRB1_1501 | 96 | GVTLRDIVHTEGPMT | IVHTEGPMT | 0.3397 | 1266.3 | 50.00 | Sequence |
| DRB1_1501 | 67 | HPAIVAVYDTGEAET | AIVAVYDTG | 0.3389 | 1278.2 | 50.00 | Sequence |
| DRB1_1501 | 43 | ADLARDPSFYLRFRR | PSFYLRFRR | 0.3387 | 1280.7 | 50.00 | Sequence |
| DRB1_1501 | 143 | IMISATNAVKVMDFG | MISATNAVK | 0.3381 | 1288.7 | 50.00 | Sequence |
| DRB1_1501 | 125 | LNFSHQNGIIHRDVK | LNFSHQNGI | 0.3377 | 1294.0 | 50.00 | Sequence |
| DRB1_1501 | 68 | PAIVAVYDTGEAETP | AIVAVYDTG | 0.3359 | 1319.4 | 50.00 | Sequence |
| DRB1_1501 | 330 | RWVAVVAVLAVLTVV | VVAVLAVLT | 0.3359 | 1320.0 | 50.00 | Sequence |
| DRB1_1501 | 129 | HQNGIIHRDVKPANI | IIHRDVKPA | 0.3357 | 1322.3 | 50.00 | Sequence |
| DRB1_1501 | 287 | LTDAERTSLLSSAAG | RTSLLSSAA | 0.3356 | 1324.4 | 50.00 | Sequence |
| DRB1_1501 | 595 | GGSQHNRVVYQNPPA | NRVVYQNPP | 0.3356 | 1324.8 | 50.00 | Sequence |
| DRB1_1501 | 127 | FSHQNGIIHRDVKPA | IIHRDVKPA | 0.3341 | 1346.7 | 50.00 | Sequence |
| DRB1_1501 | 342 | TVVVTIAINTFGGIT | VVVTIAINT | 0.3339 | 1348.5 | 50.00 | Sequence |
| DRB1_1501 | 578 | RALGWTGMLDKGADV | RALGWTGML | 0.3335 | 1354.5 | 50.00 | Sequence |
| DRB1_1501 | 175 | VIGTAQYLSPEQARG | VIGTAQYLS | 0.3329 | 1363.9 | 50.00 | Sequence |
| DRB1_1501 | 340 | VLTVVVTIAINTFGG | VVVTIAINT | 0.3320 | 1377.6 | 50.00 | Sequence |
| DRB1_1501 | 194 | ARSDVYSLGCVLYEV | DVYSLGCVL | 0.3318 | 1379.6 | 50.00 | Sequence |
| DRB1_1501 | 172 | TAAVIGTAQYLSPEQ | VIGTAQYLS | 0.3310 | 1392.6 | 50.00 | Sequence |
| DRB1_1501 | 102 | IVHTEGPMTPKRAIE | IVHTEGPMT | 0.3307 | 1396.9 | 50.00 | Sequence |
| DRB1_1501 | 198 | VYSLGCVLYEVLTGE | VLYEVLTGE | 0.3306 | 1398.6 | 50.00 | Sequence |
| DRB1_1501 | 200 | SLGCVLYEVLTGEPP | CVLYEVLTG | 0.3304 | 1400.3 | 50.00 | Sequence |
| DRB1_1501 | 92 | EYVDGVTLRDIVHTE | EYVDGVTLR | 0.3299 | 1408.3 | 50.00 | Sequence |
| DRB1_1501 | 174 | AVIGTAQYLSPEQAR | VIGTAQYLS | 0.3293 | 1417.4 | 50.00 | Sequence |
| DRB1_1501 | 293 | TSLLSSAAGNLSGPR | SLLSSAAGN | 0.3280 | 1437.6 | 50.00 | Sequence |
| DRB1_1501 | 549 | VIELQVSKGNQFVMP | VIELQVSKG | 0.3277 | 1442.4 | 50.00 | Sequence |
| DRB1_1501 | 457 | PSTPELVGKVIGTNP | LVGKVIGTN | 0.3272 | 1450.3 | 50.00 | Sequence |
| DRB1_1501 | 195 | RSDVYSLGCVLYEVL | DVYSLGCVL | 0.3272 | 1451.1 | 50.00 | Sequence |
| DRB1_1501 | 477 | SAITNVVIIIVGSGP | VVIIIVGSG | 0.3269 | 1455.3 | 50.00 | Sequence |
| DRB1_1501 | 39 | KVLRADLARDPSFYL | KVLRADLAR | 0.3256 | 1475.4 | 50.00 | Sequence |
| DRB1_1501 | 485 | IIVGSGPATKDIPDV | IIVGSGPAT | 0.3250 | 1485.4 | 50.00 | Sequence |
| DRB1_1501 | 87 | PYIVMEYVDGVTLRD | EYVDGVTLR | 0.3249 | 1486.9 | 50.00 | Sequence |
| DRB1_1501 | 116 | EVIADACQALNFSHQ | ACQALNFSH | 0.3246 | 1492.1 | 50.00 | Sequence |
| DRB1_1501 | 69 | AIVAVYDTGEAETPA | AIVAVYDTG | 0.3244 | 1495.2 | 50.00 | Sequence |
| DRB1_1501 | 199 | YSLGCVLYEVLTGEP | CVLYEVLTG | 0.3240 | 1501.3 | 50.00 | Sequence |
| DRB1_1501 | 267 | EMRADLVRVHNGEPP | EMRADLVRV | 0.3236 | 1508.0 | 50.00 | Sequence |
| DRB1_1501 | 502 | QTVDVAQKNLNVYGF | VAQKNLNVY | 0.3233 | 1512.4 | 50.00 | Sequence |
| DRB1_1501 | 346 | TIAINTFGGITRDVQ | AINTFGGIT | 0.3229 | 1518.8 | 50.00 | Sequence |
| DRB1_1501 | 144 | MISATNAVKVMDFGI | AVKVMDFGI | 0.3227 | 1522.4 | 50.00 | Sequence |
| DRB1_1501 | 128 | SHQNGIIHRDVKPAN | IIHRDVKPA | 0.3211 | 1548.7 | 50.00 | Sequence |
| DRB1_1501 | 564 | DLSGMFWVDAEPRLR | MFWVDAEPR | 0.3188 | 1587.7 | 50.00 | Sequence |
| DRB1_1501 | 600 | NRVVYQNPPAGTGVN | RVVYQNPPA | 0.3181 | 1601.0 | 50.00 | Sequence |
| DRB1_1501 | 567 | GMFWVDAEPRLRALG | MFWVDAEPR | 0.3165 | 1628.0 | 50.00 | Sequence |
| DRB1_1501 | 266 | AEMRADLVRVHNGEP | EMRADLVRV | 0.3157 | 1642.8 | 50.00 | Sequence |
| DRB1_1501 | 203 | CVLYEVLTGEPPFTG | EVLTGEPPF | 0.3151 | 1652.9 | 50.00 | Sequence |
| DRB1_1501 | 171 | QTAAVIGTAQYLSPE | VIGTAQYLS | 0.3150 | 1655.3 | 50.00 | Sequence |
| DRB1_1501 | 328 | VGRWVAVVAVLAVLT | VGRWVAVVA | 0.3146 | 1661.3 | 50.00 | Sequence |
| DRB1_1501 | 329 | GRWVAVVAVLAVLTV | AVVAVLAVL | 0.3146 | 1662.4 | 50.00 | Sequence |
| DRB1_1501 | 145 | ISATNAVKVMDFGIA | AVKVMDFGI | 0.3135 | 1682.8 | 50.00 | Sequence |
| DRB1_1501 | 563 | PDLSGMFWVDAEPRL | MFWVDAEPR | 0.3132 | 1688.4 | 50.00 | Sequence |
| DRB1_1501 | 545 | PVDSVIELQVSKGNQ | VIELQVSKG | 0.3116 | 1716.4 | 50.00 | Sequence |
| DRB1_1501 | 514 | YGFTKFSQASVDSPR | GFTKFSQAS | 0.3107 | 1733.2 | 50.00 | Sequence |
| DRB1_1501 | 501 | GQTVDVAQKNLNVYG | VAQKNLNVY | 0.3097 | 1751.7 | 50.00 | Sequence |
| DRB1_1501 | 565 | LSGMFWVDAEPRLRA | MFWVDAEPR | 0.3095 | 1756.8 | 50.00 | Sequence |
| DRB1_1501 | 456 | SPSTPELVGKVIGTN | LVGKVIGTN | 0.3072 | 1800.5 | 50.00 | Sequence |
| DRB1_1501 | 347 | IAINTFGGITRDVQV | AINTFGGIT | 0.3067 | 1811.2 | 50.00 | Sequence |
| DRB1_1501 | 176 | IGTAQYLSPEQARGD | IGTAQYLSP | 0.3062 | 1820.4 | 50.00 | Sequence |
| DRB1_1501 | 86 | LPYIVMEYVDGVTLR | EYVDGVTLR | 0.3052 | 1840.9 | 50.00 | Sequence |
| DRB1_1501 | 170 | TQTAAVIGTAQYLSP | VIGTAQYLS | 0.3048 | 1848.4 | 50.00 | Sequence |
| DRB1_1501 | 318 | DTDRDRSIGSVGRWV | SIGSVGRWV | 0.3046 | 1851.3 | 50.00 | Sequence |
| DRB1_1501 | 264 | TAAEMRADLVRVHNG | EMRADLVRV | 0.3041 | 1861.8 | 50.00 | Sequence |
| DRB1_1501 | 17 | GFGGMSEVHLARDLR | GFGGMSEVH | 0.3034 | 1876.0 | 50.00 | Sequence |
| DRB1_1501 | 262 | YQTAAEMRADLVRVH | EMRADLVRV | 0.3019 | 1907.9 | 50.00 | Sequence |

```
DRB1_1501  133  IIHRDVKPANIMISA  IIHRDVKPA         0.3009       1927.4              50.00      Sequence
DRB1_1501  265  AAEMRADLVRVHNGE  EMRADLVRV         0.3003       1940.4              50.00      Sequence
DRB1_1501  103  VHTEGPMTPKRAIEV  TEGPMTPKR         0.2996       1954.8              50.00      Sequence
DRB1_1501  136  RDVKPANIMISATNA  ANIMISATN         0.2974       2001.1              50.00      Sequence
DRB1_1501  568  MFWVDAEPRLRALGW  MFWVDAEPR         0.2967       2017.2              50.00      Sequence
DRB1_1501  104  HTEGPMTPKRAIEVI  TEGPMTPKR         0.2960       2032.6              50.00      Sequence
DRB1_1501  126  NFSHQNGIIHRDVKP  NFSHQNGII         0.2955       2044.5              50.00      Sequence
DRB1_1501  263  QTAAEMRADLVRVHN  EMRADLVRV         0.2952       2050.7              50.00      Sequence
DRB1_1501  348  AINTFGGITRDVQVP  AINTFGGIT         0.2942       2072.1              50.00      Sequence
DRB1_1501  115  IEVIADACQALNFSH  ACQALNFSH         0.2933       2092.2              50.00      Sequence
DRB1_1501   60  QNAAALNHPAIVAVY  ALNHPAIVA         0.2930       2099.4              50.00      Sequence
DRB1_1501  476  TSAITNVVIIIVGSG  VVIIIVGSG         0.2913       2138.0              50.00      Sequence
DRB1_1501  566  SGMFWVDAEPRLRAL  MFWVDAEPR         0.2896       2178.6              50.00      Sequence
DRB1_1501  562  MPDLSGMFWVDAEPR  MFWVDAEPR         0.2893       2186.7              50.00      Sequence
DRB1_1501  544  VPVDSVIELQVSKGN  VIELQVSKG         0.2892       2186.9              50.00      Sequence
DRB1_1501    7  SDRYELGEILGFGGM  ELGEILGFG         0.2885       2204.5              50.00      Sequence
DRB1_1501  241  GLSADLDAVVLKALA  DAVVLKALA         0.2884       2207.2              50.00      Sequence
DRB1_1501  608  PAGTGVNRDGIITLR  VNRDGIITL         0.2881       2213.6              50.00      Sequence
DRB1_1501   52  YLRFRREAQNAAALN  YLRFRREAQ         0.2863       2257.8              50.00      Sequence
DRB1_1501   85  PLPYIVMEYVDGVTL  YIVMEYVDG         0.2851       2285.9              50.00      Sequence
DRB1_1501  190  DSVDARSDVYSLGCV  ARSDVYSLG         0.2848       2294.1              50.00      Sequence
DRB1_1501  286  VLTDAERTSLLSSAA  RTSLLSSAA         0.2841       2310.9              50.00      Sequence
DRB1_1501  261  RYQTAAEMRADLVRV  EMRADLVRV         0.2839       2317.7              50.00      Sequence
DRB1_1501   59  AQNAAALNHPAIVAV  AALNHPAIV         0.2823       2356.8              50.00      Sequence
DRB1_1501  561  VMPDLSGMFWVDAEP  VMPDLSGMF         0.2803       2409.1              50.00      Sequence
DRB1_1501  196  SDVYSLGCVLYEVLT  DVYSLGCVL         0.2793       2436.1              50.00      Sequence
DRB1_1501   84  GPLPYIVMEYVDGVT  YIVMEYVDG         0.2787       2450.8              50.00      Sequence
DRB1_1501   61  NAAALNHPAIVAVYD  ALNHPAIVA         0.2783       2461.3              50.00      Sequence
DRB1_1501   83  AGPLPYIVMEYVDGV  PLPYIVMEY         0.2776       2481.7              50.00      Sequence
DRB1_1501  153  VMDFGIARAIADSGN  VMDFGIARA         0.2772       2491.9              50.00      Sequence
DRB1_1501  268  MRADLVRVHNGEPPE  LVRVHNGEP         0.2763       2515.1              50.00      Sequence
DRB1_1501  189  GDSVDARSDVYSLGC  ARSDVYSLG         0.2757       2531.6              50.00      Sequence
DRB1_1501  169  VTQTAAVIGTAQYLS  AAVIGTAQY         0.2747       2560.0              50.00      Sequence
DRB1_1501  111  PKRAIEVIADACQAL  AIEVIADAC         0.2743       2569.5              50.00      Sequence
DRB1_1501  294  SLLSSAAGNLSGPRT  SLLSSAAGN         0.2742       2572.2              50.00      Sequence
DRB1_1501  380  GFKIRTLQKPDSTIP  FKIRTLQKP         0.2739       2583.0              50.00      Sequence
DRB1_1501   95  DGVTLRDIVHTEGPM  GVTLRDIVH         0.2733       2598.4              50.00      Sequence
DRB1_1501   18  FGGMSEVHLARDLRL  EVHLARDLR         0.2728       2612.8              50.00      Sequence
DRB1_1501  559  QFVMPDLSGMFWVDA  VMPDLSGMF         0.2726       2619.7              50.00      Sequence
DRB1_1501  112  KRAIEVIADACQALN  AIEVIADAC         0.2716       2647.7              50.00      Sequence
DRB1_1501  113  RAIEVIADACQALNF  RAIEVIADA         0.2709       2665.9              50.00      Sequence
DRB1_1501  432  STLTYAEAVKKLTAA  TLTYAEAVK         0.2699       2695.5              50.00      Sequence
DRB1_1501   42  RADLARDPSFYLRFR  RDPSFYLRF         0.2681       2749.2              50.00      Sequence
DRB1_1501  560  FVMPDLSGMFWVDAE  VMPDLSGMF         0.2674       2769.6              50.00      Sequence
DRB1_1501  177  GTAQYLSPEQARGDS  QYLSPEQAR         0.2671       2780.0              50.00      Sequence
DRB1_1501   62  AAALNHPAIVAVYDT  ALNHPAIVA         0.2668       2787.9              50.00      Sequence
DRB1_1501  204  VLYEVLTGEPPFTGD  EVLTGEPPF         0.2668       2788.2              50.00      Sequence
DRB1_1501   93  YVDGVTLRDIVHTEG  VTLRDIVHT         0.2647       2850.5              50.00      Sequence
DRB1_1501  594  AGGSQHNRVVYQNPP  GSQHNRVVY         0.2635       2887.8              50.00      Sequence
DRB1_1501  543  TVPVDSVIELQVSKG  SVIELQVSK         0.2628       2910.4              50.00      Sequence
DRB1_1501  515  GFTKFSQASVDSPRP  GFTKFSQAS         0.2617       2944.6              50.00      Sequence
DRB1_1501    6  LSDRYELGEILGFGG  ELGEILGFG         0.2617       2944.8              50.00      Sequence
DRB1_1501  269  RADLVRVHNGEPPEA  LVRVHNGEP         0.2604       2987.5              50.00      Sequence
DRB1_1501  601  RVVYQNPPAGTGVNR  RVVYQNPPA         0.2600       3000.7              50.00      Sequence
DRB1_1501  558  NQFVMPDLSGMFWVD  VMPDLSGMF         0.2592       3026.6              50.00      Sequence
DRB1_1501  108  PMTPKRAIEVIADAC  AIEVIADAC         0.2574       3087.2              50.00      Sequence
DRB1_1501   41  LRADLARDPSFYLRF  LARDPSFYL         0.2571       3097.0              50.00      Sequence
DRB1_1501  105  TEGPMTPKRAIEVIA  PMTPKRAIE         0.2565       3117.7              50.00      Sequence
DRB1_1501   82  PAGPLPYIVMEYVDG  PLPYIVMEY         0.2559       3137.0              50.00      Sequence
DRB1_1501   40  VLRADLARDPSFYLR  VLRADLARD         0.2553       3158.2              50.00      Sequence
DRB1_1501  426  REIPDVSTLTYAEAV  EIPDVSTLT         0.2525       3253.2              50.00      Sequence
DRB1_1501  463  VGKVIGTNPPANQTS  KVIGTNPPA         0.2525       3256.2              50.00      Sequence
DRB1_1501   58  EAQNAAALNHPAIVA  ALNHPAIVA         0.2523       3261.7              50.00      Sequence
DRB1_1501  425  QREIPDVSTLTYAEA  EIPDVSTLT         0.2517       3284.5              50.00      Sequence
DRB1_1501  569  FWVDAEPRLRALGWT  AEPRLRALG         0.2501       3339.8              50.00      Sequence
DRB1_1501  270  ADLVRVHNGEPPEAP  LVRVHNGEP         0.2496       3359.9              50.00      Sequence
```

```
DRB1_1501  591  DVDAGGSQHNRVVYQ  DVDAGGSQH        0.2493       3367.7              50.00     Sequence
DRB1_1501  381  FKIRTLQKPDSTIPP  KIRTLQKPD        0.2487       3390.8              50.00     Sequence
DRB1_1501  424  EQREIPDVSTLTYAE  EIPDVSTLT        0.2434       3591.2              50.00     Sequence
DRB1_1501   94  VDGVTLRDIVHTEGP  VTLRDIVHT        0.2431       3601.1              50.00     Sequence
DRB1_1501  110  TPKRAIEVIADACQA  AIEVIADAC        0.2419       3648.6              50.00     Sequence
DRB1_1501  427  EIPDVSTLTYAEAVK  EIPDVSTLT        0.2418       3654.4              50.00     Sequence
DRB1_1501    5  HLSDRYELGEILGFG  ELGEILGFG        0.2416       3662.8              50.00     Sequence
DRB1_1501  135  HRDVKPANIMISATN  ANIMISATN        0.2408       3692.0              50.00     Sequence
DRB1_1501  271  DLVRVHNGEPPEAPK  LVRVHNGEP        0.2398       3732.0              50.00     Sequence
DRB1_1501  349  INTFGGITRDVQVPD  INTFGGITR        0.2395       3747.2              50.00     Sequence
DRB1_1501  579  ALGWTGMLDKGADVD  ALGWTGMLD        0.2393       3755.2              50.00     Sequence
DRB1_1501  429  PDVSTLTYAEAVKKL  STLTYAEAV        0.2391       3763.2              50.00     Sequence
DRB1_1501  428  IPDVSTLTYAEAVKK  TLTYAEAVK        0.2354       3916.4              50.00     Sequence
DRB1_1501  423  PEQREIPDVSTLTYA  EIPDVSTLT        0.2327       4032.0              50.00     Sequence
DRB1_1501  500  AGQTVDVAQKNLNVY  VAQKNLNVY        0.2326       4034.6              50.00     Sequence
DRB1_1501  109  MTPKRAIEVIADACQ  AIEVIADAC        0.2320       4061.6              50.00     Sequence
DRB1_1501  178  TAQYLSPEQARGDSV  YLSPEQARG        0.2317       4075.6              50.00     Sequence
DRB1_1501  240  EGLSADLDAVVLKAL  DLDAVVLKA        0.2313       4093.3              50.00     Sequence
DRB1_1501  168  SVTQTAAVIGTAQYL  AAVIGTAQY        0.2297       4164.7              50.00     Sequence
DRB1_1501  607  PPAGTGVNRDGIITL  VNRDGIITL        0.2291       4192.8              50.00     Sequence
DRB1_1501  382  KIRTLQKPDSTIPPD  KIRTLQKPD        0.2289       4203.5              50.00     Sequence
DRB1_1501  297  SSAAGNLSGPRTDPL  AAGNLSGPR        0.2287       4212.0              50.00     Sequence
DRB1_1501  250  VLKALAKNPENRYQT  VLKALAKNP        0.2278       4252.9              50.00     Sequence
DRB1_1501  107  GPMTPKRAIEVIADA  RAIEVIADA        0.2270       4289.2              50.00     Sequence
DRB1_1501  593  DAGGSQHNRVVYQNP  GSQHNRVVY        0.2265       4309.9              50.00     Sequence
DRB1_1501  188  RGDSVDARSDVYSLG  SVDARSDVY        0.2261       4328.5              50.00     Sequence
DRB1_1501  205  LYEVLTGEPPFTGDS  EVLTGEPPF        0.2253       4369.0              50.00     Sequence
DRB1_1501  592  VDAGGSQHNRVVYQN  GSQHNRVVY        0.2248       4394.0              50.00     Sequence
DRB1_1501  430  DVSTLTYAEAVKKLT  TLTYAEAVK        0.2248       4394.0              50.00     Sequence
DRB1_1501  114  AIEVIADACQALNFS  DACQALNFS        0.2245       4404.3              50.00     Sequence
DRB1_1501  361  VPDVRGQSSADAIAT  DVRGQSSAD        0.2243       4416.5              50.00     Sequence
DRB1_1501  464  GKVIGTNPPANQTSA  KVIGTNPPA        0.2241       4425.4              50.00     Sequence
DRB1_1501  431  VSTLTYAEAVKKLTA  TLTYAEAVK        0.2236       4449.4              50.00     Sequence
DRB1_1501  260  NRYQTAAEMRADLVR  AAEMRADLV        0.2235       4453.4              50.00     Sequence
DRB1_1501  360  QVPDVRGQSSADAIA  DVRGQSSAD        0.2231       4473.4              50.00     Sequence
DRB1_1501  299  AAGNLSGPRTDPLPR  AAGNLSGPR        0.2225       4502.5              50.00     Sequence
DRB1_1501  448  FGRFKQANSPSTPEL  RFKQANSPS        0.2221       4524.4              50.00     Sequence
DRB1_1501  180  QYLSPEQARGDSVDA  YLSPEQARG        0.2219       4532.4              50.00     Sequence
DRB1_1501  298  SAAGNLSGPRTDPLP  AAGNLSGPR        0.2213       4559.8              50.00     Sequence
DRB1_1501  551  ELQVSKGNQFVMPDL  LQVSKGNQF        0.2207       4593.2              50.00     Sequence
DRB1_1501  590  ADVDAGGSQHNRVVY  DVDAGGSQH        0.2203       4612.5              50.00     Sequence
DRB1_1501   81  TPAGPLPYIVMEYVD  PLPYIVMEY        0.2202       4614.0              50.00     Sequence
DRB1_1501  557  GNQFVMPDLSGMFWV  VMPDLSGMF        0.2178       4734.8              50.00     Sequence
DRB1_1501  555  SKGNQFVMPDLSGMF  VMPDLSGMF        0.2162       4821.4              50.00     Sequence
DRB1_1501  550  IELQVSKGNQFVMPD  LQVSKGNQF        0.2160       4831.2              50.00     Sequence
DRB1_1501   80  ETPAGPLPYIVMEYV  PLPYIVMEY        0.2155       4855.6              50.00     Sequence
DRB1_1501  359  VQVPDVRGQSSADAI  DVRGQSSAD        0.2151       4875.7              50.00     Sequence
DRB1_1501  106  EGPMTPKRAIEVIAD  PMTPKRAIE        0.2149       4890.5              50.00     Sequence
DRB1_1501  259  ENRYQTAAEMRADLV  RYQTAAEMR        0.2138       4947.1              50.00     Sequence
DRB1_1501  258  PENRYQTAAEMRADL  RYQTAAEMR        0.2130       4987.8              50.00     Sequence
DRB1_1501  179  AQYLSPEQARGDSVD  YLSPEQARG        0.2130       4990.6              50.00     Sequence
DRB1_1501  422  GPEQREIPDVSTLTY  EIPDVSTLT        0.2117       5062.9              50.00     Sequence
DRB1_1501  412  GDEITVNVSTGPEQR  EITVNVSTG        0.2104       5133.3              50.00     Sequence
DRB1_1501  556  KGNQFVMPDLSGMFW  VMPDLSGMF        0.2102       5140.8              50.00     Sequence
DRB1_1501  167  NSVTQTAAVIGTAQY  AAVIGTAQY        0.2090       5208.9              50.00     Sequence
DRB1_1501  413  DEITVNVSTGPEQRE  EITVNVSTG        0.2087       5227.1              50.00     Sequence
DRB1_1501  362  PDVRGQSSADAIATL  DVRGQSSAD        0.2080       5264.9              50.00     Sequence
DRB1_1501  414  EITVNVSTGPEQREI  ITVNVSTGP        0.2080       5267.5              50.00     Sequence
DRB1_1501  285  KVLTDAERTSLLSSA  ERTSLLSSA        0.2071       5318.0              50.00     Sequence
DRB1_1501  392  TIPPDHVIGTDPAAN  TIPPDHVIG        0.2057       5401.4              50.00     Sequence
DRB1_1501  552  LQVSKGNQFVMPDLS  VSKGNQFVM        0.2052       5427.0              50.00     Sequence
DRB1_1501  272  LVRVHNGEPPEAPKV  LVRVHNGEP        0.2044       5477.1              50.00     Sequence
DRB1_1501  542  TTVPVDSVIELQVSK  SVIELQVSK        0.2021       5611.9              50.00     Sequence
DRB1_1501  395  PDHVIGTDPAANTSV  VIGTDPAAN        0.2016       5647.4              50.00     Sequence
DRB1_1501  239  HEGLSADLDAVVLKA  DLDAVVLKA        0.2010       5683.6              50.00     Sequence
DRB1_1501  155  DFGIARAIADSGNSV  DFGIARAIA        0.1998       5752.9              50.00     Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_1501 | 134 | IHRDVKPANIMISAT | DVKPANIMI | 0.1990 | 5808.1 | 50.00 | Sequence |
| DRB1_1501 | 580 | LGWTGMLDKGADVDA | LGWTGMLDK | 0.1987 | 5825.3 | 50.00 | Sequence |
| DRB1_1501 | 449 | GRFKQANSPSTPELV | RFKQANSPS | 0.1984 | 5846.8 | 50.00 | Sequence |
| DRB1_1501 | 396 | DHVIGTDPAANTSVS | VIGTDPAAN | 0.1979 | 5877.5 | 50.00 | Sequence |
| DRB1_1501 | 358 | DVQVPDVRGQSSADA | DVRGQSSAD | 0.1977 | 5887.6 | 50.00 | Sequence |
| DRB1_1501 | 257 | NPENRYQTAAEMRAD | RYQTAAEMR | 0.1976 | 5892.0 | 50.00 | Sequence |
| DRB1_1501 | 350 | NTFGGITRDVQVPDV | TFGGITRDV | 0.1975 | 5900.0 | 50.00 | Sequence |
| DRB1_1501 | 351 | TFGGITRDVQVPDVR | TFGGITRDV | 0.1965 | 5966.2 | 50.00 | Sequence |
| DRB1_1501 | 187 | ARGDSVDARSDVYSL | SVDARSDVY | 0.1945 | 6096.5 | 50.00 | Sequence |
| DRB1_1501 | 475 | QTSAITNVVIIIVGS | NVVIIIVGS | 0.1940 | 6130.0 | 50.00 | Sequence |
| DRB1_1501 | 394 | PPDHVIGTDPAANTS | VIGTDPAAN | 0.1930 | 6194.1 | 50.00 | Sequence |
| DRB1_1501 | 256 | KNPENRYQTAAEMRA | RYQTAAEMR | 0.1929 | 6205.1 | 50.00 | Sequence |
| DRB1_1501 | 157 | GIARAIADSGNSVTQ | AIADSGNSV | 0.1928 | 6207.9 | 50.00 | Sequence |
| DRB1_1501 | 220 | PVSVAYQHVREDPIP | VSVAYQHVR | 0.1925 | 6229.4 | 50.00 | Sequence |
| DRB1_1501 | 411 | AGDEITVNVSTGPEQ | EITVNVSTG | 0.1924 | 6237.8 | 50.00 | Sequence |
| DRB1_1501 | 472 | PANQTSAITNVVIII | QTSAITNVV | 0.1923 | 6242.9 | 50.00 | Sequence |
| DRB1_1501 | 219 | SPVSVAYQHVREDPI | VSVAYQHVR | 0.1917 | 6281.7 | 50.00 | Sequence |
| DRB1_1501 | 553 | QVSKGNQFVMPDLSG | QVSKGNQFV | 0.1914 | 6306.7 | 50.00 | Sequence |
| DRB1_1501 | 455 | NSPSTPELVGKVIGT | ELVGKVIGT | 0.1910 | 6333.0 | 50.00 | Sequence |
| DRB1_1501 | 221 | VSVAYQHVREDPIPP | VSVAYQHVR | 0.1906 | 6356.6 | 50.00 | Sequence |
| DRB1_1501 | 317 | DDTDRDRSIGSVGRW | RDRSIGSVG | 0.1906 | 6358.7 | 50.00 | Sequence |
| DRB1_1501 | 156 | FGIARAIADSGNSVT | IARAIADSG | 0.1903 | 6378.9 | 50.00 | Sequence |
| DRB1_1501 | 295 | LLSSAAGNLSGPRTD | AAGNLSGPR | 0.1899 | 6404.9 | 50.00 | Sequence |
| DRB1_1501 | 471 | PPANQTSAITNVVII | QTSAITNVV | 0.1896 | 6426.0 | 50.00 | Sequence |
| DRB1_1501 | 465 | KVIGTNPPANQTSAI | KVIGTNPPA | 0.1890 | 6471.9 | 50.00 | Sequence |
| DRB1_1501 | 473 | ANQTSAITNVVIIIV | AITNVVIII | 0.1883 | 6520.7 | 50.00 | Sequence |
| DRB1_1501 | 79 | AETPAGPLPYIVMEY | PLPYIVMEY | 0.1876 | 6564.9 | 50.00 | Sequence |
| DRB1_1501 | 1 | TTPSHLSDRYELGEI | HLSDRYELG | 0.1876 | 6570.8 | 50.00 | Sequence |
| DRB1_1501 | 581 | GWTGMLDKGADVDAG | GMLDKGADV | 0.1874 | 6580.5 | 50.00 | Sequence |
| DRB1_1501 | 165 | SGNSVTQTAAVIGTA | VTQTAAVIG | 0.1854 | 6725.4 | 50.00 | Sequence |
| DRB1_1501 | 255 | AKNPENRYQTAAEMR | ENRYQTAAE | 0.1846 | 6786.0 | 50.00 | Sequence |
| DRB1_1501 | 393 | IPPDHVIGTDPAANT | VIGTDPAAN | 0.1845 | 6790.4 | 50.00 | Sequence |
| DRB1_1501 | 53 | LRFRREAQNAAALNH | RFRREAQNA | 0.1840 | 6826.6 | 50.00 | Sequence |
| DRB1_1501 | 397 | HVIGTDPAANTSVSA | VIGTDPAAN | 0.1833 | 6879.8 | 50.00 | Sequence |
| DRB1_1501 | 57 | REAQNAAALNHPAIV | NAAALNHPA | 0.1830 | 6906.2 | 50.00 | Sequence |
| DRB1_1501 | 158 | IARAIADSGNSVTQT | AIADSGNSV | 0.1829 | 6907.6 | 50.00 | Sequence |
| DRB1_1501 | 164 | DSGNSVTQTAAVIGT | NSVTQTAAV | 0.1828 | 6916.6 | 50.00 | Sequence |
| DRB1_1501 | 554 | VSKGNQFVMPDLSGM | FVMPDLSGM | 0.1817 | 7002.1 | 50.00 | Sequence |
| DRB1_1501 | 238 | RHEGLSADLDAVVLK | GLSADLDAV | 0.1811 | 7043.1 | 50.00 | Sequence |
| DRB1_1501 | 582 | WTGMLDKGADVDAGG | GMLDKGADV | 0.1809 | 7062.0 | 50.00 | Sequence |
| DRB1_1501 | 296 | LSSAAGNLSGPRTDP | AAGNLSGPR | 0.1799 | 7137.6 | 50.00 | Sequence |
| DRB1_1501 | 154 | MDFGIARAIADSGNS | DFGIARAIA | 0.1795 | 7173.5 | 50.00 | Sequence |
| DRB1_1501 | 206 | YEVLTGEPPFTGDSP | EVLTGEPPF | 0.1789 | 7217.7 | 50.00 | Sequence |
| DRB1_1501 | 4 | SHLSDRYELGEILGF | HLSDRYELG | 0.1780 | 7288.8 | 50.00 | Sequence |
| DRB1_1501 | 410 | SAGDEITVNVSTGPE | EITVNVSTG | 0.1778 | 7303.7 | 50.00 | Sequence |
| DRB1_1501 | 166 | GNSVTQTAAVIGTAQ | VTQTAAVIG | 0.1773 | 7341.8 | 50.00 | Sequence |
| DRB1_1501 | 0 | MTTPSHLSDRYELGE | HLSDRYELG | 0.1770 | 7369.0 | 50.00 | Sequence |
| DRB1_1501 | 316 | LDDTDRDRSIGSVGR | RDRSIGSVG | 0.1767 | 7394.1 | 50.00 | Sequence |
| DRB1_1501 | 163 | ADSGNSVTQTAAVIG | NSVTQTAAV | 0.1762 | 7426.4 | 50.00 | Sequence |
| DRB1_1501 | 218 | DSPVSVAYQHVREDP | VSVAYQHVR | 0.1762 | 7432.5 | 50.00 | Sequence |
| DRB1_1501 | 254 | LAKNPENRYQTAAEM | LAKNPENRY | 0.1746 | 7561.8 | 50.00 | Sequence |
| DRB1_1501 | 357 | RDVQVPDVRGQSSAD | DVRGQSSAD | 0.1727 | 7714.9 | 50.00 | Sequence |
| DRB1_1501 | 365 | RGQSSADAIATLQNR | DAIATLQNR | 0.1723 | 7746.8 | 50.00 | Sequence |
| DRB1_1501 | 353 | GGITRDVQVPDVRGQ | GITRDVQVP | 0.1718 | 7793.4 | 50.00 | Sequence |
| DRB1_1501 | 486 | IVGSGPATKDIPDVA | IVGSGPATK | 0.1712 | 7844.7 | 50.00 | Sequence |
| DRB1_1501 | 207 | EVLTGEPPFTGDSPV | EVLTGEPPF | 0.1702 | 7932.5 | 50.00 | Sequence |
| DRB1_1501 | 363 | DVRGQSSADAIATLQ | DVRGQSSAD | 0.1697 | 7969.2 | 50.00 | Sequence |
| DRB1_1501 | 300 | AGNLSGPRTDPLPRQ | NLSGPRTDP | 0.1697 | 7971.0 | 50.00 | Sequence |
| DRB1_1501 | 584 | GMLDKGADVDAGGSQ | GMLDKGADV | 0.1689 | 8044.8 | 50.00 | Sequence |
| DRB1_1501 | 474 | NQTSAITNVVIIIVG | AITNVVIII | 0.1681 | 8107.5 | 50.00 | Sequence |
| DRB1_1501 | 589 | GADVDAGGSQHNRVV | DVDAGGSQH | 0.1677 | 8142.7 | 50.00 | Sequence |
| DRB1_1501 | 237 | ARHEGLSADLDAVVL | RHEGLSADL | 0.1677 | 8148.1 | 50.00 | Sequence |
| DRB1_1501 | 315 | DLDDTDRDRSIGSVG | RDRSIGSVG | 0.1668 | 8221.7 | 50.00 | Sequence |
| DRB1_1501 | 159 | ARAIADSGNSVTQTA | AIADSGNSV | 0.1668 | 8225.4 | 50.00 | Sequence |
| DRB1_1501 | 2 | TPSHLSDRYELGEIL | HLSDRYELG | 0.1668 | 8227.3 | 50.00 | Sequence |
| DRB1_1501 | 409 | VSAGDEITVNVSTGP | EITVNVSTG | 0.1649 | 8395.7 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB1_1501 | 391 | STIPPDHVIGTDPAA | TIPPDHVIG | 0.1648 | 8403.9 | 50.00 | Sequence |
| DRB1_1501 | 583 | TGMLDKGADVDAGGS | GMLDKGADV | 0.1643 | 8447.7 | 50.00 | Sequence |
| DRB1_1501 | 160 | RAIADSGNSVTQTAA | AIADSGNSV | 0.1641 | 8466.8 | 50.00 | Sequence |
| DRB1_1501 | 383 | IRTLQKPDSTIPPDH | TLQKPDSTI | 0.1638 | 8498.6 | 50.00 | Sequence |
| DRB1_1501 | 284 | PKVLTDAERTSLLSS | AERTSLLSS | 0.1626 | 8612.1 | 50.00 | Sequence |
| DRB1_1501 | 398 | VIGTDPAANTSVSAG | VIGTDPAAN | 0.1625 | 8618.0 | 50.00 | Sequence |
| DRB1_1501 | 421 | TGPEQREIPDVSTLT | EIPDVSTLT | 0.1618 | 8683.2 | 50.00 | Sequence |
| DRB1_1501 | 3 | PSHLSDRYELGEILG | HLSDRYELG | 0.1615 | 8708.9 | 50.00 | Sequence |
| DRB1_1501 | 236 | SARHEGLSADLDAVV | SARHEGLSA | 0.1599 | 8867.7 | 50.00 | Sequence |
| DRB1_1501 | 181 | YLSPEQARGDSVDAR | YLSPEQARG | 0.1594 | 8916.3 | 50.00 | Sequence |
| DRB1_1501 | 384 | RTLQKPDSTIPPDHV | TLQKPDSTI | 0.1593 | 8917.5 | 50.00 | Sequence |
| DRB1_1501 | 56 | RREAQNAAALNHPAI | NAAALNHPA | 0.1586 | 8991.9 | 50.00 | Sequence |
| DRB1_1501 | 217 | GDSPVSVAYQHVRED | VSVAYQHVR | 0.1575 | 9100.7 | 50.00 | Sequence |
| DRB1_1501 | 352 | FGGITRDVQVPDVRG | GITRDVQVP | 0.1574 | 9105.8 | 50.00 | Sequence |
| DRB1_1501 | 161 | AIADSGNSVTQTAAV | AIADSGNSV | 0.1525 | 9600.3 | 50.00 | Sequence |
| DRB1_1501 | 253 | ALAKNPENRYQTAAE | LAKNPENRY | 0.1508 | 9777.0 | 50.00 | Sequence |
| DRB1_1501 | 222 | SVAYQHVREDPIPPS | HVREDPIPP | 0.1504 | 9818.0 | 50.00 | Sequence |
| DRB1_1501 | 54 | RFRREAQNAAALNHP | RFRREAQNA | 0.1503 | 9837.2 | 50.00 | Sequence |
| DRB1_1501 | 235 | PSARHEGLSADLDAV | SARHEGLSA | 0.1494 | 9932.6 | 50.00 | Sequence |
| DRB1_1501 | 408 | SVSAGDEITVNVSTG | EITVNVSTG | 0.1474 | 10149.9 | 50.00 | Sequence |
| DRB1_1501 | 354 | GITRDVQVPDVRGQS | GITRDVQVP | 0.1466 | 10238.7 | 50.00 | Sequence |
| DRB1_1501 | 216 | TGDSPVSVAYQHVRE | VSVAYQHVR | 0.1462 | 10276.4 | 50.00 | Sequence |
| DRB1_1501 | 496 | IPDVAGQTVDVAQKN | DVAGQTVDV | 0.1461 | 10290.6 | 50.00 | Sequence |
| DRB1_1501 | 211 | GEPPFTGDSPVSVAY | PFTGDSPVS | 0.1460 | 10302.2 | 50.00 | Sequence |
| DRB1_1501 | 498 | DVAGQTVDVAQKNLN | DVAGQTVDV | 0.1456 | 10350.3 | 50.00 | Sequence |
| DRB1_1501 | 529 | PAGEVTGTNPPAGTT | EVTGTNPPA | 0.1454 | 10367.1 | 50.00 | Sequence |
| DRB1_1501 | 470 | NPPANQTSAITNVVI | QTSAITNVV | 0.1453 | 10385.8 | 50.00 | Sequence |
| DRB1_1501 | 588 | KGADVDAGGSQHNRV | DVDAGGSQH | 0.1451 | 10404.7 | 50.00 | Sequence |
| DRB1_1501 | 252 | KALAKNPENRYQTAA | LAKNPENRY | 0.1450 | 10416.2 | 50.00 | Sequence |
| DRB1_1501 | 528 | RPAGEVTGTNPPAGT | EVTGTNPPA | 0.1449 | 10421.3 | 50.00 | Sequence |
| DRB1_1501 | 186 | QARGDSVDARSDVYS | SVDARSDVY | 0.1444 | 10486.4 | 50.00 | Sequence |
| DRB1_1501 | 162 | IADSGNSVTQTAAVI | SVTQTAAVI | 0.1436 | 10577.9 | 50.00 | Sequence |
| DRB1_1501 | 499 | VAGQTVDVAQKNLNV | VDVAQKNLN | 0.1425 | 10700.4 | 50.00 | Sequence |
| DRB1_1501 | 301 | GNLSGPRTDPLPRQD | LSGPRTDPL | 0.1409 | 10885.8 | 50.00 | Sequence |
| DRB1_1501 | 495 | DIPDVAGQTVDVAQK | DVAGQTVDV | 0.1406 | 10922.4 | 50.00 | Sequence |
| DRB1_1501 | 530 | AGEVTGTNPPAGTTV | EVTGTNPPA | 0.1398 | 11022.2 | 50.00 | Sequence |
| DRB1_1501 | 415 | ITVNVSTGPEQREIP | ITVNVSTGP | 0.1390 | 11110.7 | 50.00 | Sequence |
| DRB1_1501 | 234 | PPSARHEGLSADLDA | SARHEGLSA | 0.1386 | 11165.0 | 50.00 | Sequence |
| DRB1_1501 | 531 | GEVTGTNPPAGTTVP | EVTGTNPPA | 0.1375 | 11292.7 | 50.00 | Sequence |
| DRB1_1501 | 210 | TGEPPFTGDSPVSVA | PFTGDSPVS | 0.1364 | 11424.4 | 50.00 | Sequence |
| DRB1_1501 | 212 | EPPFTGDSPVSVAYQ | PFTGDSPVS | 0.1364 | 11424.9 | 50.00 | Sequence |
| DRB1_1501 | 314 | QDLDDTDRDRSIGSV | DTDRDRSIG | 0.1362 | 11452.7 | 50.00 | Sequence |
| DRB1_1501 | 223 | VAYQHVREDPIPPSA | AYQHVREDP | 0.1361 | 11461.4 | 50.00 | Sequence |
| DRB1_1501 | 390 | DSTIPPDHVIGTDPA | TIPPDHVIG | 0.1340 | 11731.3 | 50.00 | Sequence |
| DRB1_1501 | 215 | FTGDSPVSVAYQHVR | VSVAYQHVR | 0.1337 | 11772.0 | 50.00 | Sequence |
| DRB1_1501 | 450 | RFKQANSPSTPELVG | RFKQANSPS | 0.1335 | 11798.8 | 50.00 | Sequence |
| DRB1_1501 | 527 | PRPAGEVTGTNPPAG | EVTGTNPPA | 0.1333 | 11820.2 | 50.00 | Sequence |
| DRB1_1501 | 403 | PAANTSVSAGDEITV | AANTSVSAG | 0.1332 | 11837.4 | 50.00 | Sequence |
| DRB1_1501 | 494 | KDIPDVAGQTVDVAQ | VAGQTVDVA | 0.1331 | 11846.1 | 50.00 | Sequence |
| DRB1_1501 | 233 | IPPSARHEGLSADLD | SARHEGLSA | 0.1327 | 11901.3 | 50.00 | Sequence |
| DRB1_1501 | 587 | DKGADVDAGGSQHNR | DVDAGGSQH | 0.1323 | 11947.6 | 50.00 | Sequence |
| DRB1_1501 | 213 | PPFTGDSPVSVAYQH | PFTGDSPVS | 0.1323 | 11951.9 | 50.00 | Sequence |
| DRB1_1501 | 497 | PDVAGQTVDVAQKNL | DVAGQTVDV | 0.1322 | 11966.8 | 50.00 | Sequence |
| DRB1_1501 | 232 | PIPPSARHEGLSADL | SARHEGLSA | 0.1307 | 12159.0 | 50.00 | Sequence |
| DRB1_1501 | 541 | GTTVPVDSVIELQVS | TTVPVDSVI | 0.1306 | 12164.7 | 50.00 | Sequence |
| DRB1_1501 | 606 | NPPAGTGVNRDGIIT | GVNRDGIIT | 0.1305 | 12182.2 | 50.00 | Sequence |
| DRB1_1501 | 185 | EQARGDSVDARSDVY | SVDARSDVY | 0.1302 | 12218.6 | 50.00 | Sequence |
| DRB1_1501 | 209 | LTGEPPFTGDSPVSV | PFTGDSPVS | 0.1299 | 12257.7 | 50.00 | Sequence |
| DRB1_1501 | 355 | ITRDVQVPDVRGQSS | ITRDVQVPD | 0.1288 | 12405.3 | 50.00 | Sequence |
| DRB1_1501 | 540 | AGTTVPVDSVIELQV | TTVPVDSVI | 0.1280 | 12517.6 | 50.00 | Sequence |
| DRB1_1501 | 70 | IVAVYDTGEAETPAG | VAVYDTGEA | 0.1280 | 12523.6 | 50.00 | Sequence |
| DRB1_1501 | 356 | TRDVQVPDVRGQSSA | QVPDVRGQS | 0.1272 | 12622.3 | 50.00 | Sequence |
| DRB1_1501 | 385 | TLQKPDSTIPPDHVI | TLQKPDSTI | 0.1268 | 12687.5 | 50.00 | Sequence |
| DRB1_1501 | 224 | AYQHVREDPIPPSAR | HVREDPIPP | 0.1256 | 12851.2 | 50.00 | Sequence |
| DRB1_1501 | 466 | VIGTNPPANQTSAIT | VIGTNPPAN | 0.1245 | 13006.1 | 50.00 | Sequence |
| DRB1_1501 | 251 | LKALAKNPENRYQTA | LAKNPENRY | 0.1240 | 13066.7 | 50.00 | Sequence |

```
DRB1_1501  493  TKDIPDVAGQTVDVA  DVAGQTVDV         0.1232      13179.2              50.00      Sequence
DRB1_1501  602  VVYQNPPAGTGVNRD  VVYQNPPAG         0.1231      13193.7              50.00      Sequence
DRB1_1501   55  FRREAQNAAALNHPA  EAQNAAALN         0.1231      13202.3              50.00      Sequence
DRB1_1501  302  NLSGPRTDPLPRQDL  NLSGPRTDP         0.1225      13279.1              50.00      Sequence
DRB1_1501  404  AANTSVSAGDEITVN  AANTSVSAG         0.1222      13322.2              50.00      Sequence
DRB1_1501  586  LDKGADVDAGGSQHN  DVDAGGSQH         0.1217      13405.2              50.00      Sequence
DRB1_1501  516  FTKFSQASVDSPRPA  FTKFSQASV         0.1206      13556.8              50.00      Sequence
DRB1_1501  539  PAGTTVPVDSVIELQ  TTVPVDSVI         0.1206      13564.9              50.00      Sequence
DRB1_1501  389  PDSTIPPDHVIGTDP  TIPPDHVIG         0.1194      13738.6              50.00      Sequence
DRB1_1501  386  LQKPDSTIPPDHVIG  TIPPDHVIG         0.1185      13871.9              50.00      Sequence
DRB1_1501  231  DPIPPSARHEGLSAD  SARHEGLSA         0.1179      13969.2              50.00      Sequence
DRB1_1501  387  QKPDSTIPPDHVIGT  TIPPDHVIG         0.1172      14064.2              50.00      Sequence
DRB1_1501  282  EAPKVLTDAERTSLL  KVLTDAERT         0.1172      14067.2              50.00      Sequence
DRB1_1501  283  APKVLTDAERTSLLS  KVLTDAERT         0.1169      14121.1              50.00      Sequence
DRB1_1501  401  TDPAANTSVSAGDEI  AANTSVSAG         0.1165      14171.9              50.00      Sequence
DRB1_1501  225  YQHVREDPIPPSARH  HVREDPIPP         0.1164      14195.4              50.00      Sequence
DRB1_1501  388  KPDSTIPPDHVIGTD  TIPPDHVIG         0.1162      14219.5              50.00      Sequence
DRB1_1501  214  PFTGDSPVSVAYQHV  PFTGDSPVS         0.1151      14393.5              50.00      Sequence
DRB1_1501  538  PPAGTTVPVDSVIEL  TVPVDSVIE         0.1142      14532.4              50.00      Sequence
DRB1_1501  402  DPAANTSVSAGDEIT  AANTSVSAG         0.1140      14569.9              50.00      Sequence
DRB1_1501  281  PEAPKVLTDAERTSL  KVLTDAERT         0.1106      15111.1              50.00      Sequence
DRB1_1501  182  LSPEQARGDSVDARS  ARGDSVDAR         0.1098      15239.9              50.00      Sequence
DRB1_1501  364  VRGQSSADAIATLQN  VRGQSSADA         0.1086      15439.7              50.00      Sequence
DRB1_1501   78  EAETPAGPLPYIVME  AGPLPYIVM         0.1078      15572.4              50.00      Sequence
DRB1_1501  585  MLDKGADVDAGGSQH  DVDAGGSQH         0.1078      15576.8              50.00      Sequence
DRB1_1501  532  EVTGTNPPAGTTVPV  EVTGTNPPA         0.1067      15753.4              50.00      Sequence
DRB1_1501  400  GTDPAANTSVSAGDE  AANTSVSAG         0.1054      15991.1              50.00      Sequence
DRB1_1501  469  TNPPANQTSAITNVV  QTSAITNVV         0.1037      16287.7              50.00      Sequence
DRB1_1501  526  SPRPAGEVTGTNPPA  EVTGTNPPA         0.1031      16383.7              50.00      Sequence
DRB1_1501  492  ATKDIPDVAGQTVDV  DVAGQTVDV         0.1030      16400.7              50.00      Sequence
DRB1_1501  230  EDPIPPSARHEGLSA  SARHEGLSA         0.1028      16436.1              50.00      Sequence
DRB1_1501  280  PPEAPKVLTDAERTS  KVLTDAERT         0.1026      16470.8              50.00      Sequence
DRB1_1501  399  IGTDPAANTSVSAGD  AANTSVSAG         0.1013      16705.9              50.00      Sequence
DRB1_1501  208  VLTGEPPFTGDSPVS  PFTGDSPVS         0.1005      16852.8              50.00      Sequence
DRB1_1501  490  GPATKDIPDVAGQTV  DIPDVAGQT         0.1002      16911.8              50.00      Sequence
DRB1_1501  491  PATKDIPDVAGQTVD  DIPDVAGQT         0.0996      17014.4              50.00      Sequence
DRB1_1501  454  ANSPSTPELVGKVIG  STPELVGKV         0.0990      17121.7              50.00      Sequence
DRB1_1501  273  VRVHNGEPPEAPKVL  VRVHNGEPP         0.0986      17211.2              50.00      Sequence
DRB1_1501  313  RQDLDDTDRDRSIGS  DTDRDRSIG         0.0969      17523.9              50.00      Sequence
DRB1_1501   71  VAVYDTGEAETPAGP  VAVYDTGEA         0.0959      17711.1              50.00      Sequence
DRB1_1501   77  GEAETPAGPLPYIVM  AGPLPYIVM         0.0952      17846.1              50.00      Sequence
DRB1_1501  537  NPPAGTTVPVDSVIE  TVPVDSVIE         0.0920      18468.6              50.00      Sequence
DRB1_1501  226  QHVREDPIPPSARHE  HVREDPIPP         0.0915      18577.9              50.00      Sequence
DRB1_1501  303  LSGPRTDPLPRQDLD  LSGPRTDPL         0.0897      18941.4              50.00      Sequence
DRB1_1501  468  GTNPPANQTSAITNV  PPANQTSAI         0.0882      19259.6              50.00      Sequence
DRB1_1501  183  SPEQARGDSVDARSD  ARGDSVDAR         0.0841      20137.4              50.00      Sequence
DRB1_1501  405  ANTSVSAGDEITVNV  SVSAGDEIT         0.0836      20235.0              50.00      Sequence
DRB1_1501  184  PEQARGDSVDARSDV  ARGDSVDAR         0.0825      20482.6              50.00      Sequence
DRB1_1501  312  PRQDLDDTDRDRSIG  DTDRDRSIG         0.0818      20632.9              50.00      Sequence
DRB1_1501  279  EPPEAPKVLTDAERT  KVLTDAERT         0.0801      21009.6              50.00      Sequence
DRB1_1501  407  TSVSAGDEITVNVST  VSAGDEITV         0.0801      21028.7              50.00      Sequence
DRB1_1501  227  HVREDPIPPSARHEG  HVREDPIPP         0.0798      21080.0              50.00      Sequence
DRB1_1501  420  STGPEQREIPDVSTL  REIPDVSTL         0.0798      21095.7              50.00      Sequence
DRB1_1501  525  DSPRPAGEVTGTNPP  PAGEVTGTN         0.0788      21305.8              50.00      Sequence
DRB1_1501  517  TKFSQASVDSPRPAG  TKFSQASVD         0.0781      21481.1              50.00      Sequence
DRB1_1501  418  NVSTGPEQREIPDVS  NVSTGPEQR         0.0773      21672.0              50.00      Sequence
DRB1_1501  274  RVHNGEPPEAPKVLT  RVHNGEPPE         0.0773      21672.0              50.00      Sequence
DRB1_1501  416  TVNVSTGPEQREIPD  NVSTGPEQR         0.0772      21690.1              50.00      Sequence
DRB1_1501  536  TNPPAGTTVPVDSVI  TTVPVDSVI         0.0768      21773.1              50.00      Sequence
DRB1_1501  605  QNPPAGTGVNRDGII  TGVNRDGII         0.0763      21899.0              50.00      Sequence
DRB1_1501  417  VNVSTGPEQREIPDV  NVSTGPEQR         0.0762      21922.2              50.00      Sequence
DRB1_1501  521  QASVDSPRPAGEVTG  SVDSPRPAG         0.0756      22073.9              50.00      Sequence
DRB1_1501  406  NTSVSAGDEITVNVS  VSAGDEITV         0.0749      22241.7              50.00      Sequence
DRB1_1501  277  NGEPPEAPKVLTDAE  NGEPPEAPK         0.0744      22353.9              50.00      Sequence
DRB1_1501  453  QANSPSTPELVGKVI  STPELVGKV         0.0738      22501.2              50.00      Sequence
DRB1_1501  533  VTGTNPPAGTTVPVD  VTGTNPPAG         0.0719      22963.3              50.00      Sequence
```

```
   DRB1_1501  467  IGTNPPANQTSAITN  PPANQTSAI        0.0716      23030.2                50.00     Sequence
   DRB1_1501  518  KFSQASVDSPRPAGE  SVDSPRPAG        0.0707      23279.3                50.00     Sequence
   DRB1_1501  519  FSQASVDSPRPAGEV  SVDSPRPAG        0.0692      23639.7                50.00     Sequence
   DRB1_1501  487  VGSGPATKDIPDVAG  ATKDIPDVA        0.0685      23826.4                50.00     Sequence
   DRB1_1501  309  DPLPRQDLDDTDRDR  PRQDLDDTD        0.0681      23938.2                50.00     Sequence
   DRB1_1501  520  SQASVDSPRPAGEVT  SVDSPRPAG        0.0677      24041.0                50.00     Sequence
   DRB1_1501  522  ASVDSPRPAGEVTGT  SVDSPRPAG        0.0669      24250.3                50.00     Sequence
   DRB1_1501  310  PLPRQDLDDTDRDRS  DLDDTDRDR        0.0668      24275.8                50.00     Sequence
   DRB1_1501  489  SGPATKDIPDVAGQT  ATKDIPDVA        0.0660      24486.3                50.00     Sequence
   DRB1_1501  278  GEPPEAPKVLTDAER  EAPKVLTDA        0.0659      24520.5                50.00     Sequence
   DRB1_1501  311  LPRQDLDDTDRDRSI  DLDDTDRDR        0.0648      24796.6                50.00     Sequence
   DRB1_1501  308  TDPLPRQDLDDTDRD  PRQDLDDTD        0.0647      24827.5                50.00     Sequence
   DRB1_1501  523  SVDSPRPAGEVTGTN  SVDSPRPAG        0.0625      25414.3                50.00     Sequence
   DRB1_1501  488  GSGPATKDIPDVAGQ  ATKDIPDVA        0.0614      25729.7                50.00     Sequence
   DRB1_1501  276  HNGEPPEAPKVLTDA  NGEPPEAPK        0.0606      25942.1                50.00     Sequence
   DRB1_1501  524  VDSPRPAGEVTGTNP  PAGEVTGTN        0.0567      27059.1                50.00     Sequence
   DRB1_1501   76  TGEAETPAGPLPYIV  PAGPLPYIV        0.0566      27092.5                50.00     Sequence
   DRB1_1501  419  VSTGPEQREIPDVST  STGPEQREI        0.0546      27681.2                50.00     Sequence
   DRB1_1501  307  RTDPLPRQDLDDTDR  DPLPRQDLD        0.0541      27853.1                50.00     Sequence
   DRB1_1501  535  GTNPPAGTTVPVDSV  TNPPAGTTV        0.0535      28031.7                50.00     Sequence
   DRB1_1501  604  YQNPPAGTGVNRDGI  PAGTGVNRD        0.0535      28038.4                50.00     Sequence
   DRB1_1501  229  REDPIPPSARHEGLS  DPIPPSARH        0.0533      28085.2                50.00     Sequence
   DRB1_1501  306  PRTDPLPRQDLDDTD  DPLPRQDLD        0.0532      28118.9                50.00     Sequence
   DRB1_1501  452  KQANSPSTPELVGKV  STPELVGKV        0.0516      28602.5                50.00     Sequence
   DRB1_1501  534  TGTNPPAGTTVPVDS  NPPAGTTVP        0.0507      28874.6                50.00     Sequence
   DRB1_1501  228  VREDPIPPSARHEGL  DPIPPSARH        0.0507      28876.8                50.00     Sequence
   DRB1_1501  603  VYQNPPAGTGVNRDG  PAGTGVNRD        0.0502      29036.3                50.00     Sequence
   DRB1_1501  275  VHNGEPPEAPKVLTD  GEPPEAPKV        0.0490      29439.3                50.00     Sequence
   DRB1_1501  305  GPRTDPLPRQDLDDT  DPLPRQDLD        0.0487      29522.9                50.00     Sequence
   DRB1_1501   72  AVYDTGEAETPAGPL  AVYDTGEAE        0.0482      29693.0                50.00     Sequence
   DRB1_1501  451  FKQANSPSTPELVGK  FKQANSPST        0.0472      30009.5                50.00     Sequence
   DRB1_1501  304  SGPRTDPLPRQDLDD  GPRTDPLPR        0.0461      30362.2                50.00     Sequence
   DRB1_1501   74  YDTGEAETPAGPLPY  DTGEAETPA        0.0439      31110.1                50.00     Sequence
   DRB1_1501   75  DTGEAETPAGPLPYI  DTGEAETPA        0.0420      31749.4                50.00     Sequence
   DRB1_1501   73  VYDTGEAETPAGPLP  VYDTGEAET        0.0407      32196.3                50.00     Sequence
-----------------------------------------------------------------------------------------------

Allele: DRB1_1501. Number of high binders 6. Number of weak binders 94. Number of peptides 612

-----------------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------------
      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
-----------------------------------------------------------------------------------------------
   DRB3_0101  209  LTGEPPFTGDSPVSV  FTGDSPVSV        0.7220         20.2          SB     0.15     Sequence
   DRB3_0101  210  TGEPPFTGDSPVSVA  FTGDSPVSV        0.7199         20.7          SB     0.20     Sequence
   DRB3_0101  211  GEPPFTGDSPVSVAY  FTGDSPVSV        0.7168         21.4          SB     0.20     Sequence
   DRB3_0101  212  EPPFTGDSPVSVAYQ  FTGDSPVSV        0.7009         25.4          SB     0.30     Sequence
   DRB3_0101  213  PPFTGDSPVSVAYQH  FTGDSPVSV        0.6619         38.8          SB     0.80     Sequence
   DRB3_0101  214  PFTGDSPVSVAYQHV  FTGDSPVSV        0.6545         42.0          SB     0.80     Sequence
   DRB3_0101  563  PDLSGMFWVDAEPRL  FWVDAEPRL        0.6374         50.5          WB     0.80     Sequence
   DRB3_0101  564  DLSGMFWVDAEPRLR  FWVDAEPRL        0.6291         55.3          WB     0.80     Sequence
   DRB3_0101  215  FTGDSPVSVAYQHVR  FTGDSPVSV        0.6255         57.5          WB     0.80     Sequence
   DRB3_0101  555  SKGNQFVMPDLSGMF  VMPDLSGMF        0.6056         71.4          WB     1.00     Sequence
   DRB3_0101  557  GNQFVMPDLSGMFWV  VMPDLSGMF        0.6029         73.4          WB     1.00     Sequence
   DRB3_0101  565  LSGMFWVDAEPRLRA  FWVDAEPRL        0.6014         74.6          WB     1.00     Sequence
   DRB3_0101  556  KGNQFVMPDLSGMFW  VMPDLSGMF        0.6009         75.1          WB     1.00     Sequence
   DRB3_0101  558  NQFVMPDLSGMFWVD  VMPDLSGMF        0.5953         79.8          WB     1.00     Sequence
   DRB3_0101  566  SGMFWVDAEPRLRAL  FWVDAEPRL        0.5853         88.9          WB     2.00     Sequence
   DRB3_0101  559  QFVMPDLSGMFWVDA  VMPDLSGMF        0.5768         97.4          WB     2.00     Sequence
   DRB3_0101  560  FVMPDLSGMFWVDAE  VMPDLSGMF        0.5613        115.1          WB     2.00     Sequence
   DRB3_0101  567  GMFWVDAEPRLRALG  FWVDAEPRL        0.5479        133.2          WB     2.00     Sequence
   DRB3_0101  561  VMPDLSGMFWVDAEP  VMPDLSGMF        0.5383        147.7          WB     2.00     Sequence
   DRB3_0101  568  MFWVDAEPRLRALGW  FWVDAEPRL        0.5148        190.5          WB     4.00     Sequence
   DRB3_0101   39  KVLRADLARDPSFYL  LARDPSFYL        0.5146        191.0          WB     4.00     Sequence
   DRB3_0101   40  VLRADLARDPSFYLR  LARDPSFYL        0.5041        213.9          WB     4.00     Sequence
   DRB3_0101   41  LRADLARDPSFYLRF  LARDPSFYL        0.4970        230.9          WB     4.00     Sequence
```

```
DRB3_0101  113  RAIEVIADACQALNF  VIADACQAL        0.4945        237.2          WB     4.00      Sequence
DRB3_0101  111  PKRAIEVIADACQAL  VIADACQAL        0.4891        251.6          WB     4.00      Sequence
DRB3_0101  112  KRAIEVIADACQALN  VIADACQAL        0.4880        254.7          WB     4.00      Sequence
DRB3_0101  137  DVKPANIMISATNAV  IMISATNAV        0.4800        277.6          WB     4.00      Sequence
DRB3_0101  114  AIEVIADACQALNFS  VIADACQAL        0.4799        278.0          WB     4.00      Sequence
DRB3_0101   42  RADLARDPSFYLRFR  LARDPSFYL        0.4752        292.5          WB     4.00      Sequence
DRB3_0101   26  LARDLRLHRDVAVKV  LHRDVAVKV        0.4717        303.7          WB     4.00      Sequence
DRB3_0101   27  ARDLRLHRDVAVKVL  LHRDVAVKV        0.4661        322.8          WB     4.00      Sequence
DRB3_0101  548  SVIELQVSKGNQFVM  LQVSKGNQF        0.4646        328.1          WB     4.00      Sequence
DRB3_0101  115  IEVIADACQALNFSH  VIADACQAL        0.4632        332.9          WB     4.00      Sequence
DRB3_0101  549  VIELQVSKGNQFVMP  LQVSKGNQF        0.4613        339.8          WB     4.00      Sequence
DRB3_0101  138  VKPANIMISATNAVK  IMISATNAV        0.4609        341.4          WB     4.00      Sequence
DRB3_0101  547  DSVIELQVSKGNQFV  LQVSKGNQF        0.4562        359.1          WB     8.00      Sequence
DRB3_0101   43  ADLARDPSFYLRFRR  LARDPSFYL        0.4546        365.5          WB     8.00      Sequence
DRB3_0101  569  FWVDAEPRLRALGWT  FWVDAEPRL        0.4511        379.7          WB     8.00      Sequence
DRB3_0101  546  VDSVIELQVSKGNQF  LQVSKGNQF        0.4496        385.7          WB     8.00      Sequence
DRB3_0101   28  RDLRLHRDVAVKVLR  LHRDVAVKV        0.4474        394.9          WB     8.00      Sequence
DRB3_0101  550  IELQVSKGNQFVMPD  LQVSKGNQF        0.4458        402.0          WB     8.00      Sequence
DRB3_0101  116  EVIADACQALNFSHQ  VIADACQAL        0.4456        402.8          WB     8.00      Sequence
DRB3_0101   83  AGPLPYIVMEYVDGV  IVMEYVDGV        0.4455        403.1          WB     8.00      Sequence
DRB3_0101   44  DLARDPSFYLRFRRE  LARDPSFYL        0.4428        415.1          WB     8.00      Sequence
DRB3_0101  139  KPANIMISATNAVKV  IMISATNAV        0.4422        417.8          WB     8.00      Sequence
DRB3_0101   45  LARDPSFYLRFRREA  LARDPSFYL        0.4369        442.7          WB     8.00      Sequence
DRB3_0101  551  ELQVSKGNQFVMPDL  LQVSKGNQF        0.4313        470.1          WB     8.00      Sequence
DRB3_0101   29  DLRLHRDVAVKVLRA  LHRDVAVKV        0.4261        497.4          WB     8.00      Sequence
DRB3_0101  237  ARHEGLSADLDAVVL  LSADLDAVV        0.4242        507.7                 8.00      Sequence
DRB3_0101   84  GPLPYIVMEYVDGVT  IVMEYVDGV        0.4225        517.0                 8.00      Sequence
DRB3_0101  238  RHEGLSADLDAVVLK  LSADLDAVV        0.4184        540.6                 8.00      Sequence
DRB3_0101  236  SARHEGLSADLDAVV  LSADLDAVV        0.4175        545.7                 8.00      Sequence
DRB3_0101  117  VIADACQALNFSHQN  VIADACQAL        0.4136        569.6                 8.00      Sequence
DRB3_0101  552  LQVSKGNQFVMPDLS  LQVSKGNQF        0.4109        586.3                 8.00      Sequence
DRB3_0101  140  PANIMISATNAVKVM  IMISATNAV        0.4105        588.7                 8.00      Sequence
DRB3_0101   30  LRLHRDVAVKVLRAD  LHRDVAVKV        0.4009        653.1                 8.00      Sequence
DRB3_0101  239  HEGLSADLDAVVLKA  LSADLDAVV        0.3978        675.8                 8.00      Sequence
DRB3_0101   85  PLPYIVMEYVDGVTL  IVMEYVDGV        0.3953        694.0                 8.00      Sequence
DRB3_0101   49  PSFYLRFRREAQNAA  FRREAQNAA        0.3909        728.2                 8.00      Sequence
DRB3_0101  141  ANIMISATNAVKVMD  IMISATNAV        0.3893        740.4                 8.00      Sequence
DRB3_0101   31  RLHRDVAVKVLRADL  LHRDVAVKV        0.3853        773.9                 8.00      Sequence
DRB3_0101   50  SFYLRFRREAQNAAA  FRREAQNAA        0.3843        782.2                 8.00      Sequence
DRB3_0101  240  EGLSADLDAVVLKAL  LSADLDAVV        0.3835        789.0                 8.00      Sequence
DRB3_0101   51  FYLRFRREAQNAAAL  FRREAQNAA        0.3831        792.5                 8.00      Sequence
DRB3_0101  241  GLSADLDAVVLKALA  LSADLDAVV        0.3722        891.7                16.00      Sequence
DRB3_0101   86  LPYIVMEYVDGVTLR  IVMEYVDGV        0.3692        920.7                16.00      Sequence
DRB3_0101  142  NIMISATNAVKVMDF  IMISATNAV        0.3676        936.4                16.00      Sequence
DRB3_0101  262  YQTAAEMRADLVRVH  MRADLVRVH        0.3610       1005.9                16.00      Sequence
DRB3_0101   32  LHRDVAVKVLRADLA  LHRDVAVKV        0.3595       1022.4                16.00      Sequence
DRB3_0101   52  YLRFRREAQNAAALN  FRREAQNAA        0.3571       1049.9                16.00      Sequence
DRB3_0101  242  LSADLDAVVLKALAK  LSADLDAVV        0.3495       1139.9                16.00      Sequence
DRB3_0101  263  QTAAEMRADLVRVHN  MRADLVRVH        0.3478       1160.6                16.00      Sequence
DRB3_0101  219  SPVSVAYQHVREDPI  YQHVREDPI        0.3452       1193.1                16.00      Sequence
DRB3_0101   87  PYIVMEYVDGVTLRD  IVMEYVDGV        0.3402       1259.4                16.00      Sequence
DRB3_0101   53  LRFRREAQNAAALNH  FRREAQNAA        0.3317       1381.6                16.00      Sequence
DRB3_0101   88  YIVMEYVDGVTLRDI  IVMEYVDGV        0.3310       1391.7                16.00      Sequence
DRB3_0101  264  TAAEMRADLVRVHNG  MRADLVRVH        0.3292       1419.5                16.00      Sequence
DRB3_0101  150  AVKVMDFGIARAIAD  FGIARAIAD        0.3282       1434.2                16.00      Sequence
DRB3_0101  220  PVSVAYQHVREDPIP  YQHVREDPI        0.3260       1470.1                16.00      Sequence
DRB3_0101  143  IMISATNAVKVMDFG  IMISATNAV        0.3249       1487.5                16.00      Sequence
DRB3_0101    4  SHLSDRYELGEILGF  YELGEILGF        0.3167       1625.5                16.00      Sequence
DRB3_0101   54  RFRREAQNAAALNHP  FRREAQNAA        0.3124       1702.0                16.00      Sequence
DRB3_0101  265  AAEMRADLVRVHNGE  MRADLVRVH        0.3096       1753.8                16.00      Sequence
DRB3_0101  607  PPAGTGVNRDGIITL  VNRDGIITL        0.3060       1825.0                16.00      Sequence
DRB3_0101  151  VKVMDFGIARAIADS  FGIARAIAD        0.3034       1877.3                16.00      Sequence
DRB3_0101  221  VSVAYQHVREDPIPP  YQHVREDPI        0.3031       1881.4                16.00      Sequence
DRB3_0101  608  PAGTGVNRDGIITLR  VNRDGIITL        0.2950       2055.7                16.00      Sequence
DRB3_0101   89  IVMEYVDGVTLRDIV  IVMEYVDGV        0.2907       2151.9                32.00      Sequence
DRB3_0101  609  AGTGVNRDGIITLRF  VNRDGIITL        0.2892       2187.4                32.00      Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB3_0101 | 24 | VHLARDLRLHRDVAV | LRLHRDVAV | 0.2872 | 2234.8 | 32.00 | Sequence |
| DRB3_0101 | 222 | SVAYQHVREDPIPPS | YQHVREDPI | 0.2835 | 2326.9 | 32.00 | Sequence |
| DRB3_0101 | 266 | AEMRADLVRVHNGEP | MRADLVRVH | 0.2827 | 2346.3 | 32.00 | Sequence |
| DRB3_0101 | 155 | DFGIARAIADSGNSV | AIADSGNSV | 0.2791 | 2441.3 | 32.00 | Sequence |
| DRB3_0101 | 282 | EAPKVLTDAERTSLL | TDAERTSLL | 0.2784 | 2457.9 | 32.00 | Sequence |
| DRB3_0101 | 152 | KVMDFGIARAIADSG | FGIARAIAD | 0.2742 | 2573.8 | 32.00 | Sequence |
| DRB3_0101 | 25 | HLARDLRLHRDVAVK | LRLHRDVAV | 0.2725 | 2621.7 | 32.00 | Sequence |
| DRB3_0101 | 156 | FGIARAIADSGNSVT | AIADSGNSV | 0.2721 | 2633.7 | 32.00 | Sequence |
| DRB3_0101 | 267 | EMRADLVRVHNGEPP | MRADLVRVH | 0.2705 | 2677.3 | 32.00 | Sequence |
| DRB3_0101 | 538 | PPAGTTVPVDSVIEL | VPVDSVIEL | 0.2701 | 2688.8 | 32.00 | Sequence |
| DRB3_0101 | 223 | VAYQHVREDPIPPSA | YQHVREDPI | 0.2694 | 2710.7 | 32.00 | Sequence |
| DRB3_0101 | 610 | GTGVNRDGIITLRFG | VNRDGIITL | 0.2679 | 2754.4 | 32.00 | Sequence |
| DRB3_0101 | 554 | VSKGNQFVMPDLSGM | FVMPDLSGM | 0.2676 | 2765.4 | 32.00 | Sequence |
| DRB3_0101 | 55 | FRREAQNAAALNHPA | FRREAQNAA | 0.2654 | 2830.7 | 32.00 | Sequence |
| DRB3_0101 | 540 | AGTTVPVDSVIELQV | VPVDSVIEL | 0.2642 | 2868.3 | 32.00 | Sequence |
| DRB3_0101 | 283 | APKVLTDAERTSLLS | TDAERTSLL | 0.2629 | 2908.7 | 32.00 | Sequence |
| DRB3_0101 | 5 | HLSDRYELGEILGFG | YELGEILGF | 0.2619 | 2938.8 | 32.00 | Sequence |
| DRB3_0101 | 539 | PAGTTVPVDSVIELQ | VPVDSVIEL | 0.2618 | 2942.4 | 32.00 | Sequence |
| DRB3_0101 | 578 | RALGWTGMLDKGADV | GMLDKGADV | 0.2610 | 2966.9 | 32.00 | Sequence |
| DRB3_0101 | 224 | AYQHVREDPIPPSAR | YQHVREDPI | 0.2522 | 3266.3 | 32.00 | Sequence |
| DRB3_0101 | 579 | ALGWTGMLDKGADVD | GMLDKGADV | 0.2518 | 3278.4 | 32.00 | Sequence |
| DRB3_0101 | 611 | TGVNRDGIITLRFGQ | VNRDGIITL | 0.2505 | 3326.1 | 32.00 | Sequence |
| DRB3_0101 | 541 | GTTVPVDSVIELQVS | VPVDSVIEL | 0.2499 | 3348.9 | 32.00 | Sequence |
| DRB3_0101 | 121 | ACQALNFSHQNGIIH | LNFSHQNGI | 0.2468 | 3462.4 | 32.00 | Sequence |
| DRB3_0101 | 268 | MRADLVRVHNGEPPE | MRADLVRVH | 0.2432 | 3599.2 | 32.00 | Sequence |
| DRB3_0101 | 580 | LGWTGMLDKGADVDA | GMLDKGADV | 0.2415 | 3665.4 | 32.00 | Sequence |
| DRB3_0101 | 153 | VMDFGIARAIADSGN | FGIARAIAD | 0.2414 | 3671.5 | 32.00 | Sequence |
| DRB3_0101 | 284 | PKVLTDAERTSLLSS | TDAERTSLL | 0.2414 | 3671.7 | 32.00 | Sequence |
| DRB3_0101 | 473 | ANQTSAITNVVIIIV | ITNVVIIIV | 0.2410 | 3684.6 | 32.00 | Sequence |
| DRB3_0101 | 123 | QALNFSHQNGIIHRD | LNFSHQNGI | 0.2360 | 3892.2 | 32.00 | Sequence |
| DRB3_0101 | 542 | TTVPVDSVIELQVSK | VPVDSVIEL | 0.2349 | 3938.7 | 32.00 | Sequence |
| DRB3_0101 | 338 | LAVLTVVVTIAINTF | LTVVVTIAI | 0.2343 | 3960.8 | 32.00 | Sequence |
| DRB3_0101 | 148 | TNAVKVMDFGIARAI | MDFGIARAI | 0.2334 | 4002.9 | 32.00 | Sequence |
| DRB3_0101 | 119 | ADACQALNFSHQNGI | LNFSHQNGI | 0.2328 | 4029.1 | 32.00 | Sequence |
| DRB3_0101 | 6 | LSDRYELGEILGFGG | YELGEILGF | 0.2326 | 4034.9 | 32.00 | Sequence |
| DRB3_0101 | 157 | GIARAIADSGNSVTQ | AIADSGNSV | 0.2300 | 4150.4 | 32.00 | Sequence |
| DRB3_0101 | 122 | CQALNFSHQNGIIHR | LNFSHQNGI | 0.2287 | 4212.1 | 32.00 | Sequence |
| DRB3_0101 | 225 | YQHVREDPIPPSARH | YQHVREDPI | 0.2287 | 4212.6 | 32.00 | Sequence |
| DRB3_0101 | 285 | KVLTDAERTSLLSSA | TDAERTSLL | 0.2277 | 4256.7 | 32.00 | Sequence |
| DRB3_0101 | 335 | VAVLAVLTVVVTIAI | LTVVVTIAI | 0.2268 | 4296.8 | 32.00 | Sequence |
| DRB3_0101 | 124 | ALNFSHQNGIIHRDV | LNFSHQNGI | 0.2249 | 4388.3 | 32.00 | Sequence |
| DRB3_0101 | 46 | ARDPSFYLRFRREAQ | FYLRFRREA | 0.2247 | 4396.9 | 32.00 | Sequence |
| DRB3_0101 | 543 | TVPVDSVIELQVSKG | VPVDSVIEL | 0.2244 | 4412.5 | 32.00 | Sequence |
| DRB3_0101 | 120 | DACQALNFSHQNGII | LNFSHQNGI | 0.2236 | 4449.7 | 32.00 | Sequence |
| DRB3_0101 | 581 | GWTGMLDKGADVDAG | GMLDKGADV | 0.2232 | 4470.0 | 32.00 | Sequence |
| DRB3_0101 | 474 | NQTSAITNVVIIIVG | ITNVVIIIV | 0.2220 | 4528.3 | 32.00 | Sequence |
| DRB3_0101 | 341 | LTVVVTIAINTFGGI | VVTIAINTF | 0.2204 | 4604.6 | 32.00 | Sequence |
| DRB3_0101 | 154 | MDFGIARAIADSGNS | FGIARAIAD | 0.2194 | 4657.5 | 32.00 | Sequence |
| DRB3_0101 | 158 | IARAIADSGNSVTQT | AIADSGNSV | 0.2192 | 4667.4 | 32.00 | Sequence |
| DRB3_0101 | 393 | IPPDHVIGTDPAANT | IGTDPAANT | 0.2191 | 4673.6 | 32.00 | Sequence |
| DRB3_0101 | 130 | QNGIIHRDVKPANIM | IHRDVKPAN | 0.2170 | 4779.0 | 32.00 | Sequence |
| DRB3_0101 | 339 | AVLTVVVTIAINTFG | LTVVVTIAI | 0.2154 | 4862.2 | 32.00 | Sequence |
| DRB3_0101 | 336 | AVLAVLTVVVTIAIN | LTVVVTIAI | 0.2149 | 4888.3 | 32.00 | Sequence |
| DRB3_0101 | 149 | NAVKVMDFGIARAIA | MDFGIARAI | 0.2138 | 4947.5 | 32.00 | Sequence |
| DRB3_0101 | 7 | SDRYELGEILGFGGM | YELGEILGF | 0.2122 | 5033.7 | 32.00 | Sequence |
| DRB3_0101 | 159 | ARAIADSGNSVTQTA | AIADSGNSV | 0.2112 | 5088.4 | 32.00 | Sequence |
| DRB3_0101 | 544 | VPVDSVIELQVSKGN | VPVDSVIEL | 0.2109 | 5103.8 | 32.00 | Sequence |
| DRB3_0101 | 582 | WTGMLDKGADVDAGG | GMLDKGADV | 0.2093 | 5195.5 | 32.00 | Sequence |
| DRB3_0101 | 131 | NGIIHRDVKPANIMI | IHRDVKPAN | 0.2086 | 5230.8 | 32.00 | Sequence |
| DRB3_0101 | 472 | PANQTSAITNVVIII | AITNVVIII | 0.2085 | 5237.1 | 32.00 | Sequence |
| DRB3_0101 | 281 | PEAPKVLTDAERTSL | VLTDAERTS | 0.2082 | 5257.7 | 32.00 | Sequence |
| DRB3_0101 | 129 | HQNGIIHRDVKPANI | IHRDVKPAN | 0.2060 | 5380.4 | 50.00 | Sequence |
| DRB3_0101 | 280 | PPEAPKVLTDAERTS | VLTDAERTS | 0.2057 | 5401.1 | 50.00 | Sequence |
| DRB3_0101 | 160 | RAIADSGNSVTQTAA | AIADSGNSV | 0.2054 | 5419.1 | 50.00 | Sequence |
| DRB3_0101 | 47 | RDPSFYLRFRREAQN | FYLRFRREA | 0.2051 | 5437.5 | 50.00 | Sequence |
| DRB3_0101 | 128 | SHQNGIIHRDVKPAN | IHRDVKPAN | 0.2041 | 5496.6 | 50.00 | Sequence |

```
DRB3_0101  394  PPDHVIGTDPAANTS  IGTDPAANT         0.2039        5506.4                50.00      Sequence
DRB3_0101   96  GVTLRDIVHTEGPMT  IVHTEGPMT         0.2038        5514.1                50.00      Sequence
DRB3_0101  475  QTSAITNVVIIIVGS  ITNVVIIIV         0.2035        5530.2                50.00      Sequence
DRB3_0101  326  GSVGRWVAVVAVLAV  VAVVAVLAV         0.2032        5547.5                50.00      Sequence
DRB3_0101   92  EYVDGVTLRDIVHTE  TLRDIVHTE         0.2024        5597.9                50.00      Sequence
DRB3_0101  133  IIHRDVKPANIMISA  IHRDVKPAN         0.2020        5618.8                50.00      Sequence
DRB3_0101   10  YELGEILGFGGMSEV  YELGEILGF         0.2014        5656.5                50.00      Sequence
DRB3_0101  583  TGMLDKGADVDAGGS  GMLDKGADV         0.2008        5694.4                50.00      Sequence
DRB3_0101  395  PDHVIGTDPAANTSV  IGTDPAANT         0.2005        5712.1                50.00      Sequence
DRB3_0101  125  LNFSHQNGIIHRDVK  LNFSHQNGI         0.1998        5757.7                50.00      Sequence
DRB3_0101  340  VLTVVVTIAINTFGG  VVTIAINTF         0.1990        5804.2                50.00      Sequence
DRB3_0101    8  DRYELGEILGFGGMS  YELGEILGF         0.1983        5851.2                50.00      Sequence
DRB3_0101  132  GIIHRDVKPANIMIS  IHRDVKPAN         0.1980        5871.8                50.00      Sequence
DRB3_0101  337  VLAVLTVVVTIAINT  LTVVVTIAI         0.1963        5980.7                50.00      Sequence
DRB3_0101   97  VTLRDIVHTEGPMTP  IVHTEGPMT         0.1962        5984.5                50.00      Sequence
DRB3_0101  187  ARGDSVDARSDVYSL  ARGDSVDAR         0.1957        6018.3                50.00      Sequence
DRB3_0101  327  SVGRWVAVVAVLAVL  VAVVAVLAV         0.1952        6049.3                50.00      Sequence
DRB3_0101  325  IGSVGRWVAVVAVLA  WVAVVAVLA         0.1951        6055.8                50.00      Sequence
DRB3_0101   93  YVDGVTLRDIVHTEG  TLRDIVHTE         0.1932        6179.6                50.00      Sequence
DRB3_0101   37  AVKVLRADLARDPSF  LRADLARDP         0.1929        6199.4                50.00      Sequence
DRB3_0101  286  VLTDAERTSLLSSAA  TDAERTSLL         0.1925        6229.9                50.00      Sequence
DRB3_0101  445  AAGFGRFKQANSPST  FKQANSPST         0.1925        6232.2                50.00      Sequence
DRB3_0101  342  TVVVTIAINTFGGIT  VVTIAINTF         0.1924        6235.5                50.00      Sequence
DRB3_0101  476  TSAITNVVIIIVGSG  ITNVVIIIV         0.1919        6268.1                50.00      Sequence
DRB3_0101  194  ARSDVYSLGCVLYEV  SLGCVLYEV         0.1917        6285.3                50.00      Sequence
DRB3_0101  195  RSDVYSLGCVLYEVL  SLGCVLYEV         0.1913        6312.0                50.00      Sequence
DRB3_0101  318  DTDRDRSIGSVGRWV  SIGSVGRWV         0.1910        6332.3                50.00      Sequence
DRB3_0101    2  TPSHLSDRYELGEIL  SHLSDRYEL         0.1904        6373.9                50.00      Sequence
DRB3_0101  188  RGDSVDARSDVYSLG  DSVDARSDV         0.1879        6544.4                50.00      Sequence
DRB3_0101  313  RQDLDDTDRDRSIGS  TDRDRSIGS         0.1877        6560.0                50.00      Sequence
DRB3_0101  498  DVAGQTVDVAQKNLN  VDVAQKNLN         0.1873        6587.1                50.00      Sequence
DRB3_0101  161  AIADSGNSVTQTAAV  AIADSGNSV         0.1872        6600.1                50.00      Sequence
DRB3_0101  185  EQARGDSVDARSDVY  DSVDARSDV         0.1865        6644.4                50.00      Sequence
DRB3_0101  584  GMLDKGADVDAGGSQ  GMLDKGADV         0.1865        6645.6                50.00      Sequence
DRB3_0101   94  VDGVTLRDIVHTEGP  TLRDIVHTE         0.1862        6671.6                50.00      Sequence
DRB3_0101   38  VKVLRADLARDPSFY  LRADLARDP         0.1860        6685.5                50.00      Sequence
DRB3_0101    9  RYELGEILGFGGMSE  YELGEILGF         0.1850        6758.3                50.00      Sequence
DRB3_0101   35  DVAVKVLRADLARDP  LRADLARDP         0.1848        6772.6                50.00      Sequence
DRB3_0101  184  PEQARGDSVDARSDV  DSVDARSDV         0.1847        6780.4                50.00      Sequence
DRB3_0101  319  TDRDRSIGSVGRWVA  SIGSVGRWV         0.1847        6780.5                50.00      Sequence
DRB3_0101  186  QARGDSVDARSDVYS  DSVDARSDV         0.1846        6783.5                50.00      Sequence
DRB3_0101  189  GDSVDARSDVYSLGC  DSVDARSDV         0.1840        6832.5                50.00      Sequence
DRB3_0101  134  IHRDVKPANIMISAT  IHRDVKPAN         0.1836        6857.8                50.00      Sequence
DRB3_0101    1  TTPSHLSDRYELGEI  SHLSDRYEL         0.1835        6862.9                50.00      Sequence
DRB3_0101    0  MTTPSHLSDRYELGE  SHLSDRYEL         0.1834        6870.5                50.00      Sequence
DRB3_0101    3  PSHLSDRYELGEILG  SHLSDRYEL         0.1832        6891.8                50.00      Sequence
DRB3_0101  190  DSVDARSDVYSLGCV  DSVDARSDV         0.1825        6941.8                50.00      Sequence
DRB3_0101  446  AGFGRFKQANSPSTP  FKQANSPST         0.1819        6986.7                50.00      Sequence
DRB3_0101  314  QDLDDTDRDRSIGSV  TDRDRSIGS         0.1818        6992.4                50.00      Sequence
DRB3_0101   48  DPSFYLRFRREAQNA  FYLRFRREA         0.1818        6995.1                50.00      Sequence
DRB3_0101   13  GEILGFGGMSEVHLA  GGMSEVHLA         0.1816        7009.6                50.00      Sequence
DRB3_0101  396  DHVIGTDPAANTSVS  IGTDPAANT         0.1816        7011.7                50.00      Sequence
DRB3_0101  421  TGPEQREIPDVSTLT  EIPDVSTLT         0.1813        7032.1                50.00      Sequence
DRB3_0101  477  SAITNVVIIIVGSGP  ITNVVIIIV         0.1811        7048.4                50.00      Sequence
DRB3_0101  196  SDVYSLGCVLYEVLT  SLGCVLYEV         0.1796        7165.7                50.00      Sequence
DRB3_0101   36  VAVKVLRADLARDPS  LRADLARDP         0.1793        7185.0                50.00      Sequence
DRB3_0101  328  VGRWVAVVAVLAVLT  VAVVAVLAV         0.1793        7187.2                50.00      Sequence
DRB3_0101  500  AGQTVDVAQKNLNVY  VDVAQKNLN         0.1791        7199.6                50.00      Sequence
DRB3_0101  197  DVYSLGCVLYEVLTG  SLGCVLYEV         0.1782        7267.6                50.00      Sequence
DRB3_0101  331  WVAVVAVLAVLTVVV  VLAVLTVVV         0.1766        7401.3                50.00      Sequence
DRB3_0101  397  HVIGTDPAANTSVSA  IGTDPAANT         0.1764        7411.5                50.00      Sequence
DRB3_0101  449  GRFKQANSPSTPELV  FKQANSPST         0.1760        7443.3                50.00      Sequence
DRB3_0101  422  GPEQREIPDVSTLTY  EIPDVSTLT         0.1748        7546.3                50.00      Sequence
DRB3_0101  499  VAGQTVDVAQKNLNV  VDVAQKNLN         0.1746        7561.0                50.00      Sequence
DRB3_0101   14  EILGFGGMSEVHLAR  GGMSEVHLA         0.1739        7613.6                50.00      Sequence
DRB3_0101   98  TLRDIVHTEGPMTPK  IVHTEGPMT         0.1738        7627.6                50.00      Sequence
```

```
DRB3_0101   15  ILGFGGMSEVHLARD  GGMSEVHLA         0.1732        7677.2                50.00      Sequence
DRB3_0101   59  AQNAAALNHPAIVAV  LNHPAIVAV         0.1728        7712.5                50.00      Sequence
DRB3_0101   90  VMEYVDGVTLRDIVH  VDGVTLRDI         0.1727        7716.3                50.00      Sequence
DRB3_0101  324  SIGSVGRWVAVVAVL  SIGSVGRWV         0.1727        7717.5                50.00      Sequence
DRB3_0101  387  QKPDSTIPPDHVIGT  STIPPDHVI         0.1718        7788.8                50.00      Sequence
DRB3_0101  447  GFGRFKQANSPSTPE  FKQANSPST         0.1718        7792.8                50.00      Sequence
DRB3_0101   16  LGFGGMSEVHLARDL  GGMSEVHLA         0.1705        7902.0                50.00      Sequence
DRB3_0101  448  FGRFKQANSPSTPEL  FKQANSPST         0.1705        7903.1                50.00      Sequence
DRB3_0101   91  MEYVDGVTLRDIVHT  VDGVTLRDI         0.1704        7909.5                50.00      Sequence
DRB3_0101  329  GRWVAVVAVLAVLTV  VAVVAVLAV         0.1698        7958.9                50.00      Sequence
DRB3_0101   18  FGGMSEVHLARDLRL  GGMSEVHLA         0.1687        8058.9                50.00      Sequence
DRB3_0101  343  VVVTIAINTFGGITR  VVTIAINTF         0.1686        8067.4                50.00      Sequence
DRB3_0101  423  PEQREIPDVSTLTYA  EIPDVSTLT         0.1679        8127.5                50.00      Sequence
DRB3_0101  501  GQTVDVAQKNLNVYG  VDVAQKNLN         0.1679        8127.8                50.00      Sequence
DRB3_0101  478  AITNVVIIIVGSGPA  ITNVVIIIV         0.1669        8221.1                50.00      Sequence
DRB3_0101  248  AVVLKALAKNPENRY  LAKNPENRY         0.1664        8265.1                50.00      Sequence
DRB3_0101  398  VIGTDPAANTSVSAG  IGTDPAANT         0.1661        8289.9                50.00      Sequence
DRB3_0101  388  KPDSTIPPDHVIGTD  STIPPDHVI         0.1654        8348.1                50.00      Sequence
DRB3_0101   60  QNAAALNHPAIVAVY  LNHPAIVAV         0.1654        8349.7                50.00      Sequence
DRB3_0101  250  VLKALAKNPENRYQT  LAKNPENRY         0.1651        8375.5                50.00      Sequence
DRB3_0101  249  VVLKALAKNPENRYQ  LAKNPENRY         0.1640        8481.4                50.00      Sequence
DRB3_0101  391  STIPPDHVIGTDPAA  IPPDHVIGT         0.1639        8487.1                50.00      Sequence
DRB3_0101  315  DLDDTDRDRSIGSVG  TDRDRSIGS         0.1639        8491.4                50.00      Sequence
DRB3_0101  169  VTQTAAVIGTAQYLS  VIGTAQYLS         0.1635        8523.9                50.00      Sequence
DRB3_0101  450  RFKQANSPSTPELVG  FKQANSPST         0.1633        8541.6                50.00      Sequence
DRB3_0101  323  RSIGSVGRWVAVVAV  SIGSVGRWV         0.1621        8658.5                50.00      Sequence
DRB3_0101   19  GGMSEVHLARDLRLH  GGMSEVHLA         0.1614        8721.4                50.00      Sequence
DRB3_0101  390  DSTIPPDHVIGTDPA  STIPPDHVI         0.1609        8766.6                50.00      Sequence
DRB3_0101  252  KALAKNPENRYQTAA  LAKNPENRY         0.1609        8771.5                50.00      Sequence
DRB3_0101  251  LKALAKNPENRYQTA  LAKNPENRY         0.1603        8822.3                50.00      Sequence
DRB3_0101  562  MPDLSGMFWVDAEPR  PDLSGMFWV         0.1601        8848.4                50.00      Sequence
DRB3_0101  389  PDSTIPPDHVIGTDP  STIPPDHVI         0.1600        8851.2                50.00      Sequence
DRB3_0101   17  GFGGMSEVHLARDLR  GGMSEVHLA         0.1594        8915.8                50.00      Sequence
DRB3_0101  198  VYSLGCVLYEVLTGE  SLGCVLYEV         0.1592        8926.2                50.00      Sequence
DRB3_0101  253  ALAKNPENRYQTAAE  LAKNPENRY         0.1587        8976.7                50.00      Sequence
DRB3_0101  316  LDDTDRDRSIGSVGR  TDRDRSIGS         0.1561        9240.4                50.00      Sequence
DRB3_0101  332  VAVVAVLAVLTVVVT  VLAVLTVVV         0.1558        9266.5                50.00      Sequence
DRB3_0101   61  NAAALNHPAIVAVYD  LNHPAIVAV         0.1551        9335.5                50.00      Sequence
DRB3_0101   62  AAALNHPAIVAVYDT  AALNHPAIV         0.1547        9372.6                50.00      Sequence
DRB3_0101  502  QTVDVAQKNLNVYGF  VDVAQKNLN         0.1546        9385.6                50.00      Sequence
DRB3_0101  321  RDRSIGSVGRWVAVV  SIGSVGRWV         0.1541        9432.9                50.00      Sequence
DRB3_0101  171  QTAAVIGTAQYLSPE  VIGTAQYLS         0.1537        9475.8                50.00      Sequence
DRB3_0101  170  TQTAAVIGTAQYLSP  VIGTAQYLS         0.1537        9477.5                50.00      Sequence
DRB3_0101  193  DARSDVYSLGCVLYE  VYSLGCVLY         0.1529        9562.3                50.00      Sequence
DRB3_0101  126  NFSHQNGIIHRDVKP  FSHQNGIIH         0.1529        9564.1                50.00      Sequence
DRB3_0101   95  DGVTLRDIVHTEGPM  TLRDIVHTE         0.1526        9587.1                50.00      Sequence
DRB3_0101  254  LAKNPENRYQTAAEM  LAKNPENRY         0.1525        9602.0                50.00      Sequence
DRB3_0101  333  AVVAVLAVLTVVVTI  VLAVLTVVV         0.1520        9651.4                50.00      Sequence
DRB3_0101  127  FSHQNGIIHRDVKPA  FSHQNGIIH         0.1520        9653.6                50.00      Sequence
DRB3_0101  606  NPPAGTGVNRDGIIT  TGVNRDGII         0.1519        9668.0                50.00      Sequence
DRB3_0101  399  IGTDPAANTSVSAGD  IGTDPAANT         0.1517        9682.6                50.00      Sequence
DRB3_0101  344  VVTIAINTFGGITRD  VVTIAINTF         0.1515        9705.1                50.00      Sequence
DRB3_0101  489  SGPATKDIPDVAGQT  ATKDIPDVA         0.1513        9726.5                50.00      Sequence
DRB3_0101  330  RWVAVVAVLAVLTVV  VAVVAVLAV         0.1504        9818.7                50.00      Sequence
DRB3_0101  605  QNPPAGTGVNRDGII  TGVNRDGII         0.1500        9867.6                50.00      Sequence
DRB3_0101  479  ITNVVIIIVGSGPAT  ITNVVIIIV         0.1499        9876.6                50.00      Sequence
DRB3_0101  424  EQREIPDVSTLTYAE  EIPDVSTLT         0.1497        9901.1                50.00      Sequence
DRB3_0101  491  PATKDIPDVAGQTVD  ATKDIPDVA         0.1491        9965.8                50.00      Sequence
DRB3_0101  192  VDARSDVYSLGCVLY  VYSLGCVLY         0.1486       10015.4                50.00      Sequence
DRB3_0101  451  FKQANSPSTPELVGK  FKQANSPST         0.1481       10074.6                50.00      Sequence
DRB3_0101   63  AALNHPAIVAVYDTG  LNHPAIVAV         0.1477       10118.6                50.00      Sequence
DRB3_0101   57  REAQNAAALNHPAIV  AALNHPAIV         0.1476       10123.4                50.00      Sequence
DRB3_0101   82  PAGPLPYIVMEYVDG  YIVMEYVDG         0.1470       10191.1                50.00      Sequence
DRB3_0101  287  LTDAERTSLLSSAAG  TDAERTSLL         0.1467       10228.9                50.00      Sequence
DRB3_0101  317  DDTDRDRSIGSVGRW  TDRDRSIGS         0.1464       10252.4                50.00      Sequence
DRB3_0101  288  TDAERTSLLSSAAGN  TDAERTSLL         0.1459       10308.5                50.00      Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB3_0101 | 349 | INTFGGITRDVQVPD | GGITRDVQV | 0.1458 | 10327.0 | 50.00 | Sequence |
| DRB3_0101 | 261 | RYQTAAEMRADLVRV | YQTAAEMRA | 0.1452 | 10395.0 | 50.00 | Sequence |
| DRB3_0101 | 490 | GPATKDIPDVAGQTV | ATKDIPDVA | 0.1448 | 10440.9 | 50.00 | Sequence |
| DRB3_0101 | 199 | YSLGCVLYEVLTGEP | SLGCVLYEV | 0.1446 | 10454.8 | 50.00 | Sequence |
| DRB3_0101 | 172 | TAAVIGTAQYLSPEQ | VIGTAQYLS | 0.1437 | 10556.1 | 50.00 | Sequence |
| DRB3_0101 | 320 | DRDRSIGSVGRWVAV | SIGSVGRWV | 0.1435 | 10581.6 | 50.00 | Sequence |
| DRB3_0101 | 351 | TFGGITRDVQVPDVR | GGITRDVQV | 0.1433 | 10613.1 | 50.00 | Sequence |
| DRB3_0101 | 486 | IVGSGPATKDIPDVA | ATKDIPDVA | 0.1424 | 10709.3 | 50.00 | Sequence |
| DRB3_0101 | 350 | NTFGGITRDVQVPDV | GGITRDVQV | 0.1424 | 10715.8 | 50.00 | Sequence |
| DRB3_0101 | 34 | RDVAVKVLRADLARD | VKVLRADLA | 0.1416 | 10801.1 | 50.00 | Sequence |
| DRB3_0101 | 58 | EAQNAAALNHPAIVA | AALNHPAIV | 0.1414 | 10829.6 | 50.00 | Sequence |
| DRB3_0101 | 322 | DRSIGSVGRWVAVVA | SIGSVGRWV | 0.1396 | 11046.6 | 50.00 | Sequence |
| DRB3_0101 | 492 | ATKDIPDVAGQTVDV | ATKDIPDVA | 0.1389 | 11130.2 | 50.00 | Sequence |
| DRB3_0101 | 173 | AAVIGTAQYLSPEQA | VIGTAQYLS | 0.1385 | 11170.6 | 50.00 | Sequence |
| DRB3_0101 | 191 | SVDARSDVYSLGCVL | SVDARSDVY | 0.1385 | 11174.1 | 50.00 | Sequence |
| DRB3_0101 | 425 | QREIPDVSTLTYAEA | EIPDVSTLT | 0.1381 | 11216.1 | 50.00 | Sequence |
| DRB3_0101 | 334 | VVAVLAVLTVVVTIA | VLAVLTVVV | 0.1375 | 11292.3 | 50.00 | Sequence |
| DRB3_0101 | 347 | IAINTFGGITRDVQV | GGITRDVQV | 0.1372 | 11333.7 | 50.00 | Sequence |
| DRB3_0101 | 12 | LGEILGFGGMSEVHL | LGFGGMSEV | 0.1369 | 11364.7 | 50.00 | Sequence |
| DRB3_0101 | 216 | TGDSPVSVAYQHVRE | VSVAYQHVR | 0.1369 | 11365.2 | 50.00 | Sequence |
| DRB3_0101 | 311 | LPRQDLDDTDRDRSI | DDTDRDRSI | 0.1369 | 11366.8 | 50.00 | Sequence |
| DRB3_0101 | 503 | TVDVAQKNLNVYGFT | VDVAQKNLN | 0.1368 | 11374.7 | 50.00 | Sequence |
| DRB3_0101 | 20 | GMSEVHLARDLRLHR | LARDLRLHR | 0.1368 | 11383.3 | 50.00 | Sequence |
| DRB3_0101 | 200 | SLGCVLYEVLTGEPP | SLGCVLYEV | 0.1364 | 11425.6 | 50.00 | Sequence |
| DRB3_0101 | 392 | TIPPDHVIGTDPAAN | IPPDHVIGT | 0.1357 | 11518.2 | 50.00 | Sequence |
| DRB3_0101 | 487 | VGSGPATKDIPDVAG | ATKDIPDVA | 0.1346 | 11650.1 | 50.00 | Sequence |
| DRB3_0101 | 217 | GDSPVSVAYQHVRED | VSVAYQHVR | 0.1346 | 11654.2 | 50.00 | Sequence |
| DRB3_0101 | 21 | MSEVHLARDLRLHRD | LARDLRLHR | 0.1345 | 11665.3 | 50.00 | Sequence |
| DRB3_0101 | 426 | REIPDVSTLTYAEAV | EIPDVSTLT | 0.1343 | 11690.6 | 50.00 | Sequence |
| DRB3_0101 | 22 | SEVHLARDLRLHRDV | VHLARDLRL | 0.1341 | 11715.9 | 50.00 | Sequence |
| DRB3_0101 | 312 | PRQDLDDTDRDRSIG | DDTDRDRSI | 0.1333 | 11819.2 | 50.00 | Sequence |
| DRB3_0101 | 23 | EVHLARDLRLHRDVA | LARDLRLHR | 0.1329 | 11874.7 | 50.00 | Sequence |
| DRB3_0101 | 33 | HRDVAVKVLRADLAR | VKVLRADLA | 0.1324 | 11933.0 | 50.00 | Sequence |
| DRB3_0101 | 226 | QHVREDPIPPSARHE | VREDPIPPS | 0.1319 | 11996.0 | 50.00 | Sequence |
| DRB3_0101 | 352 | FGGITRDVQVPDVRG | GGITRDVQV | 0.1316 | 12034.0 | 50.00 | Sequence |
| DRB3_0101 | 404 | AANTSVSAGDEITVN | TSVSAGDEI | 0.1314 | 12064.8 | 50.00 | Sequence |
| DRB3_0101 | 403 | PAANTSVSAGDEITV | TSVSAGDEI | 0.1310 | 12114.7 | 50.00 | Sequence |
| DRB3_0101 | 504 | VDVAQKNLNVYGFTK | VDVAQKNLN | 0.1309 | 12126.6 | 50.00 | Sequence |
| DRB3_0101 | 497 | PDVAGQTVDVAQKNL | QTVDVAQKN | 0.1298 | 12276.0 | 50.00 | Sequence |
| DRB3_0101 | 259 | ENRYQTAAEMRADLV | YQTAAEMRA | 0.1284 | 12467.3 | 50.00 | Sequence |
| DRB3_0101 | 496 | IPDVAGQTVDVAQKN | QTVDVAQKN | 0.1283 | 12476.5 | 50.00 | Sequence |
| DRB3_0101 | 488 | GSGPATKDIPDVAGQ | ATKDIPDVA | 0.1282 | 12488.6 | 50.00 | Sequence |
| DRB3_0101 | 203 | CVLYEVLTGEPPFTG | LTGEPPFTG | 0.1277 | 12562.2 | 50.00 | Sequence |
| DRB3_0101 | 208 | VLTGEPPFTGDSPVS | LTGEPPFTG | 0.1275 | 12579.1 | 50.00 | Sequence |
| DRB3_0101 | 256 | KNPENRYQTAAEMRA | YQTAAEMRA | 0.1273 | 12607.3 | 50.00 | Sequence |
| DRB3_0101 | 227 | HVREDPIPPSARHEG | VREDPIPPS | 0.1273 | 12612.9 | 50.00 | Sequence |
| DRB3_0101 | 174 | AVIGTAQYLSPEQAR | VIGTAQYLS | 0.1271 | 12643.9 | 50.00 | Sequence |
| DRB3_0101 | 516 | FTKFSQASVDSPRPA | ASVDSPRPA | 0.1270 | 12657.5 | 50.00 | Sequence |
| DRB3_0101 | 385 | TLQKPDSTIPPDHVI | STIPPDHVI | 0.1269 | 12660.6 | 50.00 | Sequence |
| DRB3_0101 | 598 | QHNRVVYQNPPAGTG | VYQNPPAGT | 0.1265 | 12720.9 | 50.00 | Sequence |
| DRB3_0101 | 146 | SATNAVKVMDFGIAR | KVMDFGIAR | 0.1257 | 12828.3 | 50.00 | Sequence |
| DRB3_0101 | 348 | AINTFGGITRDVQVP | GGITRDVQV | 0.1252 | 12895.5 | 50.00 | Sequence |
| DRB3_0101 | 258 | PENRYQTAAEMRADL | YQTAAEMRA | 0.1246 | 12985.5 | 50.00 | Sequence |
| DRB3_0101 | 362 | PDVRGQSSADAIATL | SSADAIATL | 0.1246 | 12986.1 | 50.00 | Sequence |
| DRB3_0101 | 405 | ANTSVSAGDEITVNV | TSVSAGDEI | 0.1245 | 12995.2 | 50.00 | Sequence |
| DRB3_0101 | 260 | NRYQTAAEMRADLVR | YQTAAEMRA | 0.1243 | 13024.6 | 50.00 | Sequence |
| DRB3_0101 | 409 | VSAGDEITVNVSTGP | VSAGDEITV | 0.1237 | 13107.9 | 50.00 | Sequence |
| DRB3_0101 | 147 | ATNAVKVMDFGIARA | KVMDFGIAR | 0.1234 | 13150.1 | 50.00 | Sequence |
| DRB3_0101 | 99 | LRDIVHTEGPMTPKR | IVHTEGPMT | 0.1225 | 13291.1 | 50.00 | Sequence |
| DRB3_0101 | 11 | ELGEILGFGGMSEVH | LGFGGMSEV | 0.1224 | 13303.7 | 50.00 | Sequence |
| DRB3_0101 | 257 | NPENRYQTAAEMRAD | YQTAAEMRA | 0.1222 | 13325.0 | 50.00 | Sequence |
| DRB3_0101 | 406 | NTSVSAGDEITVNVS | TSVSAGDEI | 0.1221 | 13339.3 | 50.00 | Sequence |
| DRB3_0101 | 218 | DSPVSVAYQHVREDP | VSVAYQHVR | 0.1214 | 13443.9 | 50.00 | Sequence |
| DRB3_0101 | 136 | RDVKPANIMISATNA | RDVKPANIM | 0.1200 | 13648.5 | 50.00 | Sequence |
| DRB3_0101 | 408 | SVSAGDEITVNVSTG | VSAGDEITV | 0.1198 | 13680.6 | 50.00 | Sequence |
| DRB3_0101 | 517 | TKFSQASVDSPRPAG | ASVDSPRPA | 0.1192 | 13769.2 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB3_0101 | 375 | TLQNRGFKIRTLQKP | FKIRTLQKP | 0.1192 | 13770.1 | 50.00 | Sequence |
| DRB3_0101 | 181 | YLSPEQARGDSVDAR | ARGDSVDAR | 0.1190 | 13795.6 | 50.00 | Sequence |
| DRB3_0101 | 599 | HNRVVYQNPPAGTGV | VYQNPPAGT | 0.1186 | 13855.9 | 50.00 | Sequence |
| DRB3_0101 | 363 | DVRGQSSADAIATLQ | SSADAIATL | 0.1186 | 13864.1 | 50.00 | Sequence |
| DRB3_0101 | 243 | SADLDAVVLKALAKN | ADLDAVVLK | 0.1180 | 13942.1 | 50.00 | Sequence |
| DRB3_0101 | 386 | LQKPDSTIPPDHVIG | STIPPDHVI | 0.1180 | 13953.8 | 50.00 | Sequence |
| DRB3_0101 | 228 | VREDPIPPSARHEGL | VREDPIPPS | 0.1173 | 14056.0 | 50.00 | Sequence |
| DRB3_0101 | 353 | GGITRDVQVPDVRGQ | GGITRDVQV | 0.1171 | 14078.0 | 50.00 | Sequence |
| DRB3_0101 | 204 | VLYEVLTGEPPFTGD | LTGEPPFTG | 0.1169 | 14110.1 | 50.00 | Sequence |
| DRB3_0101 | 354 | GITRDVQVPDVRGQS | QVPDVRGQS | 0.1166 | 14164.4 | 50.00 | Sequence |
| DRB3_0101 | 290 | AERTSLLSSAAGNLS | LSSAAGNLS | 0.1163 | 14209.8 | 50.00 | Sequence |
| DRB3_0101 | 100 | RDIVHTEGPMTPKRA | IVHTEGPMT | 0.1162 | 14216.0 | 50.00 | Sequence |
| DRB3_0101 | 183 | SPEQARGDSVDARSD | ARGDSVDAR | 0.1162 | 14221.3 | 50.00 | Sequence |
| DRB3_0101 | 510 | NLNVYGFTKFSQASV | YGFTKFSQA | 0.1157 | 14298.2 | 50.00 | Sequence |
| DRB3_0101 | 346 | TIAINTFGGITRDVQ | IAINTFGGI | 0.1155 | 14332.1 | 50.00 | Sequence |
| DRB3_0101 | 182 | LSPEQARGDSVDARS | ARGDSVDAR | 0.1154 | 14348.2 | 50.00 | Sequence |
| DRB3_0101 | 407 | TSVSAGDEITVNVST | TSVSAGDEI | 0.1150 | 14409.8 | 50.00 | Sequence |
| DRB3_0101 | 518 | KFSQASVDSPRPAGE | ASVDSPRPA | 0.1142 | 14538.7 | 50.00 | Sequence |
| DRB3_0101 | 508 | QKNLNVYGFTKFSQA | YGFTKFSQA | 0.1141 | 14547.7 | 50.00 | Sequence |
| DRB3_0101 | 135 | HRDVKPANIMISATN | RDVKPANIM | 0.1129 | 14744.0 | 50.00 | Sequence |
| DRB3_0101 | 597 | SQHNRVVYQNPPAGT | VYQNPPAGT | 0.1126 | 14779.6 | 50.00 | Sequence |
| DRB3_0101 | 511 | LNVYGFTKFSQASVD | YGFTKFSQA | 0.1125 | 14804.4 | 50.00 | Sequence |
| DRB3_0101 | 430 | DVSTLTYAEAVKKLT | YAEAVKKLT | 0.1116 | 14944.1 | 50.00 | Sequence |
| DRB3_0101 | 519 | FSQASVDSPRPAGEV | ASVDSPRPA | 0.1116 | 14950.1 | 50.00 | Sequence |
| DRB3_0101 | 505 | DVAQKNLNVYGFTKF | VAQKNLNVY | 0.1106 | 15112.6 | 50.00 | Sequence |
| DRB3_0101 | 570 | WVDAEPRLRALGWTG | WVDAEPRLR | 0.1104 | 15138.8 | 50.00 | Sequence |
| DRB3_0101 | 471 | PPANQTSAITNVVII | SAITNVVII | 0.1103 | 15162.1 | 50.00 | Sequence |
| DRB3_0101 | 493 | TKDIPDVAGQTVDVA | DIPDVAGQT | 0.1101 | 15188.5 | 50.00 | Sequence |
| DRB3_0101 | 65 | LNHPAIVAVYDTGEA | LNHPAIVAV | 0.1100 | 15200.5 | 50.00 | Sequence |
| DRB3_0101 | 235 | PSARHEGLSADLDAV | GLSADLDAV | 0.1100 | 15204.8 | 50.00 | Sequence |
| DRB3_0101 | 427 | EIPDVSTLTYAEAVK | EIPDVSTLT | 0.1099 | 15221.2 | 50.00 | Sequence |
| DRB3_0101 | 364 | VRGQSSADAIATLQN | SSADAIATL | 0.1099 | 15222.4 | 50.00 | Sequence |
| DRB3_0101 | 600 | NRVVYQNPPAGTGVN | YQNPPAGTG | 0.1098 | 15240.5 | 50.00 | Sequence |
| DRB3_0101 | 376 | LQNRGFKIRTLQKPD | FKIRTLQKP | 0.1098 | 15241.5 | 50.00 | Sequence |
| DRB3_0101 | 572 | DAEPRLRALGWTGML | RALGWTGML | 0.1090 | 15365.9 | 50.00 | Sequence |
| DRB3_0101 | 207 | EVLTGEPPFTGDSPV | LTGEPPFTG | 0.1083 | 15488.4 | 50.00 | Sequence |
| DRB3_0101 | 359 | VQVPDVRGQSSADAI | RGQSSADAI | 0.1081 | 15518.9 | 50.00 | Sequence |
| DRB3_0101 | 206 | YEVLTGEPPFTGDSP | LTGEPPFTG | 0.1077 | 15585.4 | 50.00 | Sequence |
| DRB3_0101 | 205 | LYEVLTGEPPFTGDS | LTGEPPFTG | 0.1076 | 15604.4 | 50.00 | Sequence |
| DRB3_0101 | 513 | VYGFTKFSQASVDSP | FSQASVDSP | 0.1076 | 15611.9 | 50.00 | Sequence |
| DRB3_0101 | 379 | RGFKIRTLQKPDSTI | FKIRTLQKP | 0.1071 | 15696.6 | 50.00 | Sequence |
| DRB3_0101 | 573 | AEPRLRALGWTGMLD | RALGWTGML | 0.1056 | 15949.8 | 50.00 | Sequence |
| DRB3_0101 | 494 | KDIPDVAGQTVDVAQ | DIPDVAGQT | 0.1055 | 15968.1 | 50.00 | Sequence |
| DRB3_0101 | 345 | VTIAINTFGGITRDV | IAINTFGGI | 0.1054 | 15987.6 | 50.00 | Sequence |
| DRB3_0101 | 291 | ERTSLLSSAAGNLSG | LSSAAGNLS | 0.1051 | 16042.2 | 50.00 | Sequence |
| DRB3_0101 | 64 | ALNHPAIVAVYDTGE | LNHPAIVAV | 0.1049 | 16077.3 | 50.00 | Sequence |
| DRB3_0101 | 506 | VAQKNLNVYGFTKFS | VAQKNLNVY | 0.1049 | 16079.7 | 50.00 | Sequence |
| DRB3_0101 | 495 | DIPDVAGQTVDVAQK | DIPDVAGQT | 0.1048 | 16085.1 | 50.00 | Sequence |
| DRB3_0101 | 360 | QVPDVRGQSSADAIA | RGQSSADAI | 0.1044 | 16158.5 | 50.00 | Sequence |
| DRB3_0101 | 377 | QNRGFKIRTLQKPDS | FKIRTLQKP | 0.1039 | 16253.1 | 50.00 | Sequence |
| DRB3_0101 | 512 | NVYGFTKFSQASVDS | YGFTKFSQA | 0.1038 | 16259.2 | 50.00 | Sequence |
| DRB3_0101 | 175 | VIGTAQYLSPEQARG | VIGTAQYLS | 0.1036 | 16297.1 | 50.00 | Sequence |
| DRB3_0101 | 574 | EPRLRALGWTGMLDK | RALGWTGML | 0.1034 | 16333.4 | 50.00 | Sequence |
| DRB3_0101 | 110 | TPKRAIEVIADACQA | EVIADACQA | 0.1031 | 16388.0 | 50.00 | Sequence |
| DRB3_0101 | 601 | RVVYQNPPAGTGVNR | VYQNPPAGT | 0.1026 | 16483.6 | 50.00 | Sequence |
| DRB3_0101 | 81 | TPAGPLPYIVMEYVD | PAGPLPYIV | 0.1024 | 16504.7 | 50.00 | Sequence |
| DRB3_0101 | 380 | GFKIRTLQKPDSTIP | FKIRTLQKP | 0.1023 | 16529.2 | 50.00 | Sequence |
| DRB3_0101 | 80 | ETPAGPLPYIVMEYV | PAGPLPYIV | 0.1016 | 16659.5 | 50.00 | Sequence |
| DRB3_0101 | 202 | GCVLYEVLTGEPPFT | VLTGEPPFT | 0.1006 | 16838.4 | 50.00 | Sequence |
| DRB3_0101 | 145 | ISATNAVKVMDFGIA | TNAVKVMDF | 0.1002 | 16901.9 | 50.00 | Sequence |
| DRB3_0101 | 410 | SAGDEITVNVSTGPE | SAGDEITVN | 0.1002 | 16915.8 | 50.00 | Sequence |
| DRB3_0101 | 168 | SVTQTAAVIGTAQYL | AVIGTAQYL | 0.1000 | 16949.2 | 50.00 | Sequence |
| DRB3_0101 | 308 | TDPLPRQDLDDTDRD | QDLDDTDRD | 0.0998 | 16973.9 | 50.00 | Sequence |
| DRB3_0101 | 101 | DIVHTEGPMTPKRAI | IVHTEGPMT | 0.0997 | 17003.7 | 50.00 | Sequence |
| DRB3_0101 | 292 | RTSLLSSAAGNLSGP | LSSAAGNLS | 0.0996 | 17019.4 | 50.00 | Sequence |
| DRB3_0101 | 365 | RGQSSADAIATLQNR | SSADAIATL | 0.0995 | 17035.9 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB3_0101 | 355 | ITRDVQVPDVRGQSS | QVPDVRGQS | 0.0993 | 17076.5 | 50.00 | Sequence |
| DRB3_0101 | 144 | MISATNAVKVMDFGI | TNAVKVMDF | 0.0993 | 17079.7 | 50.00 | Sequence |
| DRB3_0101 | 520 | SQASVDSPRPAGEVT | ASVDSPRPA | 0.0985 | 17228.0 | 50.00 | Sequence |
| DRB3_0101 | 431 | VSTLTYAEAVKKLTA | YAEAVKKLT | 0.0981 | 17290.3 | 50.00 | Sequence |
| DRB3_0101 | 545 | PVDSVIELQVSKGNQ | VDSVIELQV | 0.0977 | 17367.4 | 50.00 | Sequence |
| DRB3_0101 | 244 | ADLDAVVLKALAKNP | ADLDAVVLK | 0.0968 | 17545.3 | 50.00 | Sequence |
| DRB3_0101 | 289 | DAERTSLLSSAAGNL | LLSSAAGNL | 0.0967 | 17568.9 | 50.00 | Sequence |
| DRB3_0101 | 509 | KNLNVYGFTKFSQAS | YGFTKFSQA | 0.0964 | 17620.3 | 50.00 | Sequence |
| DRB3_0101 | 401 | TDPAANTSVSAGDEI | TSVSAGDEI | 0.0964 | 17624.7 | 50.00 | Sequence |
| DRB3_0101 | 402 | DPAANTSVSAGDEIT | TSVSAGDEI | 0.0963 | 17630.4 | 50.00 | Sequence |
| DRB3_0101 | 361 | VPDVRGQSSADAIAT | RGQSSADAI | 0.0963 | 17646.8 | 50.00 | Sequence |
| DRB3_0101 | 309 | DPLPRQDLDDTDRDR | QDLDDTDRD | 0.0960 | 17688.5 | 50.00 | Sequence |
| DRB3_0101 | 521 | QASVDSPRPAGEVTG | ASVDSPRPA | 0.0955 | 17787.1 | 50.00 | Sequence |
| DRB3_0101 | 576 | RLRALGWTGMLDKGA | RALGWTGML | 0.0949 | 17903.7 | 50.00 | Sequence |
| DRB3_0101 | 310 | PLPRQDLDDTDRDRS | QDLDDTDRD | 0.0949 | 17904.9 | 50.00 | Sequence |
| DRB3_0101 | 514 | YGFTKFSQASVDSPR | FSQASVDSP | 0.0949 | 17915.2 | 50.00 | Sequence |
| DRB3_0101 | 575 | PRLRALGWTGMLDKG | RALGWTGML | 0.0945 | 17979.6 | 50.00 | Sequence |
| DRB3_0101 | 577 | LRALGWTGMLDKGAD | RALGWTGML | 0.0944 | 18012.6 | 50.00 | Sequence |
| DRB3_0101 | 378 | NRGFKIRTLQKPDST | FKIRTLQKP | 0.0943 | 18024.6 | 50.00 | Sequence |
| DRB3_0101 | 482 | VVIIIVGSGPATKDI | IIVGSGPAT | 0.0935 | 18183.5 | 50.00 | Sequence |
| DRB3_0101 | 480 | TNVVIIIVGSGPATK | IIVGSGPAT | 0.0931 | 18261.2 | 50.00 | Sequence |
| DRB3_0101 | 107 | GPMTPKRAIEVIADA | MTPKRAIEV | 0.0929 | 18300.7 | 50.00 | Sequence |
| DRB3_0101 | 293 | TSLLSSAAGNLSGPR | LSSAAGNLS | 0.0918 | 18515.4 | 50.00 | Sequence |
| DRB3_0101 | 481 | NVVIIIVGSGPATKD | IIVGSGPAT | 0.0917 | 18537.3 | 50.00 | Sequence |
| DRB3_0101 | 537 | NPPAGTTVPVDSVIE | GTTVPVDSV | 0.0911 | 18661.2 | 50.00 | Sequence |
| DRB3_0101 | 79 | AETPAGPLPYIVMEY | PAGPLPYIV | 0.0909 | 18695.6 | 50.00 | Sequence |
| DRB3_0101 | 536 | TNPPAGTTVPVDSVI | GTTVPVDSV | 0.0908 | 18713.2 | 50.00 | Sequence |
| DRB3_0101 | 602 | VVYQNPPAGTGVNRD | VYQNPPAGT | 0.0903 | 18817.2 | 50.00 | Sequence |
| DRB3_0101 | 105 | TEGPMTPKRAIEVIA | MTPKRAIEV | 0.0899 | 18902.1 | 50.00 | Sequence |
| DRB3_0101 | 78 | EAETPAGPLPYIVME | PAGPLPYIV | 0.0897 | 18945.1 | 50.00 | Sequence |
| DRB3_0101 | 102 | IVHTEGPMTPKRAIE | IVHTEGPMT | 0.0890 | 19080.8 | 50.00 | Sequence |
| DRB3_0101 | 434 | LTYAEAVKKLTAAGF | VKKLTAAGF | 0.0880 | 19291.7 | 50.00 | Sequence |
| DRB3_0101 | 108 | PMTPKRAIEVIADAC | MTPKRAIEV | 0.0876 | 19372.9 | 50.00 | Sequence |
| DRB3_0101 | 201 | LGCVLYEVLTGEPPF | LGCVLYEVL | 0.0867 | 19563.5 | 50.00 | Sequence |
| DRB3_0101 | 118 | IADACQALNFSHQNG | QALNFSHQN | 0.0864 | 19627.1 | 50.00 | Sequence |
| DRB3_0101 | 294 | SLLSSAAGNLSGPRT | LSSAAGNLS | 0.0863 | 19659.2 | 50.00 | Sequence |
| DRB3_0101 | 106 | EGPMTPKRAIEVIAD | MTPKRAIEV | 0.0857 | 19773.1 | 50.00 | Sequence |
| DRB3_0101 | 432 | STLTYAEAVKKLTAA | YAEAVKKLT | 0.0854 | 19845.4 | 50.00 | Sequence |
| DRB3_0101 | 367 | QSSADAIATLQNRGF | SSADAIATL | 0.0847 | 20004.9 | 50.00 | Sequence |
| DRB3_0101 | 356 | TRDVQVPDVRGQSSA | QVPDVRGQS | 0.0842 | 20095.6 | 50.00 | Sequence |
| DRB3_0101 | 483 | VIIIVGSGPATKDIP | IIVGSGPAT | 0.0835 | 20259.5 | 50.00 | Sequence |
| DRB3_0101 | 109 | MTPKRAIEVIADACQ | MTPKRAIEV | 0.0834 | 20286.1 | 50.00 | Sequence |
| DRB3_0101 | 435 | TYAEAVKKLTAAGFG | VKKLTAAGF | 0.0830 | 20376.0 | 50.00 | Sequence |
| DRB3_0101 | 420 | STGPEQREIPDVSTL | EQREIPDVS | 0.0821 | 20564.5 | 50.00 | Sequence |
| DRB3_0101 | 515 | GFTKFSQASVDSPRP | FSQASVDSP | 0.0819 | 20617.3 | 50.00 | Sequence |
| DRB3_0101 | 357 | RDVQVPDVRGQSSAD | QVPDVRGQS | 0.0813 | 20741.3 | 50.00 | Sequence |
| DRB3_0101 | 103 | VHTEGPMTPKRAIEV | MTPKRAIEV | 0.0810 | 20813.2 | 50.00 | Sequence |
| DRB3_0101 | 411 | AGDEITVNVSTGPEQ | AGDEITVNV | 0.0809 | 20835.1 | 50.00 | Sequence |
| DRB3_0101 | 358 | DVQVPDVRGQSSADA | QVPDVRGQS | 0.0809 | 20847.2 | 50.00 | Sequence |
| DRB3_0101 | 104 | HTEGPMTPKRAIEVI | MTPKRAIEV | 0.0805 | 20920.9 | 50.00 | Sequence |
| DRB3_0101 | 368 | SSADAIATLQNRGFK | SSADAIATL | 0.0803 | 20970.8 | 50.00 | Sequence |
| DRB3_0101 | 381 | FKIRTLQKPDSTIPP | FKIRTLQKP | 0.0799 | 21057.0 | 50.00 | Sequence |
| DRB3_0101 | 66 | NHPAIVAVYDTGEAE | VAVYDTGEA | 0.0793 | 21190.0 | 50.00 | Sequence |
| DRB3_0101 | 76 | TGEAETPAGPLPYIV | PAGPLPYIV | 0.0791 | 21253.6 | 50.00 | Sequence |
| DRB3_0101 | 553 | QVSKGNQFVMPDLSG | NQFVMPDLS | 0.0787 | 21334.7 | 50.00 | Sequence |
| DRB3_0101 | 522 | ASVDSPRPAGEVTGT | ASVDSPRPA | 0.0786 | 21362.2 | 50.00 | Sequence |
| DRB3_0101 | 77 | GEAETPAGPLPYIVM | PAGPLPYIV | 0.0785 | 21382.7 | 50.00 | Sequence |
| DRB3_0101 | 603 | VYQNPPAGTGVNRDG | VYQNPPAGT | 0.0774 | 21641.6 | 50.00 | Sequence |
| DRB3_0101 | 452 | KQANSPSTPELVGKV | STPELVGKV | 0.0770 | 21746.0 | 50.00 | Sequence |
| DRB3_0101 | 68 | PAIVAVYDTGEAETP | VAVYDTGEA | 0.0762 | 21913.0 | 50.00 | Sequence |
| DRB3_0101 | 162 | IADSGNSVTQTAAVI | NSVTQTAAV | 0.0759 | 21985.9 | 50.00 | Sequence |
| DRB3_0101 | 369 | SADAIATLQNRGFKI | TLQNRGFKI | 0.0758 | 22014.5 | 50.00 | Sequence |
| DRB3_0101 | 67 | HPAIVAVYDTGEAET | VAVYDTGEA | 0.0758 | 22018.0 | 50.00 | Sequence |
| DRB3_0101 | 295 | LLSSAAGNLSGPRTD | LSSAAGNLS | 0.0754 | 22121.0 | 50.00 | Sequence |
| DRB3_0101 | 453 | QANSPSTPELVGKVI | NSPSTPELV | 0.0737 | 22513.8 | 50.00 | Sequence |
| DRB3_0101 | 176 | IGTAQYLSPEQARGD | QYLSPEQAR | 0.0737 | 22532.3 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB3_0101 | 535 | GTNPPAGTTVPVDSV | GTTVPVDSV | 0.0725 | 22821.1 | 50.00 | Sequence |
| DRB3_0101 | 366 | GQSSADAIATLQNRG | SSADAIATL | 0.0723 | 22875.5 | 50.00 | Sequence |
| DRB3_0101 | 436 | YAEAVKKLTAAGFGR | VKKLTAAGF | 0.0721 | 22921.6 | 50.00 | Sequence |
| DRB3_0101 | 454 | ANSPSTPELVGKVIG | NSPSTPELV | 0.0713 | 23111.8 | 50.00 | Sequence |
| DRB3_0101 | 412 | GDEITVNVSTGPEQR | VNVSTGPEQ | 0.0711 | 23163.4 | 50.00 | Sequence |
| DRB3_0101 | 370 | ADAIATLQNRGFKIR | TLQNRGFKI | 0.0709 | 23206.3 | 50.00 | Sequence |
| DRB3_0101 | 485 | IIVGSGPATKDIPDV | IIVGSGPAT | 0.0709 | 23212.3 | 50.00 | Sequence |
| DRB3_0101 | 177 | GTAQYLSPEQARGDS | QYLSPEQAR | 0.0700 | 23450.4 | 50.00 | Sequence |
| DRB3_0101 | 484 | IIIVGSGPATKDIPD | IIVGSGPAT | 0.0699 | 23469.4 | 50.00 | Sequence |
| DRB3_0101 | 433 | TLTYAEAVKKLTAAG | YAEAVKKLT | 0.0694 | 23597.8 | 50.00 | Sequence |
| DRB3_0101 | 507 | AQKNLNVYGFTKFSQ | QKNLNVYGF | 0.0694 | 23605.7 | 50.00 | Sequence |
| DRB3_0101 | 269 | RADLVRVHNGEPPEA | VHNGEPPEA | 0.0687 | 23785.9 | 50.00 | Sequence |
| DRB3_0101 | 455 | NSPSTPELVGKVIGT | NSPSTPELV | 0.0686 | 23794.4 | 50.00 | Sequence |
| DRB3_0101 | 178 | TAQYLSPEQARGDSV | LSPEQARGD | 0.0685 | 23830.5 | 50.00 | Sequence |
| DRB3_0101 | 596 | GSQHNRVVYQNPPAG | QHNRVVYQN | 0.0683 | 23869.2 | 50.00 | Sequence |
| DRB3_0101 | 306 | PRTDPLPRQDLDDTD | PRQDLDDTD | 0.0682 | 23914.4 | 50.00 | Sequence |
| DRB3_0101 | 470 | NPPANQTSAITNVVI | QTSAITNVV | 0.0670 | 24226.2 | 50.00 | Sequence |
| DRB3_0101 | 69 | AIVAVYDTGEAETPA | VAVYDTGEA | 0.0670 | 24226.4 | 50.00 | Sequence |
| DRB3_0101 | 270 | ADLVRVHNGEPPEAP | VHNGEPPEA | 0.0670 | 24230.6 | 50.00 | Sequence |
| DRB3_0101 | 245 | DLDAVVLKALAKNPE | LDAVVLKAL | 0.0667 | 24291.0 | 50.00 | Sequence |
| DRB3_0101 | 371 | DAIATLQNRGFKIRT | TLQNRGFKI | 0.0663 | 24406.9 | 50.00 | Sequence |
| DRB3_0101 | 307 | RTDPLPRQDLDDTDR | PRQDLDDTD | 0.0662 | 24441.0 | 50.00 | Sequence |
| DRB3_0101 | 179 | AQYLSPEQARGDSVD | LSPEQARGD | 0.0660 | 24491.3 | 50.00 | Sequence |
| DRB3_0101 | 418 | NVSTGPEQREIPDVS | EQREIPDVS | 0.0658 | 24542.5 | 50.00 | Sequence |
| DRB3_0101 | 456 | SPSTPELVGKVIGTN | STPELVGKV | 0.0657 | 24549.7 | 50.00 | Sequence |
| DRB3_0101 | 592 | VDAGGSQHNRVVYQN | QHNRVVYQN | 0.0656 | 24585.3 | 50.00 | Sequence |
| DRB3_0101 | 469 | TNPPANQTSAITNVV | QTSAITNVV | 0.0654 | 24629.5 | 50.00 | Sequence |
| DRB3_0101 | 437 | AEAVKKLTAAGFGRF | VKKLTAAGF | 0.0646 | 24867.5 | 50.00 | Sequence |
| DRB3_0101 | 180 | QYLSPEQARGDSVDA | QYLSPEQAR | 0.0642 | 24958.1 | 50.00 | Sequence |
| DRB3_0101 | 275 | VHNGEPPEAPKVLTD | VHNGEPPEA | 0.0639 | 25053.9 | 50.00 | Sequence |
| DRB3_0101 | 246 | LDAVVLKALAKNPEN | LDAVVLKAL | 0.0636 | 25127.4 | 50.00 | Sequence |
| DRB3_0101 | 429 | PDVSTLTYAEAVKKL | TYAEAVKKL | 0.0636 | 25133.4 | 50.00 | Sequence |
| DRB3_0101 | 419 | VSTGPEQREIPDVST | EQREIPDVS | 0.0635 | 25163.1 | 50.00 | Sequence |
| DRB3_0101 | 302 | NLSGPRTDPLPRQDL | LSGPRTDPL | 0.0632 | 25238.3 | 50.00 | Sequence |
| DRB3_0101 | 372 | AIATLQNRGFKIRTL | TLQNRGFKI | 0.0625 | 25416.7 | 50.00 | Sequence |
| DRB3_0101 | 457 | PSTPELVGKVIGTNP | STPELVGKV | 0.0625 | 25417.3 | 50.00 | Sequence |
| DRB3_0101 | 70 | IVAVYDTGEAETPAG | VAVYDTGEA | 0.0623 | 25468.8 | 50.00 | Sequence |
| DRB3_0101 | 462 | LVGKVIGTNPPANQT | VIGTNPPAN | 0.0622 | 25510.7 | 50.00 | Sequence |
| DRB3_0101 | 383 | IRTLQKPDSTIPPDH | TLQKPDSTI | 0.0617 | 25635.2 | 50.00 | Sequence |
| DRB3_0101 | 374 | ATLQNRGFKIRTLQK | TLQNRGFKI | 0.0617 | 25646.6 | 50.00 | Sequence |
| DRB3_0101 | 438 | EAVKKLTAAGFGRFK | VKKLTAAGF | 0.0616 | 25667.4 | 50.00 | Sequence |
| DRB3_0101 | 593 | DAGGSQHNRVVYQNP | QHNRVVYQN | 0.0612 | 25781.0 | 50.00 | Sequence |
| DRB3_0101 | 296 | LSSAAGNLSGPRTDP | LSSAAGNLS | 0.0612 | 25785.7 | 50.00 | Sequence |
| DRB3_0101 | 272 | LVRVHNGEPPEAPKV | VHNGEPPEA | 0.0606 | 25945.2 | 50.00 | Sequence |
| DRB3_0101 | 458 | STPELVGKVIGTNPP | STPELVGKV | 0.0605 | 25983.7 | 50.00 | Sequence |
| DRB3_0101 | 303 | LSGPRTDPLPRQDLD | LSGPRTDPL | 0.0601 | 26082.0 | 50.00 | Sequence |
| DRB3_0101 | 595 | GGSQHNRVVYQNPPA | QHNRVVYQN | 0.0600 | 26120.7 | 50.00 | Sequence |
| DRB3_0101 | 164 | DSGNSVTQTAAVIGT | SVTQTAAVI | 0.0597 | 26220.9 | 50.00 | Sequence |
| DRB3_0101 | 279 | EPPEAPKVLTDAERT | KVLTDAERT | 0.0596 | 26244.2 | 50.00 | Sequence |
| DRB3_0101 | 439 | AVKKLTAAGFGRFKQ | VKKLTAAGF | 0.0595 | 26277.2 | 50.00 | Sequence |
| DRB3_0101 | 589 | GADVDAGGSQHNRVV | GGSQHNRVV | 0.0595 | 26277.7 | 50.00 | Sequence |
| DRB3_0101 | 460 | PELVGKVIGTNPPAN | VIGTNPPAN | 0.0594 | 26284.3 | 50.00 | Sequence |
| DRB3_0101 | 271 | DLVRVHNGEPPEAPK | VHNGEPPEA | 0.0592 | 26357.8 | 50.00 | Sequence |
| DRB3_0101 | 373 | IATLQNRGFKIRTLQ | TLQNRGFKI | 0.0591 | 26384.9 | 50.00 | Sequence |
| DRB3_0101 | 163 | ADSGNSVTQTAAVIG | NSVTQTAAV | 0.0591 | 26389.2 | 50.00 | Sequence |
| DRB3_0101 | 167 | NSVTQTAAVIGTAQY | AAVIGTAQY | 0.0589 | 26422.3 | 50.00 | Sequence |
| DRB3_0101 | 382 | KIRTLQKPDSTIPPD | TLQKPDSTI | 0.0589 | 26422.9 | 50.00 | Sequence |
| DRB3_0101 | 384 | RTLQKPDSTIPPDHV | TLQKPDSTI | 0.0588 | 26456.9 | 50.00 | Sequence |
| DRB3_0101 | 594 | AGGSQHNRVVYQNPP | QHNRVVYQN | 0.0584 | 26591.2 | 50.00 | Sequence |
| DRB3_0101 | 461 | ELVGKVIGTNPPANQ | VIGTNPPAN | 0.0583 | 26605.9 | 50.00 | Sequence |
| DRB3_0101 | 440 | VKKLTAAGFGRFKQA | VKKLTAAGF | 0.0581 | 26653.1 | 50.00 | Sequence |
| DRB3_0101 | 590 | ADVDAGGSQHNRVVY | GGSQHNRVV | 0.0580 | 26683.7 | 50.00 | Sequence |
| DRB3_0101 | 604 | YQNPPAGTGVNRDGI | YQNPPAGTG | 0.0580 | 26687.8 | 50.00 | Sequence |
| DRB3_0101 | 274 | RVHNGEPPEAPKVLT | VHNGEPPEA | 0.0579 | 26717.5 | 50.00 | Sequence |
| DRB3_0101 | 71 | VAVYDTGEAETPAGP | VAVYDTGEA | 0.0578 | 26744.7 | 50.00 | Sequence |
| DRB3_0101 | 165 | SGNSVTQTAAVIGTA | NSVTQTAAV | 0.0578 | 26746.2 | 50.00 | Sequence |

```
   DRB3_0101  465  KVIGTNPPANQTSAI  VIGTNPPAN        0.0578      26758.9                 50.00     Sequence
   DRB3_0101  463  VGKVIGTNPPANQTS  VIGTNPPAN        0.0576      26811.1                 50.00     Sequence
   DRB3_0101  591  DVDAGGSQHNRVVYQ  GGSQHNRVV        0.0570      26995.6                 50.00     Sequence
   DRB3_0101  413  DEITVNVSTGPEQRE  VNVSTGPEQ        0.0540      27861.5                 50.00     Sequence
   DRB3_0101  273  VRVHNGEPPEAPKVL  VHNGEPPEA        0.0538      27950.6                 50.00     Sequence
   DRB3_0101  428  IPDVSTLTYAEAVKK  STLTYAEAV        0.0537      27964.2                 50.00     Sequence
   DRB3_0101  166  GNSVTQTAAVIGTAQ  NSVTQTAAV        0.0533      28086.7                 50.00     Sequence
   DRB3_0101  297  SSAAGNLSGPRTDPL  LSGPRTDPL        0.0529      28202.1                 50.00     Sequence
   DRB3_0101  414  EITVNVSTGPEQREI  VNVSTGPEQ        0.0510      28808.8                 50.00     Sequence
   DRB3_0101  234  PPSARHEGLSADLDA  HEGLSADLD        0.0501      29071.5                 50.00     Sequence
   DRB3_0101  300  AGNLSGPRTDPLPRQ  LSGPRTDPL        0.0501      29074.0                 50.00     Sequence
   DRB3_0101  305  GPRTDPLPRQDLDDT  TDPLPRQDL        0.0495      29268.1                 50.00     Sequence
   DRB3_0101  464  GKVIGTNPPANQTSA  VIGTNPPAN        0.0495      29280.4                 50.00     Sequence
   DRB3_0101  298  SAAGNLSGPRTDPLP  LSGPRTDPL        0.0494      29312.5                 50.00     Sequence
   DRB3_0101  255  AKNPENRYQTAAEMR  KNPENRYQT        0.0491      29382.0                 50.00     Sequence
   DRB3_0101  301  GNLSGPRTDPLPRQD  LSGPRTDPL        0.0490      29411.3                 50.00     Sequence
   DRB3_0101  585  MLDKGADVDAGGSQH  ADVDAGGSQ        0.0490      29432.3                 50.00     Sequence
   DRB3_0101  233  IPPSARHEGLSADLD  HEGLSADLD        0.0484      29621.7                 50.00     Sequence
   DRB3_0101  459  TPELVGKVIGTNPPA  LVGKVIGTN        0.0477      29852.1                 50.00     Sequence
   DRB3_0101  588  KGADVDAGGSQHNRV  AGGSQHNRV        0.0475      29913.5                 50.00     Sequence
   DRB3_0101  466  VIGTNPPANQTSAIT  VIGTNPPAN        0.0475      29915.5                 50.00     Sequence
   DRB3_0101   72  AVYDTGEAETPAGPL  AVYDTGEAE        0.0472      29996.2                 50.00     Sequence
   DRB3_0101  299  AAGNLSGPRTDPLPR  LSGPRTDPL        0.0471      30048.1                 50.00     Sequence
   DRB3_0101  304  SGPRTDPLPRQDLDD  TDPLPRQDL        0.0468      30121.7                 50.00     Sequence
   DRB3_0101  276  HNGEPPEAPKVLTDA  HNGEPPEAP        0.0447      30818.0                 50.00     Sequence
   DRB3_0101  468  GTNPPANQTSAITNV  NQTSAITNV        0.0439      31102.4                 50.00     Sequence
   DRB3_0101  586  LDKGADVDAGGSQHN  ADVDAGGSQ        0.0424      31606.5                 50.00     Sequence
   DRB3_0101  528  RPAGEVTGTNPPAGT  TGTNPPAGT        0.0417      31846.8                 50.00     Sequence
   DRB3_0101  532  EVTGTNPPAGTTVPV  TGTNPPAGT        0.0416      31869.9                 50.00     Sequence
   DRB3_0101  232  PIPPSARHEGLSADL  RHEGLSADL        0.0414      31940.6                 50.00     Sequence
   DRB3_0101  534  TGTNPPAGTTVPVDS  AGTTVPVDS        0.0411      32052.1                 50.00     Sequence
   DRB3_0101  442  KLTAAGFGRFKQANS  LTAAGFGRF        0.0405      32251.4                 50.00     Sequence
   DRB3_0101  571  VDAEPRLRALGWTGM  VDAEPRLRA        0.0399      32472.7                 50.00     Sequence
   DRB3_0101  529  PAGEVTGTNPPAGTT  TGTNPPAGT        0.0394      32636.2                 50.00     Sequence
   DRB3_0101  443  LTAAGFGRFKQANSP  FGRFKQANS        0.0391      32738.4                 50.00     Sequence
   DRB3_0101  278  GEPPEAPKVLTDAER  GEPPEAPKV        0.0389      32840.2                 50.00     Sequence
   DRB3_0101   73  VYDTGEAETPAGPLP  VYDTGEAET        0.0388      32847.3                 50.00     Sequence
   DRB3_0101  415  ITVNVSTGPEQREIP  ITVNVSTGP        0.0378      33199.6                 50.00     Sequence
   DRB3_0101  530  AGEVTGTNPPAGTTV  TGTNPPAGT        0.0376      33303.2                 50.00     Sequence
   DRB3_0101  277  NGEPPEAPKVLTDAE  GEPPEAPKV        0.0373      33406.1                 50.00     Sequence
   DRB3_0101  417  VNVSTGPEQREIPDV  PEQREIPDV        0.0369      33551.7                 50.00     Sequence
   DRB3_0101  533  VTGTNPPAGTTVPVD  TGTNPPAGT        0.0364      33706.0                 50.00     Sequence
   DRB3_0101  587  DKGADVDAGGSQHNR  ADVDAGGSQ        0.0360      33875.6                 50.00     Sequence
   DRB3_0101  416  TVNVSTGPEQREIPD  VNVSTGPEQ        0.0343      34513.8                 50.00     Sequence
   DRB3_0101  441  KKLTAAGFGRFKQAN  LTAAGFGRF        0.0328      35066.0                 50.00     Sequence
   DRB3_0101   74  YDTGEAETPAGPLPY  YDTGEAETP        0.0326      35143.5                 50.00     Sequence
   DRB3_0101  444  TAAGFGRFKQANSPS  FGRFKQANS        0.0325      35161.7                 50.00     Sequence
   DRB3_0101  531  GEVTGTNPPAGTTVP  TGTNPPAGT        0.0321      35314.2                 50.00     Sequence
   DRB3_0101  400  GTDPAANTSVSAGDE  TDPAANTSV        0.0321      35323.8                 50.00     Sequence
   DRB3_0101  467  IGTNPPANQTSAITN  GTNPPANQT        0.0319      35423.3                 50.00     Sequence
   DRB3_0101  231  DPIPPSARHEGLSAD  ARHEGLSAD        0.0303      36029.8                 50.00     Sequence
   DRB3_0101  247  DAVVLKALAKNPENR  VVLKALAKN        0.0300      36126.2                 50.00     Sequence
   DRB3_0101  523  SVDSPRPAGEVTGTN  DSPRPAGEV        0.0276      37094.3                 50.00     Sequence
   DRB3_0101   75  DTGEAETPAGPLPYI  TPAGPLPYI        0.0258      37806.2                 50.00     Sequence
   DRB3_0101  229  REDPIPPSARHEGLS  IPPSARHEG        0.0251      38090.7                 50.00     Sequence
   DRB3_0101   56  RREAQNAAALNHPAI  AQNAAALNH        0.0251      38095.2                 50.00     Sequence
   DRB3_0101  230  EDPIPPSARHEGLSA  SARHEGLSA        0.0246      38317.2                 50.00     Sequence
   DRB3_0101  527  PRPAGEVTGTNPPAG  VTGTNPPAG        0.0245      38360.8                 50.00     Sequence
   DRB3_0101  524  VDSPRPAGEVTGTNP  DSPRPAGEV        0.0243      38459.3                 50.00     Sequence
   DRB3_0101  525  DSPRPAGEVTGTNPP  DSPRPAGEV        0.0240      38562.6                 50.00     Sequence
   DRB3_0101  526  SPRPAGEVTGTNPPA  PAGEVTGTN        0.0205      40035.4                 50.00     Sequence
-----------------------------------------------------------------------------------------------

Allele: DRB3_0101. Number of high binders 6. Number of weak binders 42. Number of peptides 612

-----------------------------------------------------------------------------------------------
```

```
--------------------------------------------------------------------------------------------------
      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
--------------------------------------------------------------------------------------------------
   DRB4_0101   83  AGPLPYIVMEYVDGV  LPYIVMEYV        0.7283         18.9          SB     0.80     Sequence
   DRB4_0101   84  GPLPYIVMEYVDGVT  LPYIVMEYV        0.7269         19.2          SB     1.00     Sequence
   DRB4_0101   85  PLPYIVMEYVDGVTL  LPYIVMEYV        0.7125         22.4          SB     2.00     Sequence
   DRB4_0101   33  HRDVAVKVLRADLAR  VKVLRADLA        0.7063         24.0          SB     2.00     Sequence
   DRB4_0101   82  PAGPLPYIVMEYVDG  LPYIVMEYV        0.7017         25.2          SB     2.00     Sequence
   DRB4_0101  378  NRGFKIRTLQKPDST  FKIRTLQKP        0.6925         27.9          SB     2.00     Sequence
   DRB4_0101   34  RDVAVKVLRADLARD  VKVLRADLA        0.6909         28.3          SB     2.00     Sequence
   DRB4_0101   32  LHRDVAVKVLRADLA  VKVLRADLA        0.6899         28.6          SB     2.00     Sequence
   DRB4_0101   81  TPAGPLPYIVMEYVD  LPYIVMEYV        0.6893         28.8          SB     2.00     Sequence
   DRB4_0101  379  RGFKIRTLQKPDSTI  FKIRTLQKP        0.6826         31.0          SB     2.00     Sequence
   DRB4_0101   36  VAVKVLRADLARDPS  VKVLRADLA        0.6799         31.9          SB     2.00     Sequence
   DRB4_0101   35  DVAVKVLRADLARDP  VKVLRADLA        0.6781         32.5          SB     2.00     Sequence
   DRB4_0101  377  QNRGFKIRTLQKPDS  FKIRTLQKP        0.6658         37.2          SB     4.00     Sequence
   DRB4_0101   37  AVKVLRADLARDPSF  VKVLRADLA        0.6572         40.8          SB     4.00     Sequence
   DRB4_0101  380  GFKIRTLQKPDSTIP  KIRTLQKPD        0.6554         41.6          SB     4.00     Sequence
   DRB4_0101  376  LQNRGFKIRTLQKPD  FKIRTLQKP        0.6369         50.8          WB     4.00     Sequence
   DRB4_0101   86  LPYIVMEYVDGVTLR  LPYIVMEYV        0.6346         52.1          WB     4.00     Sequence
   DRB4_0101   80  ETPAGPLPYIVMEYV  LPYIVMEYV        0.6302         54.7          WB     4.00     Sequence
   DRB4_0101  121  ACQALNFSHQNGIIH  ALNFSHQNG        0.6053         71.6          WB     8.00     Sequence
   DRB4_0101  219  SPVSVAYQHVREDPI  SPVSVAYQH        0.5894         85.0          WB     8.00     Sequence
   DRB4_0101  120  DACQALNFSHQNGII  LNFSHQNGI        0.5871         87.1          WB     8.00     Sequence
   DRB4_0101  122  CQALNFSHQNGIIHR  LNFSHQNGI        0.5847         89.4          WB     8.00     Sequence
   DRB4_0101  556  KGNQFVMPDLSGMFW  NQFVMPDLS        0.5830         91.1          WB     8.00     Sequence
   DRB4_0101   22  SEVHLARDLRLHRDV  VHLARDLRL        0.5811         93.0          WB     8.00     Sequence
   DRB4_0101  381  FKIRTLQKPDSTIPP  KIRTLQKPD        0.5810         93.1          WB     8.00     Sequence
   DRB4_0101  557  GNQFVMPDLSGMFWV  NQFVMPDLS        0.5805         93.6          WB     8.00     Sequence
   DRB4_0101  546  VDSVIELQVSKGNQF  SVIELQVSK        0.5758         98.5          WB     8.00     Sequence
   DRB4_0101  218  DSPVSVAYQHVREDP  SPVSVAYQH        0.5699        105.0          WB    16.00     Sequence
   DRB4_0101  119  ADACQALNFSHQNGI  LNFSHQNGI        0.5665        108.9          WB    16.00     Sequence
   DRB4_0101  123  QALNFSHQNGIIHRD  LNFSHQNGI        0.5660        109.5          WB    16.00     Sequence
   DRB4_0101  375  TLQNRGFKIRTLQKP  FKIRTLQKP        0.5655        110.1          WB    16.00     Sequence
   DRB4_0101  545  PVDSVIELQVSKGNQ  DSVIELQVS        0.5646        111.1          WB    16.00     Sequence
   DRB4_0101   24  VHLARDLRLHRDVAV  RDLRLHRDV        0.5642        111.7          WB    16.00     Sequence
   DRB4_0101  217  GDSPVSVAYQHVRED  SPVSVAYQH        0.5628        113.3          WB    16.00     Sequence
   DRB4_0101   23  EVHLARDLRLHRDVA  VHLARDLRL        0.5588        118.3          WB    16.00     Sequence
   DRB4_0101  544  VPVDSVIELQVSKGN  SVIELQVSK        0.5562        121.8          WB    16.00     Sequence
   DRB4_0101  555  SKGNQFVMPDLSGMF  NQFVMPDLS        0.5440        138.9          WB    16.00     Sequence
   DRB4_0101   49  PSFYLRFRREAQNAA  LRFRREAQN        0.5429        140.5          WB    16.00     Sequence
   DRB4_0101   50  SFYLRFRREAQNAAA  LRFRREAQN        0.5425        141.2          WB    16.00     Sequence
   DRB4_0101   38  VKVLRADLARDPSFY  VKVLRADLA        0.5412        143.1          WB    16.00     Sequence
   DRB4_0101   20  GMSEVHLARDLRLHR  VHLARDLRL        0.5403        144.6          WB    16.00     Sequence
   DRB4_0101   19  GGMSEVHLARDLRLH  VHLARDLRL        0.5391        146.4          WB    16.00     Sequence
   DRB4_0101  543  TVPVDSVIELQVSKG  SVIELQVSK        0.5359        151.6          WB    16.00     Sequence
   DRB4_0101   21  MSEVHLARDLRLHRD  VHLARDLRL        0.5351        153.0          WB    16.00     Sequence
   DRB4_0101   95  DGVTLRDIVHTEGPM  LRDIVHTEG        0.5349        153.4          WB    16.00     Sequence
   DRB4_0101   94  VDGVTLRDIVHTEGP  LRDIVHTEG        0.5307        160.3          WB    16.00     Sequence
   DRB4_0101   48  DPSFYLRFRREAQNA  LRFRREAQN        0.5280        165.2          WB    16.00     Sequence
   DRB4_0101   93  YVDGVTLRDIVHTEG  DGVTLRDIV        0.5273        166.5          WB    16.00     Sequence
   DRB4_0101  598  QHNRVVYQNPPAGTG  NRVVYQNPP        0.5268        167.4          WB    16.00     Sequence
   DRB4_0101  216  TGDSPVSVAYQHVRE  SPVSVAYQH        0.5265        167.9          WB    16.00     Sequence
   DRB4_0101  148  TNAVKVMDFGIARAI  AVKVMDFGI        0.5245        171.6          WB    16.00     Sequence
   DRB4_0101   27  ARDLRLHRDVAVKVL  RDLRLHRDV        0.5242        172.1          WB    16.00     Sequence
   DRB4_0101   18  FGGMSEVHLARDLRL  VHLARDLRL        0.5205        179.1          WB    16.00     Sequence
   DRB4_0101   31  RLHRDVAVKVLRADL  LHRDVAVKV        0.5203        179.6          WB    16.00     Sequence
   DRB4_0101  215  FTGDSPVSVAYQHVR  SPVSVAYQH        0.5180        184.0          WB    16.00     Sequence
   DRB4_0101   26  LARDLRLHRDVAVKV  RDLRLHRDV        0.5177        184.6          WB    16.00     Sequence
   DRB4_0101  547  DSVIELQVSKGNQFV  DSVIELQVS        0.5175        185.0          WB    16.00     Sequence
   DRB4_0101   97  VTLRDIVHTEGPMTP  LRDIVHTEG        0.5168        186.5          WB    16.00     Sequence
   DRB4_0101  558  NQFVMPDLSGMFWVD  NQFVMPDLS        0.5164        187.2          WB    16.00     Sequence
   DRB4_0101  147  ATNAVKVMDFGIARA  VKVMDFGIA        0.5158        188.4          WB    16.00     Sequence
   DRB4_0101   51  FYLRFRREAQNAAAL  LRFRREAQN        0.5158        188.5          WB    16.00     Sequence
   DRB4_0101  597  SQHNRVVYQNPPAGT  HNRVVYQNP        0.5149        190.4          WB    16.00     Sequence
   DRB4_0101   96  GVTLRDIVHTEGPMT  LRDIVHTEG        0.5127        194.9          WB    16.00     Sequence
```

```
DRB4_0101  146  SATNAVKVMDFGIAR  VKVMDFGIA        0.5118        196.9          WB    16.00      Sequence
DRB4_0101   25  HLARDLRLHRDVAVK  RDLRLHRDV        0.5110        198.5          WB    16.00      Sequence
DRB4_0101  542  TTVPVDSVIELQVSK  DSVIELQVS        0.5104        199.8          WB    16.00      Sequence
DRB4_0101   47  RDPSFYLRFRREAQN  LRFRREAQN        0.5100        200.7          WB    16.00      Sequence
DRB4_0101  554  VSKGNQFVMPDLSGM  NQFVMPDLS        0.5099        200.8          WB    16.00      Sequence
DRB4_0101   99  LRDIVHTEGPMTPKR  LRDIVHTEG        0.5068        207.8          WB    16.00      Sequence
DRB4_0101   98  TLRDIVHTEGPMTPK  LRDIVHTEG        0.5068        207.9          WB    16.00      Sequence
DRB4_0101   52  YLRFRREAQNAAALN  LRFRREAQN        0.5055        210.7          WB    16.00      Sequence
DRB4_0101  145  ISATNAVKVMDFGIA  VKVMDFGIA        0.4985        227.4          WB    32.00      Sequence
DRB4_0101  599  HNRVVYQNPPAGTGV  HNRVVYQNP        0.4970        230.9          WB    32.00      Sequence
DRB4_0101  382  KIRTLQKPDSTIPPD  KIRTLQKPD        0.4957        234.4          WB    32.00      Sequence
DRB4_0101  596  GSQHNRVVYQNPPAG  HNRVVYQNP        0.4955        234.7          WB    32.00      Sequence
DRB4_0101  124  ALNFSHQNGIIHRDV  LNFSHQNGI        0.4952        235.4          WB    32.00      Sequence
DRB4_0101  246  LDAVVLKALAKNPEN  DAVVLKALA        0.4913        245.6          WB    32.00      Sequence
DRB4_0101  553  QVSKGNQFVMPDLSG  NQFVMPDLS        0.4904        248.1          WB    32.00      Sequence
DRB4_0101   28  RDLRLHRDVAVKVLR  RDLRLHRDV        0.4901        248.9          WB    32.00      Sequence
DRB4_0101  245  DLDAVVLKALAKNPE  DAVVLKALA        0.4871        257.1          WB    32.00      Sequence
DRB4_0101  576  RLRALGWTGMLDKGA  LRALGWTGM        0.4861        259.8          WB    32.00      Sequence
DRB4_0101  574  EPRLRALGWTGMLDK  LRALGWTGM        0.4861        260.0          WB    32.00      Sequence
DRB4_0101  611  TGVNRDGIITLRFGQ  GIITLRFGQ        0.4829        269.2          WB    32.00      Sequence
DRB4_0101  149  NAVKVMDFGIARAIA  VKVMDFGIA        0.4790        280.6          WB    32.00      Sequence
DRB4_0101  575  PRLRALGWTGMLDKG  LRALGWTGM        0.4774        285.6          WB    32.00      Sequence
DRB4_0101   92  EYVDGVTLRDIVHTE  VTLRDIVHT        0.4752        292.5          WB    32.00      Sequence
DRB4_0101  244  ADLDAVVLKALAKNP  DAVVLKALA        0.4736        297.6          WB    32.00      Sequence
DRB4_0101   53  LRFRREAQNAAALNH  LRFRREAQN        0.4707        306.9          WB    32.00      Sequence
DRB4_0101  214  PFTGDSPVSVAYQHV  SPVSVAYQH        0.4700        309.4          WB    32.00      Sequence
DRB4_0101  118  IADACQALNFSHQNG  ALNFSHQNG        0.4691        312.5          WB    32.00      Sequence
DRB4_0101  552  LQVSKGNQFVMPDLS  NQFVMPDLS        0.4645        328.2          WB    32.00      Sequence
DRB4_0101  130  QNGIIHRDVKPANIM  QNGIIHRDV        0.4617        338.3          WB    32.00      Sequence
DRB4_0101  247  DAVVLKALAKNPENR  DAVVLKALA        0.4595        346.4          WB    32.00      Sequence
DRB4_0101  573  AEPRLRALGWTGMLD  LRALGWTGM        0.4575        354.3          WB    32.00      Sequence
DRB4_0101  329  GRWVAVVAVLAVLTV  AVVAVLAVL        0.4558        360.5          WB    32.00      Sequence
DRB4_0101   91  MEYVDGVTLRDIVHT  GVTLRDIVH        0.4553        362.8          WB    32.00      Sequence
DRB4_0101  360  QVPDVRGQSSADAIA  VPDVRGQSS        0.4540        367.9          WB    32.00      Sequence
DRB4_0101  150  AVKVMDFGIARAIAD  VKVMDFGIA        0.4528        372.6          WB    32.00      Sequence
DRB4_0101  115  IEVIADACQALNFSH  IEVIADACQ        0.4507        381.0          WB    32.00      Sequence
DRB4_0101  129  HQNGIIHRDVKPANI  QNGIIHRDV        0.4504        382.6          WB    32.00      Sequence
DRB4_0101  361  VPDVRGQSSADAIAT  VPDVRGQSS        0.4498        384.7          WB    32.00      Sequence
DRB4_0101  220  PVSVAYQHVREDPIP  PVSVAYQHV        0.4497        385.2          WB    32.00      Sequence
DRB4_0101  548  SVIELQVSKGNQFVM  SVIELQVSK        0.4484        391.0          WB    32.00      Sequence
DRB4_0101   87  PYIVMEYVDGVTLRD  IVMEYVDGV        0.4476        394.1          WB    32.00      Sequence
DRB4_0101  173  AAVIGTAQYLSPEQA  AQYLSPEQA        0.4467        398.2          WB    32.00      Sequence
DRB4_0101  138  VKPANIMISATNAVK  ANIMISATN        0.4461        400.5          WB    32.00      Sequence
DRB4_0101  359  VQVPDVRGQSSADAI  VPDVRGQSS        0.4458        401.9          WB    32.00      Sequence
DRB4_0101  595  GGSQHNRVVYQNPPA  HNRVVYQNP        0.4457        402.5          WB    32.00      Sequence
DRB4_0101  496  IPDVAGQTVDVAQKN  IPDVAGQTV        0.4430        414.4          WB    32.00      Sequence
DRB4_0101  132  GIIHRDVKPANIMIS  GIIHRDVKP        0.4419        419.4          WB    32.00      Sequence
DRB4_0101  110  TPKRAIEVIADACQA  IEVIADACQ        0.4402        426.8          WB    32.00      Sequence
DRB4_0101   30  LRLHRDVAVKVLRAD  LRLHRDVAV        0.4388        433.5          WB    32.00      Sequence
DRB4_0101  327  SVGRWVAVVAVLAVL  VAVVAVLAV        0.4372        441.0          WB    32.00      Sequence
DRB4_0101  572  DAEPRLRALGWTGML  LRALGWTGM        0.4363        445.2          WB    32.00      Sequence
DRB4_0101  127  FSHQNGIIHRDVKPA  QNGIIHRDV        0.4346        453.9          WB    32.00      Sequence
DRB4_0101  111  PKRAIEVIADACQAL  IEVIADACQ        0.4343        455.2          WB    32.00      Sequence
DRB4_0101  125  LNFSHQNGIIHRDVK  QNGIIHRDV        0.4340        456.7          WB    32.00      Sequence
DRB4_0101  330  RWVAVVAVLAVLTVV  AVVAVLAVL        0.4338        457.5          WB    32.00      Sequence
DRB4_0101  113  RAIEVIADACQALNF  IEVIADACQ        0.4332        460.7          WB    32.00      Sequence
DRB4_0101  478  AITNVVIIIVGSGPA  NVVIIIVGS        0.4331        461.3          WB    32.00      Sequence
DRB4_0101  116  EVIADACQALNFSHQ  CQALNFSHQ        0.4324        464.7          WB    32.00      Sequence
DRB4_0101  197  DVYSLGCVLYEVLTG  VYSLGCVLY        0.4322        465.7          WB    32.00      Sequence
DRB4_0101  358  DVQVPDVRGQSSADA  VPDVRGQSS        0.4315        469.4          WB    32.00      Sequence
DRB4_0101  328  VGRWVAVVAVLAVLT  VAVVAVLAV        0.4309        472.4          WB    32.00      Sequence
DRB4_0101  479  ITNVVIIIVGSGPAT  NVVIIIVGS        0.4304        474.7          WB    32.00      Sequence
DRB4_0101  495  DIPDVAGQTVDVAQK  IPDVAGQTV        0.4301        476.1          WB    32.00      Sequence
DRB4_0101  178  TAQYLSPEQARGDSV  AQYLSPEQA        0.4299        477.6          WB    32.00      Sequence
DRB4_0101  559  QFVMPDLSGMFWVDA  MPDLSGMFW        0.4285        484.8          WB    32.00      Sequence
DRB4_0101   29  DLRLHRDVAVKVLRA  LRLHRDVAV        0.4283        485.5          WB    32.00      Sequence
```

```
DRB4_0101   89  IVMEYVDGVTLRDIV  IVMEYVDGV        0.4279       487.7       WB    32.00      Sequence
DRB4_0101  117  VIADACQALNFSHQN  CQALNFSHQ        0.4278       488.6       WB    32.00      Sequence
DRB4_0101   90  VMEYVDGVTLRDIVH  DGVTLRDIV        0.4277       488.8       WB    32.00      Sequence
DRB4_0101   88  YIVMEYVDGVTLRDI  IVMEYVDGV        0.4273       491.0       WB    32.00      Sequence
DRB4_0101  174  AVIGTAQYLSPEQAR  AQYLSPEQA        0.4271       491.9       WB    32.00      Sequence
DRB4_0101  128  SHQNGIIHRDVKPAN  QNGIIHRDV        0.4264       495.6       WB    32.00      Sequence
DRB4_0101  141  ANIMISATNAVKVMD  ANIMISATN        0.4258       499.2       WB    32.00      Sequence
DRB4_0101  243  SADLDAVVLKALAKN  DAVVLKALA        0.4254       501.2             32.00      Sequence
DRB4_0101  561  VMPDLSGMFWVDAEP  MPDLSGMFW        0.4254       501.4             32.00      Sequence
DRB4_0101  114  AIEVIADACQALNFS  IEVIADACQ        0.4248       504.3             32.00      Sequence
DRB4_0101  137  DVKPANIMISATNAV  ANIMISATN        0.4245       506.1             32.00      Sequence
DRB4_0101  341  LTVVVTIAINTFGGI  LTVVVTIAI        0.4237       510.7             32.00      Sequence
DRB4_0101  332  VAVVAVLAVLTVVVT  AVVAVLAVL        0.4232       513.3             32.00      Sequence
DRB4_0101  494  KDIPDVAGQTVDVAQ  IPDVAGQTV        0.4223       518.1             32.00      Sequence
DRB4_0101  333  AVVAVLAVLTVVVTI  VAVLAVLTV        0.4217       521.4             32.00      Sequence
DRB4_0101  355  ITRDVQVPDVRGQSS  VPDVRGQSS        0.4216       522.3             32.00      Sequence
DRB4_0101  136  RDVKPANIMISATNA  VKPANIMIS        0.4205       528.6             32.00      Sequence
DRB4_0101  426  REIPDVSTLTYAEAV  IPDVSTLTY        0.4190       537.4             32.00      Sequence
DRB4_0101  340  VLTVVVTIAINTFGG  LTVVVTIAI        0.4187       539.2             32.00      Sequence
DRB4_0101  112  KRAIEVIADACQALN  IEVIADACQ        0.4184       540.4             32.00      Sequence
DRB4_0101  427  EIPDVSTLTYAEAVK  IPDVSTLTY        0.4182       541.6             32.00      Sequence
DRB4_0101  428  IPDVSTLTYAEAVKK  IPDVSTLTY        0.4172       547.9             32.00      Sequence
DRB4_0101  331  WVAVVAVLAVLTVVV  VAVLAVLTV        0.4170       548.8             32.00      Sequence
DRB4_0101  374  ATLQNRGFKIRTLQK  RGFKIRTLQ        0.4169       549.5             32.00      Sequence
DRB4_0101  562  MPDLSGMFWVDAEPR  MPDLSGMFW        0.4168       549.9             32.00      Sequence
DRB4_0101  198  VYSLGCVLYEVLTGE  VYSLGCVLY        0.4166       551.4             32.00      Sequence
DRB4_0101  177  GTAQYLSPEQARGDS  AQYLSPEQA        0.4165       551.9             32.00      Sequence
DRB4_0101  356  TRDVQVPDVRGQSSA  VPDVRGQSS        0.4159       555.5             32.00      Sequence
DRB4_0101  142  NIMISATNAVKVMDF  NIMISATNA        0.4159       555.6             32.00      Sequence
DRB4_0101  339  AVLTVVVTIAINTFG  LTVVVTIAI        0.4154       558.3             32.00      Sequence
DRB4_0101  357  RDVQVPDVRGQSSAD  VPDVRGQSS        0.4145       563.7             32.00      Sequence
DRB4_0101  560  FVMPDLSGMFWVDAE  MPDLSGMFW        0.4138       568.0             32.00      Sequence
DRB4_0101  477  SAITNVVIIIVGSGP  ITNVVIIIV        0.4138       568.2             32.00      Sequence
DRB4_0101  109  MTPKRAIEVIADACQ  RAIEVIADA        0.4138       568.4             32.00      Sequence
DRB4_0101  139  KPANIMISATNAVKV  ANIMISATN        0.4125       576.0             32.00      Sequence
DRB4_0101  480  TNVVIIIVGSGPATK  IIIVGSGPA        0.4122       578.4             32.00      Sequence
DRB4_0101  144  MISATNAVKVMDFGI  TNAVKVMDF        0.4120       579.2             32.00      Sequence
DRB4_0101  140  PANIMISATNAVKVM  ANIMISATN        0.4120       579.5             32.00      Sequence
DRB4_0101  481  NVVIIIVGSGPATKD  VIIIVGSGP        0.4115       582.7             32.00      Sequence
DRB4_0101  577  LRALGWTGMLDKGAD  RALGWTGML        0.4112       584.4             32.00      Sequence
DRB4_0101  338  LAVLTVVVTIAINTF  LTVVVTIAI        0.4104       589.3             32.00      Sequence
DRB4_0101  133  IIHRDVKPANIMISA  HRDVKPANI        0.4092       597.5             32.00      Sequence
DRB4_0101  493  TKDIPDVAGQTVDVA  IPDVAGQTV        0.4086       601.1             32.00      Sequence
DRB4_0101  131  NGIIHRDVKPANIMI  NGIIHRDVK        0.4076       607.8             32.00      Sequence
DRB4_0101  325  IGSVGRWVAVVAVLA  IGSVGRWVA        0.4070       611.5             32.00      Sequence
DRB4_0101  326  GSVGRWVAVVAVLAV  VAVVAVLAV        0.4063       616.0             32.00      Sequence
DRB4_0101  126  NFSHQNGIIHRDVKP  QNGIIHRDV        0.4055       621.5             32.00      Sequence
DRB4_0101  541  GTTVPVDSVIELQVS  VDSVIELQV        0.4044       629.1             32.00      Sequence
DRB4_0101  324  SIGSVGRWVAVVAVL  IGSVGRWVA        0.4043       629.5             32.00      Sequence
DRB4_0101  179  AQYLSPEQARGDSVD  AQYLSPEQA        0.4042       630.2             32.00      Sequence
DRB4_0101  135  HRDVKPANIMISATN  ANIMISATN        0.4034       636.2             32.00      Sequence
DRB4_0101  335  VAVLAVLTVVVTIAI  VAVLAVLTV        0.4021       644.7             32.00      Sequence
DRB4_0101  151  VKVMDFGIARAIADS  VKVMDFGIA        0.4012       651.3             50.00      Sequence
DRB4_0101  196  SDVYSLGCVLYEVLT  VYSLGCVLY        0.4010       652.4             50.00      Sequence
DRB4_0101   17  GFGGMSEVHLARDLR  SEVHLARDL        0.4007       655.0             50.00      Sequence
DRB4_0101  425  QREIPDVSTLTYAEA  IPDVSTLTY        0.4000       659.4             50.00      Sequence
DRB4_0101  195  RSDVYSLGCVLYEVL  YSLGCVLYE        0.3998       660.9             50.00      Sequence
DRB4_0101  571  VDAEPRLRALGWTGM  LRALGWTGM        0.3987       669.1             50.00      Sequence
DRB4_0101  502  QTVDVAQKNLNVYGF  VDVAQKNLN        0.3984       671.3             50.00      Sequence
DRB4_0101  600  NRVVYQNPPAGTGVN  NRVVYQNPP        0.3981       673.5             50.00      Sequence
DRB4_0101  134  IHRDVKPANIMISAT  VKPANIMIS        0.3977       676.2             50.00      Sequence
DRB4_0101   16  LGFGGMSEVHLARDL  SEVHLARDL        0.3975       677.9             50.00      Sequence
DRB4_0101  201  LGCVLYEVLTGEPPF  LGCVLYEVL        0.3966       684.2             50.00      Sequence
DRB4_0101  248  AVVLKALAKNPENRY  VVLKALAKN        0.3959       689.4             50.00      Sequence
DRB4_0101   14  EILGFGGMSEVHLAR  LGFGGMSEV        0.3936       707.1             50.00      Sequence
DRB4_0101  242  LSADLDAVVLKALAK  DAVVLKALA        0.3927       713.7             50.00      Sequence
```

```
DRB4_0101  143  IMISATNAVKVMDFG  IMISATNAV        0.3923        716.8              50.00     Sequence
DRB4_0101  505  DVAQKNLNVYGFTKF  LNVYGFTKF        0.3886        746.6              50.00     Sequence
DRB4_0101  175  VIGTAQYLSPEQARG  AQYLSPEQA        0.3873        756.6              50.00     Sequence
DRB4_0101  176  IGTAQYLSPEQARGD  AQYLSPEQA        0.3865        763.3              50.00     Sequence
DRB4_0101  194  ARSDVYSLGCVLYEV  VYSLGCVLY        0.3858        769.5              50.00     Sequence
DRB4_0101  334  VVAVLAVLTVVVTIA  VAVLAVLTV        0.3857        770.0              50.00     Sequence
DRB4_0101  503  TVDVAQKNLNVYGFT  VDVAQKNLN        0.3857        770.4              50.00     Sequence
DRB4_0101  504  VDVAQKNLNVYGFTK  VDVAQKNLN        0.3848        777.4              50.00     Sequence
DRB4_0101  337  VLAVLTVVVTIAINT  LTVVVTIAI        0.3845        780.0              50.00     Sequence
DRB4_0101  267  EMRADLVRVHNGEPP  MRADLVRVH        0.3795        823.2              50.00     Sequence
DRB4_0101  342  TVVVTIAINTFGGIT  VVTIAINTF        0.3790        828.1              50.00     Sequence
DRB4_0101  476  TSAITNVVIIIVGSG  VVIIIVGSG        0.3785        832.4              50.00     Sequence
DRB4_0101  492  ATKDIPDVAGQTVDV  IPDVAGQTV        0.3777        840.0              50.00     Sequence
DRB4_0101   12  LGEILGFGGMSEVHL  LGFGGMSEV        0.3745        869.6              50.00     Sequence
DRB4_0101  307  RTDPLPRQDLDDTDR  PLPRQDLDD        0.3743        871.7              50.00     Sequence
DRB4_0101  336  AVLAVLTVVVTIAIN  LTVVVTIAI        0.3737        877.0              50.00     Sequence
DRB4_0101  482  VVIIIVGSGPATKDI  VIIIVGSGP        0.3735        878.8              50.00     Sequence
DRB4_0101  200  SLGCVLYEVLTGEPP  CVLYEVLTG        0.3734        879.9              50.00     Sequence
DRB4_0101  199  YSLGCVLYEVLTGEP  YSLGCVLYE        0.3731        882.5              50.00     Sequence
DRB4_0101  268  MRADLVRVHNGEPPE  MRADLVRVH        0.3721        892.6              50.00     Sequence
DRB4_0101   13  GEILGFGGMSEVHLA  EILGFGGMS        0.3717        896.2              50.00     Sequence
DRB4_0101  491  PATKDIPDVAGQTVD  IPDVAGQTV        0.3713        899.8              50.00     Sequence
DRB4_0101  308  TDPLPRQDLDDTDRD  LPRQDLDDT        0.3709        904.4              50.00     Sequence
DRB4_0101  152  KVMDFGIARAIADSG  MDFGIARAI        0.3700        912.6              50.00     Sequence
DRB4_0101  100  RDIVHTEGPMTPKRA  RDIVHTEGP        0.3688        924.6              50.00     Sequence
DRB4_0101  501  GQTVDVAQKNLNVYG  VDVAQKNLN        0.3682        930.9              50.00     Sequence
DRB4_0101  594  AGGSQHNRVVYQNPP  HNRVVYQNP        0.3682        931.0              50.00     Sequence
DRB4_0101  203  CVLYEVLTGEPPFTG  YEVLTGEPP        0.3676        936.4              50.00     Sequence
DRB4_0101  490  GPATKDIPDVAGQTV  IPDVAGQTV        0.3657        955.8              50.00     Sequence
DRB4_0101  193  DARSDVYSLGCVLYE  VYSLGCVLY        0.3654        959.7              50.00     Sequence
DRB4_0101  202  GCVLYEVLTGEPPFT  YEVLTGEPP        0.3651        962.1              50.00     Sequence
DRB4_0101  153  VMDFGIARAIADSGN  MDFGIARAI        0.3648        965.6              50.00     Sequence
DRB4_0101  249  VVLKALAKNPENRYQ  VVLKALAKN        0.3640        974.1              50.00     Sequence
DRB4_0101   11  ELGEILGFGGMSEVH  LGFGGMSEV        0.3632        982.3              50.00     Sequence
DRB4_0101  266  AEMRADLVRVHNGEP  MRADLVRVH        0.3611       1004.6              50.00     Sequence
DRB4_0101  424  EQREIPDVSTLTYAE  IPDVSTLTY        0.3609       1007.7              50.00     Sequence
DRB4_0101  499  VAGQTVDVAQKNLNV  VAGQTVDVA        0.3599       1018.3              50.00     Sequence
DRB4_0101  422  GPEQREIPDVSTLTY  IPDVSTLTY        0.3596       1021.6              50.00     Sequence
DRB4_0101  265  AAEMRADLVRVHNGE  MRADLVRVH        0.3594       1023.5              50.00     Sequence
DRB4_0101  306  PRTDPLPRQDLDDTD  TDPLPRQDL        0.3592       1025.4              50.00     Sequence
DRB4_0101  343  VVVTIAINTFGGITR  VVTIAINTF        0.3570       1050.5              50.00     Sequence
DRB4_0101  241  GLSADLDAVVLKALA  DAVVLKALA        0.3559       1063.1              50.00     Sequence
DRB4_0101  507  AQKNLNVYGFTKFSQ  LNVYGFTKF        0.3559       1063.6              50.00     Sequence
DRB4_0101  305  GPRTDPLPRQDLDDT  LPRQDLDDT        0.3552       1071.1              50.00     Sequence
DRB4_0101  264  TAAEMRADLVRVHNG  MRADLVRVH        0.3543       1082.0              50.00     Sequence
DRB4_0101  506  VAQKNLNVYGFTKFS  LNVYGFTKF        0.3542       1082.8              50.00     Sequence
DRB4_0101   10  YELGEILGFGGMSEV  EILGFGGMS        0.3540       1084.8              50.00     Sequence
DRB4_0101  610  GTGVNRDGIITLRFG  RDGIITLRF        0.3538       1087.3              50.00     Sequence
DRB4_0101  323  RSIGSVGRWVAVVAV  IGSVGRWVA        0.3522       1106.0              50.00     Sequence
DRB4_0101  423  PEQREIPDVSTLTYA  IPDVSTLTY        0.3478       1161.0              50.00     Sequence
DRB4_0101  205  LYEVLTGEPPFTGDS  YEVLTGEPP        0.3468       1172.9              50.00     Sequence
DRB4_0101  551  ELQVSKGNQFVMPDL  GNQFVMPDL        0.3460       1183.0              50.00     Sequence
DRB4_0101  263  QTAAEMRADLVRVHN  MRADLVRVH        0.3453       1191.9              50.00     Sequence
DRB4_0101  204  VLYEVLTGEPPFTGD  YEVLTGEPP        0.3450       1195.9              50.00     Sequence
DRB4_0101  221  VSVAYQHVREDPIPP  VSVAYQHVR        0.3445       1202.4              50.00     Sequence
DRB4_0101  213  PPFTGDSPVSVAYQH  SPVSVAYQH        0.3440       1209.9              50.00     Sequence
DRB4_0101   15  ILGFGGMSEVHLARD  LGFGGMSEV        0.3438       1211.8              50.00     Sequence
DRB4_0101  483  VIIIVGSGPATKDIP  VIIIVGSGP        0.3432       1219.9              50.00     Sequence
DRB4_0101  498  DVAGQTVDVAQKNLN  VAGQTVDVA        0.3410       1248.8              50.00     Sequence
DRB4_0101  383  IRTLQKPDSTIPPDH  IRTLQKPDS        0.3406       1254.5              50.00     Sequence
DRB4_0101  351  TFGGITRDVQVPDVR  FGGITRDVQ        0.3401       1262.0              50.00     Sequence
DRB4_0101  352  FGGITRDVQVPDVRG  FGGITRDVQ        0.3384       1285.2              50.00     Sequence
DRB4_0101   79  AETPAGPLPYIVMEY  PLPYIVMEY        0.3366       1309.5              50.00     Sequence
DRB4_0101    8  DRYELGEILGFGGMS  DRYELGEIL        0.3359       1320.7              50.00     Sequence
DRB4_0101  508  QKNLNVYGFTKFSQA  LNVYGFTKF        0.3357       1322.6              50.00     Sequence
DRB4_0101   63  AALNHPAIVAVYDTG  PAIVAVYDT        0.3357       1322.7              50.00     Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB4_0101 | 322 | DRSIGSVGRWVAVVA | IGSVGRWVA | 0.3353 | 1329.3 | 50.00 | Sequence |
| DRB4_0101 | 373 | IATLQNRGFKIRTLQ | RGFKIRTLQ | 0.3334 | 1356.4 | 50.00 | Sequence |
| DRB4_0101 | 500 | AGQTVDVAQKNLNVY | VDVAQKNLN | 0.3330 | 1362.5 | 50.00 | Sequence |
| DRB4_0101 | 566 | SGMFWVDAEPRLRAL | GMFWVDAEP | 0.3329 | 1363.9 | 50.00 | Sequence |
| DRB4_0101 | 565 | LSGMFWVDAEPRLRA | GMFWVDAEP | 0.3313 | 1387.2 | 50.00 | Sequence |
| DRB4_0101 | 108 | PMTPKRAIEVIADAC | RAIEVIADA | 0.3254 | 1479.0 | 50.00 | Sequence |
| DRB4_0101 | 395 | PDHVIGTDPAANTSV | DHVIGTDPA | 0.3253 | 1479.9 | 50.00 | Sequence |
| DRB4_0101 | 269 | RADLVRVHNGEPPEA | ADLVRVHNG | 0.3251 | 1484.0 | 50.00 | Sequence |
| DRB4_0101 | 567 | GMFWVDAEPRLRALG | GMFWVDAEP | 0.3248 | 1489.2 | 50.00 | Sequence |
| DRB4_0101 | 429 | PDVSTLTYAEAVKKL | VSTLTYAEA | 0.3247 | 1489.9 | 50.00 | Sequence |
| DRB4_0101 | 497 | PDVAGQTVDVAQKNL | VAGQTVDVA | 0.3240 | 1502.0 | 50.00 | Sequence |
| DRB4_0101 | 262 | YQTAAEMRADLVRVH | MRADLVRVH | 0.3234 | 1511.7 | 50.00 | Sequence |
| DRB4_0101 | 172 | TAAVIGTAQYLSPEQ | AAVIGTAQY | 0.3233 | 1512.8 | 50.00 | Sequence |
| DRB4_0101 | 563 | PDLSGMFWVDAEPRL | GMFWVDAEP | 0.3232 | 1513.9 | 50.00 | Sequence |
| DRB4_0101 | 394 | PPDHVIGTDPAANTS | DHVIGTDPA | 0.3231 | 1515.5 | 50.00 | Sequence |
| DRB4_0101 | 107 | GPMTPKRAIEVIADA | RAIEVIADA | 0.3227 | 1522.0 | 50.00 | Sequence |
| DRB4_0101 | 350 | NTFGGITRDVQVPDV | FGGITRDVQ | 0.3210 | 1550.9 | 50.00 | Sequence |
| DRB4_0101 | 2 | TPSHLSDRYELGEIL | SHLSDRYEL | 0.3203 | 1562.4 | 50.00 | Sequence |
| DRB4_0101 | 540 | AGTTVPVDSVIELQV | VDSVIELQV | 0.3191 | 1582.7 | 50.00 | Sequence |
| DRB4_0101 | 101 | DIVHTEGPMTPKRAI | VHTEGPMTP | 0.3181 | 1599.9 | 50.00 | Sequence |
| DRB4_0101 | 353 | GGITRDVQVPDVRGQ | GGITRDVQV | 0.3172 | 1616.8 | 50.00 | Sequence |
| DRB4_0101 | 4 | SHLSDRYELGEILGF | SHLSDRYEL | 0.3159 | 1639.2 | 50.00 | Sequence |
| DRB4_0101 | 593 | DAGGSQHNRVVYQNP | HNRVVYQNP | 0.3137 | 1678.5 | 50.00 | Sequence |
| DRB4_0101 | 475 | QTSAITNVVIIIVGS | ITNVVIIIV | 0.3133 | 1685.1 | 50.00 | Sequence |
| DRB4_0101 | 393 | IPPDHVIGTDPAANT | DHVIGTDPA | 0.3131 | 1688.7 | 50.00 | Sequence |
| DRB4_0101 | 549 | VIELQVSKGNQFVMP | IELQVSKGN | 0.3124 | 1702.7 | 50.00 | Sequence |
| DRB4_0101 | 344 | VVTIAINTFGGITRD | VVTIAINTF | 0.3122 | 1705.6 | 50.00 | Sequence |
| DRB4_0101 | 3 | PSHLSDRYELGEILG | SHLSDRYEL | 0.3118 | 1714.1 | 50.00 | Sequence |
| DRB4_0101 | 509 | KNLNVYGFTKFSQAS | LNVYGFTKF | 0.3109 | 1729.9 | 50.00 | Sequence |
| DRB4_0101 | 270 | ADLVRVHNGEPPEAP | ADLVRVHNG | 0.3104 | 1738.5 | 50.00 | Sequence |
| DRB4_0101 | 430 | DVSTLTYAEAVKKLT | VSTLTYAEA | 0.3102 | 1743.4 | 50.00 | Sequence |
| DRB4_0101 | 321 | RDRSIGSVGRWVAVV | IGSVGRWVA | 0.3090 | 1766.3 | 50.00 | Sequence |
| DRB4_0101 | 349 | INTFGGITRDVQVPD | FGGITRDVQ | 0.3085 | 1774.7 | 50.00 | Sequence |
| DRB4_0101 | 564 | DLSGMFWVDAEPRLR | GMFWVDAEP | 0.3085 | 1776.4 | 50.00 | Sequence |
| DRB4_0101 | 578 | RALGWTGMLDKGADV | RALGWTGML | 0.3079 | 1786.3 | 50.00 | Sequence |
| DRB4_0101 | 39 | KVLRADLARDPSFYL | KVLRADLAR | 0.3076 | 1793.6 | 50.00 | Sequence |
| DRB4_0101 | 192 | VDARSDVYSLGCVLY | VYSLGCVLY | 0.3076 | 1793.8 | 50.00 | Sequence |
| DRB4_0101 | 309 | DPLPRQDLDDTDRDR | LPRQDLDDT | 0.3068 | 1807.8 | 50.00 | Sequence |
| DRB4_0101 | 463 | VGKVIGTNPPANQTS | GKVIGTNPP | 0.3055 | 1834.3 | 50.00 | Sequence |
| DRB4_0101 | 9 | RYELGEILGFGGMSE | EILGFGGMS | 0.3047 | 1850.7 | 50.00 | Sequence |
| DRB4_0101 | 362 | PDVRGQSSADAIATL | VRGQSSADA | 0.3046 | 1853.0 | 50.00 | Sequence |
| DRB4_0101 | 392 | TIPPDHVIGTDPAAN | DHVIGTDPA | 0.3011 | 1923.1 | 50.00 | Sequence |
| DRB4_0101 | 46 | ARDPSFYLRFRREAQ | FYLRFRREA | 0.3011 | 1924.1 | 50.00 | Sequence |
| DRB4_0101 | 250 | VLKALAKNPENRYQT | LKALAKNPE | 0.3006 | 1933.5 | 50.00 | Sequence |
| DRB4_0101 | 154 | MDFGIARAIADSGNS | MDFGIARAI | 0.3002 | 1942.8 | 50.00 | Sequence |
| DRB4_0101 | 510 | NLNVYGFTKFSQASV | LNVYGFTKF | 0.2996 | 1955.0 | 50.00 | Sequence |
| DRB4_0101 | 240 | EGLSADLDAVVLKAL | LDAVVLKAL | 0.2989 | 1969.1 | 50.00 | Sequence |
| DRB4_0101 | 396 | DHVIGTDPAANTSVS | DHVIGTDPA | 0.2986 | 1975.8 | 50.00 | Sequence |
| DRB4_0101 | 459 | TPELVGKVIGTNPPA | GKVIGTNPP | 0.2986 | 1977.0 | 50.00 | Sequence |
| DRB4_0101 | 462 | LVGKVIGTNPPANQT | GKVIGTNPP | 0.2983 | 1983.5 | 50.00 | Sequence |
| DRB4_0101 | 550 | IELQVSKGNQFVMPD | IELQVSKGN | 0.2981 | 1986.4 | 50.00 | Sequence |
| DRB4_0101 | 461 | ELVGKVIGTNPPANQ | GKVIGTNPP | 0.2973 | 2005.1 | 50.00 | Sequence |
| DRB4_0101 | 238 | RHEGLSADLDAVVLK | RHEGLSADL | 0.2971 | 2007.7 | 50.00 | Sequence |
| DRB4_0101 | 391 | STIPPDHVIGTDPAA | DHVIGTDPA | 0.2961 | 2030.1 | 50.00 | Sequence |
| DRB4_0101 | 171 | QTAAVIGTAQYLSPE | AAVIGTAQY | 0.2960 | 2031.9 | 50.00 | Sequence |
| DRB4_0101 | 438 | EAVKKLTAAGFGRFK | VKKLTAAGF | 0.2957 | 2039.4 | 50.00 | Sequence |
| DRB4_0101 | 62 | AAALNHPAIVAVYDT | PAIVAVYDT | 0.2957 | 2039.5 | 50.00 | Sequence |
| DRB4_0101 | 609 | AGTGVNRDGIITLRF | RDGIITLRF | 0.2954 | 2046.1 | 50.00 | Sequence |
| DRB4_0101 | 348 | AINTFGGITRDVQVP | FGGITRDVQ | 0.2939 | 2079.6 | 50.00 | Sequence |
| DRB4_0101 | 237 | ARHEGLSADLDAVVL | RHEGLSADL | 0.2933 | 2092.4 | 50.00 | Sequence |
| DRB4_0101 | 7 | SDRYELGEILGFGGM | DRYELGEIL | 0.2932 | 2096.2 | 50.00 | Sequence |
| DRB4_0101 | 464 | GKVIGTNPPANQTSA | GKVIGTNPP | 0.2931 | 2096.6 | 50.00 | Sequence |
| DRB4_0101 | 347 | IAINTFGGITRDVQV | FGGITRDVQ | 0.2910 | 2145.0 | 50.00 | Sequence |
| DRB4_0101 | 67 | HPAIVAVYDTGEAET | PAIVAVYDT | 0.2908 | 2150.7 | 50.00 | Sequence |
| DRB4_0101 | 431 | VSTLTYAEAVKKLTA | VSTLTYAEA | 0.2896 | 2177.3 | 50.00 | Sequence |
| DRB4_0101 | 64 | ALNHPAIVAVYDTGE | PAIVAVYDT | 0.2896 | 2177.4 | 50.00 | Sequence |

```
DRB4_0101  511  LNVYGFTKFSQASVD  LNVYGFTKF         0.2887        2199.0                 50.00     Sequence
DRB4_0101  320  DRDRSIGSVGRWVAV  IGSVGRWVA         0.2887        2200.6                 50.00     Sequence
DRB4_0101  206  YEVLTGEPPFTGDSP  YEVLTGEPP         0.2884        2206.7                 50.00     Sequence
DRB4_0101  390  DSTIPPDHVIGTDPA  DHVIGTDPA         0.2883        2210.2                 50.00     Sequence
DRB4_0101  354  GITRDVQVPDVRGQS  RDVQVPDVR         0.2880        2216.0                 50.00     Sequence
DRB4_0101   66  NHPAIVAVYDTGEAE  PAIVAVYDT         0.2880        2216.9                 50.00     Sequence
DRB4_0101   65  LNHPAIVAVYDTGEA  PAIVAVYDT         0.2871        2237.7                 50.00     Sequence
DRB4_0101  437  AEAVKKLTAAGFGRF  VKKLTAAGF         0.2863        2258.4                 50.00     Sequence
DRB4_0101  291  ERTSLLSSAAGNLSG  TSLLSSAAG         0.2838        2318.6                 50.00     Sequence
DRB4_0101  439  AVKKLTAAGFGRFKQ  VKKLTAAGF         0.2838        2320.5                 50.00     Sequence
DRB4_0101  570  WVDAEPRLRALGWTG  EPRLRALGW         0.2828        2344.2                 50.00     Sequence
DRB4_0101  256  KNPENRYQTAAEMRA  NRYQTAAEM         0.2815        2378.6                 50.00     Sequence
DRB4_0101  458  STPELVGKVIGTNPP  GKVIGTNPP         0.2813        2382.3                 50.00     Sequence
DRB4_0101  460  PELVGKVIGTNPPAN  GKVIGTNPP         0.2810        2390.9                 50.00     Sequence
DRB4_0101  236  SARHEGLSADLDAVV  RHEGLSADL         0.2804        2407.1                 50.00     Sequence
DRB4_0101  601  RVVYQNPPAGTGVNR  RVVYQNPPA         0.2799        2419.4                 50.00     Sequence
DRB4_0101  255  AKNPENRYQTAAEMR  NRYQTAAEM         0.2789        2445.1                 50.00     Sequence
DRB4_0101  345  VTIAINTFGGITRDV  VTIAINTFG         0.2783        2462.1                 50.00     Sequence
DRB4_0101  170  TQTAAVIGTAQYLSP  AAVIGTAQY         0.2770        2497.1                 50.00     Sequence
DRB4_0101  254  LAKNPENRYQTAAEM  NRYQTAAEM         0.2746        2563.5                 50.00     Sequence
DRB4_0101  290  AERTSLLSSAAGNLS  LSSAAGNLS         0.2743        2570.0                 50.00     Sequence
DRB4_0101  304  SGPRTDPLPRQDLDD  TDPLPRQDL         0.2735        2593.9                 50.00     Sequence
DRB4_0101  222  SVAYQHVREDPIPPS  YQHVREDPI         0.2733        2599.7                 50.00     Sequence
DRB4_0101  436  YAEAVKKLTAAGFGR  VKKLTAAGF         0.2726        2617.2                 50.00     Sequence
DRB4_0101  292  RTSLLSSAAGNLSGP  LSSAAGNLS         0.2726        2618.7                 50.00     Sequence
DRB4_0101  169  VTQTAAVIGTAQYLS  AAVIGTAQY         0.2702        2688.1                 50.00     Sequence
DRB4_0101  271  DLVRVHNGEPPEAPK  VRVHNGEPP         0.2700        2692.2                 50.00     Sequence
DRB4_0101  346  TIAINTFGGITRDVQ  FGGITRDVQ         0.2698        2699.8                 50.00     Sequence
DRB4_0101  106  EGPMTPKRAIEVIAD  EGPMTPKRA         0.2694        2710.6                 50.00     Sequence
DRB4_0101  257  NPENRYQTAAEMRAD  NRYQTAAEM         0.2690        2722.5                 50.00     Sequence
DRB4_0101  474  NQTSAITNVVIIIVG  ITNVVIIIV         0.2686        2733.1                 50.00     Sequence
DRB4_0101  319  TDRDRSIGSVGRWVA  IGSVGRWVA         0.2683        2742.1                 50.00     Sequence
DRB4_0101  258  PENRYQTAAEMRADL  NRYQTAAEM         0.2668        2787.2                 50.00     Sequence
DRB4_0101    5  HLSDRYELGEILGFG  DRYELGEIL         0.2668        2787.8                 50.00     Sequence
DRB4_0101   68  PAIVAVYDTGEAETP  PAIVAVYDT         0.2654        2832.0                 50.00     Sequence
DRB4_0101  293  TSLLSSAAGNLSGPR  TSLLSSAAG         0.2652        2837.8                 50.00     Sequence
DRB4_0101  239  HEGLSADLDAVVLKA  EGLSADLDA         0.2644        2862.1                 50.00     Sequence
DRB4_0101    6  LSDRYELGEILGFGG  DRYELGEIL         0.2626        2917.0                 50.00     Sequence
DRB4_0101  223  VAYQHVREDPIPPSA  YQHVREDPI         0.2609        2971.7                 50.00     Sequence
DRB4_0101  435  TYAEAVKKLTAAGFG  VKKLTAAGF         0.2605        2985.1                 50.00     Sequence
DRB4_0101  168  SVTQTAAVIGTAQYL  AAVIGTAQY         0.2598        3008.2                 50.00     Sequence
DRB4_0101  310  PLPRQDLDDTDRDRS  LPRQDLDDT         0.2594        3020.8                 50.00     Sequence
DRB4_0101  260  NRYQTAAEMRADLVR  NRYQTAAEM         0.2591        3029.1                 50.00     Sequence
DRB4_0101  434  LTYAEAVKKLTAAGF  VKKLTAAGF         0.2583        3055.2                 50.00     Sequence
DRB4_0101  259  ENRYQTAAEMRADLV  NRYQTAAEM         0.2578        3072.1                 50.00     Sequence
DRB4_0101  363  DVRGQSSADAIATLQ  VRGQSSADA         0.2572        3094.2                 50.00     Sequence
DRB4_0101  103  VHTEGPMTPKRAIEV  VHTEGPMTP         0.2563        3123.1                 50.00     Sequence
DRB4_0101  484  IIIVGSGPATKDIPD  IIIVGSGPA         0.2557        3142.3                 50.00     Sequence
DRB4_0101  372  AIATLQNRGFKIRTL  NRGFKIRTL         0.2554        3153.8                 50.00     Sequence
DRB4_0101  105  TEGPMTPKRAIEVIA  EGPMTPKRA         0.2547        3177.7                 50.00     Sequence
DRB4_0101    1  TTPSHLSDRYELGEI  SHLSDRYEL         0.2533        3226.2                 50.00     Sequence
DRB4_0101  102  IVHTEGPMTPKRAIE  VHTEGPMTP         0.2531        3234.4                 50.00     Sequence
DRB4_0101  303  LSGPRTDPLPRQDLD  TDPLPRQDL         0.2530        3237.9                 50.00     Sequence
DRB4_0101  473  ANQTSAITNVVIIIV  ITNVVIIIV         0.2519        3276.9                 50.00     Sequence
DRB4_0101  261  RYQTAAEMRADLVRV  AAEMRADLV         0.2516        3286.2                 50.00     Sequence
DRB4_0101  364  VRGQSSADAIATLQN  VRGQSSADA         0.2504        3329.1                 50.00     Sequence
DRB4_0101  412  GDEITVNVSTGPEQR  DEITVNVST         0.2502        3337.2                 50.00     Sequence
DRB4_0101  224  AYQHVREDPIPPSAR  YQHVREDPI         0.2493        3368.6                 50.00     Sequence
DRB4_0101  384  RTLQKPDSTIPPDHV  RTLQKPDST         0.2487        3391.0                 50.00     Sequence
DRB4_0101   40  VLRADLARDPSFYLR  RADLARDPS         0.2455        3512.4                 50.00     Sequence
DRB4_0101  440  VKKLTAAGFGRFKQA  VKKLTAAGF         0.2433        3595.2                 50.00     Sequence
DRB4_0101  370  ADAIATLQNRGFKIR  IATLQNRGF         0.2432        3597.2                 50.00     Sequence
DRB4_0101  457  PSTPELVGKVIGTNP  VGKVIGTNP         0.2429        3611.0                 50.00     Sequence
DRB4_0101  411  AGDEITVNVSTGPEQ  DEITVNVST         0.2427        3620.3                 50.00     Sequence
DRB4_0101  235  PSARHEGLSADLDAV  RHEGLSADL         0.2423        3635.9                 50.00     Sequence
DRB4_0101  413  DEITVNVSTGPEQRE  EITVNVSTG         0.2420        3644.8                 50.00     Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB4_0101 | 41 | LRADLARDPSFYLRF | RADLARDPS | 0.2412 | 3679.0 | 50.00 | Sequence |
| DRB4_0101 | 580 | LGWTGMLDKGADVDA | LGWTGMLDK | 0.2406 | 3701.7 | 50.00 | Sequence |
| DRB4_0101 | 58 | EAQNAAALNHPAIVA | AALNHPAIV | 0.2401 | 3721.9 | 50.00 | Sequence |
| DRB4_0101 | 59 | AQNAAALNHPAIVAV | AALNHPAIV | 0.2397 | 3738.9 | 50.00 | Sequence |
| DRB4_0101 | 516 | FTKFSQASVDSPRPA | FTKFSQASV | 0.2381 | 3804.7 | 50.00 | Sequence |
| DRB4_0101 | 272 | LVRVHNGEPPEAPKV | VRVHNGEPP | 0.2350 | 3931.3 | 50.00 | Sequence |
| DRB4_0101 | 289 | DAERTSLLSSAAGNL | TSLLSSAAG | 0.2344 | 3959.1 | 50.00 | Sequence |
| DRB4_0101 | 61 | NAAALNHPAIVAVYD | AALNHPAIV | 0.2340 | 3977.8 | 50.00 | Sequence |
| DRB4_0101 | 302 | NLSGPRTDPLPRQDL | LSGPRTDPL | 0.2338 | 3984.0 | 50.00 | Sequence |
| DRB4_0101 | 592 | VDAGGSQHNRVVYQN | QHNRVVYQN | 0.2320 | 4061.6 | 50.00 | Sequence |
| DRB4_0101 | 0 | MTTPSHLSDRYELGE | SHLSDRYEL | 0.2316 | 4081.4 | 50.00 | Sequence |
| DRB4_0101 | 45 | LARDPSFYLRFRREA | FYLRFRREA | 0.2310 | 4106.6 | 50.00 | Sequence |
| DRB4_0101 | 167 | NSVTQTAAVIGTAQY | AAVIGTAQY | 0.2305 | 4128.4 | 50.00 | Sequence |
| DRB4_0101 | 512 | NVYGFTKFSQASVDS | YGFTKFSQA | 0.2304 | 4131.5 | 50.00 | Sequence |
| DRB4_0101 | 155 | DFGIARAIADSGNSV | IARAIADSG | 0.2303 | 4137.8 | 50.00 | Sequence |
| DRB4_0101 | 579 | ALGWTGMLDKGADVD | LGWTGMLDK | 0.2288 | 4207.3 | 50.00 | Sequence |
| DRB4_0101 | 57 | REAQNAAALNHPAIV | AALNHPAIV | 0.2261 | 4330.1 | 50.00 | Sequence |
| DRB4_0101 | 410 | SAGDEITVNVSTGPE | DEITVNVST | 0.2261 | 4332.3 | 50.00 | Sequence |
| DRB4_0101 | 514 | YGFTKFSQASVDSPR | FTKFSQASV | 0.2254 | 4361.2 | 50.00 | Sequence |
| DRB4_0101 | 156 | FGIARAIADSGNSVT | IARAIADSG | 0.2241 | 4425.3 | 50.00 | Sequence |
| DRB4_0101 | 445 | AAGFGRFKQANSPST | GRFKQANSP | 0.2238 | 4437.5 | 50.00 | Sequence |
| DRB4_0101 | 433 | TLTYAEAVKKLTAAG | LTYAEAVKK | 0.2229 | 4483.4 | 50.00 | Sequence |
| DRB4_0101 | 369 | SADAIATLQNRGFKI | IATLQNRGF | 0.2227 | 4494.6 | 50.00 | Sequence |
| DRB4_0101 | 513 | VYGFTKFSQASVDSP | FTKFSQASV | 0.2225 | 4504.1 | 50.00 | Sequence |
| DRB4_0101 | 294 | SLLSSAAGNLSGPRT | LSSAAGNLS | 0.2222 | 4516.8 | 50.00 | Sequence |
| DRB4_0101 | 539 | PAGTTVPVDSVIELQ | VPVDSVIEL | 0.2218 | 4535.0 | 50.00 | Sequence |
| DRB4_0101 | 409 | VSAGDEITVNVSTGP | DEITVNVST | 0.2217 | 4542.5 | 50.00 | Sequence |
| DRB4_0101 | 465 | KVIGTNPPANQTSAI | KVIGTNPPA | 0.2205 | 4599.8 | 50.00 | Sequence |
| DRB4_0101 | 389 | PDSTIPPDHVIGTDP | DSTIPPDHV | 0.2202 | 4616.4 | 50.00 | Sequence |
| DRB4_0101 | 371 | DAIATLQNRGFKIRT | IATLQNRGF | 0.2200 | 4625.1 | 50.00 | Sequence |
| DRB4_0101 | 60 | QNAAALNHPAIVAVY | AALNHPAIV | 0.2196 | 4645.6 | 50.00 | Sequence |
| DRB4_0101 | 446 | AGFGRFKQANSPSTP | GRFKQANSP | 0.2193 | 4659.6 | 50.00 | Sequence |
| DRB4_0101 | 444 | TAAGFGRFKQANSPS | FGRFKQANS | 0.2190 | 4676.5 | 50.00 | Sequence |
| DRB4_0101 | 414 | EITVNVSTGPEQREI | ITVNVSTGP | 0.2189 | 4681.0 | 50.00 | Sequence |
| DRB4_0101 | 42 | RADLARDPSFYLRFR | RADLARDPS | 0.2185 | 4703.9 | 50.00 | Sequence |
| DRB4_0101 | 517 | TKFSQASVDSPRPAG | ASVDSPRPA | 0.2183 | 4711.4 | 50.00 | Sequence |
| DRB4_0101 | 432 | STLTYAEAVKKLTAA | LTYAEAVKK | 0.2179 | 4730.1 | 50.00 | Sequence |
| DRB4_0101 | 207 | EVLTGEPPFTGDSPV | EVLTGEPPF | 0.2172 | 4768.4 | 50.00 | Sequence |
| DRB4_0101 | 568 | MFWVDAEPRLRALGW | EPRLRALGW | 0.2163 | 4817.3 | 50.00 | Sequence |
| DRB4_0101 | 515 | GFTKFSQASVDSPRP | FTKFSQASV | 0.2139 | 4941.4 | 50.00 | Sequence |
| DRB4_0101 | 608 | PAGTGVNRDGIITLR | GTGVNRDGI | 0.2137 | 4953.9 | 50.00 | Sequence |
| DRB4_0101 | 251 | LKALAKNPENRYQTA | LKALAKNPE | 0.2117 | 5059.1 | 50.00 | Sequence |
| DRB4_0101 | 104 | HTEGPMTPKRAIEVI | GPMTPKRAI | 0.2115 | 5070.2 | 50.00 | Sequence |
| DRB4_0101 | 388 | KPDSTIPPDHVIGTD | DSTIPPDHV | 0.2106 | 5121.9 | 50.00 | Sequence |
| DRB4_0101 | 212 | EPPFTGDSPVSVAYQ | PPFTGDSPV | 0.2103 | 5137.3 | 50.00 | Sequence |
| DRB4_0101 | 443 | LTAAGFGRFKQANSP | FGRFKQANS | 0.2102 | 5142.1 | 50.00 | Sequence |
| DRB4_0101 | 225 | YQHVREDPIPPSARH | YQHVREDPI | 0.2098 | 5164.2 | 50.00 | Sequence |
| DRB4_0101 | 368 | SSADAIATLQNRGFK | IATLQNRGF | 0.2097 | 5171.0 | 50.00 | Sequence |
| DRB4_0101 | 191 | SVDARSDVYSLGCVL | ARSDVYSLG | 0.2064 | 5362.0 | 50.00 | Sequence |
| DRB4_0101 | 456 | SPSTPELVGKVIGTN | ELVGKVIGT | 0.2061 | 5374.7 | 50.00 | Sequence |
| DRB4_0101 | 288 | TDAERTSLLSSAAGN | TSLLSSAAG | 0.2058 | 5394.0 | 50.00 | Sequence |
| DRB4_0101 | 387 | QKPDSTIPPDHVIGT | DSTIPPDHV | 0.2056 | 5404.5 | 50.00 | Sequence |
| DRB4_0101 | 447 | GFGRFKQANSPSTPE | GRFKQANSP | 0.2052 | 5430.0 | 50.00 | Sequence |
| DRB4_0101 | 234 | PPSARHEGLSADLDA | RHEGLSADL | 0.2042 | 5485.8 | 50.00 | Sequence |
| DRB4_0101 | 157 | GIARAIADSGNSVTQ | GIARAIADS | 0.2033 | 5543.8 | 50.00 | Sequence |
| DRB4_0101 | 386 | LQKPDSTIPPDHVIG | DSTIPPDHV | 0.2009 | 5686.7 | 50.00 | Sequence |
| DRB4_0101 | 190 | DSVDARSDVYSLGCV | DSVDARSDV | 0.2005 | 5713.0 | 50.00 | Sequence |
| DRB4_0101 | 44 | DLARDPSFYLRFRRE | LARDPSFYL | 0.2004 | 5720.7 | 50.00 | Sequence |
| DRB4_0101 | 287 | LTDAERTSLLSSAAG | TSLLSSAAG | 0.1993 | 5789.3 | 50.00 | Sequence |
| DRB4_0101 | 421 | TGPEQREIPDVSTLT | QREIPDVST | 0.1979 | 5874.6 | 50.00 | Sequence |
| DRB4_0101 | 518 | KFSQASVDSPRPAGE | KFSQASVDS | 0.1975 | 5899.8 | 50.00 | Sequence |
| DRB4_0101 | 189 | GDSVDARSDVYSLGC | DSVDARSDV | 0.1971 | 5928.3 | 50.00 | Sequence |
| DRB4_0101 | 165 | SGNSVTQTAAVIGTA | GNSVTQTAA | 0.1962 | 5981.8 | 50.00 | Sequence |
| DRB4_0101 | 273 | VRVHNGEPPEAPKVL | VRVHNGEPP | 0.1961 | 5991.9 | 50.00 | Sequence |
| DRB4_0101 | 311 | LPRQDLDDTDRDRSI | LPRQDLDDT | 0.1956 | 6022.6 | 50.00 | Sequence |
| DRB4_0101 | 582 | WTGMLDKGADVDAGG | GMLDKGADV | 0.1951 | 6054.2 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB4_0101 | 367 | QSSADAIATLQNRGF | IATLQNRGF | 0.1950 | 6064.0 | 50.00 | Sequence |
| DRB4_0101 | 43 | ADLARDPSFYLRFRR | ADLARDPSF | 0.1937 | 6148.0 | 50.00 | Sequence |
| DRB4_0101 | 54 | RFRREAQNAAALNHP | RFRREAQNA | 0.1911 | 6322.9 | 50.00 | Sequence |
| DRB4_0101 | 569 | FWVDAEPRLRALGWT | EPRLRALGW | 0.1906 | 6358.6 | 50.00 | Sequence |
| DRB4_0101 | 408 | SVSAGDEITVNVSTG | DEITVNVST | 0.1903 | 6380.4 | 50.00 | Sequence |
| DRB4_0101 | 164 | DSGNSVTQTAAVIGT | GNSVTQTAA | 0.1900 | 6398.5 | 50.00 | Sequence |
| DRB4_0101 | 581 | GWTGMLDKGADVDAG | GMLDKGADV | 0.1893 | 6447.7 | 50.00 | Sequence |
| DRB4_0101 | 607 | PPAGTGVNRDGIITL | VNRDGIITL | 0.1892 | 6453.5 | 50.00 | Sequence |
| DRB4_0101 | 448 | FGRFKQANSPSTPEL | GRFKQANSP | 0.1882 | 6527.1 | 50.00 | Sequence |
| DRB4_0101 | 538 | PPAGTTVPVDSVIEL | VPVDSVIEL | 0.1863 | 6659.5 | 50.00 | Sequence |
| DRB4_0101 | 442 | KLTAAGFGRFKQANS | AGFGRFKQA | 0.1863 | 6660.4 | 50.00 | Sequence |
| DRB4_0101 | 166 | GNSVTQTAAVIGTAQ | GNSVTQTAA | 0.1862 | 6668.2 | 50.00 | Sequence |
| DRB4_0101 | 299 | AAGNLSGPRTDPLPR | LSGPRTDPL | 0.1858 | 6697.5 | 50.00 | Sequence |
| DRB4_0101 | 455 | NSPSTPELVGKVIGT | PELVGKVIG | 0.1855 | 6715.9 | 50.00 | Sequence |
| DRB4_0101 | 300 | AGNLSGPRTDPLPRQ | LSGPRTDPL | 0.1853 | 6734.5 | 50.00 | Sequence |
| DRB4_0101 | 283 | APKVLTDAERTSLLS | LTDAERTSL | 0.1848 | 6770.2 | 50.00 | Sequence |
| DRB4_0101 | 385 | TLQKPDSTIPPDHVI | DSTIPPDHV | 0.1846 | 6782.9 | 50.00 | Sequence |
| DRB4_0101 | 282 | EAPKVLTDAERTSLL | KVLTDAERT | 0.1829 | 6910.1 | 50.00 | Sequence |
| DRB4_0101 | 211 | GEPPFTGDSPVSVAY | PPFTGDSPV | 0.1829 | 6911.1 | 50.00 | Sequence |
| DRB4_0101 | 441 | KKLTAAGFGRFKQAN | AGFGRFKQA | 0.1812 | 7039.6 | 50.00 | Sequence |
| DRB4_0101 | 232 | PIPPSARHEGLSADL | RHEGLSADL | 0.1808 | 7066.5 | 50.00 | Sequence |
| DRB4_0101 | 397 | HVIGTDPAANTSVSA | HVIGTDPAA | 0.1805 | 7090.0 | 50.00 | Sequence |
| DRB4_0101 | 285 | KVLTDAERTSLLSSA | ERTSLLSSA | 0.1801 | 7124.1 | 50.00 | Sequence |
| DRB4_0101 | 297 | SSAAGNLSGPRTDPL | LSGPRTDPL | 0.1797 | 7153.1 | 50.00 | Sequence |
| DRB4_0101 | 519 | FSQASVDSPRPAGEV | FSQASVDSP | 0.1797 | 7156.0 | 50.00 | Sequence |
| DRB4_0101 | 284 | PKVLTDAERTSLLSS | KVLTDAERT | 0.1795 | 7170.2 | 50.00 | Sequence |
| DRB4_0101 | 163 | ADSGNSVTQTAAVIG | GNSVTQTAA | 0.1785 | 7250.6 | 50.00 | Sequence |
| DRB4_0101 | 301 | GNLSGPRTDPLPRQD | LSGPRTDPL | 0.1774 | 7336.9 | 50.00 | Sequence |
| DRB4_0101 | 233 | IPPSARHEGLSADLD | RHEGLSADL | 0.1773 | 7338.6 | 50.00 | Sequence |
| DRB4_0101 | 188 | RGDSVDARSDVYSLG | DSVDARSDV | 0.1763 | 7423.8 | 50.00 | Sequence |
| DRB4_0101 | 298 | SAAGNLSGPRTDPLP | LSGPRTDPL | 0.1762 | 7434.2 | 50.00 | Sequence |
| DRB4_0101 | 415 | ITVNVSTGPEQREIP | ITVNVSTGP | 0.1743 | 7582.6 | 50.00 | Sequence |
| DRB4_0101 | 252 | KALAKNPENRYQTAA | KNPENRYQT | 0.1742 | 7594.8 | 50.00 | Sequence |
| DRB4_0101 | 281 | PEAPKVLTDAERTSL | KVLTDAERT | 0.1739 | 7619.8 | 50.00 | Sequence |
| DRB4_0101 | 419 | VSTGPEQREIPDVST | QREIPDVST | 0.1723 | 7746.8 | 50.00 | Sequence |
| DRB4_0101 | 158 | IARAIADSGNSVTQT | IARAIADSG | 0.1723 | 7751.2 | 50.00 | Sequence |
| DRB4_0101 | 286 | VLTDAERTSLLSSAA | ERTSLLSSA | 0.1702 | 7932.2 | 50.00 | Sequence |
| DRB4_0101 | 420 | STGPEQREIPDVSTL | QREIPDVST | 0.1698 | 7965.2 | 50.00 | Sequence |
| DRB4_0101 | 521 | QASVDSPRPAGEVTG | ASVDSPRPA | 0.1682 | 8102.7 | 50.00 | Sequence |
| DRB4_0101 | 78 | EAETPAGPLPYIVME | AGPLPYIVM | 0.1681 | 8114.7 | 50.00 | Sequence |
| DRB4_0101 | 520 | SQASVDSPRPAGEVT | ASVDSPRPA | 0.1673 | 8184.9 | 50.00 | Sequence |
| DRB4_0101 | 472 | PANQTSAITNVVIII | SAITNVVII | 0.1664 | 8262.6 | 50.00 | Sequence |
| DRB4_0101 | 162 | IADSGNSVTQTAAVI | IADSGNSVT | 0.1656 | 8330.2 | 50.00 | Sequence |
| DRB4_0101 | 295 | LLSSAAGNLSGPRTD | LSSAAGNLS | 0.1645 | 8436.1 | 50.00 | Sequence |
| DRB4_0101 | 253 | ALAKNPENRYQTAAE | PENRYQTAA | 0.1635 | 8524.9 | 50.00 | Sequence |
| DRB4_0101 | 187 | ARGDSVDARSDVYSL | DSVDARSDV | 0.1632 | 8550.0 | 50.00 | Sequence |
| DRB4_0101 | 583 | TGMLDKGADVDAGGS | GMLDKGADV | 0.1625 | 8616.1 | 50.00 | Sequence |
| DRB4_0101 | 318 | DTDRDRSIGSVGRWV | DRSIGSVGR | 0.1623 | 8632.7 | 50.00 | Sequence |
| DRB4_0101 | 449 | GRFKQANSPSTPELV | GRFKQANSP | 0.1613 | 8731.6 | 50.00 | Sequence |
| DRB4_0101 | 296 | LSSAAGNLSGPRTDP | LSSAAGNLS | 0.1589 | 8958.3 | 50.00 | Sequence |
| DRB4_0101 | 210 | TGEPPFTGDSPVSVA | PPFTGDSPV | 0.1587 | 8977.7 | 50.00 | Sequence |
| DRB4_0101 | 56 | RREAQNAAALNHPAI | AQNAAALNH | 0.1581 | 9038.2 | 50.00 | Sequence |
| DRB4_0101 | 226 | QHVREDPIPPSARHE | VREDPIPPS | 0.1549 | 9356.6 | 50.00 | Sequence |
| DRB4_0101 | 606 | NPPAGTGVNRDGIIT | GTGVNRDGI | 0.1547 | 9373.2 | 50.00 | Sequence |
| DRB4_0101 | 584 | GMLDKGADVDAGGSQ | GMLDKGADV | 0.1546 | 9384.8 | 50.00 | Sequence |
| DRB4_0101 | 280 | PPEAPKVLTDAERTS | PKVLTDAER | 0.1543 | 9413.9 | 50.00 | Sequence |
| DRB4_0101 | 186 | QARGDSVDARSDVYS | DSVDARSDV | 0.1536 | 9493.0 | 50.00 | Sequence |
| DRB4_0101 | 522 | ASVDSPRPAGEVTGT | ASVDSPRPA | 0.1527 | 9580.3 | 50.00 | Sequence |
| DRB4_0101 | 366 | GQSSADAIATLQNRG | ADAIATLQN | 0.1517 | 9685.8 | 50.00 | Sequence |
| DRB4_0101 | 231 | DPIPPSARHEGLSAD | DPIPPSARH | 0.1516 | 9694.3 | 50.00 | Sequence |
| DRB4_0101 | 209 | LTGEPPFTGDSPVSV | FTGDSPVSV | 0.1511 | 9753.0 | 50.00 | Sequence |
| DRB4_0101 | 317 | DDTDRDRSIGSVGRW | DRSIGSVGR | 0.1477 | 10110.9 | 50.00 | Sequence |
| DRB4_0101 | 407 | TSVSAGDEITVNVST | DEITVNVST | 0.1471 | 10184.5 | 50.00 | Sequence |
| DRB4_0101 | 591 | DVDAGGSQHNRVVYQ | VDAGGSQHN | 0.1465 | 10246.4 | 50.00 | Sequence |
| DRB4_0101 | 605 | QNPPAGTGVNRDGII | GTGVNRDGI | 0.1461 | 10290.7 | 50.00 | Sequence |
| DRB4_0101 | 160 | RAIADSGNSVTQTAA | RAIADSGNS | 0.1455 | 10355.1 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB4_0101 | 417 | VNVSTGPEQREIPDV | GPEQREIPD | 0.1454 | 10373.1 | 50.00 | Sequence |
| DRB4_0101 | 279 | EPPEAPKVLTDAERT | PKVLTDAER | 0.1453 | 10379.2 | 50.00 | Sequence |
| DRB4_0101 | 489 | SGPATKDIPDVAGQT | ATKDIPDVA | 0.1452 | 10394.6 | 50.00 | Sequence |
| DRB4_0101 | 55 | FRREAQNAAALNHPA | FRREAQNAA | 0.1437 | 10565.1 | 50.00 | Sequence |
| DRB4_0101 | 185 | EQARGDSVDARSDVY | DSVDARSDV | 0.1428 | 10670.2 | 50.00 | Sequence |
| DRB4_0101 | 227 | HVREDPIPPSARHEG | VREDPIPPS | 0.1421 | 10750.2 | 50.00 | Sequence |
| DRB4_0101 | 590 | ADVDAGGSQHNRVVY | VDAGGSQHN | 0.1416 | 10803.3 | 50.00 | Sequence |
| DRB4_0101 | 365 | RGQSSADAIATLQNR | ADAIATLQN | 0.1412 | 10854.3 | 50.00 | Sequence |
| DRB4_0101 | 316 | LDDTDRDRSIGSVGR | DRSIGSVGR | 0.1411 | 10860.5 | 50.00 | Sequence |
| DRB4_0101 | 418 | NVSTGPEQREIPDVS | GPEQREIPD | 0.1409 | 10890.7 | 50.00 | Sequence |
| DRB4_0101 | 69 | AIVAVYDTGEAETPA | AIVAVYDTG | 0.1405 | 10936.0 | 50.00 | Sequence |
| DRB4_0101 | 471 | PPANQTSAITNVVII | SAITNVVII | 0.1385 | 11172.1 | 50.00 | Sequence |
| DRB4_0101 | 184 | PEQARGDSVDARSDV | DSVDARSDV | 0.1384 | 11179.5 | 50.00 | Sequence |
| DRB4_0101 | 604 | YQNPPAGTGVNRDGI | GTGVNRDGI | 0.1370 | 11354.0 | 50.00 | Sequence |
| DRB4_0101 | 416 | TVNVSTGPEQREIPD | VNVSTGPEQ | 0.1367 | 11398.0 | 50.00 | Sequence |
| DRB4_0101 | 180 | QYLSPEQARGDSVDA | QYLSPEQAR | 0.1358 | 11503.3 | 50.00 | Sequence |
| DRB4_0101 | 161 | AIADSGNSVTQTAAV | IADSGNSVT | 0.1329 | 11867.4 | 50.00 | Sequence |
| DRB4_0101 | 230 | EDPIPPSARHEGLSA | DPIPPSARH | 0.1327 | 11898.6 | 50.00 | Sequence |
| DRB4_0101 | 488 | GSGPATKDIPDVAGQ | ATKDIPDVA | 0.1320 | 11992.2 | 50.00 | Sequence |
| DRB4_0101 | 589 | GADVDAGGSQHNRVV | VDAGGSQHN | 0.1309 | 12131.0 | 50.00 | Sequence |
| DRB4_0101 | 278 | GEPPEAPKVLTDAER | PKVLTDAER | 0.1289 | 12389.2 | 50.00 | Sequence |
| DRB4_0101 | 228 | VREDPIPPSARHEGL | VREDPIPPS | 0.1281 | 12508.1 | 50.00 | Sequence |
| DRB4_0101 | 454 | ANSPSTPELVGKVIG | PELVGKVIG | 0.1258 | 12824.4 | 50.00 | Sequence |
| DRB4_0101 | 77 | GEAETPAGPLPYIVM | AGPLPYIVM | 0.1255 | 12866.9 | 50.00 | Sequence |
| DRB4_0101 | 588 | KGADVDAGGSQHNRV | VDAGGSQHN | 0.1245 | 13002.4 | 50.00 | Sequence |
| DRB4_0101 | 229 | REDPIPPSARHEGLS | DPIPPSARH | 0.1235 | 13137.6 | 50.00 | Sequence |
| DRB4_0101 | 208 | VLTGEPPFTGDSPVS | PPFTGDSPV | 0.1231 | 13193.1 | 50.00 | Sequence |
| DRB4_0101 | 183 | SPEQARGDSVDARSD | SPEQARGDS | 0.1230 | 13208.6 | 50.00 | Sequence |
| DRB4_0101 | 313 | RQDLDDTDRDRSIGS | RQDLDDTDR | 0.1219 | 13372.6 | 50.00 | Sequence |
| DRB4_0101 | 159 | ARAIADSGNSVTQTA | ARAIADSGN | 0.1200 | 13645.7 | 50.00 | Sequence |
| DRB4_0101 | 312 | PRQDLDDTDRDRSIG | RQDLDDTDR | 0.1175 | 14016.8 | 50.00 | Sequence |
| DRB4_0101 | 181 | YLSPEQARGDSVDAR | ARGDSVDAR | 0.1175 | 14028.3 | 50.00 | Sequence |
| DRB4_0101 | 466 | VIGTNPPANQTSAIT | IGTNPPANQ | 0.1171 | 14082.8 | 50.00 | Sequence |
| DRB4_0101 | 602 | VVYQNPPAGTGVNRD | VVYQNPPAG | 0.1158 | 14285.2 | 50.00 | Sequence |
| DRB4_0101 | 530 | AGEVTGTNPPAGTTV | AGEVTGTNP | 0.1156 | 14313.0 | 50.00 | Sequence |
| DRB4_0101 | 529 | PAGEVTGTNPPAGTT | AGEVTGTNP | 0.1147 | 14449.6 | 50.00 | Sequence |
| DRB4_0101 | 485 | IIVGSGPATKDIPDV | IIVGSGPAT | 0.1144 | 14507.5 | 50.00 | Sequence |
| DRB4_0101 | 274 | RVHNGEPPEAPKVLT | VHNGEPPEA | 0.1139 | 14580.5 | 50.00 | Sequence |
| DRB4_0101 | 487 | VGSGPATKDIPDVAG | ATKDIPDVA | 0.1139 | 14585.0 | 50.00 | Sequence |
| DRB4_0101 | 537 | NPPAGTTVPVDSVIE | GTTVPVDSV | 0.1138 | 14592.6 | 50.00 | Sequence |
| DRB4_0101 | 486 | IVGSGPATKDIPDVA | ATKDIPDVA | 0.1122 | 14853.5 | 50.00 | Sequence |
| DRB4_0101 | 586 | LDKGADVDAGGSQHN | VDAGGSQHN | 0.1117 | 14926.9 | 50.00 | Sequence |
| DRB4_0101 | 528 | RPAGEVTGTNPPAGT | AGEVTGTNP | 0.1116 | 14944.1 | 50.00 | Sequence |
| DRB4_0101 | 467 | IGTNPPANQTSAITN | IGTNPPANQ | 0.1100 | 15208.6 | 50.00 | Sequence |
| DRB4_0101 | 527 | PRPAGEVTGTNPPAG | AGEVTGTNP | 0.1098 | 15241.3 | 50.00 | Sequence |
| DRB4_0101 | 182 | LSPEQARGDSVDARS | SPEQARGDS | 0.1087 | 15416.6 | 50.00 | Sequence |
| DRB4_0101 | 470 | NPPANQTSAITNVVI | TSAITNVVI | 0.1086 | 15445.2 | 50.00 | Sequence |
| DRB4_0101 | 406 | NTSVSAGDEITVNVS | AGDEITVNV | 0.1072 | 15676.9 | 50.00 | Sequence |
| DRB4_0101 | 450 | RFKQANSPSTPELVG | FKQANSPST | 0.1058 | 15911.3 | 50.00 | Sequence |
| DRB4_0101 | 536 | TNPPAGTTVPVDSVI | GTTVPVDSV | 0.1022 | 16555.7 | 50.00 | Sequence |
| DRB4_0101 | 277 | NGEPPEAPKVLTDAE | APKVLTDAE | 0.1017 | 16630.4 | 50.00 | Sequence |
| DRB4_0101 | 587 | DKGADVDAGGSQHNR | VDAGGSQHN | 0.1015 | 16676.1 | 50.00 | Sequence |
| DRB4_0101 | 315 | DLDDTDRDRSIGSVG | LDDTDRDRS | 0.1009 | 16782.2 | 50.00 | Sequence |
| DRB4_0101 | 469 | TNPPANQTSAITNVV | NPPANQTSA | 0.0999 | 16955.6 | 50.00 | Sequence |
| DRB4_0101 | 314 | QDLDDTDRDRSIGSV | LDDTDRDRS | 0.0999 | 16972.1 | 50.00 | Sequence |
| DRB4_0101 | 585 | MLDKGADVDAGGSQH | LDKGADVDA | 0.0997 | 17006.8 | 50.00 | Sequence |
| DRB4_0101 | 405 | ANTSVSAGDEITVNV | TSVSAGDEI | 0.0956 | 17765.8 | 50.00 | Sequence |
| DRB4_0101 | 531 | GEVTGTNPPAGTTVP | GEVTGTNPP | 0.0943 | 18024.6 | 50.00 | Sequence |
| DRB4_0101 | 526 | SPRPAGEVTGTNPPA | AGEVTGTNP | 0.0936 | 18167.6 | 50.00 | Sequence |
| DRB4_0101 | 451 | FKQANSPSTPELVGK | FKQANSPST | 0.0931 | 18268.9 | 50.00 | Sequence |
| DRB4_0101 | 276 | HNGEPPEAPKVLTDA | EAPKVLTDA | 0.0916 | 18551.5 | 50.00 | Sequence |
| DRB4_0101 | 532 | EVTGTNPPAGTTVPV | EVTGTNPPA | 0.0911 | 18660.9 | 50.00 | Sequence |
| DRB4_0101 | 535 | GTNPPAGTTVPVDSV | GTTVPVDSV | 0.0899 | 18901.2 | 50.00 | Sequence |
| DRB4_0101 | 523 | SVDSPRPAGEVTGTN | VDSPRPAGE | 0.0899 | 18902.3 | 50.00 | Sequence |
| DRB4_0101 | 76 | TGEAETPAGPLPYIV | ETPAGPLPY | 0.0898 | 18918.6 | 50.00 | Sequence |
| DRB4_0101 | 468 | GTNPPANQTSAITNV | NPPANQTSA | 0.0897 | 18945.3 | 50.00 | Sequence |

```
   DRB4_0101  275  VHNGEPPEAPKVLTD  VHNGEPPEA        0.0891      19069.1                50.00     Sequence
   DRB4_0101  453  QANSPSTPELVGKVI  TPELVGKVI        0.0875      19394.3                50.00     Sequence
   DRB4_0101  603  VYQNPPAGTGVNRDG  AGTGVNRDG        0.0862      19668.4                50.00     Sequence
   DRB4_0101  524  VDSPRPAGEVTGTNP  VDSPRPAGE        0.0835      20266.5                50.00     Sequence
   DRB4_0101  404  AANTSVSAGDEITVN  TSVSAGDEI        0.0818      20637.0                50.00     Sequence
   DRB4_0101  403  PAANTSVSAGDEITV  TSVSAGDEI        0.0817      20661.3                50.00     Sequence
   DRB4_0101  525  DSPRPAGEVTGTNPP  GEVTGTNPP        0.0803      20962.2                50.00     Sequence
   DRB4_0101   75  DTGEAETPAGPLPYI  ETPAGPLPY        0.0792      21219.6                50.00     Sequence
   DRB4_0101  398  VIGTDPAANTSVSAG  IGTDPAANT        0.0776      21584.3                50.00     Sequence
   DRB4_0101   70  IVAVYDTGEAETPAG  VAVYDTGEA        0.0755      22091.8                50.00     Sequence
   DRB4_0101  399  IGTDPAANTSVSAGD  IGTDPAANT        0.0741      22433.6                50.00     Sequence
   DRB4_0101  452  KQANSPSTPELVGKV  KQANSPSTP        0.0711      23177.7                50.00     Sequence
   DRB4_0101  401  TDPAANTSVSAGDEI  TSVSAGDEI        0.0710      23199.3                50.00     Sequence
   DRB4_0101  402  DPAANTSVSAGDEIT  TSVSAGDEI        0.0704      23346.1                50.00     Sequence
   DRB4_0101   71  VAVYDTGEAETPAGP  VAVYDTGEA        0.0647      24825.6                50.00     Sequence
   DRB4_0101   74  YDTGEAETPAGPLPY  ETPAGPLPY        0.0645      24871.3                50.00     Sequence
   DRB4_0101  533  VTGTNPPAGTTVPVD  VTGTNPPAG        0.0624      25466.3                50.00     Sequence
   DRB4_0101  534  TGTNPPAGTTVPVDS  AGTTVPVDS        0.0528      28235.7                50.00     Sequence
   DRB4_0101  400  GTDPAANTSVSAGDE  NTSVSAGDE        0.0521      28460.8                50.00     Sequence
   DRB4_0101   73  VYDTGEAETPAGPLP  VYDTGEAET        0.0479      29791.1                50.00     Sequence
   DRB4_0101   72  AVYDTGEAETPAGPL  VYDTGEAET        0.0458      30449.1                50.00     Sequence
-----------------------------------------------------------------------------------------------------

Allele: DRB4_0101. Number of high binders 15. Number of weak binders 121. Number of peptides 612

-----------------------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------------------
      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
-----------------------------------------------------------------------------------------------------
   DRB5_0101  432  STLTYAEAVKKLTAA  LTYAEAVKK        0.8104          7.8          SB     0.40     Sequence
   DRB5_0101  431  VSTLTYAEAVKKLTA  LTYAEAVKK        0.8104          7.8          SB     0.40     Sequence
   DRB5_0101  430  DVSTLTYAEAVKKLT  LTYAEAVKK        0.7974          9.0          SB     0.80     Sequence
   DRB5_0101  433  TLTYAEAVKKLTAAG  LTYAEAVKK        0.7949          9.2          SB     0.80     Sequence
   DRB5_0101  567  GMFWVDAEPRLRALG  WVDAEPRLR        0.7898          9.7          SB     0.80     Sequence
   DRB5_0101  566  SGMFWVDAEPRLRAL  WVDAEPRLR        0.7874         10.0          SB     0.80     Sequence
   DRB5_0101  568  MFWVDAEPRLRALGW  WVDAEPRLR        0.7749         11.4          SB     0.80     Sequence
   DRB5_0101  565  LSGMFWVDAEPRLRA  WVDAEPRLR        0.7712         11.9          SB     1.00     Sequence
   DRB5_0101  429  PDVSTLTYAEAVKKL  LTYAEAVKK        0.7494         15.0          SB     2.00     Sequence
   DRB5_0101  434  LTYAEAVKKLTAAGF  LTYAEAVKK        0.7447         15.8          SB     2.00     Sequence
   DRB5_0101  564  DLSGMFWVDAEPRLR  WVDAEPRLR        0.7403         16.6          SB     2.00     Sequence
   DRB5_0101  569  FWVDAEPRLRALGWT  WVDAEPRLR        0.7198         20.7          SB     4.00     Sequence
   DRB5_0101  428  IPDVSTLTYAEAVKK  LTYAEAVKK        0.6704         35.4          SB     4.00     Sequence
   DRB5_0101   18  FGGMSEVHLARDLRL  VHLARDLRL        0.6621         38.7          SB     8.00     Sequence
   DRB5_0101  140  PANIMISATNAVKVM  MISATNAVK        0.6596         39.8          SB     8.00     Sequence
   DRB5_0101  141  ANIMISATNAVKVMD  MISATNAVK        0.6440         47.1          SB     8.00     Sequence
   DRB5_0101  139  KPANIMISATNAVKV  MISATNAVK        0.6388         49.8          SB     8.00     Sequence
   DRB5_0101  142  NIMISATNAVKVMDF  ISATNAVKV        0.6250         57.8          WB     8.00     Sequence
   DRB5_0101   20  GMSEVHLARDLRLHR  VHLARDLRL        0.6105         67.6          WB     8.00     Sequence
   DRB5_0101  570  WVDAEPRLRALGWTG  WVDAEPRLR        0.5982         77.3          WB    16.00     Sequence
   DRB5_0101  246  LDAVVLKALAKNPEN  AVVLKALAK        0.5890         85.4          WB    16.00     Sequence
   DRB5_0101  370  ADAIATLQNRGFKIR  AIATLQNRG        0.5875         86.8          WB    16.00     Sequence
   DRB5_0101  378  NRGFKIRTLQKPDST  FKIRTLQKP        0.5866         87.6          WB    16.00     Sequence
   DRB5_0101  143  IMISATNAVKVMDFG  ISATNAVKV        0.5860         88.2          WB    16.00     Sequence
   DRB5_0101  379  RGFKIRTLQKPDSTI  FKIRTLQKP        0.5859         88.3          WB    16.00     Sequence
   DRB5_0101  245  DLDAVVLKALAKNPE  AVVLKALAK        0.5842         90.0          WB    16.00     Sequence
   DRB5_0101  377  QNRGFKIRTLQKPDS  FKIRTLQKP        0.5823         91.8          WB    16.00     Sequence
   DRB5_0101  369  SADAIATLQNRGFKI  AIATLQNRG        0.5817         92.4          WB    16.00     Sequence
   DRB5_0101  124  ALNFSHQNGIIHRDV  FSHQNGIIH        0.5809         93.2          WB    16.00     Sequence
   DRB5_0101  152  KVMDFGIARAIADSG  FGIARAIAD        0.5805         93.6          WB    16.00     Sequence
   DRB5_0101   49  PSFYLRFRREAQNAA  LRFRREAQN        0.5802         93.9          WB    16.00     Sequence
   DRB5_0101  123  QALNFSHQNGIIHRD  FSHQNGIIH        0.5800         94.1          WB    16.00     Sequence
   DRB5_0101   50  SFYLRFRREAQNAAA  LRFRREAQN        0.5798         94.3          WB    16.00     Sequence
   DRB5_0101   48  DPSFYLRFRREAQNA  FYLRFRREA        0.5784         95.8          WB    16.00     Sequence
   DRB5_0101   19  GGMSEVHLARDLRLH  VHLARDLRL        0.5782         96.0          WB    16.00     Sequence
   DRB5_0101  247  DAVVLKALAKNPENR  AVVLKALAK        0.5775         96.7          WB    16.00     Sequence
   DRB5_0101  151  VKVMDFGIARAIADS  FGIARAIAD        0.5724        102.2          WB    16.00     Sequence
```

```
DRB5_0101  122  CQALNFSHQNGIIHR  FSHQNGIIH        0.5721        102.5        WB    16.00     Sequence
DRB5_0101   47  RDPSFYLRFRREAQN  PSFYLRFRR        0.5708        104.0        WB    16.00     Sequence
DRB5_0101   21  MSEVHLARDLRLHRD  VHLARDLRL        0.5704        104.4        WB    16.00     Sequence
DRB5_0101  380  GFKIRTLQKPDSTIP  FKIRTLQKP        0.5696        105.3        WB    16.00     Sequence
DRB5_0101  448  FGRFKQANSPSTPEL  FKQANSPST        0.5676        107.6        WB    16.00     Sequence
DRB5_0101  371  DAIATLQNRGFKIRT  AIATLQNRG        0.5663        109.1        WB    16.00     Sequence
DRB5_0101  244  ADLDAVVLKALAKNP  AVVLKALAK        0.5657        109.8        WB    16.00     Sequence
DRB5_0101  447  GFGRFKQANSPSTPE  FKQANSPST        0.5643        111.5        WB    16.00     Sequence
DRB5_0101  138  VKPANIMISATNAVK  MISATNAVK        0.5627        113.4        WB    16.00     Sequence
DRB5_0101  125  LNFSHQNGIIHRDVK  FSHQNGIIH        0.5619        114.5        WB    16.00     Sequence
DRB5_0101  150  AVKVMDFGIARAIAD  FGIARAIAD        0.5551        123.2        WB    16.00     Sequence
DRB5_0101  449  GRFKQANSPSTPELV  FKQANSPST        0.5536        125.2        WB    16.00     Sequence
DRB5_0101   22  SEVHLARDLRLHRDV  VHLARDLRL        0.5534        125.5        WB    16.00     Sequence
DRB5_0101  248  AVVLKALAKNPENRY  AVVLKALAK        0.5497        130.5        WB    16.00     Sequence
DRB5_0101   51  FYLRFRREAQNAAAL  LRFRREAQN        0.5480        133.1        WB    16.00     Sequence
DRB5_0101  446  AGFGRFKQANSPSTP  FKQANSPST        0.5471        134.3        WB    16.00     Sequence
DRB5_0101  376  LQNRGFKIRTLQKPD  FKIRTLQKP        0.5459        136.0        WB    16.00     Sequence
DRB5_0101  101  DIVHTEGPMTPKRAI  IVHTEGPMT        0.5452        137.1        WB    16.00     Sequence
DRB5_0101  153  VMDFGIARAIADSGN  FGIARAIAD        0.5429        140.5        WB    16.00     Sequence
DRB5_0101  368  SSADAIATLQNRGFK  AIATLQNRG        0.5398        145.3        WB    16.00     Sequence
DRB5_0101   31  RLHRDVAVKVLRADL  LHRDVAVKV        0.5381        148.0        WB    16.00     Sequence
DRB5_0101  243  SADLDAVVLKALAKN  AVVLKALAK        0.5368        150.2        WB    16.00     Sequence
DRB5_0101  102  IVHTEGPMTPKRAIE  IVHTEGPMT        0.5354        152.4        WB    16.00     Sequence
DRB5_0101  121  ACQALNFSHQNGIIH  FSHQNGIIH        0.5338        155.1        WB    16.00     Sequence
DRB5_0101  375  TLQNRGFKIRTLQKP  FKIRTLQKP        0.5338        155.2        WB    16.00     Sequence
DRB5_0101   46  ARDPSFYLRFRREAQ  PSFYLRFRR        0.5313        159.4        WB    16.00     Sequence
DRB5_0101  100  RDIVHTEGPMTPKRA  IVHTEGPMT        0.5272        166.6        WB    16.00     Sequence
DRB5_0101   34  RDVAVKVLRADLARD  DVAVKVLRA        0.5267        167.5        WB    16.00     Sequence
DRB5_0101   30  LRLHRDVAVKVLRAD  LHRDVAVKV        0.5266        167.6        WB    16.00     Sequence
DRB5_0101   17  GFGGMSEVHLARDLR  FGGMSEVHL        0.5246        171.3        WB    16.00     Sequence
DRB5_0101   23  EVHLARDLRLHRDVA  VHLARDLRL        0.5216        177.1        WB    32.00     Sequence
DRB5_0101   29  DLRLHRDVAVKVLRA  LHRDVAVKV        0.5212        177.8        WB    32.00     Sequence
DRB5_0101   32  LHRDVAVKVLRADLA  LHRDVAVKV        0.5199        180.3        WB    32.00     Sequence
DRB5_0101  259  ENRYQTAAEMRADLV  YQTAAEMRA        0.5190        182.1        WB    32.00     Sequence
DRB5_0101  445  AAGFGRFKQANSPST  FKQANSPST        0.5149        190.3        WB    32.00     Sequence
DRB5_0101   99  LRDIVHTEGPMTPKR  IVHTEGPMT        0.5093        202.2        WB    32.00     Sequence
DRB5_0101   52  YLRFRREAQNAAALN  LRFRREAQN        0.5084        204.1        WB    32.00     Sequence
DRB5_0101  258  PENRYQTAAEMRADL  YQTAAEMRA        0.5059        209.8        WB    32.00     Sequence
DRB5_0101   45  LARDPSFYLRFRREA  PSFYLRFRR        0.5008        221.7        WB    32.00     Sequence
DRB5_0101  599  HNRVVYQNPPAGTGV  VVYQNPPAG        0.4935        239.9        WB    32.00     Sequence
DRB5_0101  381  FKIRTLQKPDSTIPP  FKIRTLQKP        0.4934        240.2        WB    32.00     Sequence
DRB5_0101  600  NRVVYQNPPAGTGVN  VVYQNPPAG        0.4911        246.1        WB    32.00     Sequence
DRB5_0101  260  NRYQTAAEMRADLVR  YQTAAEMRA        0.4904        248.2        WB    32.00     Sequence
DRB5_0101   35  DVAVKVLRADLARDP  DVAVKVLRA        0.4895        250.6        WB    32.00     Sequence
DRB5_0101  178  TAQYLSPEQARGDSV  YLSPEQARG        0.4879        254.9        WB    32.00     Sequence
DRB5_0101  144  MISATNAVKVMDFGI  ISATNAVKV        0.4874        256.3        WB    32.00     Sequence
DRB5_0101  126  NFSHQNGIIHRDVKP  FSHQNGIIH        0.4872        256.7        WB    32.00     Sequence
DRB5_0101  372  AIATLQNRGFKIRTL  AIATLQNRG        0.4859        260.5        WB    32.00     Sequence
DRB5_0101   28  RDLRLHRDVAVKVLR  LHRDVAVKV        0.4846        264.1        WB    32.00     Sequence
DRB5_0101  450  RFKQANSPSTPELVG  FKQANSPST        0.4807        275.5        WB    32.00     Sequence
DRB5_0101  367  QSSADAIATLQNRGF  AIATLQNRG        0.4801        277.3        WB    32.00     Sequence
DRB5_0101  179  AQYLSPEQARGDSVD  YLSPEQARG        0.4790        280.6        WB    32.00     Sequence
DRB5_0101   33  HRDVAVKVLRADLAR  RDVAVKVLR        0.4778        284.3        WB    32.00     Sequence
DRB5_0101  154  MDFGIARAIADSGNS  FGIARAIAD        0.4733        298.4        WB    32.00     Sequence
DRB5_0101   53  LRFRREAQNAAALNH  LRFRREAQN        0.4716        304.2        WB    32.00     Sequence
DRB5_0101  563  PDLSGMFWVDAEPRL  MFWVDAEPR        0.4714        304.7        WB    32.00     Sequence
DRB5_0101  257  NPENRYQTAAEMRAD  YQTAAEMRA        0.4713        304.9        WB    32.00     Sequence
DRB5_0101  483  VIIIVGSGPATKDIP  IVGSGPATK        0.4688        313.4        WB    32.00     Sequence
DRB5_0101  598  QHNRVVYQNPPAGTG  VVYQNPPAG        0.4658        323.7        WB    32.00     Sequence
DRB5_0101  482  VVIIIVGSGPATKDI  IVGSGPATK        0.4646        327.8        WB    32.00     Sequence
DRB5_0101   24  VHLARDLRLHRDVAV  VHLARDLRL        0.4637        331.1        WB    32.00     Sequence
DRB5_0101  177  GTAQYLSPEQARGDS  YLSPEQARG        0.4610        341.0        WB    32.00     Sequence
DRB5_0101   16  LGFGGMSEVHLARDL  FGGMSEVHL        0.4580        352.1        WB    32.00     Sequence
DRB5_0101  601  RVVYQNPPAGTGVNR  VVYQNPPAG        0.4565        358.0        WB    32.00     Sequence
DRB5_0101  435  TYAEAVKKLTAAGFG  VKKLTAAGF        0.4550        364.0        WB    32.00     Sequence
DRB5_0101  205  LYEVLTGEPPFTGDS  VLTGEPPFT        0.4537        368.9        WB    32.00     Sequence
```

```
DRB5_0101   14  EILGFGGMSEVHLAR  FGGMSEVHL        0.4532        371.0          WB    32.00       Sequence
DRB5_0101   98  TLRDIVHTEGPMTPK  IVHTEGPMT        0.4530        372.0          WB    32.00       Sequence
DRB5_0101  261  RYQTAAEMRADLVRV  YQTAAEMRA        0.4481        392.0          WB    32.00       Sequence
DRB5_0101   15  ILGFGGMSEVHLARD  FGGMSEVHL        0.4480        392.6          WB    32.00       Sequence
DRB5_0101  204  VLYEVLTGEPPFTGD  VLTGEPPFT        0.4474        395.1          WB    32.00       Sequence
DRB5_0101  546  VDSVIELQVSKGNQF  SVIELQVSK        0.4457        402.5          WB    32.00       Sequence
DRB5_0101  256  KNPENRYQTAAEMRA  YQTAAEMRA        0.4454        403.6          WB    32.00       Sequence
DRB5_0101  249  VVLKALAKNPENRYQ  VVLKALAKN        0.4450        405.3          WB    32.00       Sequence
DRB5_0101  149  NAVKVMDFGIARAIA  KVMDFGIAR        0.4441        409.2          WB    32.00       Sequence
DRB5_0101  180  QYLSPEQARGDSVDA  YLSPEQARG        0.4425        416.5          WB    32.00       Sequence
DRB5_0101  547  DSVIELQVSKGNQFV  SVIELQVSK        0.4391        432.0          WB    32.00       Sequence
DRB5_0101   36  VAVKVLRADLARDPS  KVLRADLAR        0.4377        438.9          WB    32.00       Sequence
DRB5_0101  203  CVLYEVLTGEPPFTG  VLTGEPPFT        0.4375        439.5          WB    32.00       Sequence
DRB5_0101   88  YIVMEYVDGVTLRDI  YIVMEYVDG        0.4362        446.0          WB    32.00       Sequence
DRB5_0101  484  IIIVGSGPATKDIPD  IVGSGPATK        0.4351        451.5          WB    32.00       Sequence
DRB5_0101   90  VMEYVDGVTLRDIVH  YVDGVTLRD        0.4344        454.7          WB    32.00       Sequence
DRB5_0101  103  VHTEGPMTPKRAIEV  VHTEGPMTP        0.4340        456.5          WB    32.00       Sequence
DRB5_0101  176  IGTAQYLSPEQARGD  YLSPEQARG        0.4334        459.7          WB    32.00       Sequence
DRB5_0101  242  LSADLDAVVLKALAK  AVVLKALAK        0.4327        463.1          WB    32.00       Sequence
DRB5_0101  597  SQHNRVVYQNPPAGT  VVYQNPPAG        0.4325        464.1          WB    32.00       Sequence
DRB5_0101  481  NVVIIIVGSGPATKD  IVGSGPATK        0.4322        465.5          WB    32.00       Sequence
DRB5_0101   44  DLARDPSFYLRFRRE  PSFYLRFRR        0.4304        474.9          WB    32.00       Sequence
DRB5_0101  137  DVKPANIMISATNAV  ANIMISATN        0.4281        486.5          WB    32.00       Sequence
DRB5_0101   89  IVMEYVDGVTLRDIV  YVDGVTLRD        0.4274        490.6          WB    32.00       Sequence
DRB5_0101  548  SVIELQVSKGNQFVM  SVIELQVSK        0.4253        501.5                32.00       Sequence
DRB5_0101  576  RLRALGWTGMLDKGA  RLRALGWTG        0.4252        502.5                32.00       Sequence
DRB5_0101   91  MEYVDGVTLRDIVHT  YVDGVTLRD        0.4246        505.4                32.00       Sequence
DRB5_0101  127  FSHQNGIIHRDVKPA  FSHQNGIIH        0.4242        507.6                32.00       Sequence
DRB5_0101   37  AVKVLRADLARDPSF  VLRADLARD        0.4235        511.4                32.00       Sequence
DRB5_0101   97  VTLRDIVHTEGPMTP  IVHTEGPMT        0.4222        518.8                32.00       Sequence
DRB5_0101  480  TNVVIIIVGSGPATK  IVGSGPATK        0.4201        530.6                32.00       Sequence
DRB5_0101  436  YAEAVKKLTAAGFGR  VKKLTAAGF        0.4196        533.8                32.00       Sequence
DRB5_0101  206  YEVLTGEPPFTGDSP  VLTGEPPFT        0.4190        537.3                32.00       Sequence
DRB5_0101   26  LARDLRLHRDVAVKV  LHRDVAVKV        0.4187        538.7                32.00       Sequence
DRB5_0101   27  ARDLRLHRDVAVKVL  LHRDVAVKV        0.4160        554.7                32.00       Sequence
DRB5_0101   38  VKVLRADLARDPSFY  VLRADLARD        0.4132        571.6                32.00       Sequence
DRB5_0101  438  EAVKKLTAAGFGRFK  VKKLTAAGF        0.4130        573.3                32.00       Sequence
DRB5_0101  292  RTSLLSSAAGNLSGP  LLSSAAGNL        0.4113        584.0                50.00       Sequence
DRB5_0101   87  PYIVMEYVDGVTLRD  YIVMEYVDG        0.4096        594.6                50.00       Sequence
DRB5_0101  437  AEAVKKLTAAGFGRF  VKKLTAAGF        0.4077        607.1                50.00       Sequence
DRB5_0101  558  NQFVMPDLSGMFWVD  FVMPDLSGM        0.4067        613.5                50.00       Sequence
DRB5_0101  574  EPRLRALGWTGMLDK  RLRALGWTG        0.4060        618.3                50.00       Sequence
DRB5_0101  439  AVKKLTAAGFGRFKQ  KLTAAGFGR        0.4051        624.6                50.00       Sequence
DRB5_0101  215  FTGDSPVSVAYQHVR  FTGDSPVSV        0.4048        626.5                50.00       Sequence
DRB5_0101  575  PRLRALGWTGMLDKG  RLRALGWTG        0.4047        627.0                50.00       Sequence
DRB5_0101  545  PVDSVIELQVSKGNQ  SVIELQVSK        0.4005        655.9                50.00       Sequence
DRB5_0101  291  ERTSLLSSAAGNLSG  LLSSAAGNL        0.3993        664.9                50.00       Sequence
DRB5_0101  557  GNQFVMPDLSGMFWV  FVMPDLSGM        0.3987        669.0                50.00       Sequence
DRB5_0101   92  EYVDGVTLRDIVHTE  YVDGVTLRD        0.3959        689.4                50.00       Sequence
DRB5_0101  544  VPVDSVIELQVSKGN  SVIELQVSK        0.3946        699.4                50.00       Sequence
DRB5_0101  485  IIVGSGPATKDIPDV  IVGSGPATK        0.3933        709.3                50.00       Sequence
DRB5_0101   39  KVLRADLARDPSFYL  VLRADLARD        0.3928        713.2                50.00       Sequence
DRB5_0101  345  VTIAINTFGGITRDV  INTFGGITR        0.3927        714.1                50.00       Sequence
DRB5_0101  374  ATLQNRGFKIRTLQK  GFKIRTLQK        0.3919        720.5                50.00       Sequence
DRB5_0101  175  VIGTAQYLSPEQARG  YLSPEQARG        0.3892        741.8                50.00       Sequence
DRB5_0101  373  IATLQNRGFKIRTLQ  IATLQNRGF        0.3873        757.0                50.00       Sequence
DRB5_0101  155  DFGIARAIADSGNSV  FGIARAIAD        0.3870        759.0                50.00       Sequence
DRB5_0101  105  TEGPMTPKRAIEVIA  MTPKRAIEV        0.3850        776.3                50.00       Sequence
DRB5_0101  556  KGNQFVMPDLSGMFW  QFVMPDLSG        0.3841        783.4                50.00       Sequence
DRB5_0101  320  DRDRSIGSVGRWVAV  DRSIGSVGR        0.3836        787.8                50.00       Sequence
DRB5_0101  290  AERTSLLSSAAGNLS  SLLSSAAGN        0.3823        799.0                50.00       Sequence
DRB5_0101  293  TSLLSSAAGNLSGPR  LLSSAAGNL        0.3818        803.4                50.00       Sequence
DRB5_0101  104  HTEGPMTPKRAIEVI  MTPKRAIEV        0.3803        816.5                50.00       Sequence
DRB5_0101  596  GSQHNRVVYQNPPAG  VVYQNPPAG        0.3785        832.3                50.00       Sequence
DRB5_0101  346  TIAINTFGGITRDVQ  INTFGGITR        0.3782        835.7                50.00       Sequence
DRB5_0101  343  VVVTIAINTFGGITR  INTFGGITR        0.3765        850.9                50.00       Sequence
```

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| DRB5_0101 | 319 | TDRDRSIGSVGRWVA | DRSIGSVGR | 0.3765 | 851.1 | 50.00 | Sequence |
| DRB5_0101 | 202 | GCVLYEVLTGEPPFT | VLTGEPPFT | 0.3734 | 879.9 | 50.00 | Sequence |
| DRB5_0101 | 344 | VVTIAINTFGGITRD | INTFGGITR | 0.3732 | 882.0 | 50.00 | Sequence |
| DRB5_0101 | 218 | DSPVSVAYQHVREDP | VSVAYQHVR | 0.3730 | 883.6 | 50.00 | Sequence |
| DRB5_0101 | 321 | RDRSIGSVGRWVAVV | DRSIGSVGR | 0.3723 | 890.0 | 50.00 | Sequence |
| DRB5_0101 | 219 | SPVSVAYQHVREDPI | VSVAYQHVR | 0.3714 | 898.9 | 50.00 | Sequence |
| DRB5_0101 | 559 | QFVMPDLSGMFWVDA | FVMPDLSGM | 0.3704 | 908.5 | 50.00 | Sequence |
| DRB5_0101 | 43 | ADLARDPSFYLRFRR | PSFYLRFRR | 0.3686 | 926.9 | 50.00 | Sequence |
| DRB5_0101 | 217 | GDSPVSVAYQHVRED | VSVAYQHVR | 0.3680 | 932.6 | 50.00 | Sequence |
| DRB5_0101 | 513 | VYGFTKFSQASVDSP | FTKFSQASV | 0.3670 | 943.3 | 50.00 | Sequence |
| DRB5_0101 | 451 | FKQANSPSTPELVGK | FKQANSPST | 0.3656 | 957.6 | 50.00 | Sequence |
| DRB5_0101 | 13 | GEILGFGGMSEVHLA | FGGMSEVHL | 0.3655 | 958.3 | 50.00 | Sequence |
| DRB5_0101 | 207 | EVLTGEPPFTGDSPV | VLTGEPPFT | 0.3652 | 961.4 | 50.00 | Sequence |
| DRB5_0101 | 573 | AEPRLRALGWTGMLD | RLRALGWTG | 0.3647 | 966.2 | 50.00 | Sequence |
| DRB5_0101 | 262 | YQTAAEMRADLVRVH | YQTAAEMRA | 0.3640 | 973.9 | 50.00 | Sequence |
| DRB5_0101 | 512 | NVYGFTKFSQASVDS | FTKFSQASV | 0.3628 | 986.7 | 50.00 | Sequence |
| DRB5_0101 | 148 | TNAVKVMDFGIARAI | VMDFGIARA | 0.3621 | 994.4 | 50.00 | Sequence |
| DRB5_0101 | 318 | DTDRDRSIGSVGRWV | DRSIGSVGR | 0.3610 | 1006.0 | 50.00 | Sequence |
| DRB5_0101 | 514 | YGFTKFSQASVDSPR | FTKFSQASV | 0.3608 | 1008.5 | 50.00 | Sequence |
| DRB5_0101 | 347 | IAINTFGGITRDVQV | INTFGGITR | 0.3607 | 1009.7 | 50.00 | Sequence |
| DRB5_0101 | 86 | LPYIVMEYVDGVTLR | YIVMEYVDG | 0.3602 | 1014.4 | 50.00 | Sequence |
| DRB5_0101 | 555 | SKGNQFVMPDLSGMF | FVMPDLSGM | 0.3600 | 1017.1 | 50.00 | Sequence |
| DRB5_0101 | 543 | TVPVDSVIELQVSKG | SVIELQVSK | 0.3599 | 1018.0 | 50.00 | Sequence |
| DRB5_0101 | 294 | SLLSSAAGNLSGPRT | SLLSSAAGN | 0.3599 | 1018.1 | 50.00 | Sequence |
| DRB5_0101 | 549 | VIELQVSKGNQFVMP | LQVSKGNQF | 0.3595 | 1023.0 | 50.00 | Sequence |
| DRB5_0101 | 611 | TGVNRDGIITLRFGQ | RDGIITLRF | 0.3572 | 1048.0 | 50.00 | Sequence |
| DRB5_0101 | 54 | RFRREAQNAAALNHP | FRREAQNAA | 0.3544 | 1081.0 | 50.00 | Sequence |
| DRB5_0101 | 136 | RDVKPANIMISATNA | ANIMISATN | 0.3538 | 1088.1 | 50.00 | Sequence |
| DRB5_0101 | 12 | LGEILGFGGMSEVHL | FGGMSEVHL | 0.3537 | 1088.5 | 50.00 | Sequence |
| DRB5_0101 | 602 | VVYQNPPAGTGVNRD | VVYQNPPAG | 0.3516 | 1114.4 | 50.00 | Sequence |
| DRB5_0101 | 511 | LNVYGFTKFSQASVD | FTKFSQASV | 0.3453 | 1191.8 | 50.00 | Sequence |
| DRB5_0101 | 120 | DACQALNFSHQNGII | ACQALNFSH | 0.3446 | 1202.0 | 50.00 | Sequence |
| DRB5_0101 | 96 | GVTLRDIVHTEGPMT | IVHTEGPMT | 0.3442 | 1207.0 | 50.00 | Sequence |
| DRB5_0101 | 322 | DRSIGSVGRWVAVVA | DRSIGSVGR | 0.3428 | 1225.3 | 50.00 | Sequence |
| DRB5_0101 | 216 | TGDSPVSVAYQHVRE | VSVAYQHVR | 0.3415 | 1241.8 | 50.00 | Sequence |
| DRB5_0101 | 348 | AINTFGGITRDVQVP | INTFGGITR | 0.3409 | 1251.0 | 50.00 | Sequence |
| DRB5_0101 | 145 | ISATNAVKVMDFGIA | ISATNAVKV | 0.3398 | 1265.2 | 50.00 | Sequence |
| DRB5_0101 | 572 | DAEPRLRALGWTGML | RLRALGWTG | 0.3393 | 1272.9 | 50.00 | Sequence |
| DRB5_0101 | 440 | VKKLTAAGFGRFKQA | KLTAAGFGR | 0.3391 | 1274.5 | 50.00 | Sequence |
| DRB5_0101 | 93 | YVDGVTLRDIVHTEG | YVDGVTLRD | 0.3390 | 1276.6 | 50.00 | Sequence |
| DRB5_0101 | 135 | HRDVKPANIMISATN | VKPANIMIS | 0.3372 | 1301.8 | 50.00 | Sequence |
| DRB5_0101 | 106 | EGPMTPKRAIEVIAD | MTPKRAIEV | 0.3358 | 1321.6 | 50.00 | Sequence |
| DRB5_0101 | 250 | VLKALAKNPENRYQT | VLKALAKNP | 0.3339 | 1349.3 | 50.00 | Sequence |
| DRB5_0101 | 366 | GQSSADAIATLQNRG | AIATLQNRG | 0.3331 | 1361.1 | 50.00 | Sequence |
| DRB5_0101 | 213 | PPFTGDSPVSVAYQH | FTGDSPVSV | 0.3320 | 1377.5 | 50.00 | Sequence |
| DRB5_0101 | 579 | ALGWTGMLDKGADVD | LGWTGMLDK | 0.3299 | 1408.0 | 50.00 | Sequence |
| DRB5_0101 | 578 | RALGWTGMLDKGADV | LGWTGMLDK | 0.3298 | 1410.8 | 50.00 | Sequence |
| DRB5_0101 | 289 | DAERTSLLSSAAGNL | RTSLLSSAA | 0.3279 | 1438.7 | 50.00 | Sequence |
| DRB5_0101 | 8 | DRYELGEILGFGGMS | YELGEILGF | 0.3270 | 1453.0 | 50.00 | Sequence |
| DRB5_0101 | 577 | LRALGWTGMLDKGAD | LGWTGMLDK | 0.3251 | 1484.1 | 50.00 | Sequence |
| DRB5_0101 | 107 | GPMTPKRAIEVIADA | MTPKRAIEV | 0.3244 | 1495.3 | 50.00 | Sequence |
| DRB5_0101 | 266 | AEMRADLVRVHNGEP | EMRADLVRV | 0.3243 | 1497.2 | 50.00 | Sequence |
| DRB5_0101 | 214 | PFTGDSPVSVAYQHV | FTGDSPVSV | 0.3229 | 1519.2 | 50.00 | Sequence |
| DRB5_0101 | 510 | NLNVYGFTKFSQASV | VYGFTKFSQ | 0.3224 | 1527.8 | 50.00 | Sequence |
| DRB5_0101 | 9 | RYELGEILGFGGMSE | YELGEILGF | 0.3199 | 1568.8 | 50.00 | Sequence |
| DRB5_0101 | 212 | EPPFTGDSPVSVAYQ | FTGDSPVSV | 0.3193 | 1580.3 | 50.00 | Sequence |
| DRB5_0101 | 25 | HLARDLRLHRDVAVK | LARDLRLHR | 0.3192 | 1582.1 | 50.00 | Sequence |
| DRB5_0101 | 220 | PVSVAYQHVREDPIP | VSVAYQHVR | 0.3187 | 1590.2 | 50.00 | Sequence |
| DRB5_0101 | 580 | LGWTGMLDKGADVDA | LGWTGMLDK | 0.3161 | 1635.8 | 50.00 | Sequence |
| DRB5_0101 | 554 | VSKGNQFVMPDLSGM | FVMPDLSGM | 0.3142 | 1669.4 | 50.00 | Sequence |
| DRB5_0101 | 85 | PLPYIVMEYVDGVTL | YIVMEYVDG | 0.3141 | 1670.5 | 50.00 | Sequence |
| DRB5_0101 | 515 | GFTKFSQASVDSPRP | FTKFSQASV | 0.3136 | 1680.9 | 50.00 | Sequence |
| DRB5_0101 | 442 | KLTAAGFGRFKQANS | KLTAAGFGR | 0.3133 | 1686.5 | 50.00 | Sequence |
| DRB5_0101 | 221 | VSVAYQHVREDPIPP | VSVAYQHVR | 0.3123 | 1704.4 | 50.00 | Sequence |
| DRB5_0101 | 571 | VDAEPRLRALGWTGM | RLRALGWTG | 0.3119 | 1711.1 | 50.00 | Sequence |
| DRB5_0101 | 255 | AKNPENRYQTAAEMR | NRYQTAAEM | 0.3105 | 1737.6 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB5_0101 | 444 | TAAGFGRFKQANSPS | GRFKQANSP | 0.3100 | 1746.3 | 50.00 | Sequence |
| DRB5_0101 | 441 | KKLTAAGFGRFKQAN | KLTAAGFGR | 0.3095 | 1756.6 | 50.00 | Sequence |
| DRB5_0101 | 40 | VLRADLARDPSFYLR | VLRADLARD | 0.3091 | 1763.7 | 50.00 | Sequence |
| DRB5_0101 | 55 | FRREAQNAAALNHPA | FRREAQNAA | 0.3088 | 1770.0 | 50.00 | Sequence |
| DRB5_0101 | 132 | GIIHRDVKPANIMIS | HRDVKPANI | 0.3079 | 1786.5 | 50.00 | Sequence |
| DRB5_0101 | 147 | ATNAVKVMDFGIARA | KVMDFGIAR | 0.3079 | 1787.9 | 50.00 | Sequence |
| DRB5_0101 | 267 | EMRADLVRVHNGEPP | EMRADLVRV | 0.3064 | 1816.6 | 50.00 | Sequence |
| DRB5_0101 | 486 | IVGSGPATKDIPDVA | IVGSGPATK | 0.3059 | 1825.8 | 50.00 | Sequence |
| DRB5_0101 | 7 | SDRYELGEILGFGGM | YELGEILGF | 0.3048 | 1848.2 | 50.00 | Sequence |
| DRB5_0101 | 181 | YLSPEQARGDSVDAR | YLSPEQARG | 0.3019 | 1906.9 | 50.00 | Sequence |
| DRB5_0101 | 134 | IHRDVKPANIMISAT | VKPANIMIS | 0.3000 | 1947.0 | 50.00 | Sequence |
| DRB5_0101 | 119 | ADACQALNFSHQNGI | ACQALNFSH | 0.2996 | 1954.5 | 50.00 | Sequence |
| DRB5_0101 | 562 | MPDLSGMFWVDAEPR | MFWVDAEPR | 0.2991 | 1965.6 | 50.00 | Sequence |
| DRB5_0101 | 463 | VGKVIGTNPPANQTS | VIGTNPPAN | 0.2983 | 1983.3 | 50.00 | Sequence |
| DRB5_0101 | 133 | IIHRDVKPANIMISA | HRDVKPANI | 0.2972 | 2006.1 | 50.00 | Sequence |
| DRB5_0101 | 349 | INTFGGITRDVQVPD | INTFGGITR | 0.2972 | 2006.4 | 50.00 | Sequence |
| DRB5_0101 | 196 | SDVYSLGCVLYEVLT | YSLGCVLYE | 0.2966 | 2019.6 | 50.00 | Sequence |
| DRB5_0101 | 211 | GEPPFTGDSPVSVAY | FTGDSPVSV | 0.2966 | 2020.0 | 50.00 | Sequence |
| DRB5_0101 | 317 | DDTDRDRSIGSVGRW | DRSIGSVGR | 0.2958 | 2036.2 | 50.00 | Sequence |
| DRB5_0101 | 208 | VLTGEPPFTGDSPVS | VLTGEPPFT | 0.2956 | 2041.9 | 50.00 | Sequence |
| DRB5_0101 | 195 | RSDVYSLGCVLYEVL | YSLGCVLYE | 0.2924 | 2113.4 | 50.00 | Sequence |
| DRB5_0101 | 462 | LVGKVIGTNPPANQT | VIGTNPPAN | 0.2919 | 2125.5 | 50.00 | Sequence |
| DRB5_0101 | 264 | TAAEMRADLVRVHNG | EMRADLVRV | 0.2916 | 2132.7 | 50.00 | Sequence |
| DRB5_0101 | 194 | ARSDVYSLGCVLYEV | DVYSLGCVL | 0.2909 | 2147.7 | 50.00 | Sequence |
| DRB5_0101 | 542 | TTVPVDSVIELQVSK | SVIELQVSK | 0.2906 | 2156.1 | 50.00 | Sequence |
| DRB5_0101 | 265 | AAEMRADLVRVHNGE | EMRADLVRV | 0.2895 | 2180.1 | 50.00 | Sequence |
| DRB5_0101 | 550 | IELQVSKGNQFVMPD | LQVSKGNQF | 0.2888 | 2196.6 | 50.00 | Sequence |
| DRB5_0101 | 464 | GKVIGTNPPANQTSA | VIGTNPPAN | 0.2888 | 2197.4 | 50.00 | Sequence |
| DRB5_0101 | 156 | FGIARAIADSGNSVT | FGIARAIAD | 0.2877 | 2222.5 | 50.00 | Sequence |
| DRB5_0101 | 174 | AVIGTAQYLSPEQAR | AVIGTAQYL | 0.2876 | 2225.7 | 50.00 | Sequence |
| DRB5_0101 | 6 | LSDRYELGEILGFGG | YELGEILGF | 0.2867 | 2247.8 | 50.00 | Sequence |
| DRB5_0101 | 443 | LTAAGFGRFKQANSP | GRFKQANSP | 0.2842 | 2309.9 | 50.00 | Sequence |
| DRB5_0101 | 201 | LGCVLYEVLTGEPPF | LYEVLTGEP | 0.2842 | 2310.5 | 50.00 | Sequence |
| DRB5_0101 | 197 | DVYSLGCVLYEVLTG | YSLGCVLYE | 0.2833 | 2332.4 | 50.00 | Sequence |
| DRB5_0101 | 84 | GPLPYIVMEYVDGVT | YIVMEYVDG | 0.2803 | 2408.9 | 50.00 | Sequence |
| DRB5_0101 | 465 | KVIGTNPPANQTSAI | VIGTNPPAN | 0.2795 | 2430.6 | 50.00 | Sequence |
| DRB5_0101 | 382 | KIRTLQKPDSTIPPD | RTLQKPDST | 0.2794 | 2433.2 | 50.00 | Sequence |
| DRB5_0101 | 610 | GTGVNRDGIITLRFG | RDGIITLRF | 0.2771 | 2494.2 | 50.00 | Sequence |
| DRB5_0101 | 461 | ELVGKVIGTNPPANQ | VIGTNPPAN | 0.2764 | 2514.2 | 50.00 | Sequence |
| DRB5_0101 | 283 | APKVLTDAERTSLLS | KVLTDAERT | 0.2760 | 2522.5 | 50.00 | Sequence |
| DRB5_0101 | 131 | NGIIHRDVKPANIMI | GIIHRDVKP | 0.2758 | 2529.0 | 50.00 | Sequence |
| DRB5_0101 | 193 | DARSDVYSLGCVLYE | YSLGCVLYE | 0.2754 | 2539.3 | 50.00 | Sequence |
| DRB5_0101 | 295 | LLSSAAGNLSGPRTD | LLSSAAGNL | 0.2746 | 2562.8 | 50.00 | Sequence |
| DRB5_0101 | 560 | FVMPDLSGMFWVDAE | FVMPDLSGM | 0.2725 | 2619.8 | 50.00 | Sequence |
| DRB5_0101 | 83 | AGPLPYIVMEYVDGV | YIVMEYVDG | 0.2695 | 2708.5 | 50.00 | Sequence |
| DRB5_0101 | 323 | RSIGSVGRWVAVVAV | GRWVAVVAV | 0.2683 | 2741.7 | 50.00 | Sequence |
| DRB5_0101 | 284 | PKVLTDAERTSLLSS | KVLTDAERT | 0.2656 | 2823.3 | 50.00 | Sequence |
| DRB5_0101 | 251 | LKALAKNPENRYQTA | ALAKNPENR | 0.2654 | 2830.1 | 50.00 | Sequence |
| DRB5_0101 | 10 | YELGEILGFGGMSEV | YELGEILGF | 0.2643 | 2863.7 | 50.00 | Sequence |
| DRB5_0101 | 11 | ELGEILGFGGMSEVH | ILGFGGMSE | 0.2636 | 2884.7 | 50.00 | Sequence |
| DRB5_0101 | 5 | HLSDRYELGEILGFG | YELGEILGF | 0.2623 | 2928.5 | 50.00 | Sequence |
| DRB5_0101 | 509 | KNLNVYGFTKFSQAS | VYGFTKFSQ | 0.2618 | 2941.4 | 50.00 | Sequence |
| DRB5_0101 | 288 | TDAERTSLLSSAAGN | RTSLLSSAA | 0.2617 | 2946.8 | 50.00 | Sequence |
| DRB5_0101 | 209 | LTGEPPFTGDSPVSV | FTGDSPVSV | 0.2602 | 2994.5 | 50.00 | Sequence |
| DRB5_0101 | 460 | PELVGKVIGTNPPAN | VIGTNPPAN | 0.2601 | 2996.2 | 50.00 | Sequence |
| DRB5_0101 | 327 | SVGRWVAVVAVLAVL | GRWVAVVAV | 0.2585 | 3049.4 | 50.00 | Sequence |
| DRB5_0101 | 172 | TAAVIGTAQYLSPEQ | AVIGTAQYL | 0.2575 | 3084.0 | 50.00 | Sequence |
| DRB5_0101 | 329 | GRWVAVVAVLAVLTV | GRWVAVVAV | 0.2570 | 3099.2 | 50.00 | Sequence |
| DRB5_0101 | 173 | AAVIGTAQYLSPEQA | AVIGTAQYL | 0.2564 | 3121.4 | 50.00 | Sequence |
| DRB5_0101 | 328 | VGRWVAVVAVLAVLT | GRWVAVVAV | 0.2559 | 3136.5 | 50.00 | Sequence |
| DRB5_0101 | 263 | QTAAEMRADLVRVHN | EMRADLVRV | 0.2551 | 3165.3 | 50.00 | Sequence |
| DRB5_0101 | 282 | EAPKVLTDAERTSLL | KVLTDAERT | 0.2545 | 3184.4 | 50.00 | Sequence |
| DRB5_0101 | 285 | KVLTDAERTSLLSSA | KVLTDAERT | 0.2531 | 3231.8 | 50.00 | Sequence |
| DRB5_0101 | 118 | IADACQALNFSHQNG | ACQALNFSH | 0.2520 | 3271.2 | 50.00 | Sequence |
| DRB5_0101 | 507 | AQKNLNVYGFTKFSQ | NLNVYGFTK | 0.2514 | 3295.1 | 50.00 | Sequence |
| DRB5_0101 | 210 | TGEPPFTGDSPVSVA | FTGDSPVSV | 0.2498 | 3349.9 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB5_0101 | 466 | VIGTNPPANQTSAIT | VIGTNPPAN | 0.2498 | 3351.2 | 50.00 | Sequence |
| DRB5_0101 | 508 | QKNLNVYGFTKFSQA | VYGFTKFSQ | 0.2483 | 3404.0 | 50.00 | Sequence |
| DRB5_0101 | 171 | QTAAVIGTAQYLSPE | AVIGTAQYL | 0.2478 | 3422.8 | 50.00 | Sequence |
| DRB5_0101 | 326 | GSVGRWVAVVAVLAV | GRWVAVVAV | 0.2475 | 3434.6 | 50.00 | Sequence |
| DRB5_0101 | 502 | QTVDVAQKNLNVYGF | VDVAQKNLN | 0.2474 | 3440.5 | 50.00 | Sequence |
| DRB5_0101 | 427 | EIPDVSTLTYAEAVK | IPDVSTLTY | 0.2468 | 3460.9 | 50.00 | Sequence |
| DRB5_0101 | 146 | SATNAVKVMDFGIAR | KVMDFGIAR | 0.2456 | 3504.9 | 50.00 | Sequence |
| DRB5_0101 | 199 | YSLGCVLYEVLTGEP | YSLGCVLYE | 0.2454 | 3513.5 | 50.00 | Sequence |
| DRB5_0101 | 130 | QNGIIHRDVKPANIM | GIIHRDVKP | 0.2453 | 3519.0 | 50.00 | Sequence |
| DRB5_0101 | 504 | VDVAQKNLNVYGFTK | VDVAQKNLN | 0.2432 | 3598.0 | 50.00 | Sequence |
| DRB5_0101 | 115 | IEVIADACQALNFSH | ACQALNFSH | 0.2431 | 3603.7 | 50.00 | Sequence |
| DRB5_0101 | 501 | GQTVDVAQKNLNVYG | VDVAQKNLN | 0.2425 | 3626.3 | 50.00 | Sequence |
| DRB5_0101 | 609 | AGTGVNRDGIITLRF | RDGIITLRF | 0.2423 | 3634.8 | 50.00 | Sequence |
| DRB5_0101 | 82 | PAGPLPYIVMEYVDG | YIVMEYVDG | 0.2417 | 3659.4 | 50.00 | Sequence |
| DRB5_0101 | 117 | VIADACQALNFSHQN | ACQALNFSH | 0.2416 | 3663.5 | 50.00 | Sequence |
| DRB5_0101 | 342 | TVVVTIAINTFGGIT | VTIAINTFG | 0.2412 | 3676.0 | 50.00 | Sequence |
| DRB5_0101 | 325 | IGSVGRWVAVVAVLA | GRWVAVVAV | 0.2401 | 3723.1 | 50.00 | Sequence |
| DRB5_0101 | 479 | ITNVVIIIVGSGPAT | IIVGSGPAT | 0.2396 | 3740.0 | 50.00 | Sequence |
| DRB5_0101 | 116 | EVIADACQALNFSHQ | ACQALNFSH | 0.2374 | 3832.7 | 50.00 | Sequence |
| DRB5_0101 | 516 | FTKFSQASVDSPRPA | FTKFSQASV | 0.2370 | 3847.2 | 50.00 | Sequence |
| DRB5_0101 | 324 | SIGSVGRWVAVVAVL | GRWVAVVAV | 0.2367 | 3862.6 | 50.00 | Sequence |
| DRB5_0101 | 503 | TVDVAQKNLNVYGFT | DVAQKNLNV | 0.2364 | 3874.6 | 50.00 | Sequence |
| DRB5_0101 | 269 | RADLVRVHNGEPPEA | LVRVHNGEP | 0.2347 | 3946.9 | 50.00 | Sequence |
| DRB5_0101 | 506 | VAQKNLNVYGFTKFS | NLNVYGFTK | 0.2346 | 3950.0 | 50.00 | Sequence |
| DRB5_0101 | 252 | KALAKNPENRYQTAA | ALAKNPENR | 0.2323 | 4051.7 | 50.00 | Sequence |
| DRB5_0101 | 200 | SLGCVLYEVLTGEPP | LYEVLTGEP | 0.2316 | 4079.8 | 50.00 | Sequence |
| DRB5_0101 | 505 | DVAQKNLNVYGFTKF | LNVYGFTKF | 0.2312 | 4099.1 | 50.00 | Sequence |
| DRB5_0101 | 198 | VYSLGCVLYEVLTGE | YSLGCVLYE | 0.2310 | 4108.4 | 50.00 | Sequence |
| DRB5_0101 | 170 | TQTAAVIGTAQYLSP | AVIGTAQYL | 0.2289 | 4203.0 | 50.00 | Sequence |
| DRB5_0101 | 581 | GWTGMLDKGADVDAG | WTGMLDKGA | 0.2273 | 4273.7 | 50.00 | Sequence |
| DRB5_0101 | 42 | RADLARDPSFYLRFR | DLARDPSFY | 0.2260 | 4335.0 | 50.00 | Sequence |
| DRB5_0101 | 595 | GGSQHNRVVYQNPPA | RVVYQNPPA | 0.2259 | 4341.1 | 50.00 | Sequence |
| DRB5_0101 | 551 | ELQVSKGNQFVMPDL | LQVSKGNQF | 0.2251 | 4378.2 | 50.00 | Sequence |
| DRB5_0101 | 128 | SHQNGIIHRDVKPAN | SHQNGIIHR | 0.2242 | 4420.6 | 50.00 | Sequence |
| DRB5_0101 | 500 | AGQTVDVAQKNLNVY | VDVAQKNLN | 0.2237 | 4443.4 | 50.00 | Sequence |
| DRB5_0101 | 241 | GLSADLDAVVLKALA | DLDAVVLKA | 0.2232 | 4468.1 | 50.00 | Sequence |
| DRB5_0101 | 268 | MRADLVRVHNGEPPE | LVRVHNGEP | 0.2232 | 4468.5 | 50.00 | Sequence |
| DRB5_0101 | 396 | DHVIGTDPAANTSVS | VIGTDPAAN | 0.2220 | 4529.3 | 50.00 | Sequence |
| DRB5_0101 | 316 | LDDTDRDRSIGSVGR | DRSIGSVGR | 0.2213 | 4560.0 | 50.00 | Sequence |
| DRB5_0101 | 4 | SHLSDRYELGEILGF | YELGEILGF | 0.2213 | 4562.0 | 50.00 | Sequence |
| DRB5_0101 | 286 | VLTDAERTSLLSSAA | RTSLLSSAA | 0.2198 | 4634.2 | 50.00 | Sequence |
| DRB5_0101 | 108 | PMTPKRAIEVIADAC | MTPKRAIEV | 0.2194 | 4656.7 | 50.00 | Sequence |
| DRB5_0101 | 365 | RGQSSADAIATLQNR | DAIATLQNR | 0.2192 | 4665.8 | 50.00 | Sequence |
| DRB5_0101 | 395 | PDHVIGTDPAANTSV | VIGTDPAAN | 0.2191 | 4670.5 | 50.00 | Sequence |
| DRB5_0101 | 129 | HQNGIIHRDVKPANI | GIIHRDVKP | 0.2185 | 4699.7 | 50.00 | Sequence |
| DRB5_0101 | 341 | LTVVVTIAINTFGGI | VTIAINTFG | 0.2158 | 4839.4 | 50.00 | Sequence |
| DRB5_0101 | 287 | LTDAERTSLLSSAAG | RTSLLSSAA | 0.2157 | 4844.6 | 50.00 | Sequence |
| DRB5_0101 | 168 | SVTQTAAVIGTAQYL | VTQTAAVIG | 0.2149 | 4890.7 | 50.00 | Sequence |
| DRB5_0101 | 296 | LSSAAGNLSGPRTDP | AAGNLSGPR | 0.2144 | 4913.2 | 50.00 | Sequence |
| DRB5_0101 | 56 | RREAQNAAALNHPAI | RREAQNAAA | 0.2141 | 4932.6 | 50.00 | Sequence |
| DRB5_0101 | 41 | LRADLARDPSFYLRF | DLARDPSFY | 0.2140 | 4933.5 | 50.00 | Sequence |
| DRB5_0101 | 363 | DVRGQSSADAIATLQ | VRGQSSADA | 0.2139 | 4939.0 | 50.00 | Sequence |
| DRB5_0101 | 383 | IRTLQKPDSTIPPDH | IRTLQKPDS | 0.2139 | 4943.2 | 50.00 | Sequence |
| DRB5_0101 | 362 | PDVRGQSSADAIATL | VRGQSSADA | 0.2132 | 4981.0 | 50.00 | Sequence |
| DRB5_0101 | 169 | VTQTAAVIGTAQYLS | AVIGTAQYL | 0.2129 | 4997.2 | 50.00 | Sequence |
| DRB5_0101 | 397 | HVIGTDPAANTSVSA | VIGTDPAAN | 0.2128 | 5003.3 | 50.00 | Sequence |
| DRB5_0101 | 361 | VPDVRGQSSADAIAT | VRGQSSADA | 0.2121 | 5036.2 | 50.00 | Sequence |
| DRB5_0101 | 192 | VDARSDVYSLGCVLY | DVYSLGCVL | 0.2116 | 5063.3 | 50.00 | Sequence |
| DRB5_0101 | 281 | PEAPKVLTDAERTSL | KVLTDAERT | 0.2111 | 5093.1 | 50.00 | Sequence |
| DRB5_0101 | 414 | EITVNVSTGPEQREI | VNVSTGPEQ | 0.2107 | 5116.3 | 50.00 | Sequence |
| DRB5_0101 | 472 | PANQTSAITNVVIII | ANQTSAITN | 0.2096 | 5175.8 | 50.00 | Sequence |
| DRB5_0101 | 270 | ADLVRVHNGEPPEAP | LVRVHNGEP | 0.2085 | 5239.2 | 50.00 | Sequence |
| DRB5_0101 | 552 | LQVSKGNQFVMPDLS | LQVSKGNQF | 0.2077 | 5286.2 | 50.00 | Sequence |
| DRB5_0101 | 473 | ANQTSAITNVVIIIV | ANQTSAITN | 0.2072 | 5313.6 | 50.00 | Sequence |
| DRB5_0101 | 471 | PPANQTSAITNVVII | ANQTSAITN | 0.2069 | 5333.2 | 50.00 | Sequence |
| DRB5_0101 | 340 | VLTVVVTIAINTFGG | VVVTIAINT | 0.2065 | 5353.1 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB5_0101 | 254 | LAKNPENRYQTAAEM | NRYQTAAEM | 0.2051 | 5434.0 | 50.00 | Sequence |
| DRB5_0101 | 330 | RWVAVVAVLAVLTVV | RWVAVVAVL | 0.2039 | 5507.8 | 50.00 | Sequence |
| DRB5_0101 | 553 | QVSKGNQFVMPDLSG | QFVMPDLSG | 0.2030 | 5562.9 | 50.00 | Sequence |
| DRB5_0101 | 339 | AVLTVVVTIAINTFG | VVVTIAINT | 0.2028 | 5569.3 | 50.00 | Sequence |
| DRB5_0101 | 499 | VAGQTVDVAQKNLNV | VDVAQKNLN | 0.2025 | 5589.4 | 50.00 | Sequence |
| DRB5_0101 | 398 | VIGTDPAANTSVSAG | VIGTDPAAN | 0.2018 | 5632.5 | 50.00 | Sequence |
| DRB5_0101 | 64 | ALNHPAIVAVYDTGE | LNHPAIVAV | 0.2017 | 5640.2 | 50.00 | Sequence |
| DRB5_0101 | 63 | AALNHPAIVAVYDTG | LNHPAIVAV | 0.2008 | 5692.1 | 50.00 | Sequence |
| DRB5_0101 | 272 | LVRVHNGEPPEAPKV | LVRVHNGEP | 0.1990 | 5808.4 | 50.00 | Sequence |
| DRB5_0101 | 394 | PPDHVIGTDPAANTS | VIGTDPAAN | 0.1977 | 5889.1 | 50.00 | Sequence |
| DRB5_0101 | 415 | ITVNVSTGPEQREIP | VNVSTGPEQ | 0.1977 | 5889.2 | 50.00 | Sequence |
| DRB5_0101 | 425 | QREIPDVSTLTYAEA | IPDVSTLTY | 0.1973 | 5910.7 | 50.00 | Sequence |
| DRB5_0101 | 299 | AAGNLSGPRTDPLPR | AAGNLSGPR | 0.1972 | 5918.6 | 50.00 | Sequence |
| DRB5_0101 | 62 | AAALNHPAIVAVYDT | LNHPAIVAV | 0.1969 | 5940.8 | 50.00 | Sequence |
| DRB5_0101 | 413 | DEITVNVSTGPEQRE | VNVSTGPEQ | 0.1965 | 5964.7 | 50.00 | Sequence |
| DRB5_0101 | 109 | MTPKRAIEVIADACQ | MTPKRAIEV | 0.1960 | 5995.5 | 50.00 | Sequence |
| DRB5_0101 | 360 | QVPDVRGQSSADAIA | VRGQSSADA | 0.1958 | 6007.7 | 50.00 | Sequence |
| DRB5_0101 | 424 | EQREIPDVSTLTYAE | IPDVSTLTY | 0.1935 | 6162.7 | 50.00 | Sequence |
| DRB5_0101 | 470 | NPPANQTSAITNVVI | ANQTSAITN | 0.1932 | 6184.1 | 50.00 | Sequence |
| DRB5_0101 | 253 | ALAKNPENRYQTAAE | ALAKNPENR | 0.1931 | 6187.4 | 50.00 | Sequence |
| DRB5_0101 | 114 | AIEVIADACQALNFS | VIADACQAL | 0.1929 | 6202.3 | 50.00 | Sequence |
| DRB5_0101 | 167 | NSVTQTAAVIGTAQY | VTQTAAVIG | 0.1927 | 6216.1 | 50.00 | Sequence |
| DRB5_0101 | 426 | REIPDVSTLTYAEAV | IPDVSTLTY | 0.1921 | 6255.0 | 50.00 | Sequence |
| DRB5_0101 | 412 | GDEITVNVSTGPEQR | ITVNVSTGP | 0.1893 | 6451.4 | 50.00 | Sequence |
| DRB5_0101 | 166 | GNSVTQTAAVIGTAQ | SVTQTAAVI | 0.1885 | 6503.2 | 50.00 | Sequence |
| DRB5_0101 | 222 | SVAYQHVREDPIPPS | YQHVREDPI | 0.1877 | 6559.6 | 50.00 | Sequence |
| DRB5_0101 | 298 | SAAGNLSGPRTDPLP | GNLSGPRTD | 0.1875 | 6574.8 | 50.00 | Sequence |
| DRB5_0101 | 271 | DLVRVHNGEPPEAPK | LVRVHNGEP | 0.1861 | 6672.1 | 50.00 | Sequence |
| DRB5_0101 | 165 | SGNSVTQTAAVIGTA | SVTQTAAVI | 0.1849 | 6759.4 | 50.00 | Sequence |
| DRB5_0101 | 517 | TKFSQASVDSPRPAG | TKFSQASVD | 0.1844 | 6797.3 | 50.00 | Sequence |
| DRB5_0101 | 297 | SSAAGNLSGPRTDPL | AAGNLSGPR | 0.1838 | 6846.0 | 50.00 | Sequence |
| DRB5_0101 | 95 | DGVTLRDIVHTEGPM | GVTLRDIVH | 0.1830 | 6899.7 | 50.00 | Sequence |
| DRB5_0101 | 423 | PEQREIPDVSTLTYA | IPDVSTLTY | 0.1826 | 6935.2 | 50.00 | Sequence |
| DRB5_0101 | 94 | VDGVTLRDIVHTEGP | GVTLRDIVH | 0.1815 | 7019.7 | 50.00 | Sequence |
| DRB5_0101 | 541 | GTTVPVDSVIELQVS | VPVDSVIEL | 0.1786 | 7236.4 | 50.00 | Sequence |
| DRB5_0101 | 273 | VRVHNGEPPEAPKVL | VHNGEPPEA | 0.1784 | 7253.6 | 50.00 | Sequence |
| DRB5_0101 | 364 | VRGQSSADAIATLQN | VRGQSSADA | 0.1780 | 7288.3 | 50.00 | Sequence |
| DRB5_0101 | 224 | AYQHVREDPIPPSAR | YQHVREDPI | 0.1779 | 7297.9 | 50.00 | Sequence |
| DRB5_0101 | 416 | TVNVSTGPEQREIPD | VNVSTGPEQ | 0.1769 | 7376.6 | 50.00 | Sequence |
| DRB5_0101 | 478 | AITNVVIIIVGSGPA | VIIIVGSGP | 0.1760 | 7448.3 | 50.00 | Sequence |
| DRB5_0101 | 225 | YQHVREDPIPPSARH | YQHVREDPI | 0.1756 | 7476.0 | 50.00 | Sequence |
| DRB5_0101 | 81 | TPAGPLPYIVMEYVD | PYIVMEYVD | 0.1754 | 7498.7 | 50.00 | Sequence |
| DRB5_0101 | 61 | NAAALNHPAIVAVYD | LNHPAIVAV | 0.1746 | 7556.1 | 50.00 | Sequence |
| DRB5_0101 | 65 | LNHPAIVAVYDTGEA | LNHPAIVAV | 0.1743 | 7582.9 | 50.00 | Sequence |
| DRB5_0101 | 359 | VQVPDVRGQSSADAI | VRGQSSADA | 0.1743 | 7584.8 | 50.00 | Sequence |
| DRB5_0101 | 561 | VMPDLSGMFWVDAEP | VMPDLSGMF | 0.1738 | 7626.3 | 50.00 | Sequence |
| DRB5_0101 | 300 | AGNLSGPRTDPLPRQ | GNLSGPRTD | 0.1712 | 7847.1 | 50.00 | Sequence |
| DRB5_0101 | 458 | STPELVGKVIGTNPP | LVGKVIGTN | 0.1694 | 7998.9 | 50.00 | Sequence |
| DRB5_0101 | 164 | DSGNSVTQTAAVIGT | SVTQTAAVI | 0.1691 | 8027.8 | 50.00 | Sequence |
| DRB5_0101 | 582 | WTGMLDKGADVDAGG | WTGMLDKGA | 0.1689 | 8040.5 | 50.00 | Sequence |
| DRB5_0101 | 280 | PPEAPKVLTDAERTS | KVLTDAERT | 0.1686 | 8064.2 | 50.00 | Sequence |
| DRB5_0101 | 60 | QNAAALNHPAIVAVY | LNHPAIVAV | 0.1685 | 8073.8 | 50.00 | Sequence |
| DRB5_0101 | 301 | GNLSGPRTDPLPRQD | GNLSGPRTD | 0.1677 | 8145.7 | 50.00 | Sequence |
| DRB5_0101 | 223 | VAYQHVREDPIPPSA | YQHVREDPI | 0.1674 | 8170.5 | 50.00 | Sequence |
| DRB5_0101 | 393 | IPPDHVIGTDPAANT | VIGTDPAAN | 0.1670 | 8212.0 | 50.00 | Sequence |
| DRB5_0101 | 113 | RAIEVIADACQALNF | EVIADACQA | 0.1659 | 8302.1 | 50.00 | Sequence |
| DRB5_0101 | 338 | LAVLTVVVTIAINTF | VVVTIAINT | 0.1657 | 8320.8 | 50.00 | Sequence |
| DRB5_0101 | 191 | SVDARSDVYSLGCVL | DVYSLGCVL | 0.1644 | 8446.0 | 50.00 | Sequence |
| DRB5_0101 | 422 | GPEQREIPDVSTLTY | IPDVSTLTY | 0.1614 | 8718.4 | 50.00 | Sequence |
| DRB5_0101 | 112 | KRAIEVIADACQALN | VIADACQAL | 0.1607 | 8788.4 | 50.00 | Sequence |
| DRB5_0101 | 457 | PSTPELVGKVIGTNP | LVGKVIGTN | 0.1583 | 9017.8 | 50.00 | Sequence |
| DRB5_0101 | 417 | VNVSTGPEQREIPDV | VNVSTGPEQ | 0.1583 | 9020.4 | 50.00 | Sequence |
| DRB5_0101 | 274 | RVHNGEPPEAPKVLT | VHNGEPPEA | 0.1581 | 9033.7 | 50.00 | Sequence |
| DRB5_0101 | 469 | TNPPANQTSAITNVV | ANQTSAITN | 0.1575 | 9096.0 | 50.00 | Sequence |
| DRB5_0101 | 3 | PSHLSDRYELGEILG | DRYELGEIL | 0.1565 | 9197.0 | 50.00 | Sequence |
| DRB5_0101 | 540 | AGTTVPVDSVIELQV | VDSVIELQV | 0.1563 | 9219.1 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB5_0101 | 459 | TPELVGKVIGTNPPA | LVGKVIGTN | 0.1560 | 9246.8 | 50.00 | Sequence |
| DRB5_0101 | 358 | DVQVPDVRGQSSADA | VRGQSSADA | 0.1550 | 9342.2 | 50.00 | Sequence |
| DRB5_0101 | 163 | ADSGNSVTQTAAVIG | SVTQTAAVI | 0.1549 | 9358.7 | 50.00 | Sequence |
| DRB5_0101 | 456 | SPSTPELVGKVIGTN | LVGKVIGTN | 0.1541 | 9438.5 | 50.00 | Sequence |
| DRB5_0101 | 66 | NHPAIVAVYDTGEAE | AIVAVYDTG | 0.1524 | 9611.4 | 50.00 | Sequence |
| DRB5_0101 | 354 | GITRDVQVPDVRGQS | RDVQVPDVR | 0.1514 | 9721.5 | 50.00 | Sequence |
| DRB5_0101 | 59 | AQNAAALNHPAIVAV | LNHPAIVAV | 0.1506 | 9799.9 | 50.00 | Sequence |
| DRB5_0101 | 498 | DVAGQTVDVAQKNLN | GQTVDVAQK | 0.1503 | 9829.3 | 50.00 | Sequence |
| DRB5_0101 | 355 | ITRDVQVPDVRGQSS | RDVQVPDVR | 0.1503 | 9829.4 | 50.00 | Sequence |
| DRB5_0101 | 240 | EGLSADLDAVVLKAL | DLDAVVLKA | 0.1498 | 9891.2 | 50.00 | Sequence |
| DRB5_0101 | 594 | AGGSQHNRVVYQNPP | SQHNRVVYQ | 0.1494 | 9926.3 | 50.00 | Sequence |
| DRB5_0101 | 331 | WVAVVAVLAVLTVVV | WVAVVAVLA | 0.1489 | 9984.6 | 50.00 | Sequence |
| DRB5_0101 | 337 | VLAVLTVVVTIAINT | VVVTIAINT | 0.1467 | 10223.8 | 50.00 | Sequence |
| DRB5_0101 | 518 | KFSQASVDSPRPAGE | FSQASVDSP | 0.1464 | 10262.8 | 50.00 | Sequence |
| DRB5_0101 | 592 | VDAGGSQHNRVVYQN | SQHNRVVYQ | 0.1454 | 10368.7 | 50.00 | Sequence |
| DRB5_0101 | 57 | REAQNAAALNHPAIV | REAQNAAAL | 0.1452 | 10396.4 | 50.00 | Sequence |
| DRB5_0101 | 353 | GGITRDVQVPDVRGQ | RDVQVPDVR | 0.1446 | 10458.4 | 50.00 | Sequence |
| DRB5_0101 | 593 | DAGGSQHNRVVYQNP | SQHNRVVYQ | 0.1436 | 10567.6 | 50.00 | Sequence |
| DRB5_0101 | 474 | NQTSAITNVVIIIVG | QTSAITNVV | 0.1433 | 10609.8 | 50.00 | Sequence |
| DRB5_0101 | 357 | RDVQVPDVRGQSSAD | RDVQVPDVR | 0.1416 | 10800.7 | 50.00 | Sequence |
| DRB5_0101 | 591 | DVDAGGSQHNRVVYQ | VDAGGSQHN | 0.1407 | 10905.2 | 50.00 | Sequence |
| DRB5_0101 | 392 | TIPPDHVIGTDPAAN | VIGTDPAAN | 0.1405 | 10931.6 | 50.00 | Sequence |
| DRB5_0101 | 275 | VHNGEPPEAPKVLTD | VHNGEPPEA | 0.1401 | 10979.5 | 50.00 | Sequence |
| DRB5_0101 | 303 | LSGPRTDPLPRQDLD | GPRTDPLPR | 0.1398 | 11014.9 | 50.00 | Sequence |
| DRB5_0101 | 80 | ETPAGPLPYIVMEYV | ETPAGPLPY | 0.1397 | 11030.6 | 50.00 | Sequence |
| DRB5_0101 | 226 | QHVREDPIPPSARHE | HVREDPIPP | 0.1392 | 11090.1 | 50.00 | Sequence |
| DRB5_0101 | 302 | NLSGPRTDPLPRQDL | GPRTDPLPR | 0.1388 | 11139.1 | 50.00 | Sequence |
| DRB5_0101 | 227 | HVREDPIPPSARHEG | HVREDPIPP | 0.1386 | 11157.0 | 50.00 | Sequence |
| DRB5_0101 | 68 | PAIVAVYDTGEAETP | IVAVYDTGE | 0.1377 | 11273.4 | 50.00 | Sequence |
| DRB5_0101 | 111 | PKRAIEVIADACQAL | KRAIEVIAD | 0.1375 | 11290.6 | 50.00 | Sequence |
| DRB5_0101 | 356 | TRDVQVPDVRGQSSA | RDVQVPDVR | 0.1369 | 11367.3 | 50.00 | Sequence |
| DRB5_0101 | 67 | HPAIVAVYDTGEAET | IVAVYDTGE | 0.1350 | 11600.0 | 50.00 | Sequence |
| DRB5_0101 | 411 | AGDEITVNVSTGPEQ | VNVSTGPEQ | 0.1348 | 11626.9 | 50.00 | Sequence |
| DRB5_0101 | 58 | EAQNAAALNHPAIVA | AQNAAALNH | 0.1329 | 11867.4 | 50.00 | Sequence |
| DRB5_0101 | 157 | GIARAIADSGNSVTQ | RAIADSGNS | 0.1303 | 12215.6 | 50.00 | Sequence |
| DRB5_0101 | 79 | AETPAGPLPYIVMEY | ETPAGPLPY | 0.1300 | 12242.6 | 50.00 | Sequence |
| DRB5_0101 | 304 | SGPRTDPLPRQDLDD | GPRTDPLPR | 0.1286 | 12440.9 | 50.00 | Sequence |
| DRB5_0101 | 305 | GPRTDPLPRQDLDDT | GPRTDPLPR | 0.1282 | 12487.4 | 50.00 | Sequence |
| DRB5_0101 | 468 | GTNPPANQTSAITNV | ANQTSAITN | 0.1268 | 12679.1 | 50.00 | Sequence |
| DRB5_0101 | 477 | SAITNVVIIIVGSGP | VIIIVGSGP | 0.1256 | 12840.5 | 50.00 | Sequence |
| DRB5_0101 | 352 | FGGITRDVQVPDVRG | RDVQVPDVR | 0.1254 | 12875.1 | 50.00 | Sequence |
| DRB5_0101 | 332 | VAVVAVLAVLTVVVT | VVAVLAVLT | 0.1248 | 12956.8 | 50.00 | Sequence |
| DRB5_0101 | 519 | FSQASVDSPRPAGEV | FSQASVDSP | 0.1245 | 12994.0 | 50.00 | Sequence |
| DRB5_0101 | 69 | AIVAVYDTGEAETPA | IVAVYDTGE | 0.1235 | 13137.7 | 50.00 | Sequence |
| DRB5_0101 | 71 | VAVYDTGEAETPAGP | VYDTGEAET | 0.1217 | 13401.5 | 50.00 | Sequence |
| DRB5_0101 | 467 | IGTNPPANQTSAITN | IGTNPPANQ | 0.1216 | 13415.5 | 50.00 | Sequence |
| DRB5_0101 | 236 | SARHEGLSADLDAVV | ARHEGLSAD | 0.1211 | 13487.3 | 50.00 | Sequence |
| DRB5_0101 | 70 | IVAVYDTGEAETPAG | VYDTGEAET | 0.1210 | 13506.7 | 50.00 | Sequence |
| DRB5_0101 | 158 | IARAIADSGNSVTQT | RAIADSGNS | 0.1207 | 13541.4 | 50.00 | Sequence |
| DRB5_0101 | 603 | VYQNPPAGTGVNRDG | VYQNPPAGT | 0.1207 | 13552.2 | 50.00 | Sequence |
| DRB5_0101 | 162 | IADSGNSVTQTAAVI | SVTQTAAVI | 0.1186 | 13850.1 | 50.00 | Sequence |
| DRB5_0101 | 350 | NTFGGITRDVQVPDV | TFGGITRDV | 0.1186 | 13856.5 | 50.00 | Sequence |
| DRB5_0101 | 235 | PSARHEGLSADLDAV | ARHEGLSAD | 0.1184 | 13888.9 | 50.00 | Sequence |
| DRB5_0101 | 78 | EAETPAGPLPYIVME | ETPAGPLPY | 0.1180 | 13951.9 | 50.00 | Sequence |
| DRB5_0101 | 159 | ARAIADSGNSVTQTA | RAIADSGNS | 0.1178 | 13974.2 | 50.00 | Sequence |
| DRB5_0101 | 384 | RTLQKPDSTIPPDHV | RTLQKPDST | 0.1171 | 14081.8 | 50.00 | Sequence |
| DRB5_0101 | 160 | RAIADSGNSVTQTAA | RAIADSGNS | 0.1170 | 14104.4 | 50.00 | Sequence |
| DRB5_0101 | 539 | PAGTTVPVDSVIELQ | VPVDSVIEL | 0.1167 | 14143.8 | 50.00 | Sequence |
| DRB5_0101 | 336 | AVLAVLTVVVTIAIN | LTVVVTIAI | 0.1153 | 14356.0 | 50.00 | Sequence |
| DRB5_0101 | 530 | AGEVTGTNPPAGTTV | VTGTNPPAG | 0.1151 | 14392.1 | 50.00 | Sequence |
| DRB5_0101 | 110 | TPKRAIEVIADACQA | KRAIEVIAD | 0.1141 | 14555.4 | 50.00 | Sequence |
| DRB5_0101 | 333 | AVVAVLAVLTVVVTI | VVAVLAVLT | 0.1139 | 14579.0 | 50.00 | Sequence |
| DRB5_0101 | 351 | TFGGITRDVQVPDVR | RDVQVPDVR | 0.1139 | 14580.3 | 50.00 | Sequence |
| DRB5_0101 | 608 | PAGTGVNRDGIITLR | VNRDGIITL | 0.1135 | 14649.7 | 50.00 | Sequence |
| DRB5_0101 | 182 | LSPEQARGDSVDARS | LSPEQARGD | 0.1132 | 14688.0 | 50.00 | Sequence |
| DRB5_0101 | 404 | AANTSVSAGDEITVN | ANTSVSAGD | 0.1131 | 14710.1 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| DRB5_0101 | 475 | QTSAITNVVIIIVGS | QTSAITNVV | 0.1121 | 14861.6 | 50.00 | Sequence |
| DRB5_0101 | 2 | TPSHLSDRYELGEIL | DRYELGEIL | 0.1117 | 14924.1 | 50.00 | Sequence |
| DRB5_0101 | 529 | PAGEVTGTNPPAGTT | VTGTNPPAG | 0.1112 | 15014.5 | 50.00 | Sequence |
| DRB5_0101 | 234 | PPSARHEGLSADLDA | ARHEGLSAD | 0.1111 | 15035.3 | 50.00 | Sequence |
| DRB5_0101 | 531 | GEVTGTNPPAGTTVP | VTGTNPPAG | 0.1109 | 15056.3 | 50.00 | Sequence |
| DRB5_0101 | 77 | GEAETPAGPLPYIVM | ETPAGPLPY | 0.1109 | 15058.4 | 50.00 | Sequence |
| DRB5_0101 | 279 | EPPEAPKVLTDAERT | KVLTDAERT | 0.1104 | 15150.3 | 50.00 | Sequence |
| DRB5_0101 | 335 | VAVLAVLTVVVTIAI | LTVVVTIAI | 0.1094 | 15306.1 | 50.00 | Sequence |
| DRB5_0101 | 228 | VREDPIPPSARHEGL | DPIPPSARH | 0.1084 | 15482.2 | 50.00 | Sequence |
| DRB5_0101 | 520 | SQASVDSPRPAGEVT | VDSPRPAGE | 0.1079 | 15561.6 | 50.00 | Sequence |
| DRB5_0101 | 528 | RPAGEVTGTNPPAGT | VTGTNPPAG | 0.1075 | 15621.3 | 50.00 | Sequence |
| DRB5_0101 | 403 | PAANTSVSAGDEITV | ANTSVSAGD | 0.1075 | 15629.6 | 50.00 | Sequence |
| DRB5_0101 | 229 | REDPIPPSARHEGLS | DPIPPSARH | 0.1062 | 15855.1 | 50.00 | Sequence |
| DRB5_0101 | 76 | TGEAETPAGPLPYIV | ETPAGPLPY | 0.1047 | 16110.4 | 50.00 | Sequence |
| DRB5_0101 | 538 | PPAGTTVPVDSVIEL | VPVDSVIEL | 0.1042 | 16197.6 | 50.00 | Sequence |
| DRB5_0101 | 232 | PIPPSARHEGLSADL | SARHEGLSA | 0.1042 | 16200.2 | 50.00 | Sequence |
| DRB5_0101 | 72 | AVYDTGEAETPAGPL | VYDTGEAET | 0.1041 | 16209.8 | 50.00 | Sequence |
| DRB5_0101 | 230 | EDPIPPSARHEGLSA | DPIPPSARH | 0.1033 | 16356.1 | 50.00 | Sequence |
| DRB5_0101 | 521 | QASVDSPRPAGEVTG | VDSPRPAGE | 0.1033 | 16358.6 | 50.00 | Sequence |
| DRB5_0101 | 233 | IPPSARHEGLSADLD | ARHEGLSAD | 0.1028 | 16431.6 | 50.00 | Sequence |
| DRB5_0101 | 276 | HNGEPPEAPKVLTDA | GEPPEAPKV | 0.1021 | 16558.5 | 50.00 | Sequence |
| DRB5_0101 | 73 | VYDTGEAETPAGPLP | YDTGEAETP | 0.1017 | 16641.9 | 50.00 | Sequence |
| DRB5_0101 | 532 | EVTGTNPPAGTTVPV | VTGTNPPAG | 0.1012 | 16719.5 | 50.00 | Sequence |
| DRB5_0101 | 590 | ADVDAGGSQHNRVVY | VDAGGSQHN | 0.1011 | 16752.6 | 50.00 | Sequence |
| DRB5_0101 | 402 | DPAANTSVSAGDEIT | ANTSVSAGD | 0.0996 | 17025.4 | 50.00 | Sequence |
| DRB5_0101 | 455 | NSPSTPELVGKVIGT | STPELVGKV | 0.0992 | 17088.0 | 50.00 | Sequence |
| DRB5_0101 | 334 | VVAVLAVLTVVVTIA | VVAVLAVLT | 0.0985 | 17223.3 | 50.00 | Sequence |
| DRB5_0101 | 1 | TTPSHLSDRYELGEI | TPSHLSDRY | 0.0983 | 17255.0 | 50.00 | Sequence |
| DRB5_0101 | 75 | DTGEAETPAGPLPYI | ETPAGPLPY | 0.0976 | 17400.5 | 50.00 | Sequence |
| DRB5_0101 | 0 | MTTPSHLSDRYELGE | TPSHLSDRY | 0.0975 | 17416.7 | 50.00 | Sequence |
| DRB5_0101 | 231 | DPIPPSARHEGLSAD | DPIPPSARH | 0.0972 | 17463.9 | 50.00 | Sequence |
| DRB5_0101 | 522 | ASVDSPRPAGEVTGT | VDSPRPAGE | 0.0953 | 17827.0 | 50.00 | Sequence |
| DRB5_0101 | 237 | ARHEGLSADLDAVVL | RHEGLSADL | 0.0950 | 17883.2 | 50.00 | Sequence |
| DRB5_0101 | 527 | PRPAGEVTGTNPPAG | VTGTNPPAG | 0.0941 | 18069.2 | 50.00 | Sequence |
| DRB5_0101 | 278 | GEPPEAPKVLTDAER | GEPPEAPKV | 0.0927 | 18347.3 | 50.00 | Sequence |
| DRB5_0101 | 589 | GADVDAGGSQHNRVV | VDAGGSQHN | 0.0925 | 18387.7 | 50.00 | Sequence |
| DRB5_0101 | 277 | NGEPPEAPKVLTDAE | GEPPEAPKV | 0.0917 | 18538.9 | 50.00 | Sequence |
| DRB5_0101 | 239 | HEGLSADLDAVVLKA | DLDAVVLKA | 0.0916 | 18550.5 | 50.00 | Sequence |
| DRB5_0101 | 74 | YDTGEAETPAGPLPY | ETPAGPLPY | 0.0913 | 18628.4 | 50.00 | Sequence |
| DRB5_0101 | 533 | VTGTNPPAGTTVPVD | VTGTNPPAG | 0.0908 | 18720.1 | 50.00 | Sequence |
| DRB5_0101 | 476 | TSAITNVVIIIVGSG | VVIIIVGSG | 0.0908 | 18722.3 | 50.00 | Sequence |
| DRB5_0101 | 418 | NVSTGPEQREIPDVS | NVSTGPEQR | 0.0905 | 18780.2 | 50.00 | Sequence |
| DRB5_0101 | 410 | SAGDEITVNVSTGPE | EITVNVSTG | 0.0890 | 19082.9 | 50.00 | Sequence |
| DRB5_0101 | 401 | TDPAANTSVSAGDEI | ANTSVSAGD | 0.0890 | 19083.3 | 50.00 | Sequence |
| DRB5_0101 | 187 | ARGDSVDARSDVYSL | ARGDSVDAR | 0.0876 | 19371.6 | 50.00 | Sequence |
| DRB5_0101 | 186 | QARGDSVDARSDVYS | RGDSVDARS | 0.0855 | 19821.5 | 50.00 | Sequence |
| DRB5_0101 | 497 | PDVAGQTVDVAQKNL | GQTVDVAQK | 0.0852 | 19891.4 | 50.00 | Sequence |
| DRB5_0101 | 454 | ANSPSTPELVGKVIG | STPELVGKV | 0.0847 | 19992.6 | 50.00 | Sequence |
| DRB5_0101 | 421 | TGPEQREIPDVSTLT | EQREIPDVS | 0.0844 | 20067.5 | 50.00 | Sequence |
| DRB5_0101 | 315 | DLDDTDRDRSIGSVG | RDRSIGSVG | 0.0840 | 20148.1 | 50.00 | Sequence |
| DRB5_0101 | 607 | PPAGTGVNRDGIITL | GVNRDGIIT | 0.0825 | 20471.3 | 50.00 | Sequence |
| DRB5_0101 | 190 | DSVDARSDVYSLGCV | VDARSDVYS | 0.0823 | 20531.0 | 50.00 | Sequence |
| DRB5_0101 | 185 | EQARGDSVDARSDVY | ARGDSVDAR | 0.0802 | 21002.8 | 50.00 | Sequence |
| DRB5_0101 | 238 | RHEGLSADLDAVVLK | RHEGLSADL | 0.0793 | 21194.3 | 50.00 | Sequence |
| DRB5_0101 | 306 | PRTDPLPRQDLDDTD | PRTDPLPRQ | 0.0786 | 21350.4 | 50.00 | Sequence |
| DRB5_0101 | 161 | AIADSGNSVTQTAAV | AIADSGNSV | 0.0780 | 21496.6 | 50.00 | Sequence |
| DRB5_0101 | 184 | PEQARGDSVDARSDV | ARGDSVDAR | 0.0779 | 21535.0 | 50.00 | Sequence |
| DRB5_0101 | 400 | GTDPAANTSVSAGDE | ANTSVSAGD | 0.0765 | 21863.5 | 50.00 | Sequence |
| DRB5_0101 | 588 | KGADVDAGGSQHNRV | VDAGGSQHN | 0.0759 | 21984.0 | 50.00 | Sequence |
| DRB5_0101 | 452 | KQANSPSTPELVGKV | STPELVGKV | 0.0758 | 22020.0 | 50.00 | Sequence |
| DRB5_0101 | 523 | SVDSPRPAGEVTGTN | VDSPRPAGE | 0.0758 | 22021.1 | 50.00 | Sequence |
| DRB5_0101 | 409 | VSAGDEITVNVSTGP | EITVNVSTG | 0.0753 | 22143.5 | 50.00 | Sequence |
| DRB5_0101 | 453 | QANSPSTPELVGKVI | STPELVGKV | 0.0747 | 22270.8 | 50.00 | Sequence |
| DRB5_0101 | 188 | RGDSVDARSDVYSLG | RGDSVDARS | 0.0740 | 22440.4 | 50.00 | Sequence |
| DRB5_0101 | 386 | LQKPDSTIPPDHVIG | DSTIPPDHV | 0.0731 | 22664.9 | 50.00 | Sequence |
| DRB5_0101 | 385 | TLQKPDSTIPPDHVI | DSTIPPDHV | 0.0727 | 22777.0 | 50.00 | Sequence |

```
   DRB5_0101  604  YQNPPAGTGVNRDGI  YQNPPAGTG        0.0719      22979.9               50.00     Sequence
   DRB5_0101  399  IGTDPAANTSVSAGD  ANTSVSAGD        0.0718      22992.6               50.00     Sequence
   DRB5_0101  420  STGPEQREIPDVSTL  EQREIPDVS        0.0688      23751.5               50.00     Sequence
   DRB5_0101  387  QKPDSTIPPDHVIGT  DSTIPPDHV        0.0683      23881.1               50.00     Sequence
   DRB5_0101  189  GDSVDARSDVYSLGC  VDARSDVYS        0.0681      23943.4               50.00     Sequence
   DRB5_0101  587  DKGADVDAGGSQHNR  VDAGGSQHN        0.0670      24211.2               50.00     Sequence
   DRB5_0101  183  SPEQARGDSVDARSD  ARGDSVDAR        0.0670      24227.7               50.00     Sequence
   DRB5_0101  496  IPDVAGQTVDVAQKN  QTVDVAQKN        0.0669      24235.9               50.00     Sequence
   DRB5_0101  405  ANTSVSAGDEITVNV  ANTSVSAGD        0.0669      24246.1               50.00     Sequence
   DRB5_0101  314  QDLDDTDRDRSIGSV  LDDTDRDRS        0.0667      24300.5               50.00     Sequence
   DRB5_0101  388  KPDSTIPPDHVIGTD  DSTIPPDHV        0.0653      24655.6               50.00     Sequence
   DRB5_0101  307  RTDPLPRQDLDDTDR  RTDPLPRQD        0.0651      24714.4               50.00     Sequence
   DRB5_0101  537  NPPAGTTVPVDSVIE  TTVPVDSVI        0.0632      25228.8               50.00     Sequence
   DRB5_0101  583  TGMLDKGADVDAGGS  GMLDKGADV        0.0628      25346.4               50.00     Sequence
   DRB5_0101  586  LDKGADVDAGGSQHN  VDAGGSQHN        0.0608      25890.0               50.00     Sequence
   DRB5_0101  389  PDSTIPPDHVIGTDP  DSTIPPDHV        0.0590      26405.1               50.00     Sequence
   DRB5_0101  495  DIPDVAGQTVDVAQK  GQTVDVAQK        0.0580      26698.5               50.00     Sequence
   DRB5_0101  606  NPPAGTGVNRDGIIT  GVNRDGIIT        0.0565      27145.9               50.00     Sequence
   DRB5_0101  408  SVSAGDEITVNVSTG  EITVNVSTG        0.0559      27299.0               50.00     Sequence
   DRB5_0101  390  DSTIPPDHVIGTDPA  DSTIPPDHV        0.0544      27751.4               50.00     Sequence
   DRB5_0101  493  TKDIPDVAGQTVDVA  IPDVAGQTV        0.0539      27898.6               50.00     Sequence
   DRB5_0101  494  KDIPDVAGQTVDVAQ  IPDVAGQTV        0.0530      28185.7               50.00     Sequence
   DRB5_0101  419  VSTGPEQREIPDVST  VSTGPEQRE        0.0524      28359.7               50.00     Sequence
   DRB5_0101  492  ATKDIPDVAGQTVDV  IPDVAGQTV        0.0506      28934.3               50.00     Sequence
   DRB5_0101  524  VDSPRPAGEVTGTNP  VDSPRPAGE        0.0492      29349.3               50.00     Sequence
   DRB5_0101  584  GMLDKGADVDAGGSQ  GMLDKGADV        0.0481      29714.2               50.00     Sequence
   DRB5_0101  526  SPRPAGEVTGTNPPA  GEVTGTNPP        0.0473      29963.7               50.00     Sequence
   DRB5_0101  585  MLDKGADVDAGGSQH  DVDAGGSQH        0.0461      30359.3               50.00     Sequence
   DRB5_0101  313  RQDLDDTDRDRSIGS  DLDDTDRDR        0.0454      30578.5               50.00     Sequence
   DRB5_0101  536  TNPPAGTTVPVDSVI  AGTTVPVDS        0.0451      30706.5               50.00     Sequence
   DRB5_0101  406  NTSVSAGDEITVNVS  TSVSAGDEI        0.0446      30857.3               50.00     Sequence
   DRB5_0101  407  TSVSAGDEITVNVST  TSVSAGDEI        0.0442      30999.9               50.00     Sequence
   DRB5_0101  491  PATKDIPDVAGQTVD  IPDVAGQTV        0.0441      31019.3               50.00     Sequence
   DRB5_0101  312  PRQDLDDTDRDRSIG  DLDDTDRDR        0.0439      31097.3               50.00     Sequence
   DRB5_0101  605  QNPPAGTGVNRDGII  PAGTGVNRD        0.0427      31515.3               50.00     Sequence
   DRB5_0101  311  LPRQDLDDTDRDRSI  DLDDTDRDR        0.0420      31738.1               50.00     Sequence
   DRB5_0101  525  DSPRPAGEVTGTNPP  GEVTGTNPP        0.0419      31764.2               50.00     Sequence
   DRB5_0101  310  PLPRQDLDDTDRDRS  DLDDTDRDR        0.0419      31787.9               50.00     Sequence
   DRB5_0101  391  STIPPDHVIGTDPAA  DHVIGTDPA        0.0413      31971.1               50.00     Sequence
   DRB5_0101  490  GPATKDIPDVAGQTV  IPDVAGQTV        0.0413      31994.9               50.00     Sequence
   DRB5_0101  309  DPLPRQDLDDTDRDR  DLDDTDRDR        0.0412      32020.9               50.00     Sequence
   DRB5_0101  308  TDPLPRQDLDDTDRD  QDLDDTDRD        0.0407      32179.3               50.00     Sequence
   DRB5_0101  535  GTNPPAGTTVPVDSV  AGTTVPVDS        0.0406      32207.8               50.00     Sequence
   DRB5_0101  534  TGTNPPAGTTVPVDS  GTNPPAGTT        0.0393      32696.6               50.00     Sequence
   DRB5_0101  487  VGSGPATKDIPDVAG  VGSGPATKD        0.0325      35167.8               50.00     Sequence
   DRB5_0101  489  SGPATKDIPDVAGQT  DIPDVAGQT        0.0283      36797.6               50.00     Sequence
   DRB5_0101  488  GSGPATKDIPDVAGQ  GSGPATKDI        0.0278      37030.9               50.00     Sequence
------------------------------------------------------------------------------------------------

Allele: DRB5_0101. Number of high binders 17. Number of weak binders 110. Number of peptides 612

------------------------------------------------------------------------------------------------
------------------------------------------------------------------------------------------------
      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
------------------------------------------------------------------------------------------------
         IAb  601  RVVYQNPPAGTGVNR  VVYQNPPAG        0.7059         24.1          SB     0.30     Sequence
         IAb  600  NRVVYQNPPAGTGVN  VVYQNPPAG        0.6996         25.8          SB     0.40     Sequence
         IAb  599  HNRVVYQNPPAGTGV  VVYQNPPAG        0.6858         29.9          SB     0.80     Sequence
         IAb  598  QHNRVVYQNPPAGTG  VVYQNPPAG        0.6495         44.4          SB     0.80     Sequence
         IAb  602  VVYQNPPAGTGVNRD  VVYQNPPAG        0.6434         47.4          SB     1.00     Sequence
         IAb  597  SQHNRVVYQNPPAGT  VVYQNPPAG        0.5942         80.7          WB     2.00     Sequence
         IAb   61  NAAALNHPAIVAVYD  AALNHPAIV        0.5917         82.9          WB     2.00     Sequence
         IAb   60  QNAAALNHPAIVAVY  AALNHPAIV        0.5869         87.3          WB     2.00     Sequence
         IAb   62  AAALNHPAIVAVYDT  AALNHPAIV        0.5815         92.6          WB     2.00     Sequence
         IAb  464  GKVIGTNPPANQTSA  VIGTNPPAN        0.5618        114.5          WB     4.00     Sequence
         IAb   59  AQNAAALNHPAIVAV  AALNHPAIV        0.5581        119.3          WB     4.00     Sequence
```

```
IAb  465  KVIGTNPPANQTSAI  VIGTNPPAN       0.5563        121.6          WB     4.00       Sequence
IAb  463  VGKVIGTNPPANQTS  VIGTNPPAN       0.5514        128.2          WB     4.00       Sequence
IAb   57  REAQNAAALNHPAIV  REAQNAAAL       0.5471        134.3          WB     4.00       Sequence
IAb  466  VIGTNPPANQTSAIT  VIGTNPPAN       0.5209        178.3          WB     4.00       Sequence
IAb  449  GRFKQANSPSTPELV  FKQANSPST       0.5187        182.6          WB     4.00       Sequence
IAb  450  RFKQANSPSTPELVG  FKQANSPST       0.5175        185.1          WB     4.00       Sequence
IAb  484  IIIVGSGPATKDIPD  IIVGSGPAT       0.5167        186.6          WB     4.00       Sequence
IAb  462  LVGKVIGTNPPANQT  VIGTNPPAN       0.5132        193.9          WB     4.00       Sequence
IAb  483  VIIIVGSGPATKDIP  IIVGSGPAT       0.5097        201.3          WB     8.00       Sequence
IAb   71  VAVYDTGEAETPAGP  AVYDTGEAE       0.5069        207.6          WB     8.00       Sequence
IAb  176  IGTAQYLSPEQARGD  AQYLSPEQA       0.5053        211.1          WB     8.00       Sequence
IAb   58  EAQNAAALNHPAIVA  AALNHPAIV       0.5038        214.7          WB     8.00       Sequence
IAb  178  TAQYLSPEQARGDSV  AQYLSPEQA       0.5026        217.4          WB     8.00       Sequence
IAb  177  GTAQYLSPEQARGDS  AQYLSPEQA       0.5013        220.4          WB     8.00       Sequence
IAb   56  RREAQNAAALNHPAI  REAQNAAAL       0.4974        230.0          WB     8.00       Sequence
IAb  259  ENRYQTAAEMRADLV  YQTAAEMRA       0.4968        231.4          WB     8.00       Sequence
IAb   70  IVAVYDTGEAETPAG  AVYDTGEAE       0.4960        233.4          WB     8.00       Sequence
IAb  448  FGRFKQANSPSTPEL  FKQANSPST       0.4954        234.9          WB     8.00       Sequence
IAb  273  VRVHNGEPPEAPKVL  RVHNGEPPE       0.4896        250.3          WB     8.00       Sequence
IAb  482  VVIIIVGSGPATKDI  IIIVGSGPA       0.4893        251.0          WB     8.00       Sequence
IAb  272  LVRVHNGEPPEAPKV  RVHNGEPPE       0.4876        255.8          WB     8.00       Sequence
IAb  451  FKQANSPSTPELVGK  FKQANSPST       0.4864        259.1          WB     8.00       Sequence
IAb  175  VIGTAQYLSPEQARG  AQYLSPEQA       0.4844        264.7          WB     8.00       Sequence
IAb  258  PENRYQTAAEMRADL  YQTAAEMRA       0.4814        273.5          WB     8.00       Sequence
IAb  260  NRYQTAAEMRADLVR  YQTAAEMRA       0.4777        284.7          WB     8.00       Sequence
IAb   69  AIVAVYDTGEAETPA  AVYDTGEAE       0.4761        289.7          WB     8.00       Sequence
IAb  596  GSQHNRVVYQNPPAG  VVYQNPPAG       0.4750        293.0          WB     8.00       Sequence
IAb  533  VTGTNPPAGTTVPVD  TGTNPPAGT       0.4742        295.6          WB     8.00       Sequence
IAb   55  FRREAQNAAALNHPA  REAQNAAAL       0.4735        297.8          WB     8.00       Sequence
IAb   63  AALNHPAIVAVYDTG  AALNHPAIV       0.4717        303.8          WB     8.00       Sequence
IAb  151  VKVMDFGIARAIADS  FGIARAIAD       0.4692        312.0          WB     8.00       Sequence
IAb  179  AQYLSPEQARGDSVD  AQYLSPEQA       0.4683        315.3          WB     8.00       Sequence
IAb  447  GFGRFKQANSPSTPE  FKQANSPST       0.4678        316.8          WB     8.00       Sequence
IAb  485  IIVGSGPATKDIPDV  IVGSGPATK       0.4665        321.3          WB     8.00       Sequence
IAb  461  ELVGKVIGTNPPANQ  VIGTNPPAN       0.4644        328.7          WB     8.00       Sequence
IAb  603  VYQNPPAGTGVNRDG  VYQNPPAGT       0.4620        337.3          WB     8.00       Sequence
IAb  152  KVMDFGIARAIADSG  FGIARAIAD       0.4603        343.7          WB     8.00       Sequence
IAb   54  RFRREAQNAAALNHP  REAQNAAAL       0.4601        344.5          WB     8.00       Sequence
IAb  257  NPENRYQTAAEMRAD  NRYQTAAEM       0.4585        350.4          WB     8.00       Sequence
IAb  532  EVTGTNPPAGTTVPV  TGTNPPAGT       0.4582        351.6          WB     8.00       Sequence
IAb  153  VMDFGIARAIADSGN  FGIARAIAD       0.4563        358.9          WB     8.00       Sequence
IAb  271  DLVRVHNGEPPEAPK  RVHNGEPPE       0.4554        362.5          WB     8.00       Sequence
IAb  174  AVIGTAQYLSPEQAR  AQYLSPEQA       0.4533        370.5          WB     8.00       Sequence
IAb  481  NVVIIIVGSGPATKD  IIIVGSGPA       0.4506        381.6          WB     8.00       Sequence
IAb  150  AVKVMDFGIARAIAD  FGIARAIAD       0.4479        392.9          WB     8.00       Sequence
IAb   68  PAIVAVYDTGEAETP  AVYDTGEAE       0.4454        403.6          WB     8.00       Sequence
IAb  531  GEVTGTNPPAGTTVP  TGTNPPAGT       0.4435        412.3          WB     8.00       Sequence
IAb   79  AETPAGPLPYIVMEY  ETPAGPLPY       0.4406        425.4          WB     8.00       Sequence
IAb   77  GEAETPAGPLPYIVM  ETPAGPLPY       0.4381        437.0          WB     8.00       Sequence
IAb  431  VSTLTYAEAVKKLTA  LTYAEAVKK       0.4379        437.9          WB     8.00       Sequence
IAb  446  AGFGRFKQANSPSTP  FKQANSPST       0.4373        440.7          WB     8.00       Sequence
IAb  397  HVIGTDPAANTSVSA  VIGTDPAAN       0.4365        444.6          WB     8.00       Sequence
IAb  398  VIGTDPAANTSVSAG  VIGTDPAAN       0.4361        446.6          WB     8.00       Sequence
IAb  212  EPPFTGDSPVSVAYQ  FTGDSPVSV       0.4358        447.9          WB     8.00       Sequence
IAb   78  EAETPAGPLPYIVME  ETPAGPLPY       0.4358        448.0          WB     8.00       Sequence
IAb  534  TGTNPPAGTTVPVDS  TNPPAGTTV       0.4327        463.4          WB    16.00       Sequence
IAb   53  LRFRREAQNAAALNH  REAQNAAAL       0.4321        466.1          WB    16.00       Sequence
IAb  256  KNPENRYQTAAEMRA  NRYQTAAEM       0.4316        468.9          WB    16.00       Sequence
IAb  270  ADLVRVHNGEPPEAP  VRVHNGEPP       0.4276        489.4          WB    16.00       Sequence
IAb  206  YEVLTGEPPFTGDSP  YEVLTGEPP       0.4242        507.9                16.00       Sequence
IAb   72  AVYDTGEAETPAGPL  AVYDTGEAE       0.4229        515.1                16.00       Sequence
IAb  432  STLTYAEAVKKLTAA  LTYAEAVKK       0.4226        516.6                16.00       Sequence
IAb  211  GEPPFTGDSPVSVAY  FTGDSPVSV       0.4202        530.5                16.00       Sequence
IAb  154  MDFGIARAIADSGNS  FGIARAIAD       0.4196        533.5                16.00       Sequence
IAb  205  LYEVLTGEPPFTGDS  YEVLTGEPP       0.4179        543.4                16.00       Sequence
IAb  173  AAVIGTAQYLSPEQA  AQYLSPEQA       0.4159        555.4                16.00       Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAb | 396 | DHVIGTDPAANTSVS | VIGTDPAAN | 0.4140 | 566.8 | 16.00 | Sequence |
| IAb | 430 | DVSTLTYAEAVKKLT | STLTYAEAV | 0.4117 | 581.3 | 16.00 | Sequence |
| IAb | 138 | VKPANIMISATNAVK | VKPANIMIS | 0.4102 | 590.8 | 16.00 | Sequence |
| IAb | 76 | TGEAETPAGPLPYIV | ETPAGPLPY | 0.4092 | 597.2 | 16.00 | Sequence |
| IAb | 516 | FTKFSQASVDSPRPA | ASVDSPRPA | 0.4069 | 612.2 | 16.00 | Sequence |
| IAb | 519 | FSQASVDSPRPAGEV | ASVDSPRPA | 0.4068 | 613.2 | 16.00 | Sequence |
| IAb | 395 | PDHVIGTDPAANTSV | VIGTDPAAN | 0.4066 | 614.3 | 16.00 | Sequence |
| IAb | 204 | VLYEVLTGEPPFTGD | YEVLTGEPP | 0.4057 | 620.1 | 16.00 | Sequence |
| IAb | 327 | SVGRWVAVVAVLAVL | GRWVAVVAV | 0.4040 | 631.6 | 16.00 | Sequence |
| IAb | 52 | YLRFRREAQNAAALN | REAQNAAAL | 0.4032 | 637.5 | 16.00 | Sequence |
| IAb | 530 | AGEVTGTNPPAGTTV | TGTNPPAGT | 0.4022 | 644.1 | 16.00 | Sequence |
| IAb | 213 | PPFTGDSPVSVAYQH | FTGDSPVSV | 0.4019 | 646.4 | 16.00 | Sequence |
| IAb | 460 | PELVGKVIGTNPPAN | VIGTNPPAN | 0.3996 | 662.7 | 16.00 | Sequence |
| IAb | 480 | TNVVIIIVGSGPATK | IIVGSGPAT | 0.3970 | 681.4 | 16.00 | Sequence |
| IAb | 102 | IVHTEGPMTPKRAIE | VHTEGPMTP | 0.3961 | 687.8 | 16.00 | Sequence |
| IAb | 274 | RVHNGEPPEAPKVLT | RVHNGEPPE | 0.3955 | 692.9 | 16.00 | Sequence |
| IAb | 137 | DVKPANIMISATNAV | VKPANIMIS | 0.3954 | 693.1 | 16.00 | Sequence |
| IAb | 515 | GFTKFSQASVDSPRP | GFTKFSQAS | 0.3940 | 703.9 | 16.00 | Sequence |
| IAb | 326 | GSVGRWVAVVAVLAV | GRWVAVVAV | 0.3937 | 706.1 | 16.00 | Sequence |
| IAb | 328 | VGRWVAVVAVLAVLT | GRWVAVVAV | 0.3935 | 707.9 | 16.00 | Sequence |
| IAb | 210 | TGEPPFTGDSPVSVA | FTGDSPVSV | 0.3934 | 708.9 | 16.00 | Sequence |
| IAb | 514 | YGFTKFSQASVDSPR | FTKFSQASV | 0.3932 | 710.4 | 16.00 | Sequence |
| IAb | 203 | CVLYEVLTGEPPFTG | YEVLTGEPP | 0.3894 | 739.9 | 16.00 | Sequence |
| IAb | 141 | ANIMISATNAVKVMD | ANIMISATN | 0.3890 | 743.5 | 16.00 | Sequence |
| IAb | 101 | DIVHTEGPMTPKRAI | VHTEGPMTP | 0.3889 | 743.7 | 16.00 | Sequence |
| IAb | 103 | VHTEGPMTPKRAIEV | VHTEGPMTP | 0.3886 | 746.3 | 16.00 | Sequence |
| IAb | 209 | LTGEPPFTGDSPVSV | FTGDSPVSV | 0.3870 | 759.4 | 16.00 | Sequence |
| IAb | 452 | KQANSPSTPELVGKV | KQANSPSTP | 0.3863 | 765.1 | 16.00 | Sequence |
| IAb | 521 | QASVDSPRPAGEVTG | ASVDSPRPA | 0.3842 | 783.1 | 16.00 | Sequence |
| IAb | 140 | PANIMISATNAVKVM | ANIMISATN | 0.3839 | 785.1 | 16.00 | Sequence |
| IAb | 292 | RTSLLSSAAGNLSGP | TSLLSSAAG | 0.3832 | 791.1 | 16.00 | Sequence |
| IAb | 517 | TKFSQASVDSPRPAG | ASVDSPRPA | 0.3826 | 796.5 | 16.00 | Sequence |
| IAb | 80 | ETPAGPLPYIVMEYV | ETPAGPLPY | 0.3822 | 799.5 | 16.00 | Sequence |
| IAb | 518 | KFSQASVDSPRPAGE | ASVDSPRPA | 0.3801 | 818.3 | 16.00 | Sequence |
| IAb | 325 | IGSVGRWVAVVAVLA | GRWVAVVAV | 0.3798 | 821.2 | 16.00 | Sequence |
| IAb | 513 | VYGFTKFSQASVDSP | FTKFSQASV | 0.3767 | 848.5 | 16.00 | Sequence |
| IAb | 293 | TSLLSSAAGNLSGPR | LSSAAGNLS | 0.3763 | 852.9 | 16.00 | Sequence |
| IAb | 445 | AAGFGRFKQANSPST | FKQANSPST | 0.3745 | 869.1 | 16.00 | Sequence |
| IAb | 100 | RDIVHTEGPMTPKRA | VHTEGPMTP | 0.3744 | 870.5 | 16.00 | Sequence |
| IAb | 155 | DFGIARAIADSGNSV | FGIARAIAD | 0.3734 | 879.4 | 16.00 | Sequence |
| IAb | 136 | RDVKPANIMISATNA | VKPANIMIS | 0.3730 | 883.4 | 16.00 | Sequence |
| IAb | 429 | PDVSTLTYAEAVKKL | STLTYAEAV | 0.3725 | 888.5 | 16.00 | Sequence |
| IAb | 394 | PPDHVIGTDPAANTS | VIGTDPAAN | 0.3717 | 896.6 | 16.00 | Sequence |
| IAb | 139 | KPANIMISATNAVKV | ANIMISATN | 0.3694 | 918.9 | 16.00 | Sequence |
| IAb | 291 | ERTSLLSSAAGNLSG | TSLLSSAAG | 0.3680 | 932.3 | 16.00 | Sequence |
| IAb | 433 | TLTYAEAVKKLTAAG | LTYAEAVKK | 0.3674 | 938.7 | 16.00 | Sequence |
| IAb | 51 | FYLRFRREAQNAAAL | REAQNAAAL | 0.3644 | 969.3 | 16.00 | Sequence |
| IAb | 522 | ASVDSPRPAGEVTGT | ASVDSPRPA | 0.3638 | 975.7 | 16.00 | Sequence |
| IAb | 300 | AGNLSGPRTDPLPRQ | GNLSGPRTD | 0.3638 | 975.7 | 16.00 | Sequence |
| IAb | 520 | SQASVDSPRPAGEVT | ASVDSPRPA | 0.3635 | 979.4 | 16.00 | Sequence |
| IAb | 299 | AAGNLSGPRTDPLPR | GNLSGPRTD | 0.3619 | 996.7 | 16.00 | Sequence |
| IAb | 269 | RADLVRVHNGEPPEA | VRVHNGEPP | 0.3577 | 1042.4 | 16.00 | Sequence |
| IAb | 486 | IVGSGPATKDIPDVA | IVGSGPATK | 0.3561 | 1061.0 | 16.00 | Sequence |
| IAb | 535 | GTNPPAGTTVPVDSV | TNPPAGTTV | 0.3557 | 1065.6 | 16.00 | Sequence |
| IAb | 296 | LSSAAGNLSGPRTDP | GNLSGPRTD | 0.3543 | 1081.4 | 16.00 | Sequence |
| IAb | 290 | AERTSLLSSAAGNLS | TSLLSSAAG | 0.3541 | 1083.5 | 16.00 | Sequence |
| IAb | 467 | IGTNPPANQTSAITN | IGTNPPANQ | 0.3536 | 1089.5 | 16.00 | Sequence |
| IAb | 275 | VHNGEPPEAPKVLTD | VHNGEPPEA | 0.3505 | 1127.4 | 16.00 | Sequence |
| IAb | 536 | TNPPAGTTVPVDSVI | TNPPAGTTV | 0.3483 | 1153.7 | 16.00 | Sequence |
| IAb | 329 | GRWVAVVAVLAVLTV | GRWVAVVAV | 0.3480 | 1158.2 | 16.00 | Sequence |
| IAb | 135 | HRDVKPANIMISATN | VKPANIMIS | 0.3473 | 1166.3 | 16.00 | Sequence |
| IAb | 156 | FGIARAIADSGNSVT | FGIARAIAD | 0.3461 | 1182.1 | 16.00 | Sequence |
| IAb | 149 | NAVKVMDFGIARAIA | MDFGIARAI | 0.3458 | 1185.7 | 32.00 | Sequence |
| IAb | 294 | SLLSSAAGNLSGPRT | SLLSSAAGN | 0.3452 | 1194.0 | 32.00 | Sequence |
| IAb | 298 | SAAGNLSGPRTDPLP | GNLSGPRTD | 0.3448 | 1199.3 | 32.00 | Sequence |
| IAb | 511 | LNVYGFTKFSQASVD | NVYGFTKFS | 0.3447 | 1199.6 | 32.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAb | 74 | YDTGEAETPAGPLPY | ETPAGPLPY | 0.3445 | 1203.1 | 32.00 | Sequence |
| IAb | 208 | VLTGEPPFTGDSPVS | VLTGEPPFT | 0.3443 | 1206.0 | 32.00 | Sequence |
| IAb | 202 | GCVLYEVLTGEPPFT | YEVLTGEPP | 0.3417 | 1240.0 | 32.00 | Sequence |
| IAb | 399 | IGTDPAANTSVSAGD | PAANTSVSA | 0.3388 | 1279.2 | 32.00 | Sequence |
| IAb | 214 | PFTGDSPVSVAYQHV | FTGDSPVSV | 0.3384 | 1284.1 | 32.00 | Sequence |
| IAb | 261 | RYQTAAEMRADLVRV | YQTAAEMRA | 0.3382 | 1287.0 | 32.00 | Sequence |
| IAb | 297 | SSAAGNLSGPRTDPL | GNLSGPRTD | 0.3378 | 1293.7 | 32.00 | Sequence |
| IAb | 75 | DTGEAETPAGPLPYI | ETPAGPLPY | 0.3371 | 1303.2 | 32.00 | Sequence |
| IAb | 400 | GTDPAANTSVSAGDE | PAANTSVSA | 0.3370 | 1303.9 | 32.00 | Sequence |
| IAb | 401 | TDPAANTSVSAGDEI | PAANTSVSA | 0.3365 | 1311.4 | 32.00 | Sequence |
| IAb | 142 | NIMISATNAVKVMDF | IMISATNAV | 0.3364 | 1312.9 | 32.00 | Sequence |
| IAb | 248 | AVVLKALAKNPENRY | AVVLKALAK | 0.3363 | 1314.1 | 32.00 | Sequence |
| IAb | 295 | LLSSAAGNLSGPRTD | LSSAAGNLS | 0.3354 | 1326.9 | 32.00 | Sequence |
| IAb | 393 | IPPDHVIGTDPAANT | VIGTDPAAN | 0.3348 | 1335.4 | 32.00 | Sequence |
| IAb | 207 | EVLTGEPPFTGDSPV | VLTGEPPFT | 0.3329 | 1364.1 | 32.00 | Sequence |
| IAb | 227 | HVREDPIPPSARHEG | HVREDPIPP | 0.3326 | 1368.2 | 32.00 | Sequence |
| IAb | 470 | NPPANQTSAITNVVI | ANQTSAITN | 0.3311 | 1389.8 | 32.00 | Sequence |
| IAb | 512 | NVYGFTKFSQASVDS | FTKFSQASV | 0.3301 | 1405.5 | 32.00 | Sequence |
| IAb | 13 | GEILGFGGMSEVHLA | LGFGGMSEV | 0.3297 | 1411.4 | 32.00 | Sequence |
| IAb | 428 | IPDVSTLTYAEAVKK | STLTYAEAV | 0.3295 | 1414.4 | 32.00 | Sequence |
| IAb | 567 | GMFWVDAEPRLRALG | MFWVDAEPR | 0.3280 | 1437.2 | 32.00 | Sequence |
| IAb | 226 | QHVREDPIPPSARHE | HVREDPIPP | 0.3276 | 1443.4 | 32.00 | Sequence |
| IAb | 566 | SGMFWVDAEPRLRAL | MFWVDAEPR | 0.3270 | 1453.2 | 32.00 | Sequence |
| IAb | 14 | EILGFGGMSEVHLAR | LGFGGMSEV | 0.3266 | 1460.2 | 32.00 | Sequence |
| IAb | 301 | GNLSGPRTDPLPRQD | GNLSGPRTD | 0.3263 | 1464.0 | 32.00 | Sequence |
| IAb | 99 | LRDIVHTEGPMTPKR | VHTEGPMTP | 0.3231 | 1515.8 | 32.00 | Sequence |
| IAb | 510 | NLNVYGFTKFSQASV | NVYGFTKFS | 0.3208 | 1554.4 | 32.00 | Sequence |
| IAb | 434 | LTYAEAVKKLTAAGF | LTYAEAVKK | 0.3194 | 1577.4 | 32.00 | Sequence |
| IAb | 469 | TNPPANQTSAITNVV | ANQTSAITN | 0.3187 | 1590.9 | 32.00 | Sequence |
| IAb | 565 | LSGMFWVDAEPRLRA | MFWVDAEPR | 0.3180 | 1601.5 | 32.00 | Sequence |
| IAb | 247 | DAVVLKALAKNPENR | AVVLKALAK | 0.3178 | 1605.4 | 32.00 | Sequence |
| IAb | 134 | IHRDVKPANIMISAT | VKPANIMIS | 0.3172 | 1616.6 | 32.00 | Sequence |
| IAb | 529 | PAGEVTGTNPPAGTT | VTGTNPPAG | 0.3156 | 1643.9 | 32.00 | Sequence |
| IAb | 67 | HPAIVAVYDTGEAET | AVYDTGEAE | 0.3156 | 1644.8 | 32.00 | Sequence |
| IAb | 143 | IMISATNAVKVMDFG | IMISATNAV | 0.3123 | 1704.6 | 32.00 | Sequence |
| IAb | 133 | IIHRDVKPANIMISA | VKPANIMIS | 0.3111 | 1726.1 | 32.00 | Sequence |
| IAb | 12 | LGEILGFGGMSEVHL | LGFGGMSEV | 0.3106 | 1735.6 | 32.00 | Sequence |
| IAb | 604 | YQNPPAGTGVNRDGI | NPPAGTGVN | 0.3049 | 1846.7 | 32.00 | Sequence |
| IAb | 148 | TNAVKVMDFGIARAI | MDFGIARAI | 0.3044 | 1856.2 | 32.00 | Sequence |
| IAb | 246 | LDAVVLKALAKNPEN | AVVLKALAK | 0.3039 | 1866.5 | 32.00 | Sequence |
| IAb | 568 | MFWVDAEPRLRALGW | MFWVDAEPR | 0.3038 | 1868.2 | 32.00 | Sequence |
| IAb | 15 | ILGFGGMSEVHLARD | LGFGGMSEV | 0.3026 | 1892.8 | 32.00 | Sequence |
| IAb | 276 | HNGEPPEAPKVLTDA | HNGEPPEAP | 0.3023 | 1898.2 | 32.00 | Sequence |
| IAb | 105 | TEGPMTPKRAIEVIA | EGPMTPKRA | 0.3016 | 1913.4 | 32.00 | Sequence |
| IAb | 106 | EGPMTPKRAIEVIAD | EGPMTPKRA | 0.3009 | 1927.3 | 32.00 | Sequence |
| IAb | 172 | TAAVIGTAQYLSPEQ | TAAVIGTAQ | 0.3002 | 1942.4 | 32.00 | Sequence |
| IAb | 364 | VRGQSSADAIATLQN | QSSADAIAT | 0.2987 | 1973.8 | 32.00 | Sequence |
| IAb | 168 | SVTQTAAVIGTAQYL | TAAVIGTAQ | 0.2977 | 1996.3 | 32.00 | Sequence |
| IAb | 228 | VREDPIPPSARHEGL | EDPIPPSAR | 0.2968 | 2014.7 | 32.00 | Sequence |
| IAb | 132 | GIIHRDVKPANIMIS | VKPANIMIS | 0.2956 | 2042.3 | 32.00 | Sequence |
| IAb | 98 | TLRDIVHTEGPMTPK | VHTEGPMTP | 0.2955 | 2044.8 | 32.00 | Sequence |
| IAb | 122 | CQALNFSHQNGIIHR | QALNFSHQN | 0.2947 | 2061.3 | 32.00 | Sequence |
| IAb | 557 | GNQFVMPDLSGMFWV | NQFVMPDLS | 0.2944 | 2068.0 | 32.00 | Sequence |
| IAb | 363 | DVRGQSSADAIATLQ | RGQSSADAI | 0.2941 | 2075.6 | 32.00 | Sequence |
| IAb | 324 | SIGSVGRWVAVVAVL | GRWVAVVAV | 0.2940 | 2077.8 | 32.00 | Sequence |
| IAb | 556 | KGNQFVMPDLSGMFW | NQFVMPDLS | 0.2931 | 2096.8 | 32.00 | Sequence |
| IAb | 468 | GTNPPANQTSAITNV | ANQTSAITN | 0.2925 | 2110.0 | 32.00 | Sequence |
| IAb | 249 | VVLKALAKNPENRYQ | VVLKALAKN | 0.2921 | 2120.2 | 32.00 | Sequence |
| IAb | 171 | QTAAVIGTAQYLSPE | TAAVIGTAQ | 0.2919 | 2125.2 | 32.00 | Sequence |
| IAb | 170 | TQTAAVIGTAQYLSP | TAAVIGTAQ | 0.2917 | 2128.9 | 32.00 | Sequence |
| IAb | 104 | HTEGPMTPKRAIEVI | EGPMTPKRA | 0.2914 | 2137.3 | 32.00 | Sequence |
| IAb | 73 | VYDTGEAETPAGPLP | YDTGEAETP | 0.2913 | 2137.8 | 32.00 | Sequence |
| IAb | 479 | ITNVVIIIVGSGPAT | IIVGSGPAT | 0.2905 | 2157.1 | 32.00 | Sequence |
| IAb | 169 | VTQTAAVIGTAQYLS | TAAVIGTAQ | 0.2901 | 2167.8 | 32.00 | Sequence |
| IAb | 225 | YQHVREDPIPPSARH | HVREDPIPP | 0.2894 | 2184.0 | 32.00 | Sequence |
| IAb | 392 | TIPPDHVIGTDPAAN | VIGTDPAAN | 0.2892 | 2188.0 | 32.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAb | 229 | REDPIPPSARHEGLS | EDPIPPSAR | 0.2887 | 2198.6 | 32.00 | Sequence |
| IAb | 289 | DAERTSLLSSAAGNL | RTSLLSSAA | 0.2883 | 2209.7 | 32.00 | Sequence |
| IAb | 402 | DPAANTSVSAGDEIT | PAANTSVSA | 0.2865 | 2251.8 | 32.00 | Sequence |
| IAb | 123 | QALNFSHQNGIIHRD | QALNFSHQN | 0.2864 | 2256.2 | 32.00 | Sequence |
| IAb | 471 | PPANQTSAITNVVII | ANQTSAITN | 0.2836 | 2325.7 | 32.00 | Sequence |
| IAb | 555 | SKGNQFVMPDLSGMF | NQFVMPDLS | 0.2834 | 2330.6 | 32.00 | Sequence |
| IAb | 564 | DLSGMFWVDAEPRLR | MFWVDAEPR | 0.2824 | 2353.9 | 32.00 | Sequence |
| IAb | 11 | ELGEILGFGGMSEVH | LGFGGMSEV | 0.2824 | 2355.3 | 32.00 | Sequence |
| IAb | 121 | ACQALNFSHQNGIIH | QALNFSHQN | 0.2806 | 2401.7 | 32.00 | Sequence |
| IAb | 362 | PDVRGQSSADAIATL | RGQSSADAI | 0.2806 | 2402.0 | 32.00 | Sequence |
| IAb | 509 | KNLNVYGFTKFSQAS | NVYGFTKFS | 0.2802 | 2412.9 | 32.00 | Sequence |
| IAb | 255 | AKNPENRYQTAAEMR | NRYQTAAEM | 0.2795 | 2430.3 | 32.00 | Sequence |
| IAb | 262 | YQTAAEMRADLVRVH | YQTAAEMRA | 0.2791 | 2440.4 | 32.00 | Sequence |
| IAb | 528 | RPAGEVTGTNPPAGT | VTGTNPPAG | 0.2790 | 2443.5 | 32.00 | Sequence |
| IAb | 167 | NSVTQTAAVIGTAQY | SVTQTAAVI | 0.2776 | 2480.5 | 32.00 | Sequence |
| IAb | 50 | SFYLRFRREAQNAAA | FRREAQNAA | 0.2766 | 2507.4 | 32.00 | Sequence |
| IAb | 66 | NHPAIVAVYDTGEAE | AVYDTGEAE | 0.2737 | 2587.5 | 32.00 | Sequence |
| IAb | 537 | NPPAGTTVPVDSVIE | NPPAGTTVP | 0.2723 | 2625.5 | 32.00 | Sequence |
| IAb | 224 | AYQHVREDPIPPSAR | HVREDPIPP | 0.2723 | 2625.7 | 32.00 | Sequence |
| IAb | 576 | RLRALGWTGMLDKGA | LGWTGMLDK | 0.2718 | 2641.9 | 32.00 | Sequence |
| IAb | 453 | QANSPSTPELVGKVI | NSPSTPELV | 0.2689 | 2726.2 | 32.00 | Sequence |
| IAb | 97 | VTLRDIVHTEGPMTP | VHTEGPMTP | 0.2682 | 2747.0 | 32.00 | Sequence |
| IAb | 554 | VSKGNQFVMPDLSGM | NQFVMPDLS | 0.2664 | 2800.4 | 32.00 | Sequence |
| IAb | 577 | LRALGWTGMLDKGAD | LGWTGMLDK | 0.2663 | 2803.6 | 32.00 | Sequence |
| IAb | 245 | DLDAVVLKALAKNPE | AVVLKALAK | 0.2656 | 2823.8 | 32.00 | Sequence |
| IAb | 472 | PANQTSAITNVVIII | ANQTSAITN | 0.2656 | 2825.0 | 32.00 | Sequence |
| IAb | 427 | EIPDVSTLTYAEAVK | STLTYAEAV | 0.2647 | 2853.3 | 32.00 | Sequence |
| IAb | 277 | NGEPPEAPKVLTDAE | EPPEAPKVL | 0.2643 | 2865.4 | 32.00 | Sequence |
| IAb | 278 | GEPPEAPKVLTDAER | EPPEAPKVL | 0.2628 | 2910.9 | 32.00 | Sequence |
| IAb | 605 | QNPPAGTGVNRDGII | NPPAGTGVN | 0.2625 | 2919.2 | 32.00 | Sequence |
| IAb | 323 | RSIGSVGRWVAVVAV | GRWVAVVAV | 0.2625 | 2921.6 | 32.00 | Sequence |
| IAb | 215 | FTGDSPVSVAYQHVR | FTGDSPVSV | 0.2621 | 2933.8 | 32.00 | Sequence |
| IAb | 330 | RWVAVVAVLAVLTVV | WVAVVAVLA | 0.2605 | 2984.9 | 32.00 | Sequence |
| IAb | 361 | VPDVRGQSSADAIAT | QSSADAIAT | 0.2600 | 2999.2 | 32.00 | Sequence |
| IAb | 166 | GNSVTQTAAVIGTAQ | SVTQTAAVI | 0.2595 | 3015.6 | 32.00 | Sequence |
| IAb | 250 | VLKALAKNPENRYQT | LKALAKNPE | 0.2591 | 3029.5 | 32.00 | Sequence |
| IAb | 558 | NQFVMPDLSGMFWVD | NQFVMPDLS | 0.2582 | 3059.5 | 32.00 | Sequence |
| IAb | 64 | ALNHPAIVAVYDTGE | LNHPAIVAV | 0.2553 | 3158.1 | 32.00 | Sequence |
| IAb | 124 | ALNFSHQNGIIHRDV | FSHQNGIIH | 0.2534 | 3224.3 | 32.00 | Sequence |
| IAb | 365 | RGQSSADAIATLQNR | QSSADAIAT | 0.2522 | 3263.7 | 32.00 | Sequence |
| IAb | 595 | GGSQHNRVVYQNPPA | RVVYQNPPA | 0.2514 | 3292.0 | 32.00 | Sequence |
| IAb | 223 | VAYQHVREDPIPPSA | VAYQHVRED | 0.2509 | 3311.3 | 32.00 | Sequence |
| IAb | 288 | TDAERTSLLSSAAGN | RTSLLSSAA | 0.2491 | 3377.4 | 32.00 | Sequence |
| IAb | 473 | ANQTSAITNVVIIIV | ANQTSAITN | 0.2470 | 3454.5 | 32.00 | Sequence |
| IAb | 120 | DACQALNFSHQNGII | QALNFSHQN | 0.2466 | 3470.5 | 32.00 | Sequence |
| IAb | 459 | TPELVGKVIGTNPPA | GKVIGTNPP | 0.2438 | 3577.1 | 50.00 | Sequence |
| IAb | 508 | QKNLNVYGFTKFSQA | NVYGFTKFS | 0.2434 | 3590.5 | 50.00 | Sequence |
| IAb | 454 | ANSPSTPELVGKVIG | NSPSTPELV | 0.2410 | 3685.3 | 50.00 | Sequence |
| IAb | 444 | TAAGFGRFKQANSPS | GRFKQANSP | 0.2410 | 3687.4 | 50.00 | Sequence |
| IAb | 403 | PAANTSVSAGDEITV | PAANTSVSA | 0.2400 | 3726.1 | 50.00 | Sequence |
| IAb | 254 | LAKNPENRYQTAAEM | NRYQTAAEM | 0.2392 | 3757.7 | 50.00 | Sequence |
| IAb | 251 | LKALAKNPENRYQTA | LKALAKNPE | 0.2388 | 3775.9 | 50.00 | Sequence |
| IAb | 230 | EDPIPPSARHEGLSA | EDPIPPSAR | 0.2384 | 3791.5 | 50.00 | Sequence |
| IAb | 10 | YELGEILGFGGMSEV | LGFGGMSEV | 0.2367 | 3860.2 | 50.00 | Sequence |
| IAb | 331 | WVAVVAVLAVLTVVV | WVAVVAVLA | 0.2352 | 3924.9 | 50.00 | Sequence |
| IAb | 575 | PRLRALGWTGMLDKG | LGWTGMLDK | 0.2352 | 3926.4 | 50.00 | Sequence |
| IAb | 49 | PSFYLRFRREAQNAA | FRREAQNAA | 0.2349 | 3938.0 | 50.00 | Sequence |
| IAb | 144 | MISATNAVKVMDFGI | ISATNAVKV | 0.2345 | 3953.4 | 50.00 | Sequence |
| IAb | 222 | SVAYQHVREDPIPPS | VAYQHVRED | 0.2341 | 3969.7 | 50.00 | Sequence |
| IAb | 527 | PRPAGEVTGTNPPAG | VTGTNPPAG | 0.2328 | 4028.9 | 50.00 | Sequence |
| IAb | 268 | MRADLVRVHNGEPPE | VRVHNGEPP | 0.2317 | 4077.7 | 50.00 | Sequence |
| IAb | 125 | LNFSHQNGIIHRDVK | FSHQNGIIH | 0.2316 | 4078.5 | 50.00 | Sequence |
| IAb | 201 | LGCVLYEVLTGEPPF | YEVLTGEPP | 0.2268 | 4297.2 | 50.00 | Sequence |
| IAb | 578 | RALGWTGMLDKGADV | LGWTGMLDK | 0.2260 | 4335.1 | 50.00 | Sequence |
| IAb | 366 | GQSSADAIATLQNRG | QSSADAIAT | 0.2252 | 4371.8 | 50.00 | Sequence |
| IAb | 426 | REIPDVSTLTYAEAV | STLTYAEAV | 0.2247 | 4394.3 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAb | 563 | PDLSGMFWVDAEPRL | MFWVDAEPR | 0.2235 | 4454.0 | 50.00 | Sequence |
| IAb | 165 | SGNSVTQTAAVIGTA | SVTQTAAVI | 0.2222 | 4514.9 | 50.00 | Sequence |
| IAb | 302 | NLSGPRTDPLPRQDL | GPRTDPLPR | 0.2216 | 4546.9 | 50.00 | Sequence |
| IAb | 244 | ADLDAVVLKALAKNP | AVVLKALAK | 0.2213 | 4562.6 | 50.00 | Sequence |
| IAb | 221 | VSVAYQHVREDPIPP | VAYQHVRED | 0.2190 | 4678.7 | 50.00 | Sequence |
| IAb | 303 | LSGPRTDPLPRQDLD | GPRTDPLPR | 0.2170 | 4780.3 | 50.00 | Sequence |
| IAb | 279 | EPPEAPKVLTDAERT | EPPEAPKVL | 0.2165 | 4805.2 | 50.00 | Sequence |
| IAb | 384 | RTLQKPDSTIPPDHV | RTLQKPDST | 0.2164 | 4809.1 | 50.00 | Sequence |
| IAb | 360 | QVPDVRGQSSADAIA | VRGQSSADA | 0.2163 | 4814.6 | 50.00 | Sequence |
| IAb | 16 | LGFGGMSEVHLARDL | LGFGGMSEV | 0.2161 | 4826.5 | 50.00 | Sequence |
| IAb | 219 | SPVSVAYQHVREDPI | VAYQHVRED | 0.2153 | 4865.9 | 50.00 | Sequence |
| IAb | 606 | NPPAGTGVNRDGIIT | NPPAGTGVN | 0.2148 | 4894.5 | 50.00 | Sequence |
| IAb | 443 | LTAAGFGRFKQANSP | GRFKQANSP | 0.2138 | 4946.3 | 50.00 | Sequence |
| IAb | 220 | PVSVAYQHVREDPIP | VAYQHVRED | 0.2129 | 4996.7 | 50.00 | Sequence |
| IAb | 65 | LNHPAIVAVYDTGEA | LNHPAIVAV | 0.2110 | 5096.8 | 50.00 | Sequence |
| IAb | 415 | ITVNVSTGPEQREIP | VNVSTGPEQ | 0.2109 | 5107.3 | 50.00 | Sequence |
| IAb | 287 | LTDAERTSLLSSAAG | RTSLLSSAA | 0.2091 | 5203.0 | 50.00 | Sequence |
| IAb | 38 | VKVLRADLARDPSFY | KVLRADLAR | 0.2089 | 5215.6 | 50.00 | Sequence |
| IAb | 195 | RSDVYSLGCVLYEVL | DVYSLGCVL | 0.2082 | 5256.2 | 50.00 | Sequence |
| IAb | 196 | SDVYSLGCVLYEVLT | DVYSLGCVL | 0.2080 | 5267.4 | 50.00 | Sequence |
| IAb | 574 | EPRLRALGWTGMLDK | RALGWTGML | 0.2076 | 5289.9 | 50.00 | Sequence |
| IAb | 383 | IRTLQKPDSTIPPDH | RTLQKPDST | 0.2058 | 5392.7 | 50.00 | Sequence |
| IAb | 36 | VAVKVLRADLARDPS | KVLRADLAR | 0.2048 | 5450.5 | 50.00 | Sequence |
| IAb | 119 | ADACQALNFSHQNGI | QALNFSHQN | 0.2048 | 5452.7 | 50.00 | Sequence |
| IAb | 145 | ISATNAVKVMDFGIA | ISATNAVKV | 0.2039 | 5509.1 | 50.00 | Sequence |
| IAb | 131 | NGIIHRDVKPANIMI | IIHRDVKPA | 0.2035 | 5529.2 | 50.00 | Sequence |
| IAb | 523 | SVDSPRPAGEVTGTN | VDSPRPAGE | 0.2025 | 5590.2 | 50.00 | Sequence |
| IAb | 524 | VDSPRPAGEVTGTNP | VDSPRPAGE | 0.2023 | 5601.3 | 50.00 | Sequence |
| IAb | 455 | NSPSTPELVGKVIGT | NSPSTPELV | 0.2019 | 5626.6 | 50.00 | Sequence |
| IAb | 194 | ARSDVYSLGCVLYEV | DVYSLGCVL | 0.2018 | 5635.2 | 50.00 | Sequence |
| IAb | 304 | SGPRTDPLPRQDLDD | GPRTDPLPR | 0.2007 | 5698.5 | 50.00 | Sequence |
| IAb | 37 | AVKVLRADLARDPSF | KVLRADLAR | 0.1995 | 5773.3 | 50.00 | Sequence |
| IAb | 378 | NRGFKIRTLQKPDST | FKIRTLQKP | 0.1986 | 5829.6 | 50.00 | Sequence |
| IAb | 507 | AQKNLNVYGFTKFSQ | NVYGFTKFS | 0.1984 | 5841.8 | 50.00 | Sequence |
| IAb | 381 | FKIRTLQKPDSTIPP | RTLQKPDST | 0.1974 | 5907.0 | 50.00 | Sequence |
| IAb | 367 | QSSADAIATLQNRGF | QSSADAIAT | 0.1973 | 5910.8 | 50.00 | Sequence |
| IAb | 435 | TYAEAVKKLTAAGFG | TYAEAVKKL | 0.1969 | 5940.0 | 50.00 | Sequence |
| IAb | 553 | QVSKGNQFVMPDLSG | NQFVMPDLS | 0.1967 | 5950.0 | 50.00 | Sequence |
| IAb | 115 | IEVIADACQALNFSH | VIADACQAL | 0.1947 | 6085.5 | 50.00 | Sequence |
| IAb | 159 | ARAIADSGNSVTQTA | AIADSGNSV | 0.1945 | 6094.0 | 50.00 | Sequence |
| IAb | 414 | EITVNVSTGPEQREI | VNVSTGPEQ | 0.1942 | 6117.2 | 50.00 | Sequence |
| IAb | 158 | IARAIADSGNSVTQT | AIADSGNSV | 0.1935 | 6160.8 | 50.00 | Sequence |
| IAb | 562 | MPDLSGMFWVDAEPR | MFWVDAEPR | 0.1927 | 6214.3 | 50.00 | Sequence |
| IAb | 382 | KIRTLQKPDSTIPPD | RTLQKPDST | 0.1918 | 6279.3 | 50.00 | Sequence |
| IAb | 35 | DVAVKVLRADLARDP | VKVLRADLA | 0.1913 | 6307.0 | 50.00 | Sequence |
| IAb | 200 | SLGCVLYEVLTGEPP | YEVLTGEPP | 0.1912 | 6319.4 | 50.00 | Sequence |
| IAb | 379 | RGFKIRTLQKPDSTI | RTLQKPDST | 0.1910 | 6328.5 | 50.00 | Sequence |
| IAb | 157 | GIARAIADSGNSVTQ | AIADSGNSV | 0.1901 | 6390.2 | 50.00 | Sequence |
| IAb | 88 | YIVMEYVDGVTLRDI | MEYVDGVTL | 0.1901 | 6390.7 | 50.00 | Sequence |
| IAb | 89 | IVMEYVDGVTLRDIV | MEYVDGVTL | 0.1899 | 6407.9 | 50.00 | Sequence |
| IAb | 526 | SPRPAGEVTGTNPPA | GEVTGTNPP | 0.1897 | 6418.5 | 50.00 | Sequence |
| IAb | 525 | DSPRPAGEVTGTNPP | PRPAGEVTG | 0.1887 | 6491.2 | 50.00 | Sequence |
| IAb | 252 | KALAKNPENRYQTAA | KALAKNPEN | 0.1879 | 6544.2 | 50.00 | Sequence |
| IAb | 380 | GFKIRTLQKPDSTIP | RTLQKPDST | 0.1872 | 6593.6 | 50.00 | Sequence |
| IAb | 164 | DSGNSVTQTAAVIGT | SVTQTAAVI | 0.1871 | 6606.3 | 50.00 | Sequence |
| IAb | 90 | VMEYVDGVTLRDIVH | MEYVDGVTL | 0.1868 | 6625.8 | 50.00 | Sequence |
| IAb | 117 | VIADACQALNFSHQN | VIADACQAL | 0.1860 | 6680.8 | 50.00 | Sequence |
| IAb | 114 | AIEVIADACQALNFS | VIADACQAL | 0.1855 | 6716.7 | 50.00 | Sequence |
| IAb | 579 | ALGWTGMLDKGADVD | LGWTGMLDK | 0.1849 | 6762.3 | 50.00 | Sequence |
| IAb | 87 | PYIVMEYVDGVTLRD | MEYVDGVTL | 0.1849 | 6763.2 | 50.00 | Sequence |
| IAb | 130 | QNGIIHRDVKPANIM | IIHRDVKPA | 0.1838 | 6846.6 | 50.00 | Sequence |
| IAb | 416 | TVNVSTGPEQREIPD | VNVSTGPEQ | 0.1833 | 6880.5 | 50.00 | Sequence |
| IAb | 180 | QYLSPEQARGDSVDA | QYLSPEQAR | 0.1828 | 6922.0 | 50.00 | Sequence |
| IAb | 193 | DARSDVYSLGCVLYE | DVYSLGCVL | 0.1816 | 7011.3 | 50.00 | Sequence |
| IAb | 442 | KLTAAGFGRFKQANS | KLTAAGFGR | 0.1810 | 7053.7 | 50.00 | Sequence |
| IAb | 391 | STIPPDHVIGTDPAA | HVIGTDPAA | 0.1801 | 7126.8 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAb | 81 | TPAGPLPYIVMEYVD | AGPLPYIVM | 0.1800 | 7133.2 | 50.00 | Sequence |
| IAb | 506 | VAQKNLNVYGFTKFS | NVYGFTKFS | 0.1798 | 7144.5 | 50.00 | Sequence |
| IAb | 573 | AEPRLRALGWTGMLD | RALGWTGML | 0.1788 | 7224.7 | 50.00 | Sequence |
| IAb | 107 | GPMTPKRAIEVIADA | MTPKRAIEV | 0.1782 | 7274.8 | 50.00 | Sequence |
| IAb | 116 | EVIADACQALNFSHQ | VIADACQAL | 0.1777 | 7312.9 | 50.00 | Sequence |
| IAb | 126 | NFSHQNGIIHRDVKP | FSHQNGIIH | 0.1774 | 7333.8 | 50.00 | Sequence |
| IAb | 231 | DPIPPSARHEGLSAD | PIPPSARHE | 0.1774 | 7337.2 | 50.00 | Sequence |
| IAb | 538 | PPAGTTVPVDSVIEL | PPAGTTVPV | 0.1766 | 7396.5 | 50.00 | Sequence |
| IAb | 127 | FSHQNGIIHRDVKPA | FSHQNGIIH | 0.1756 | 7477.1 | 50.00 | Sequence |
| IAb | 552 | LQVSKGNQFVMPDLS | NQFVMPDLS | 0.1755 | 7484.5 | 50.00 | Sequence |
| IAb | 386 | LQKPDSTIPPDHVIG | QKPDSTIPP | 0.1750 | 7529.7 | 50.00 | Sequence |
| IAb | 359 | VQVPDVRGQSSADAI | RGQSSADAI | 0.1747 | 7548.6 | 50.00 | Sequence |
| IAb | 590 | ADVDAGGSQHNRVVY | VDAGGSQHN | 0.1743 | 7583.7 | 50.00 | Sequence |
| IAb | 385 | TLQKPDSTIPPDHVI | QKPDSTIPP | 0.1738 | 7626.8 | 50.00 | Sequence |
| IAb | 377 | QNRGFKIRTLQKPDS | FKIRTLQKP | 0.1737 | 7637.7 | 50.00 | Sequence |
| IAb | 413 | DEITVNVSTGPEQRE | VNVSTGPEQ | 0.1732 | 7675.7 | 50.00 | Sequence |
| IAb | 113 | RAIEVIADACQALNF | EVIADACQA | 0.1728 | 7711.3 | 50.00 | Sequence |
| IAb | 82 | PAGPLPYIVMEYVDG | AGPLPYIVM | 0.1724 | 7744.1 | 50.00 | Sequence |
| IAb | 160 | RAIADSGNSVTQTAA | AIADSGNSV | 0.1722 | 7756.6 | 50.00 | Sequence |
| IAb | 375 | TLQNRGFKIRTLQKP | FKIRTLQKP | 0.1721 | 7769.9 | 50.00 | Sequence |
| IAb | 147 | ATNAVKVMDFGIARA | KVMDFGIAR | 0.1718 | 7788.5 | 50.00 | Sequence |
| IAb | 376 | LQNRGFKIRTLQKPD | FKIRTLQKP | 0.1706 | 7897.1 | 50.00 | Sequence |
| IAb | 305 | GPRTDPLPRQDLDDT | GPRTDPLPR | 0.1692 | 8014.7 | 50.00 | Sequence |
| IAb | 589 | GADVDAGGSQHNRVV | VDAGGSQHN | 0.1690 | 8034.1 | 50.00 | Sequence |
| IAb | 458 | STPELVGKVIGTNPP | GKVIGTNPP | 0.1689 | 8043.4 | 50.00 | Sequence |
| IAb | 197 | DVYSLGCVLYEVLTG | DVYSLGCVL | 0.1688 | 8050.5 | 50.00 | Sequence |
| IAb | 286 | VLTDAERTSLLSSAA | RTSLLSSAA | 0.1686 | 8064.9 | 50.00 | Sequence |
| IAb | 118 | IADACQALNFSHQNG | QALNFSHQN | 0.1675 | 8160.6 | 50.00 | Sequence |
| IAb | 478 | AITNVVIIIVGSGPA | IIIVGSGPA | 0.1666 | 8244.7 | 50.00 | Sequence |
| IAb | 161 | AIADSGNSVTQTAAV | AIADSGNSV | 0.1663 | 8270.8 | 50.00 | Sequence |
| IAb | 232 | PIPPSARHEGLSADL | PIPPSARHE | 0.1656 | 8328.9 | 50.00 | Sequence |
| IAb | 163 | ADSGNSVTQTAAVIG | SVTQTAAVI | 0.1649 | 8395.0 | 50.00 | Sequence |
| IAb | 218 | DSPVSVAYQHVREDP | VAYQHVRED | 0.1647 | 8410.8 | 50.00 | Sequence |
| IAb | 162 | IADSGNSVTQTAAVI | GNSVTQTAA | 0.1645 | 8433.2 | 50.00 | Sequence |
| IAb | 39 | KVLRADLARDPSFYL | KVLRADLAR | 0.1642 | 8460.0 | 50.00 | Sequence |
| IAb | 34 | RDVAVKVLRADLARD | VKVLRADLA | 0.1640 | 8478.7 | 50.00 | Sequence |
| IAb | 332 | VAVVAVLAVLTVVVT | VAVVAVLAV | 0.1638 | 8493.8 | 50.00 | Sequence |
| IAb | 48 | DPSFYLRFRREAQNA | FYLRFRREA | 0.1634 | 8534.8 | 50.00 | Sequence |
| IAb | 417 | VNVSTGPEQREIPDV | VNVSTGPEQ | 0.1631 | 8563.7 | 50.00 | Sequence |
| IAb | 236 | SARHEGLSADLDAVV | SARHEGLSA | 0.1624 | 8625.3 | 50.00 | Sequence |
| IAb | 559 | QFVMPDLSGMFWVDA | FVMPDLSGM | 0.1622 | 8645.6 | 50.00 | Sequence |
| IAb | 112 | KRAIEVIADACQALN | VIADACQAL | 0.1619 | 8674.3 | 50.00 | Sequence |
| IAb | 592 | VDAGGSQHNRVVYQN | VDAGGSQHN | 0.1604 | 8814.5 | 50.00 | Sequence |
| IAb | 91 | MEYVDGVTLRDIVHT | MEYVDGVTL | 0.1604 | 8819.6 | 50.00 | Sequence |
| IAb | 436 | YAEAVKKLTAAGFGR | EAVKKLTAA | 0.1601 | 8843.3 | 50.00 | Sequence |
| IAb | 267 | EMRADLVRVHNGEPP | VRVHNGEPP | 0.1594 | 8915.9 | 50.00 | Sequence |
| IAb | 387 | QKPDSTIPPDHVIGT | QKPDSTIPP | 0.1589 | 8959.9 | 50.00 | Sequence |
| IAb | 438 | EAVKKLTAAGFGRFK | EAVKKLTAA | 0.1582 | 9024.5 | 50.00 | Sequence |
| IAb | 440 | VKKLTAAGFGRFKQA | VKKLTAAGF | 0.1581 | 9037.6 | 50.00 | Sequence |
| IAb | 253 | ALAKNPENRYQTAAE | ALAKNPENR | 0.1578 | 9062.7 | 50.00 | Sequence |
| IAb | 591 | DVDAGGSQHNRVVYQ | VDAGGSQHN | 0.1576 | 9089.8 | 50.00 | Sequence |
| IAb | 569 | FWVDAEPRLRALGWT | WVDAEPRLR | 0.1565 | 9195.5 | 50.00 | Sequence |
| IAb | 572 | DAEPRLRALGWTGML | RALGWTGML | 0.1564 | 9207.3 | 50.00 | Sequence |
| IAb | 441 | KKLTAAGFGRFKQAN | TAAGFGRFK | 0.1550 | 9344.3 | 50.00 | Sequence |
| IAb | 412 | GDEITVNVSTGPEQR | VNVSTGPEQ | 0.1546 | 9391.0 | 50.00 | Sequence |
| IAb | 580 | LGWTGMLDKGADVDA | LGWTGMLDK | 0.1542 | 9429.9 | 50.00 | Sequence |
| IAb | 235 | PSARHEGLSADLDAV | SARHEGLSA | 0.1540 | 9452.4 | 50.00 | Sequence |
| IAb | 345 | VTIAINTFGGITRDV | INTFGGITR | 0.1535 | 9496.0 | 50.00 | Sequence |
| IAb | 243 | SADLDAVVLKALAKN | AVVLKALAK | 0.1526 | 9594.0 | 50.00 | Sequence |
| IAb | 549 | VIELQVSKGNQFVMP | IELQVSKGN | 0.1521 | 9645.3 | 50.00 | Sequence |
| IAb | 86 | LPYIVMEYVDGVTLR | MEYVDGVTL | 0.1518 | 9670.2 | 50.00 | Sequence |
| IAb | 109 | MTPKRAIEVIADACQ | MTPKRAIEV | 0.1515 | 9711.4 | 50.00 | Sequence |
| IAb | 439 | AVKKLTAAGFGRFKQ | KLTAAGFGR | 0.1513 | 9724.4 | 50.00 | Sequence |
| IAb | 368 | SSADAIATLQNRGFK | ADAIATLQN | 0.1510 | 9759.1 | 50.00 | Sequence |
| IAb | 369 | SADAIATLQNRGFKI | ADAIATLQN | 0.1503 | 9831.7 | 50.00 | Sequence |
| IAb | 347 | IAINTFGGITRDVQV | INTFGGITR | 0.1501 | 9859.9 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAb | 83 | AGPLPYIVMEYVDGV | AGPLPYIVM | 0.1499 | 9880.4 | 50.00 | Sequence |
| IAb | 322 | DRSIGSVGRWVAVVA | VGRWVAVVA | 0.1498 | 9884.5 | 50.00 | Sequence |
| IAb | 588 | KGADVDAGGSQHNRV | VDAGGSQHN | 0.1491 | 9967.0 | 50.00 | Sequence |
| IAb | 146 | SATNAVKVMDFGIAR | SATNAVKVM | 0.1489 | 9981.8 | 50.00 | Sequence |
| IAb | 344 | VVTIAINTFGGITRD | VVTIAINTF | 0.1488 | 9995.5 | 50.00 | Sequence |
| IAb | 333 | AVVAVLAVLTVVVTI | VVAVLAVLT | 0.1482 | 10056.5 | 50.00 | Sequence |
| IAb | 550 | IELQVSKGNQFVMPD | IELQVSKGN | 0.1470 | 10194.9 | 50.00 | Sequence |
| IAb | 111 | PKRAIEVIADACQAL | VIADACQAL | 0.1468 | 10212.0 | 50.00 | Sequence |
| IAb | 348 | AINTFGGITRDVQVP | INTFGGITR | 0.1461 | 10296.3 | 50.00 | Sequence |
| IAb | 33 | HRDVAVKVLRADLAR | VKVLRADLA | 0.1460 | 10303.2 | 50.00 | Sequence |
| IAb | 349 | INTFGGITRDVQVPD | INTFGGITR | 0.1460 | 10304.5 | 50.00 | Sequence |
| IAb | 346 | TIAINTFGGITRDVQ | INTFGGITR | 0.1458 | 10329.0 | 50.00 | Sequence |
| IAb | 437 | AEAVKKLTAAGFGRF | EAVKKLTAA | 0.1454 | 10364.5 | 50.00 | Sequence |
| IAb | 570 | WVDAEPRLRALGWTG | WVDAEPRLR | 0.1446 | 10454.2 | 50.00 | Sequence |
| IAb | 334 | VVAVLAVLTVVVTIA | VVAVLAVLT | 0.1444 | 10485.7 | 50.00 | Sequence |
| IAb | 9 | RYELGEILGFGGMSE | ILGFGGMSE | 0.1437 | 10563.3 | 50.00 | Sequence |
| IAb | 217 | GDSPVSVAYQHVRED | VAYQHVRED | 0.1427 | 10671.5 | 50.00 | Sequence |
| IAb | 425 | QREIPDVSTLTYAEA | EIPDVSTLT | 0.1422 | 10740.1 | 50.00 | Sequence |
| IAb | 548 | SVIELQVSKGNQFVM | IELQVSKGN | 0.1419 | 10765.9 | 50.00 | Sequence |
| IAb | 341 | LTVVVTIAINTFGGI | TVVVTIAIN | 0.1419 | 10768.7 | 50.00 | Sequence |
| IAb | 85 | PLPYIVMEYVDGVTL | MEYVDGVTL | 0.1411 | 10865.7 | 50.00 | Sequence |
| IAb | 8 | DRYELGEILGFGGMS | DRYELGEIL | 0.1410 | 10878.8 | 50.00 | Sequence |
| IAb | 370 | ADAIATLQNRGFKIR | ADAIATLQN | 0.1404 | 10950.2 | 50.00 | Sequence |
| IAb | 487 | VGSGPATKDIPDVAG | VGSGPATKD | 0.1401 | 10980.4 | 50.00 | Sequence |
| IAb | 340 | VLTVVVTIAINTFGG | TVVVTIAIN | 0.1398 | 11013.9 | 50.00 | Sequence |
| IAb | 237 | ARHEGLSADLDAVVL | ARHEGLSAD | 0.1397 | 11023.6 | 50.00 | Sequence |
| IAb | 108 | PMTPKRAIEVIADAC | MTPKRAIEV | 0.1394 | 11066.7 | 50.00 | Sequence |
| IAb | 335 | VAVLAVLTVVVTIAI | VAVLAVLTV | 0.1394 | 11068.3 | 50.00 | Sequence |
| IAb | 539 | PAGTTVPVDSVIELQ | PAGTTVPVD | 0.1377 | 11272.7 | 50.00 | Sequence |
| IAb | 342 | TVVVTIAINTFGGIT | TVVVTIAIN | 0.1375 | 11299.9 | 50.00 | Sequence |
| IAb | 47 | RDPSFYLRFRREAQN | FYLRFRREA | 0.1367 | 11397.5 | 50.00 | Sequence |
| IAb | 343 | VVVTIAINTFGGITR | VVTIAINTF | 0.1364 | 11427.5 | 50.00 | Sequence |
| IAb | 7 | SDRYELGEILGFGGM | DRYELGEIL | 0.1351 | 11594.2 | 50.00 | Sequence |
| IAb | 234 | PPSARHEGLSADLDA | SARHEGLSA | 0.1344 | 11685.4 | 50.00 | Sequence |
| IAb | 129 | HQNGIIHRDVKPANI | IIHRDVKPA | 0.1334 | 11803.9 | 50.00 | Sequence |
| IAb | 339 | AVLTVVVTIAINTFG | TVVVTIAIN | 0.1327 | 11901.7 | 50.00 | Sequence |
| IAb | 547 | DSVIELQVSKGNQFV | IELQVSKGN | 0.1313 | 12083.9 | 50.00 | Sequence |
| IAb | 374 | ATLQNRGFKIRTLQK | NRGFKIRTL | 0.1309 | 12132.8 | 50.00 | Sequence |
| IAb | 233 | IPPSARHEGLSADLD | SARHEGLSA | 0.1303 | 12215.1 | 50.00 | Sequence |
| IAb | 338 | LAVLTVVVTIAINTF | TVVVTIAIN | 0.1284 | 12466.9 | 50.00 | Sequence |
| IAb | 30 | LRLHRDVAVKVLRAD | LRLHRDVAV | 0.1279 | 12527.8 | 50.00 | Sequence |
| IAb | 587 | DKGADVDAGGSQHNR | VDAGGSQHN | 0.1277 | 12559.2 | 50.00 | Sequence |
| IAb | 560 | FVMPDLSGMFWVDAE | FVMPDLSGM | 0.1275 | 12580.5 | 50.00 | Sequence |
| IAb | 474 | NQTSAITNVVIIIVG | QTSAITNVV | 0.1273 | 12608.4 | 50.00 | Sequence |
| IAb | 32 | LHRDVAVKVLRADLA | VAVKVLRAD | 0.1273 | 12617.8 | 50.00 | Sequence |
| IAb | 198 | VYSLGCVLYEVLTGE | VYSLGCVLY | 0.1255 | 12859.4 | 50.00 | Sequence |
| IAb | 6 | LSDRYELGEILGFGG | DRYELGEIL | 0.1255 | 12862.6 | 50.00 | Sequence |
| IAb | 110 | TPKRAIEVIADACQA | KRAIEVIAD | 0.1237 | 13120.0 | 50.00 | Sequence |
| IAb | 192 | VDARSDVYSLGCVLY | DVYSLGCVL | 0.1236 | 13120.7 | 50.00 | Sequence |
| IAb | 411 | AGDEITVNVSTGPEQ | VNVSTGPEQ | 0.1228 | 13248.4 | 50.00 | Sequence |
| IAb | 96 | GVTLRDIVHTEGPMT | IVHTEGPMT | 0.1215 | 13428.9 | 50.00 | Sequence |
| IAb | 390 | DSTIPPDHVIGTDPA | DSTIPPDHV | 0.1211 | 13481.2 | 50.00 | Sequence |
| IAb | 540 | AGTTVPVDSVIELQV | AGTTVPVDS | 0.1209 | 13515.3 | 50.00 | Sequence |
| IAb | 418 | NVSTGPEQREIPDVS | NVSTGPEQR | 0.1209 | 13517.2 | 50.00 | Sequence |
| IAb | 336 | AVLAVLTVVVTIAIN | AVLAVLTVV | 0.1208 | 13532.0 | 50.00 | Sequence |
| IAb | 5 | HLSDRYELGEILGFG | DRYELGEIL | 0.1206 | 13560.9 | 50.00 | Sequence |
| IAb | 502 | QTVDVAQKNLNVYGF | VDVAQKNLN | 0.1196 | 13701.4 | 50.00 | Sequence |
| IAb | 17 | GFGGMSEVHLARDLR | GFGGMSEVH | 0.1171 | 14089.9 | 50.00 | Sequence |
| IAb | 242 | LSADLDAVVLKALAK | AVVLKALAK | 0.1166 | 14161.1 | 50.00 | Sequence |
| IAb | 388 | KPDSTIPPDHVIGTD | DSTIPPDHV | 0.1165 | 14182.2 | 50.00 | Sequence |
| IAb | 29 | DLRLHRDVAVKVLRA | LRLHRDVAV | 0.1163 | 14207.8 | 50.00 | Sequence |
| IAb | 181 | YLSPEQARGDSVDAR | LSPEQARGD | 0.1159 | 14262.3 | 50.00 | Sequence |
| IAb | 586 | LDKGADVDAGGSQHN | VDAGGSQHN | 0.1147 | 14451.7 | 50.00 | Sequence |
| IAb | 424 | EQREIPDVSTLTYAE | REIPDVSTL | 0.1147 | 14460.1 | 50.00 | Sequence |
| IAb | 321 | RDRSIGSVGRWVAVV | DRSIGSVGR | 0.1134 | 14659.9 | 50.00 | Sequence |
| IAb | 404 | AANTSVSAGDEITVN | SVSAGDEIT | 0.1133 | 14668.3 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAb | 500 | AGQTVDVAQKNLNVY | VDVAQKNLN | 0.1129 | 14731.3 | 50.00 | Sequence |
| IAb | 551 | ELQVSKGNQFVMPDL | LQVSKGNQF | 0.1128 | 14757.6 | 50.00 | Sequence |
| IAb | 499 | VAGQTVDVAQKNLNV | QTVDVAQKN | 0.1126 | 14792.8 | 50.00 | Sequence |
| IAb | 501 | GQTVDVAQKNLNVYG | VDVAQKNLN | 0.1125 | 14806.2 | 50.00 | Sequence |
| IAb | 496 | IPDVAGQTVDVAQKN | PDVAGQTVD | 0.1125 | 14808.0 | 50.00 | Sequence |
| IAb | 495 | DIPDVAGQTVDVAQK | PDVAGQTVD | 0.1121 | 14872.4 | 50.00 | Sequence |
| IAb | 4 | SHLSDRYELGEILGF | DRYELGEIL | 0.1117 | 14932.3 | 50.00 | Sequence |
| IAb | 423 | PEQREIPDVSTLTYA | EQREIPDVS | 0.1116 | 14953.5 | 50.00 | Sequence |
| IAb | 373 | IATLQNRGFKIRTLQ | NRGFKIRTL | 0.1110 | 15048.1 | 50.00 | Sequence |
| IAb | 571 | VDAEPRLRALGWTGM | LRALGWTGM | 0.1109 | 15064.3 | 50.00 | Sequence |
| IAb | 543 | TVPVDSVIELQVSKG | TVPVDSVIE | 0.1107 | 15086.5 | 50.00 | Sequence |
| IAb | 216 | TGDSPVSVAYQHVRE | TGDSPVSVA | 0.1107 | 15101.6 | 50.00 | Sequence |
| IAb | 494 | KDIPDVAGQTVDVAQ | PDVAGQTVD | 0.1101 | 15188.0 | 50.00 | Sequence |
| IAb | 337 | VLAVLTVVVTIAINT | VLTVVVTIA | 0.1100 | 15204.6 | 50.00 | Sequence |
| IAb | 46 | ARDPSFYLRFRREAQ | FYLRFRREA | 0.1100 | 15207.2 | 50.00 | Sequence |
| IAb | 497 | PDVAGQTVDVAQKNL | PDVAGQTVD | 0.1092 | 15342.3 | 50.00 | Sequence |
| IAb | 239 | HEGLSADLDAVVLKA | HEGLSADLD | 0.1085 | 15454.1 | 50.00 | Sequence |
| IAb | 358 | DVQVPDVRGQSSADA | VRGQSSADA | 0.1078 | 15569.0 | 50.00 | Sequence |
| IAb | 285 | KVLTDAERTSLLSSA | KVLTDAERT | 0.1072 | 15683.1 | 50.00 | Sequence |
| IAb | 263 | QTAAEMRADLVRVHN | QTAAEMRAD | 0.1071 | 15692.1 | 50.00 | Sequence |
| IAb | 405 | ANTSVSAGDEITVNV | SVSAGDEIT | 0.1060 | 15881.2 | 50.00 | Sequence |
| IAb | 546 | VDSVIELQVSKGNQF | IELQVSKGN | 0.1051 | 16034.0 | 50.00 | Sequence |
| IAb | 84 | GPLPYIVMEYVDGVT | LPYIVMEYV | 0.1049 | 16071.5 | 50.00 | Sequence |
| IAb | 238 | RHEGLSADLDAVVLK | HEGLSADLD | 0.1025 | 16491.5 | 50.00 | Sequence |
| IAb | 541 | GTTVPVDSVIELQVS | TVPVDSVIE | 0.1025 | 16492.2 | 50.00 | Sequence |
| IAb | 475 | QTSAITNVVIIIVGS | QTSAITNVV | 0.1022 | 16549.0 | 50.00 | Sequence |
| IAb | 389 | PDSTIPPDHVIGTDP | DSTIPPDHV | 0.1018 | 16617.2 | 50.00 | Sequence |
| IAb | 457 | PSTPELVGKVIGTNP | LVGKVIGTN | 0.1002 | 16906.1 | 50.00 | Sequence |
| IAb | 320 | DRDRSIGSVGRWVAV | DRSIGSVGR | 0.1001 | 16936.3 | 50.00 | Sequence |
| IAb | 493 | TKDIPDVAGQTVDVA | PDVAGQTVD | 0.0996 | 17023.0 | 50.00 | Sequence |
| IAb | 498 | DVAGQTVDVAQKNLN | QTVDVAQKN | 0.0995 | 17030.8 | 50.00 | Sequence |
| IAb | 31 | RLHRDVAVKVLRADL | VAVKVLRAD | 0.0995 | 17033.5 | 50.00 | Sequence |
| IAb | 199 | YSLGCVLYEVLTGEP | YSLGCVLYE | 0.0992 | 17087.1 | 50.00 | Sequence |
| IAb | 406 | NTSVSAGDEITVNVS | SVSAGDEIT | 0.0981 | 17291.8 | 50.00 | Sequence |
| IAb | 128 | SHQNGIIHRDVKPAN | IIHRDVKPA | 0.0978 | 17347.9 | 50.00 | Sequence |
| IAb | 505 | DVAQKNLNVYGFTKF | LNVYGFTKF | 0.0978 | 17362.0 | 50.00 | Sequence |
| IAb | 28 | RDLRLHRDVAVKVLR | LRLHRDVAV | 0.0977 | 17370.6 | 50.00 | Sequence |
| IAb | 542 | TTVPVDSVIELQVSK | TVPVDSVIE | 0.0973 | 17451.6 | 50.00 | Sequence |
| IAb | 319 | TDRDRSIGSVGRWVA | DRSIGSVGR | 0.0972 | 17474.1 | 50.00 | Sequence |
| IAb | 282 | EAPKVLTDAERTSLL | KVLTDAERT | 0.0970 | 17514.6 | 50.00 | Sequence |
| IAb | 561 | VMPDLSGMFWVDAEP | GMFWVDAEP | 0.0961 | 17677.2 | 50.00 | Sequence |
| IAb | 410 | SAGDEITVNVSTGPE | TVNVSTGPE | 0.0956 | 17766.7 | 50.00 | Sequence |
| IAb | 45 | LARDPSFYLRFRREA | FYLRFRREA | 0.0955 | 17785.8 | 50.00 | Sequence |
| IAb | 280 | PPEAPKVLTDAERTS | KVLTDAERT | 0.0951 | 17863.1 | 50.00 | Sequence |
| IAb | 504 | VDVAQKNLNVYGFTK | VDVAQKNLN | 0.0947 | 17942.5 | 50.00 | Sequence |
| IAb | 408 | SVSAGDEITVNVSTG | SVSAGDEIT | 0.0945 | 17975.6 | 50.00 | Sequence |
| IAb | 607 | PPAGTGVNRDGIITL | VNRDGIITL | 0.0942 | 18051.0 | 50.00 | Sequence |
| IAb | 372 | AIATLQNRGFKIRTL | NRGFKIRTL | 0.0938 | 18121.6 | 50.00 | Sequence |
| IAb | 407 | TSVSAGDEITVNVST | SVSAGDEIT | 0.0935 | 18180.3 | 50.00 | Sequence |
| IAb | 27 | ARDLRLHRDVAVKVL | LRLHRDVAV | 0.0928 | 18310.6 | 50.00 | Sequence |
| IAb | 283 | APKVLTDAERTSLLS | KVLTDAERT | 0.0926 | 18350.5 | 50.00 | Sequence |
| IAb | 182 | LSPEQARGDSVDARS | LSPEQARGD | 0.0922 | 18440.1 | 50.00 | Sequence |
| IAb | 284 | PKVLTDAERTSLLSS | KVLTDAERT | 0.0918 | 18524.5 | 50.00 | Sequence |
| IAb | 240 | EGLSADLDAVVLKAL | EGLSADLDA | 0.0912 | 18640.1 | 50.00 | Sequence |
| IAb | 281 | PEAPKVLTDAERTSL | KVLTDAERT | 0.0906 | 18764.9 | 50.00 | Sequence |
| IAb | 503 | TVDVAQKNLNVYGFT | VDVAQKNLN | 0.0901 | 18868.9 | 50.00 | Sequence |
| IAb | 422 | GPEQREIPDVSTLTY | REIPDVSTL | 0.0900 | 18889.2 | 50.00 | Sequence |
| IAb | 421 | TGPEQREIPDVSTLT | REIPDVSTL | 0.0898 | 18916.2 | 50.00 | Sequence |
| IAb | 456 | SPSTPELVGKVIGTN | LVGKVIGTN | 0.0888 | 19131.3 | 50.00 | Sequence |
| IAb | 44 | DLARDPSFYLRFRRE | LARDPSFYL | 0.0879 | 19319.1 | 50.00 | Sequence |
| IAb | 191 | SVDARSDVYSLGCVL | DVYSLGCVL | 0.0875 | 19397.2 | 50.00 | Sequence |
| IAb | 92 | EYVDGVTLRDIVHTE | EYVDGVTLR | 0.0866 | 19584.5 | 50.00 | Sequence |
| IAb | 492 | ATKDIPDVAGQTVDV | PDVAGQTVD | 0.0849 | 19945.0 | 50.00 | Sequence |
| IAb | 544 | VPVDSVIELQVSKGN | IELQVSKGN | 0.0848 | 19977.9 | 50.00 | Sequence |
| IAb | 357 | RDVQVPDVRGQSSAD | RDVQVPDVR | 0.0847 | 19999.5 | 50.00 | Sequence |
| IAb | 581 | GWTGMLDKGADVDAG | WTGMLDKGA | 0.0838 | 20201.1 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAb | 43 | ADLARDPSFYLRFRR | LARDPSFYL | 0.0820 | 20585.9 | 50.00 | Sequence |
| IAb | 489 | SGPATKDIPDVAGQT | ATKDIPDVA | 0.0820 | 20595.3 | 50.00 | Sequence |
| IAb | 491 | PATKDIPDVAGQTVD | ATKDIPDVA | 0.0819 | 20614.4 | 50.00 | Sequence |
| IAb | 241 | GLSADLDAVVLKALA | LDAVVLKAL | 0.0815 | 20690.9 | 50.00 | Sequence |
| IAb | 266 | AEMRADLVRVHNGEP | AEMRADLVR | 0.0815 | 20701.6 | 50.00 | Sequence |
| IAb | 490 | GPATKDIPDVAGQTV | ATKDIPDVA | 0.0806 | 20893.1 | 50.00 | Sequence |
| IAb | 545 | PVDSVIELQVSKGNQ | IELQVSKGN | 0.0806 | 20900.1 | 50.00 | Sequence |
| IAb | 318 | DTDRDRSIGSVGRWV | DRSIGSVGR | 0.0806 | 20905.5 | 50.00 | Sequence |
| IAb | 40 | VLRADLARDPSFYLR | LRADLARDP | 0.0787 | 21337.2 | 50.00 | Sequence |
| IAb | 354 | GITRDVQVPDVRGQS | RDVQVPDVR | 0.0781 | 21468.0 | 50.00 | Sequence |
| IAb | 594 | AGGSQHNRVVYQNPP | NRVVYQNPP | 0.0767 | 21794.3 | 50.00 | Sequence |
| IAb | 420 | STGPEQREIPDVSTL | EQREIPDVS | 0.0761 | 21957.9 | 50.00 | Sequence |
| IAb | 582 | WTGMLDKGADVDAGG | WTGMLDKGA | 0.0760 | 21971.4 | 50.00 | Sequence |
| IAb | 41 | LRADLARDPSFYLRF | LARDPSFYL | 0.0758 | 22018.0 | 50.00 | Sequence |
| IAb | 371 | DAIATLQNRGFKIRT | DAIATLQNR | 0.0757 | 22042.8 | 50.00 | Sequence |
| IAb | 356 | TRDVQVPDVRGQSSA | RDVQVPDVR | 0.0757 | 22044.5 | 50.00 | Sequence |
| IAb | 184 | PEQARGDSVDARSDV | EQARGDSVD | 0.0754 | 22104.5 | 50.00 | Sequence |
| IAb | 3 | PSHLSDRYELGEILG | DRYELGEIL | 0.0743 | 22390.4 | 50.00 | Sequence |
| IAb | 350 | NTFGGITRDVQVPDV | NTFGGITRD | 0.0741 | 22437.5 | 50.00 | Sequence |
| IAb | 18 | FGGMSEVHLARDLRL | FGGMSEVHL | 0.0740 | 22458.8 | 50.00 | Sequence |
| IAb | 185 | EQARGDSVDARSDVY | QARGDSVDA | 0.0740 | 22459.1 | 50.00 | Sequence |
| IAb | 355 | ITRDVQVPDVRGQSS | RDVQVPDVR | 0.0739 | 22475.6 | 50.00 | Sequence |
| IAb | 409 | VSAGDEITVNVSTGP | ITVNVSTGP | 0.0738 | 22502.9 | 50.00 | Sequence |
| IAb | 488 | GSGPATKDIPDVAGQ | SGPATKDIP | 0.0736 | 22556.0 | 50.00 | Sequence |
| IAb | 183 | SPEQARGDSVDARSD | EQARGDSVD | 0.0734 | 22590.7 | 50.00 | Sequence |
| IAb | 265 | AAEMRADLVRVHNGE | AEMRADLVR | 0.0729 | 22730.2 | 50.00 | Sequence |
| IAb | 42 | RADLARDPSFYLRFR | LARDPSFYL | 0.0726 | 22785.6 | 50.00 | Sequence |
| IAb | 608 | PAGTGVNRDGIITLR | VNRDGIITL | 0.0715 | 23079.1 | 50.00 | Sequence |
| IAb | 26 | LARDLRLHRDVAVKV | LRLHRDVAV | 0.0703 | 23357.5 | 50.00 | Sequence |
| IAb | 264 | TAAEMRADLVRVHNG | AEMRADLVR | 0.0701 | 23411.1 | 50.00 | Sequence |
| IAb | 95 | DGVTLRDIVHTEGPM | VTLRDIVHT | 0.0686 | 23791.1 | 50.00 | Sequence |
| IAb | 419 | VSTGPEQREIPDVST | EQREIPDVS | 0.0684 | 23859.6 | 50.00 | Sequence |
| IAb | 353 | GGITRDVQVPDVRGQ | RDVQVPDVR | 0.0684 | 23860.4 | 50.00 | Sequence |
| IAb | 611 | TGVNRDGIITLRFGQ | VNRDGIITL | 0.0683 | 23878.7 | 50.00 | Sequence |
| IAb | 306 | PRTDPLPRQDLDDTD | PRTDPLPRQ | 0.0680 | 23960.0 | 50.00 | Sequence |
| IAb | 610 | GTGVNRDGIITLRFG | VNRDGIITL | 0.0670 | 24207.3 | 50.00 | Sequence |
| IAb | 585 | MLDKGADVDAGGSQH | ADVDAGGSQ | 0.0669 | 24247.1 | 50.00 | Sequence |
| IAb | 584 | GMLDKGADVDAGGSQ | ADVDAGGSQ | 0.0657 | 24551.3 | 50.00 | Sequence |
| IAb | 583 | TGMLDKGADVDAGGS | TGMLDKGAD | 0.0655 | 24623.1 | 50.00 | Sequence |
| IAb | 19 | GGMSEVHLARDLRLH | VHLARDLRL | 0.0651 | 24725.6 | 50.00 | Sequence |
| IAb | 93 | YVDGVTLRDIVHTEG | YVDGVTLRD | 0.0636 | 25118.8 | 50.00 | Sequence |
| IAb | 351 | TFGGITRDVQVPDVR | RDVQVPDVR | 0.0630 | 25290.0 | 50.00 | Sequence |
| IAb | 20 | GMSEVHLARDLRLHR | VHLARDLRL | 0.0625 | 25416.5 | 50.00 | Sequence |
| IAb | 609 | AGTGVNRDGIITLRF | VNRDGIITL | 0.0614 | 25733.0 | 50.00 | Sequence |
| IAb | 352 | FGGITRDVQVPDVRG | RDVQVPDVR | 0.0601 | 26091.6 | 50.00 | Sequence |
| IAb | 21 | MSEVHLARDLRLHRD | VHLARDLRL | 0.0594 | 26289.1 | 50.00 | Sequence |
| IAb | 24 | VHLARDLRLHRDVAV | VHLARDLRL | 0.0578 | 26748.5 | 50.00 | Sequence |
| IAb | 22 | SEVHLARDLRLHRDV | VHLARDLRL | 0.0564 | 27165.6 | 50.00 | Sequence |
| IAb | 476 | TSAITNVVIIIVGSG | TSAITNVVI | 0.0562 | 27216.2 | 50.00 | Sequence |
| IAb | 94 | VDGVTLRDIVHTEGP | VTLRDIVHT | 0.0557 | 27353.7 | 50.00 | Sequence |
| IAb | 317 | DDTDRDRSIGSVGRW | DRSIGSVGR | 0.0532 | 28110.7 | 50.00 | Sequence |
| IAb | 23 | EVHLARDLRLHRDVA | VHLARDLRL | 0.0532 | 28132.6 | 50.00 | Sequence |
| IAb | 186 | QARGDSVDARSDVYS | QARGDSVDA | 0.0522 | 28415.3 | 50.00 | Sequence |
| IAb | 477 | SAITNVVIIIVGSGP | SAITNVVII | 0.0506 | 28932.5 | 50.00 | Sequence |
| IAb | 2 | TPSHLSDRYELGEIL | DRYELGEIL | 0.0500 | 29097.0 | 50.00 | Sequence |
| IAb | 25 | HLARDLRLHRDVAVK | LRLHRDVAV | 0.0451 | 30678.2 | 50.00 | Sequence |
| IAb | 593 | DAGGSQHNRVVYQNP | GGSQHNRVV | 0.0443 | 30951.3 | 50.00 | Sequence |
| IAb | 190 | DSVDARSDVYSLGCV | SDVYSLGCV | 0.0433 | 31283.3 | 50.00 | Sequence |
| IAb | 187 | ARGDSVDARSDVYSL | GDSVDARSD | 0.0416 | 31871.9 | 50.00 | Sequence |
| IAb | 307 | RTDPLPRQDLDDTDR | RTDPLPRQD | 0.0393 | 32696.2 | 50.00 | Sequence |
| IAb | 0 | MTTPSHLSDRYELGE | MTTPSHLSD | 0.0379 | 33174.1 | 50.00 | Sequence |
| IAb | 316 | LDDTDRDRSIGSVGR | DRSIGSVGR | 0.0361 | 33831.6 | 50.00 | Sequence |
| IAb | 188 | RGDSVDARSDVYSLG | GDSVDARSD | 0.0322 | 35310.0 | 50.00 | Sequence |
| IAb | 189 | GDSVDARSDVYSLGC | GDSVDARSD | 0.0281 | 36895.7 | 50.00 | Sequence |
| IAb | 1 | TTPSHLSDRYELGEI | TTPSHLSDR | 0.0259 | 37762.8 | 50.00 | Sequence |
| IAb | 315 | DLDDTDRDRSIGSVG | RDRSIGSVG | 0.0221 | 39351.2 | 50.00 | Sequence |

```
      IAb  308  TDPLPRQDLDDTDRD  TDPLPRQDL        0.0189     40758.7             50.00     Sequence
      IAb  310  PLPRQDLDDTDRDRS  PLPRQDLDD        0.0177     41280.7             50.00     Sequence
      IAb  309  DPLPRQDLDDTDRDR  PLPRQDLDD        0.0145     42747.4             50.00     Sequence
      IAb  314  QDLDDTDRDRSIGSV  TDRDRSIGS        0.0134     43262.5             50.00     Sequence
      IAb  311  LPRQDLDDTDRDRSI  LPRQDLDDT        0.0118     43992.3             50.00     Sequence
      IAb  313  RQDLDDTDRDRSIGS  TDRDRSIGS        0.0116     44097.6             50.00     Sequence
      IAb  312  PRQDLDDTDRDRSIG  QDLDDTDRD        0.0094     45151.6             50.00     Sequence
-----------------------------------------------------------------------------------------------

Allele: IAb. Number of high binders 5. Number of weak binders 65. Number of peptides 612

-----------------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------------
    Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
-----------------------------------------------------------------------------------------------
      IAd  329  GRWVAVVAVLAVLTV  GRWVAVVAV        0.6192        61.5          WB     0.05     Sequence
      IAd  328  VGRWVAVVAVLAVLT  WVAVVAVLA        0.5874        86.8          WB     0.10     Sequence
      IAd  327  SVGRWVAVVAVLAVL  WVAVVAVLA        0.5759        98.4          WB     0.15     Sequence
      IAd  326  GSVGRWVAVVAVLAV  WVAVVAVLA        0.5623       114.0          WB     0.15     Sequence
      IAd  330  RWVAVVAVLAVLTVV  WVAVVAVLA        0.5499       130.3          WB     0.20     Sequence
      IAd   30  LRLHRDVAVKVLRAD  LHRDVAVKV        0.5188       182.5          WB     0.40     Sequence
      IAd   27  ARDLRLHRDVAVKVL  LHRDVAVKV        0.5183       183.5          WB     0.40     Sequence
      IAd   29  DLRLHRDVAVKVLRA  LHRDVAVKV        0.5072       206.9          WB     0.40     Sequence
      IAd  331  WVAVVAVLAVLTVVV  WVAVVAVLA        0.5052       211.3          WB     0.40     Sequence
      IAd   31  RLHRDVAVKVLRADL  LHRDVAVKV        0.5045       213.0          WB     0.40     Sequence
      IAd  325  IGSVGRWVAVVAVLA  WVAVVAVLA        0.4952       235.4          WB     0.80     Sequence
      IAd   28  RDLRLHRDVAVKVLR  LHRDVAVKV        0.4891       251.7          WB     0.80     Sequence
      IAd  262  YQTAAEMRADLVRVH  YQTAAEMRA        0.4786       281.9          WB     0.80     Sequence
      IAd   32  LHRDVAVKVLRADLA  LHRDVAVKV        0.4717       303.9          WB     0.80     Sequence
      IAd  261  RYQTAAEMRADLVRV  YQTAAEMRA        0.4686       314.1          WB     0.80     Sequence
      IAd   26  LARDLRLHRDVAVKV  LHRDVAVKV        0.4614       339.4          WB     1.00     Sequence
      IAd  259  ENRYQTAAEMRADLV  YQTAAEMRA        0.4574       354.5          WB     1.00     Sequence
      IAd  260  NRYQTAAEMRADLVR  YQTAAEMRA        0.4472       396.0          WB     2.00     Sequence
      IAd  332  VAVVAVLAVLTVVVT  VAVVAVLAV        0.4438       410.9          WB     2.00     Sequence
      IAd  109  MTPKRAIEVIADACQ  KRAIEVIAD        0.4417       420.2          WB     2.00     Sequence
      IAd  108  PMTPKRAIEVIADAC  KRAIEVIAD        0.4394       430.6          WB     2.00     Sequence
      IAd  258  PENRYQTAAEMRADL  YQTAAEMRA        0.4374       440.1          WB     2.00     Sequence
      IAd  257  NPENRYQTAAEMRAD  YQTAAEMRA        0.4296       479.1          WB     2.00     Sequence
      IAd  167  NSVTQTAAVIGTAQY  QTAAVIGTA        0.4213       524.2                 2.00     Sequence
      IAd  333  AVVAVLAVLTVVVTI  VAVLAVLTV        0.4199       531.8                 2.00     Sequence
      IAd  264  TAAEMRADLVRVHNG  AEMRADLVR        0.4197       533.1                 2.00     Sequence
      IAd  166  GNSVTQTAAVIGTAQ  QTAAVIGTA        0.4140       567.2                 2.00     Sequence
      IAd  107  GPMTPKRAIEVIADA  RAIEVIADA        0.4138       568.3                 2.00     Sequence
      IAd  165  SGNSVTQTAAVIGTA  QTAAVIGTA        0.4088       599.7                 2.00     Sequence
      IAd  263  QTAAEMRADLVRVHN  AEMRADLVR        0.4081       604.7                 2.00     Sequence
      IAd  168  SVTQTAAVIGTAQYL  QTAAVIGTA        0.4021       645.2                 4.00     Sequence
      IAd  334  VVAVLAVLTVVVTIA  VAVLAVLTV        0.3978       675.7                 4.00     Sequence
      IAd  265  AAEMRADLVRVHNGE  EMRADLVRV        0.3861       766.5                 4.00     Sequence
      IAd  256  KNPENRYQTAAEMRA  YQTAAEMRA        0.3818       803.4                 4.00     Sequence
      IAd  434  LTYAEAVKKLTAAGF  LTYAEAVKK        0.3788       829.9                 4.00     Sequence
      IAd  364  VRGQSSADAIATLQN  QSSADAIAT        0.3783       833.9                 4.00     Sequence
      IAd  110  TPKRAIEVIADACQA  RAIEVIADA        0.3747       867.3                 4.00     Sequence
      IAd  169  VTQTAAVIGTAQYLS  QTAAVIGTA        0.3746       868.6                 4.00     Sequence
      IAd  323  RSIGSVGRWVAVVAV  GRWVAVVAV        0.3674       939.0                 4.00     Sequence
      IAd  266  AEMRADLVRVHNGEP  EMRADLVRV        0.3594      1023.8                 4.00     Sequence
      IAd  145  ISATNAVKVMDFGIA  ISATNAVKV        0.3586      1032.9                 4.00     Sequence
      IAd  324  SIGSVGRWVAVVAVL  GRWVAVVAV        0.3563      1058.4                 4.00     Sequence
      IAd  363  DVRGQSSADAIATLQ  QSSADAIAT        0.3550      1073.0                 4.00     Sequence
      IAd  139  KPANIMISATNAVKV  PANIMISAT        0.3497      1136.6                 8.00     Sequence
      IAd  111  PKRAIEVIADACQAL  KRAIEVIAD        0.3474      1165.9                 8.00     Sequence
      IAd   21  MSEVHLARDLRLHRD  VHLARDLRL        0.3473      1166.4                 8.00     Sequence
      IAd  335  VAVLAVLTVVVTIAI  VAVLAVLTV        0.3468      1173.3                 8.00     Sequence
      IAd  516  FTKFSQASVDSPRPA  QASVDSPRP        0.3441      1207.3                 8.00     Sequence
      IAd  240  EGLSADLDAVVLKAL  LDAVVLKAL        0.3427      1226.5                 8.00     Sequence
      IAd   22  SEVHLARDLRLHRDV  VHLARDLRL        0.3425      1229.7                 8.00     Sequence
      IAd   33  HRDVAVKVLRADLAR  HRDVAVKVL        0.3405      1255.6                 8.00     Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAd | 23 | EVHLARDLRLHRDVA | VHLARDLRL | 0.3393 | 1272.7 | 8.00 | Sequence |
| IAd | 170 | TQTAAVIGTAQYLSP | QTAAVIGTA | 0.3389 | 1277.7 | 8.00 | Sequence |
| IAd | 362 | PDVRGQSSADAIATL | QSSADAIAT | 0.3364 | 1312.6 | 8.00 | Sequence |
| IAd | 241 | GLSADLDAVVLKALA | LDAVVLKAL | 0.3358 | 1322.0 | 8.00 | Sequence |
| IAd | 431 | VSTLTYAEAVKKLTA | LTYAEAVKK | 0.3329 | 1364.1 | 8.00 | Sequence |
| IAd | 517 | TKFSQASVDSPRPAG | QASVDSPRP | 0.3327 | 1365.9 | 8.00 | Sequence |
| IAd | 24 | VHLARDLRLHRDVAV | VHLARDLRL | 0.3305 | 1399.4 | 8.00 | Sequence |
| IAd | 25 | HLARDLRLHRDVAVK | ARDLRLHRD | 0.3283 | 1432.4 | 8.00 | Sequence |
| IAd | 148 | TNAVKVMDFGIARAI | VMDFGIARA | 0.3280 | 1437.3 | 8.00 | Sequence |
| IAd | 433 | TLTYAEAVKKLTAAG | EAVKKLTAA | 0.3258 | 1473.0 | 8.00 | Sequence |
| IAd | 106 | EGPMTPKRAIEVIAD | KRAIEVIAD | 0.3236 | 1507.6 | 8.00 | Sequence |
| IAd | 140 | PANIMISATNAVKVM | ISATNAVKV | 0.3190 | 1585.5 | 8.00 | Sequence |
| IAd | 437 | AEAVKKLTAAGFGRF | AEAVKKLTA | 0.3168 | 1622.8 | 8.00 | Sequence |
| IAd | 144 | MISATNAVKVMDFGI | ISATNAVKV | 0.3167 | 1625.6 | 8.00 | Sequence |
| IAd | 429 | PDVSTLTYAEAVKKL | VSTLTYAEA | 0.3158 | 1640.3 | 8.00 | Sequence |
| IAd | 365 | RGQSSADAIATLQNR | QSSADAIAT | 0.3138 | 1676.0 | 8.00 | Sequence |
| IAd | 435 | TYAEAVKKLTAAGFG | AEAVKKLTA | 0.3129 | 1693.1 | 8.00 | Sequence |
| IAd | 143 | IMISATNAVKVMDFG | ISATNAVKV | 0.3116 | 1716.9 | 8.00 | Sequence |
| IAd | 361 | VPDVRGQSSADAIAT | QSSADAIAT | 0.3115 | 1719.8 | 8.00 | Sequence |
| IAd | 403 | PAANTSVSAGDEITV | PAANTSVSA | 0.3102 | 1744.0 | 8.00 | Sequence |
| IAd | 430 | DVSTLTYAEAVKKLT | VSTLTYAEA | 0.3089 | 1767.8 | 8.00 | Sequence |
| IAd | 518 | KFSQASVDSPRPAGE | QASVDSPRP | 0.3081 | 1783.1 | 8.00 | Sequence |
| IAd | 267 | EMRADLVRVHNGEPP | EMRADLVRV | 0.3080 | 1785.7 | 8.00 | Sequence |
| IAd | 432 | STLTYAEAVKKLTAA | AEAVKKLTA | 0.3026 | 1893.0 | 8.00 | Sequence |
| IAd | 428 | IPDVSTLTYAEAVKK | LTYAEAVKK | 0.3020 | 1905.9 | 8.00 | Sequence |
| IAd | 242 | LSADLDAVVLKALAK | LDAVVLKAL | 0.3007 | 1931.1 | 16.00 | Sequence |
| IAd | 142 | NIMISATNAVKVMDF | ISATNAVKV | 0.2988 | 1971.3 | 16.00 | Sequence |
| IAd | 147 | ATNAVKVMDFGIARA | VMDFGIARA | 0.2932 | 2095.8 | 16.00 | Sequence |
| IAd | 515 | GFTKFSQASVDSPRP | KFSQASVDS | 0.2932 | 2096.3 | 16.00 | Sequence |
| IAd | 322 | DRSIGSVGRWVAVVA | VGRWVAVVA | 0.2897 | 2175.7 | 16.00 | Sequence |
| IAd | 36 | VAVKVLRADLARDPS | VKVLRADLA | 0.2892 | 2187.2 | 16.00 | Sequence |
| IAd | 565 | LSGMFWVDAEPRLRA | VDAEPRLRA | 0.2891 | 2189.6 | 16.00 | Sequence |
| IAd | 436 | YAEAVKKLTAAGFGR | AEAVKKLTA | 0.2889 | 2194.1 | 16.00 | Sequence |
| IAd | 35 | DVAVKVLRADLARDP | DVAVKVLRA | 0.2885 | 2204.0 | 16.00 | Sequence |
| IAd | 62 | AAALNHPAIVAVYDT | LNHPAIVAV | 0.2884 | 2206.9 | 16.00 | Sequence |
| IAd | 65 | LNHPAIVAVYDTGEA | PAIVAVYDT | 0.2834 | 2330.2 | 16.00 | Sequence |
| IAd | 290 | AERTSLLSSAAGNLS | ERTSLLSSA | 0.2820 | 2364.0 | 16.00 | Sequence |
| IAd | 171 | QTAAVIGTAQYLSPE | QTAAVIGTA | 0.2809 | 2394.6 | 16.00 | Sequence |
| IAd | 243 | SADLDAVVLKALAKN | LDAVVLKAL | 0.2807 | 2399.5 | 16.00 | Sequence |
| IAd | 438 | EAVKKLTAAGFGRFK | EAVKKLTAA | 0.2807 | 2399.8 | 16.00 | Sequence |
| IAd | 55 | FRREAQNAAALNHPA | REAQNAAAL | 0.2795 | 2429.7 | 16.00 | Sequence |
| IAd | 538 | PPAGTTVPVDSVIEL | PPAGTTVPV | 0.2791 | 2439.9 | 16.00 | Sequence |
| IAd | 425 | QREIPDVSTLTYAEA | VSTLTYAEA | 0.2782 | 2465.0 | 16.00 | Sequence |
| IAd | 63 | AALNHPAIVAVYDTG | PAIVAVYDT | 0.2774 | 2486.3 | 16.00 | Sequence |
| IAd | 112 | KRAIEVIADACQALN | KRAIEVIAD | 0.2754 | 2539.8 | 16.00 | Sequence |
| IAd | 366 | GQSSADAIATLQNRG | QSSADAIAT | 0.2754 | 2540.5 | 16.00 | Sequence |
| IAd | 133 | IIHRDVKPANIMISA | KPANIMISA | 0.2752 | 2545.6 | 16.00 | Sequence |
| IAd | 64 | ALNHPAIVAVYDTGE | PAIVAVYDT | 0.2742 | 2573.4 | 16.00 | Sequence |
| IAd | 136 | RDVKPANIMISATNA | VKPANIMIS | 0.2726 | 2617.6 | 16.00 | Sequence |
| IAd | 289 | DAERTSLLSSAAGNL | ERTSLLSSA | 0.2718 | 2641.1 | 16.00 | Sequence |
| IAd | 338 | LAVLTVVVTIAINTF | LAVLTVVVT | 0.2718 | 2642.5 | 16.00 | Sequence |
| IAd | 244 | ADLDAVVLKALAKNP | LDAVVLKAL | 0.2710 | 2664.4 | 16.00 | Sequence |
| IAd | 137 | DVKPANIMISATNAV | KPANIMISA | 0.2696 | 2705.1 | 16.00 | Sequence |
| IAd | 135 | HRDVKPANIMISATN | KPANIMISA | 0.2693 | 2714.3 | 16.00 | Sequence |
| IAd | 56 | RREAQNAAALNHPAI | RREAQNAAA | 0.2685 | 2737.0 | 16.00 | Sequence |
| IAd | 288 | TDAERTSLLSSAAGN | ERTSLLSSA | 0.2682 | 2744.8 | 16.00 | Sequence |
| IAd | 367 | QSSADAIATLQNRGF | QSSADAIAT | 0.2678 | 2757.4 | 16.00 | Sequence |
| IAd | 566 | SGMFWVDAEPRLRAL | VDAEPRLRA | 0.2670 | 2783.2 | 16.00 | Sequence |
| IAd | 519 | FSQASVDSPRPAGEV | QASVDSPRP | 0.2667 | 2790.8 | 16.00 | Sequence |
| IAd | 164 | DSGNSVTQTAAVIGT | TQTAAVIGT | 0.2664 | 2800.3 | 16.00 | Sequence |
| IAd | 138 | VKPANIMISATNAVK | VKPANIMIS | 0.2662 | 2804.6 | 16.00 | Sequence |
| IAd | 134 | IHRDVKPANIMISAT | KPANIMISA | 0.2662 | 2807.0 | 16.00 | Sequence |
| IAd | 319 | TDRDRSIGSVGRWVA | RSIGSVGRW | 0.2659 | 2814.2 | 16.00 | Sequence |
| IAd | 317 | DDTDRDRSIGSVGRW | RSIGSVGRW | 0.2649 | 2844.8 | 16.00 | Sequence |
| IAd | 318 | DTDRDRSIGSVGRWV | RSIGSVGRW | 0.2634 | 2891.9 | 16.00 | Sequence |
| IAd | 426 | REIPDVSTLTYAEAV | VSTLTYAEA | 0.2611 | 2966.4 | 16.00 | Sequence |

|  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|
| IAd | 401 | TDPAANTSVSAGDEI | PAANTSVSA | 0.2607 | 2977.8 | 16.00 | Sequence |
| IAd | 54 | RFRREAQNAAALNHP | REAQNAAAL | 0.2606 | 2981.5 | 16.00 | Sequence |
| IAd | 287 | LTDAERTSLLSSAAG | ERTSLLSSA | 0.2604 | 2987.3 | 16.00 | Sequence |
| IAd | 402 | DPAANTSVSAGDEIT | PAANTSVSA | 0.2594 | 3019.4 | 16.00 | Sequence |
| IAd | 291 | ERTSLLSSAAGNLSG | ERTSLLSSA | 0.2594 | 3020.7 | 16.00 | Sequence |
| IAd | 34 | RDVAVKVLRADLARD | DVAVKVLRA | 0.2586 | 3045.4 | 16.00 | Sequence |
| IAd | 149 | NAVKVMDFGIARAIA | VKVMDFGIA | 0.2582 | 3061.2 | 16.00 | Sequence |
| IAd | 400 | GTDPAANTSVSAGDE | PAANTSVSA | 0.2571 | 3096.2 | 16.00 | Sequence |
| IAd | 245 | DLDAVVLKALAKNPE | LDAVVLKAL | 0.2566 | 3113.6 | 16.00 | Sequence |
| IAd | 399 | IGTDPAANTSVSAGD | PAANTSVSA | 0.2540 | 3201.3 | 16.00 | Sequence |
| IAd | 141 | ANIMISATNAVKVMD | ISATNAVKV | 0.2536 | 3215.1 | 16.00 | Sequence |
| IAd | 60 | QNAAALNHPAIVAVY | LNHPAIVAV | 0.2530 | 3235.2 | 16.00 | Sequence |
| IAd | 286 | VLTDAERTSLLSSAA | ERTSLLSSA | 0.2528 | 3245.5 | 16.00 | Sequence |
| IAd | 536 | TNPPAGTTVPVDSVI | PPAGTTVPV | 0.2524 | 3259.0 | 16.00 | Sequence |
| IAd | 336 | AVLAVLTVVVTIAIN | AVLAVLTVV | 0.2521 | 3267.8 | 16.00 | Sequence |
| IAd | 535 | GTNPPAGTTVPVDSV | PPAGTTVPV | 0.2521 | 3267.9 | 16.00 | Sequence |
| IAd | 18 | FGGMSEVHLARDLRL | VHLARDLRL | 0.2506 | 3321.8 | 16.00 | Sequence |
| IAd | 66 | NHPAIVAVYDTGEAE | PAIVAVYDT | 0.2503 | 3334.5 | 16.00 | Sequence |
| IAd | 61 | NAAALNHPAIVAVYD | LNHPAIVAV | 0.2502 | 3337.6 | 16.00 | Sequence |
| IAd | 537 | NPPAGTTVPVDSVIE | AGTTVPVDS | 0.2484 | 3400.8 | 16.00 | Sequence |
| IAd | 37 | AVKVLRADLARDPSF | VKVLRADLA | 0.2477 | 3428.5 | 16.00 | Sequence |
| IAd | 20 | GMSEVHLARDLRLHR | VHLARDLRL | 0.2475 | 3434.0 | 16.00 | Sequence |
| IAd | 398 | VIGTDPAANTSVSAG | PAANTSVSA | 0.2435 | 3586.1 | 32.00 | Sequence |
| IAd | 105 | TEGPMTPKRAIEVIA | EGPMTPKRA | 0.2428 | 3613.1 | 32.00 | Sequence |
| IAd | 57 | REAQNAAALNHPAIV | REAQNAAAL | 0.2392 | 3756.8 | 32.00 | Sequence |
| IAd | 19 | GGMSEVHLARDLRLH | VHLARDLRL | 0.2384 | 3789.2 | 32.00 | Sequence |
| IAd | 562 | MPDLSGMFWVDAEPR | LSGMFWVDA | 0.2376 | 3822.4 | 32.00 | Sequence |
| IAd | 146 | SATNAVKVMDFGIAR | VKVMDFGIA | 0.2353 | 3918.7 | 32.00 | Sequence |
| IAd | 539 | PAGTTVPVDSVIELQ | GTTVPVDSV | 0.2339 | 3982.0 | 32.00 | Sequence |
| IAd | 239 | HEGLSADLDAVVLKA | DLDAVVLKA | 0.2326 | 4036.2 | 32.00 | Sequence |
| IAd | 320 | DRDRSIGSVGRWVAV | RSIGSVGRW | 0.2311 | 4102.4 | 32.00 | Sequence |
| IAd | 246 | LDAVVLKALAKNPEN | LDAVVLKAL | 0.2296 | 4169.2 | 32.00 | Sequence |
| IAd | 150 | AVKVMDFGIARAIAD | VKVMDFGIA | 0.2283 | 4226.8 | 32.00 | Sequence |
| IAd | 285 | KVLTDAERTSLLSSA | ERTSLLSSA | 0.2280 | 4240.1 | 32.00 | Sequence |
| IAd | 609 | AGTGVNRDGIITLRF | VNRDGIITL | 0.2269 | 4294.5 | 32.00 | Sequence |
| IAd | 564 | DLSGMFWVDAEPRLR | MFWVDAEPR | 0.2267 | 4302.6 | 32.00 | Sequence |
| IAd | 103 | VHTEGPMTPKRAIEV | VHTEGPMTP | 0.2265 | 4311.8 | 32.00 | Sequence |
| IAd | 59 | AQNAAALNHPAIVAV | LNHPAIVAV | 0.2265 | 4312.2 | 32.00 | Sequence |
| IAd | 280 | PPEAPKVLTDAERTS | KVLTDAERT | 0.2264 | 4314.9 | 32.00 | Sequence |
| IAd | 53 | LRFRREAQNAAALNH | RREAQNAAA | 0.2251 | 4377.3 | 32.00 | Sequence |
| IAd | 281 | PEAPKVLTDAERTSL | KVLTDAERT | 0.2249 | 4389.3 | 32.00 | Sequence |
| IAd | 611 | TGVNRDGIITLRFGQ | VNRDGIITL | 0.2240 | 4428.9 | 32.00 | Sequence |
| IAd | 337 | VLAVLTVVVTIAINT | LAVLTVVVT | 0.2237 | 4446.2 | 32.00 | Sequence |
| IAd | 124 | ALNFSHQNGIIHRDV | SHQNGIIHR | 0.2230 | 4478.8 | 32.00 | Sequence |
| IAd | 321 | RDRSIGSVGRWVAVV | RSIGSVGRW | 0.2230 | 4479.8 | 32.00 | Sequence |
| IAd | 520 | SQASVDSPRPAGEVT | QASVDSPRP | 0.2224 | 4506.2 | 32.00 | Sequence |
| IAd | 610 | GTGVNRDGIITLRFG | VNRDGIITL | 0.2211 | 4571.7 | 32.00 | Sequence |
| IAd | 404 | AANTSVSAGDEITVN | AANTSVSAG | 0.2210 | 4575.0 | 32.00 | Sequence |
| IAd | 17 | GFGGMSEVHLARDLR | FGGMSEVHL | 0.2206 | 4595.1 | 32.00 | Sequence |
| IAd | 557 | GNQFVMPDLSGMFWV | GNQFVMPDL | 0.2206 | 4595.7 | 32.00 | Sequence |
| IAd | 237 | ARHEGLSADLDAVVL | RHEGLSADL | 0.2198 | 4634.4 | 32.00 | Sequence |
| IAd | 556 | KGNQFVMPDLSGMFW | GNQFVMPDL | 0.2191 | 4670.7 | 32.00 | Sequence |
| IAd | 427 | EIPDVSTLTYAEAVK | VSTLTYAEA | 0.2184 | 4704.2 | 32.00 | Sequence |
| IAd | 582 | WTGMLDKGADVDAGG | DKGADVDAG | 0.2183 | 4712.2 | 32.00 | Sequence |
| IAd | 521 | QASVDSPRPAGEVTG | ASVDSPRPA | 0.2176 | 4748.3 | 32.00 | Sequence |
| IAd | 581 | GWTGMLDKGADVDAG | WTGMLDKGA | 0.2168 | 4790.2 | 32.00 | Sequence |
| IAd | 514 | YGFTKFSQASVDSPR | KFSQASVDS | 0.2159 | 4836.2 | 32.00 | Sequence |
| IAd | 567 | GMFWVDAEPRLRALG | VDAEPRLRA | 0.2154 | 4861.6 | 32.00 | Sequence |
| IAd | 522 | ASVDSPRPAGEVTGT | ASVDSPRPA | 0.2148 | 4893.4 | 32.00 | Sequence |
| IAd | 123 | QALNFSHQNGIIHRD | SHQNGIIHR | 0.2148 | 4893.6 | 32.00 | Sequence |
| IAd | 125 | LNFSHQNGIIHRDVK | SHQNGIIHR | 0.2147 | 4898.9 | 32.00 | Sequence |
| IAd | 563 | PDLSGMFWVDAEPRL | MFWVDAEPR | 0.2140 | 4934.5 | 32.00 | Sequence |
| IAd | 544 | VPVDSVIELQVSKGN | DSVIELQVS | 0.2138 | 4945.8 | 32.00 | Sequence |
| IAd | 397 | HVIGTDPAANTSVSA | PAANTSVSA | 0.2132 | 4978.5 | 32.00 | Sequence |
| IAd | 38 | VKVLRADLARDPSFY | VKVLRADLA | 0.2125 | 5018.6 | 32.00 | Sequence |
| IAd | 127 | FSHQNGIIHRDVKPA | SHQNGIIHR | 0.2116 | 5067.4 | 32.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAd | 16 | LGFGGMSEVHLARDL | FGGMSEVHL | 0.2115 | 5073.4 | 32.00 | Sequence |
| IAd | 193 | DARSDVYSLGCVLYE | YSLGCVLYE | 0.2089 | 5218.9 | 32.00 | Sequence |
| IAd | 543 | TVPVDSVIELQVSKG | DSVIELQVS | 0.2086 | 5233.1 | 32.00 | Sequence |
| IAd | 279 | EPPEAPKVLTDAERT | KVLTDAERT | 0.2082 | 5257.4 | 32.00 | Sequence |
| IAd | 113 | RAIEVIADACQALNF | RAIEVIADA | 0.2081 | 5260.0 | 32.00 | Sequence |
| IAd | 15 | ILGFGGMSEVHLARD | FGGMSEVHL | 0.2078 | 5278.0 | 32.00 | Sequence |
| IAd | 282 | EAPKVLTDAERTSLL | KVLTDAERT | 0.2066 | 5349.6 | 32.00 | Sequence |
| IAd | 85 | PLPYIVMEYVDGVTL | MEYVDGVTL | 0.2050 | 5440.5 | 32.00 | Sequence |
| IAd | 235 | PSARHEGLSADLDAV | SARHEGLSA | 0.2043 | 5482.2 | 32.00 | Sequence |
| IAd | 236 | SARHEGLSADLDAVV | SARHEGLSA | 0.2041 | 5491.5 | 32.00 | Sequence |
| IAd | 568 | MFWVDAEPRLRALGW | VDAEPRLRA | 0.2037 | 5516.4 | 32.00 | Sequence |
| IAd | 339 | AVLTVVVTIAINTFG | VLTVVVTIA | 0.2033 | 5544.9 | 32.00 | Sequence |
| IAd | 238 | RHEGLSADLDAVVLK | RHEGLSADL | 0.2031 | 5555.1 | 32.00 | Sequence |
| IAd | 151 | VKVMDFGIARAIADS | VKVMDFGIA | 0.2018 | 5629.7 | 32.00 | Sequence |
| IAd | 268 | MRADLVRVHNGEPPE | MRADLVRVH | 0.2016 | 5647.2 | 32.00 | Sequence |
| IAd | 423 | PEQREIPDVSTLTYA | PEQREIPDV | 0.2006 | 5705.2 | 32.00 | Sequence |
| IAd | 104 | HTEGPMTPKRAIEVI | MTPKRAIEV | 0.2004 | 5719.0 | 32.00 | Sequence |
| IAd | 126 | NFSHQNGIIHRDVKP | SHQNGIIHR | 0.1991 | 5797.1 | 32.00 | Sequence |
| IAd | 128 | SHQNGIIHRDVKPAN | SHQNGIIHR | 0.1985 | 5839.0 | 32.00 | Sequence |
| IAd | 353 | GGITRDVQVPDVRGQ | TRDVQVPDV | 0.1984 | 5841.6 | 32.00 | Sequence |
| IAd | 541 | GTTVPVDSVIELQVS | VPVDSVIEL | 0.1979 | 5873.4 | 32.00 | Sequence |
| IAd | 534 | TGTNPPAGTTVPVDS | AGTTVPVDS | 0.1973 | 5913.5 | 32.00 | Sequence |
| IAd | 284 | PKVLTDAERTSLLSS | AERTSLLSS | 0.1967 | 5953.5 | 32.00 | Sequence |
| IAd | 86 | LPYIVMEYVDGVTLR | MEYVDGVTL | 0.1961 | 5994.0 | 32.00 | Sequence |
| IAd | 545 | PVDSVIELQVSKGNQ | DSVIELQVS | 0.1955 | 6028.5 | 32.00 | Sequence |
| IAd | 352 | FGGITRDVQVPDVRG | TRDVQVPDV | 0.1949 | 6066.4 | 32.00 | Sequence |
| IAd | 561 | VMPDLSGMFWVDAEP | LSGMFWVDA | 0.1948 | 6075.8 | 32.00 | Sequence |
| IAd | 360 | QVPDVRGQSSADAIA | VRGQSSADA | 0.1948 | 6075.9 | 32.00 | Sequence |
| IAd | 424 | EQREIPDVSTLTYAE | REIPDVSTL | 0.1942 | 6115.3 | 32.00 | Sequence |
| IAd | 343 | VVVTIAINTFGGITR | VVTIAINTF | 0.1934 | 6167.4 | 32.00 | Sequence |
| IAd | 422 | GPEQREIPDVSTLTY | PEQREIPDV | 0.1925 | 6229.3 | 32.00 | Sequence |
| IAd | 7 | SDRYELGEILGFGGM | SDRYELGEI | 0.1924 | 6233.0 | 32.00 | Sequence |
| IAd | 82 | PAGPLPYIVMEYVDG | YIVMEYVDG | 0.1921 | 6257.2 | 32.00 | Sequence |
| IAd | 351 | TFGGITRDVQVPDVR | TRDVQVPDV | 0.1920 | 6261.1 | 32.00 | Sequence |
| IAd | 192 | VDARSDVYSLGCVLY | DARSDVYSL | 0.1920 | 6262.9 | 32.00 | Sequence |
| IAd | 560 | FVMPDLSGMFWVDAE | LSGMFWVDA | 0.1908 | 6346.9 | 32.00 | Sequence |
| IAd | 407 | TSVSAGDEITVNVST | VSAGDEITV | 0.1906 | 6356.1 | 32.00 | Sequence |
| IAd | 292 | RTSLLSSAAGNLSGP | RTSLLSSAA | 0.1900 | 6399.4 | 32.00 | Sequence |
| IAd | 540 | AGTTVPVDSVIELQV | GTTVPVDSV | 0.1899 | 6407.9 | 32.00 | Sequence |
| IAd | 101 | DIVHTEGPMTPKRAI | VHTEGPMTP | 0.1896 | 6430.3 | 32.00 | Sequence |
| IAd | 58 | EAQNAAALNHPAIVA | NAAALNHPA | 0.1895 | 6434.4 | 32.00 | Sequence |
| IAd | 498 | DVAGQTVDVAQKNLN | GQTVDVAQK | 0.1887 | 6492.0 | 32.00 | Sequence |
| IAd | 546 | VDSVIELQVSKGNQF | DSVIELQVS | 0.1881 | 6535.0 | 32.00 | Sequence |
| IAd | 584 | GMLDKGADVDAGGSQ | DKGADVDAG | 0.1878 | 6554.2 | 32.00 | Sequence |
| IAd | 408 | SVSAGDEITVNVSTG | VSAGDEITV | 0.1874 | 6581.0 | 32.00 | Sequence |
| IAd | 368 | SSADAIATLQNRGFK | ADAIATLQN | 0.1873 | 6588.4 | 32.00 | Sequence |
| IAd | 52 | YLRFRREAQNAAALN | RREAQNAAA | 0.1851 | 6748.6 | 32.00 | Sequence |
| IAd | 499 | VAGQTVDVAQKNLNV | GQTVDVAQK | 0.1847 | 6774.9 | 32.00 | Sequence |
| IAd | 350 | NTFGGITRDVQVPDV | TRDVQVPDV | 0.1845 | 6790.3 | 32.00 | Sequence |
| IAd | 586 | LDKGADVDAGGSQHN | DKGADVDAG | 0.1843 | 6805.6 | 32.00 | Sequence |
| IAd | 559 | QFVMPDLSGMFWVDA | LSGMFWVDA | 0.1839 | 6837.2 | 32.00 | Sequence |
| IAd | 359 | VQVPDVRGQSSADAI | VRGQSSADA | 0.1839 | 6838.6 | 32.00 | Sequence |
| IAd | 354 | GITRDVQVPDVRGQS | TRDVQVPDV | 0.1836 | 6859.1 | 32.00 | Sequence |
| IAd | 100 | RDIVHTEGPMTPKRA | VHTEGPMTP | 0.1834 | 6874.2 | 32.00 | Sequence |
| IAd | 497 | PDVAGQTVDVAQKNL | GQTVDVAQK | 0.1830 | 6899.7 | 32.00 | Sequence |
| IAd | 583 | TGMLDKGADVDAGGS | LDKGADVDA | 0.1821 | 6970.0 | 32.00 | Sequence |
| IAd | 608 | PAGTGVNRDGIITLR | VNRDGIITL | 0.1810 | 7057.5 | 32.00 | Sequence |
| IAd | 406 | NTSVSAGDEITVNVS | VSAGDEITV | 0.1808 | 7066.7 | 32.00 | Sequence |
| IAd | 6 | LSDRYELGEILGFGG | YELGEILGF | 0.1807 | 7078.5 | 32.00 | Sequence |
| IAd | 186 | QARGDSVDARSDVYS | QARGDSVDA | 0.1805 | 7092.8 | 32.00 | Sequence |
| IAd | 571 | VDAEPRLRALGWTGM | VDAEPRLRA | 0.1793 | 7184.3 | 32.00 | Sequence |
| IAd | 83 | AGPLPYIVMEYVDGV | YIVMEYVDG | 0.1781 | 7275.5 | 50.00 | Sequence |
| IAd | 513 | VYGFTKFSQASVDSP | KFSQASVDS | 0.1768 | 7380.1 | 50.00 | Sequence |
| IAd | 496 | IPDVAGQTVDVAQKN | GQTVDVAQK | 0.1760 | 7450.5 | 50.00 | Sequence |
| IAd | 439 | AVKKLTAAGFGRFKQ | VKKLTAAGF | 0.1756 | 7476.0 | 50.00 | Sequence |
| IAd | 4 | SHLSDRYELGEILGF | YELGEILGF | 0.1754 | 7492.3 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAd | 473 | ANQTSAITNVVIIIV | ANQTSAITN | 0.1751 | 7516.9 | 50.00 | Sequence |
| IAd | 39 | KVLRADLARDPSFYL | LRADLARDP | 0.1746 | 7558.1 | 50.00 | Sequence |
| IAd | 269 | RADLVRVHNGEPPEA | VHNGEPPEA | 0.1740 | 7608.4 | 50.00 | Sequence |
| IAd | 40 | VLRADLARDPSFYLR | RADLARDPS | 0.1740 | 7608.8 | 50.00 | Sequence |
| IAd | 222 | SVAYQHVREDPIPPS | VREDPIPPS | 0.1738 | 7622.1 | 50.00 | Sequence |
| IAd | 80 | ETPAGPLPYIVMEYV | LPYIVMEYV | 0.1738 | 7628.0 | 50.00 | Sequence |
| IAd | 585 | MLDKGADVDAGGSQH | LDKGADVDA | 0.1737 | 7634.8 | 50.00 | Sequence |
| IAd | 505 | DVAQKNLNVYGFTKF | QKNLNVYGF | 0.1735 | 7646.5 | 50.00 | Sequence |
| IAd | 14 | EILGFGGMSEVHLAR | GGMSEVHLA | 0.1734 | 7657.4 | 50.00 | Sequence |
| IAd | 195 | RSDVYSLGCVLYEVL | YSLGCVLYE | 0.1722 | 7757.4 | 50.00 | Sequence |
| IAd | 555 | SKGNQFVMPDLSGMF | GNQFVMPDL | 0.1720 | 7774.8 | 50.00 | Sequence |
| IAd | 223 | VAYQHVREDPIPPSA | VREDPIPPS | 0.1715 | 7819.6 | 50.00 | Sequence |
| IAd | 409 | VSAGDEITVNVSTGP | VSAGDEITV | 0.1714 | 7824.1 | 50.00 | Sequence |
| IAd | 547 | DSVIELQVSKGNQFV | DSVIELQVS | 0.1707 | 7882.8 | 50.00 | Sequence |
| IAd | 523 | SVDSPRPAGEVTGTN | RPAGEVTGT | 0.1706 | 7896.5 | 50.00 | Sequence |
| IAd | 132 | GIIHRDVKPANIMIS | VKPANIMIS | 0.1703 | 7916.4 | 50.00 | Sequence |
| IAd | 476 | TSAITNVVIIIVGSG | ITNVVIIIV | 0.1698 | 7961.9 | 50.00 | Sequence |
| IAd | 344 | VVTIAINTFGGITRD | INTFGGITR | 0.1685 | 8079.5 | 50.00 | Sequence |
| IAd | 81 | TPAGPLPYIVMEYVD | LPYIVMEYV | 0.1682 | 8100.9 | 50.00 | Sequence |
| IAd | 5 | HLSDRYELGEILGFG | YELGEILGF | 0.1681 | 8109.8 | 50.00 | Sequence |
| IAd | 471 | PPANQTSAITNVVII | ANQTSAITN | 0.1680 | 8124.0 | 50.00 | Sequence |
| IAd | 91 | MEYVDGVTLRDIVHT | MEYVDGVTL | 0.1674 | 8174.5 | 50.00 | Sequence |
| IAd | 196 | SDVYSLGCVLYEVLT | YSLGCVLYE | 0.1672 | 8188.4 | 50.00 | Sequence |
| IAd | 255 | AKNPENRYQTAAEMR | RYQTAAEMR | 0.1667 | 8231.0 | 50.00 | Sequence |
| IAd | 554 | VSKGNQFVMPDLSGM | GNQFVMPDL | 0.1666 | 8239.9 | 50.00 | Sequence |
| IAd | 84 | GPLPYIVMEYVDGVT | YIVMEYVDG | 0.1637 | 8506.7 | 50.00 | Sequence |
| IAd | 569 | FWVDAEPRLRALGWT | VDAEPRLRA | 0.1636 | 8517.9 | 50.00 | Sequence |
| IAd | 200 | SLGCVLYEVLTGEPP | YEVLTGEPP | 0.1633 | 8538.8 | 50.00 | Sequence |
| IAd | 184 | PEQARGDSVDARSDV | QARGDSVDA | 0.1631 | 8563.0 | 50.00 | Sequence |
| IAd | 97 | VTLRDIVHTEGPMTP | VTLRDIVHT | 0.1629 | 8580.7 | 50.00 | Sequence |
| IAd | 102 | IVHTEGPMTPKRAIE | VHTEGPMTP | 0.1625 | 8619.3 | 50.00 | Sequence |
| IAd | 51 | FYLRFRREAQNAAAL | RREAQNAAA | 0.1622 | 8646.7 | 50.00 | Sequence |
| IAd | 234 | PPSARHEGLSADLDA | SARHEGLSA | 0.1616 | 8702.3 | 50.00 | Sequence |
| IAd | 580 | LGWTGMLDKGADVDA | WTGMLDKGA | 0.1615 | 8712.7 | 50.00 | Sequence |
| IAd | 576 | RLRALGWTGMLDKGA | LRALGWTGM | 0.1615 | 8714.3 | 50.00 | Sequence |
| IAd | 67 | HPAIVAVYDTGEAET | PAIVAVYDT | 0.1613 | 8725.5 | 50.00 | Sequence |
| IAd | 190 | DSVDARSDVYSLGCV | DARSDVYSL | 0.1613 | 8728.4 | 50.00 | Sequence |
| IAd | 542 | TTVPVDSVIELQVSK | VPVDSVIEL | 0.1607 | 8787.5 | 50.00 | Sequence |
| IAd | 187 | ARGDSVDARSDVYSL | DARSDVYSL | 0.1606 | 8795.2 | 50.00 | Sequence |
| IAd | 570 | WVDAEPRLRALGWTG | VDAEPRLRA | 0.1603 | 8824.7 | 50.00 | Sequence |
| IAd | 340 | VLTVVVTIAINTFGG | LTVVVTIAI | 0.1600 | 8858.5 | 50.00 | Sequence |
| IAd | 421 | TGPEQREIPDVSTLT | QREIPDVST | 0.1592 | 8934.2 | 50.00 | Sequence |
| IAd | 341 | LTVVVTIAINTFGGI | LTVVVTIAI | 0.1591 | 8937.1 | 50.00 | Sequence |
| IAd | 358 | DVQVPDVRGQSSADA | VRGQSSADA | 0.1582 | 9027.2 | 50.00 | Sequence |
| IAd | 75 | DTGEAETPAGPLPYI | TGEAETPAG | 0.1577 | 9074.1 | 50.00 | Sequence |
| IAd | 278 | GEPPEAPKVLTDAER | PKVLTDAER | 0.1571 | 9137.4 | 50.00 | Sequence |
| IAd | 283 | APKVLTDAERTSLLS | PKVLTDAER | 0.1570 | 9149.6 | 50.00 | Sequence |
| IAd | 163 | ADSGNSVTQTAAVIG | VTQTAAVIG | 0.1567 | 9172.3 | 50.00 | Sequence |
| IAd | 201 | LGCVLYEVLTGEPPF | YEVLTGEPP | 0.1566 | 9188.4 | 50.00 | Sequence |
| IAd | 188 | RGDSVDARSDVYSLG | DARSDVYSL | 0.1558 | 9263.4 | 50.00 | Sequence |
| IAd | 152 | KVMDFGIARAIADSG | VMDFGIARA | 0.1558 | 9266.5 | 50.00 | Sequence |
| IAd | 214 | PFTGDSPVSVAYQHV | FTGDSPVSV | 0.1555 | 9291.2 | 50.00 | Sequence |
| IAd | 215 | FTGDSPVSVAYQHVR | FTGDSPVSV | 0.1555 | 9296.0 | 50.00 | Sequence |
| IAd | 185 | EQARGDSVDARSDVY | QARGDSVDA | 0.1555 | 9297.3 | 50.00 | Sequence |
| IAd | 533 | VTGTNPPAGTTVPVD | PPAGTTVPV | 0.1553 | 9313.8 | 50.00 | Sequence |
| IAd | 197 | DVYSLGCVLYEVLTG | CVLYEVLTG | 0.1552 | 9321.0 | 50.00 | Sequence |
| IAd | 470 | NPPANQTSAITNVVI | ANQTSAITN | 0.1543 | 9413.7 | 50.00 | Sequence |
| IAd | 472 | PANQTSAITNVVIII | ANQTSAITN | 0.1540 | 9445.8 | 50.00 | Sequence |
| IAd | 587 | DKGADVDAGGSQHNR | DKGADVDAG | 0.1540 | 9447.1 | 50.00 | Sequence |
| IAd | 577 | LRALGWTGMLDKGAD | LRALGWTGM | 0.1540 | 9447.9 | 50.00 | Sequence |
| IAd | 41 | LRADLARDPSFYLRF | RADLARDPS | 0.1540 | 9449.7 | 50.00 | Sequence |
| IAd | 504 | VDVAQKNLNVYGFTK | QKNLNVYGF | 0.1535 | 9500.5 | 50.00 | Sequence |
| IAd | 474 | NQTSAITNVVIIIVG | ITNVVIIIV | 0.1534 | 9511.5 | 50.00 | Sequence |
| IAd | 88 | YIVMEYVDGVTLRDI | YIVMEYVDG | 0.1525 | 9600.2 | 50.00 | Sequence |
| IAd | 99 | LRDIVHTEGPMTPKR | VHTEGPMTP | 0.1521 | 9641.3 | 50.00 | Sequence |
| IAd | 194 | ARSDVYSLGCVLYEV | YSLGCVLYE | 0.1511 | 9747.3 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAd | 506 | VAQKNLNVYGFTKFS | QKNLNVYGF | 0.1510 | 9761.1 | 50.00 | Sequence |
| IAd | 13 | GEILGFGGMSEVHLA | GGMSEVHLA | 0.1509 | 9770.3 | 50.00 | Sequence |
| IAd | 503 | TVDVAQKNLNVYGFT | QKNLNVYGF | 0.1508 | 9778.5 | 50.00 | Sequence |
| IAd | 475 | QTSAITNVVIIIVGS | ITNVVIIIV | 0.1507 | 9793.6 | 50.00 | Sequence |
| IAd | 183 | SPEQARGDSVDARSD | QARGDSVDA | 0.1505 | 9809.1 | 50.00 | Sequence |
| IAd | 191 | SVDARSDVYSLGCVL | DARSDVYSL | 0.1500 | 9860.3 | 50.00 | Sequence |
| IAd | 553 | QVSKGNQFVMPDLSG | GNQFVMPDL | 0.1496 | 9906.6 | 50.00 | Sequence |
| IAd | 478 | AITNVVIIIVGSGPA | ITNVVIIIV | 0.1495 | 9917.3 | 50.00 | Sequence |
| IAd | 355 | ITRDVQVPDVRGQSS | TRDVQVPDV | 0.1495 | 9924.4 | 50.00 | Sequence |
| IAd | 477 | SAITNVVIIIVGSGP | ITNVVIIIV | 0.1487 | 10002.6 | 50.00 | Sequence |
| IAd | 349 | INTFGGITRDVQVPD | INTFGGITR | 0.1485 | 10029.1 | 50.00 | Sequence |
| IAd | 420 | STGPEQREIPDVSTL | QREIPDVST | 0.1484 | 10039.7 | 50.00 | Sequence |
| IAd | 495 | DIPDVAGQTVDVAQK | GQTVDVAQK | 0.1483 | 10046.4 | 50.00 | Sequence |
| IAd | 98 | TLRDIVHTEGPMTPK | VHTEGPMTP | 0.1479 | 10089.7 | 50.00 | Sequence |
| IAd | 153 | VMDFGIARAIADSGN | VMDFGIARA | 0.1478 | 10102.9 | 50.00 | Sequence |
| IAd | 502 | QTVDVAQKNLNVYGF | QKNLNVYGF | 0.1469 | 10198.7 | 50.00 | Sequence |
| IAd | 87 | PYIVMEYVDGVTLRD | MEYVDGVTL | 0.1462 | 10280.9 | 50.00 | Sequence |
| IAd | 189 | GDSVDARSDVYSLGC | DARSDVYSL | 0.1461 | 10289.2 | 50.00 | Sequence |
| IAd | 154 | MDFGIARAIADSGNS | FGIARAIAD | 0.1453 | 10378.0 | 50.00 | Sequence |
| IAd | 440 | VKKLTAAGFGRFKQA | VKKLTAAGF | 0.1451 | 10400.9 | 50.00 | Sequence |
| IAd | 552 | LQVSKGNQFVMPDLS | GNQFVMPDL | 0.1441 | 10515.7 | 50.00 | Sequence |
| IAd | 369 | SADAIATLQNRGFKI | ADAIATLQN | 0.1436 | 10575.7 | 50.00 | Sequence |
| IAd | 524 | VDSPRPAGEVTGTNP | RPAGEVTGT | 0.1434 | 10592.1 | 50.00 | Sequence |
| IAd | 76 | TGEAETPAGPLPYIV | TGEAETPAG | 0.1427 | 10671.0 | 50.00 | Sequence |
| IAd | 405 | ANTSVSAGDEITVNV | VSAGDEITV | 0.1424 | 10705.5 | 50.00 | Sequence |
| IAd | 122 | CQALNFSHQNGIIHR | SHQNGIIHR | 0.1424 | 10714.4 | 50.00 | Sequence |
| IAd | 233 | IPPSARHEGLSADLD | RHEGLSADL | 0.1421 | 10742.5 | 50.00 | Sequence |
| IAd | 356 | TRDVQVPDVRGQSSA | TRDVQVPDV | 0.1421 | 10750.6 | 50.00 | Sequence |
| IAd | 216 | TGDSPVSVAYQHVRE | PVSVAYQHV | 0.1413 | 10836.4 | 50.00 | Sequence |
| IAd | 558 | NQFVMPDLSGMFWVD | QFVMPDLSG | 0.1409 | 10891.8 | 50.00 | Sequence |
| IAd | 182 | LSPEQARGDSVDARS | QARGDSVDA | 0.1407 | 10910.6 | 50.00 | Sequence |
| IAd | 174 | AVIGTAQYLSPEQAR | AQYLSPEQA | 0.1403 | 10955.0 | 50.00 | Sequence |
| IAd | 175 | VIGTAQYLSPEQARG | AQYLSPEQA | 0.1400 | 10987.5 | 50.00 | Sequence |
| IAd | 176 | IGTAQYLSPEQARGD | AQYLSPEQA | 0.1398 | 11014.5 | 50.00 | Sequence |
| IAd | 68 | PAIVAVYDTGEAETP | PAIVAVYDT | 0.1391 | 11098.6 | 50.00 | Sequence |
| IAd | 578 | RALGWTGMLDKGADV | WTGMLDKGA | 0.1388 | 11138.1 | 50.00 | Sequence |
| IAd | 348 | AINTFGGITRDVQVP | INTFGGITR | 0.1382 | 11207.6 | 50.00 | Sequence |
| IAd | 342 | TVVVTIAINTFGGIT | VVVTIAINT | 0.1379 | 11243.5 | 50.00 | Sequence |
| IAd | 572 | DAEPRLRALGWTGML | LRALGWTGM | 0.1379 | 11245.3 | 50.00 | Sequence |
| IAd | 575 | PRLRALGWTGMLDKG | LRALGWTGM | 0.1378 | 11256.1 | 50.00 | Sequence |
| IAd | 316 | LDDTDRDRSIGSVGR | DRSIGSVGR | 0.1367 | 11386.4 | 50.00 | Sequence |
| IAd | 270 | ADLVRVHNGEPPEAP | VHNGEPPEA | 0.1365 | 11411.4 | 50.00 | Sequence |
| IAd | 597 | SQHNRVVYQNPPAGT | QHNRVVYQN | 0.1363 | 11440.7 | 50.00 | Sequence |
| IAd | 203 | CVLYEVLTGEPPFTG | YEVLTGEPP | 0.1360 | 11480.5 | 50.00 | Sequence |
| IAd | 526 | SPRPAGEVTGTNPPA | RPAGEVTGT | 0.1359 | 11489.6 | 50.00 | Sequence |
| IAd | 479 | ITNVVIIIVGSGPAT | ITNVVIIIV | 0.1357 | 11514.0 | 50.00 | Sequence |
| IAd | 551 | ELQVSKGNQFVMPDL | GNQFVMPDL | 0.1353 | 11565.1 | 50.00 | Sequence |
| IAd | 525 | DSPRPAGEVTGTNPP | RPAGEVTGT | 0.1350 | 11608.2 | 50.00 | Sequence |
| IAd | 224 | AYQHVREDPIPPSAR | VREDPIPPS | 0.1348 | 11630.6 | 50.00 | Sequence |
| IAd | 177 | GTAQYLSPEQARGDS | AQYLSPEQA | 0.1347 | 11640.3 | 50.00 | Sequence |
| IAd | 181 | YLSPEQARGDSVDAR | QARGDSVDA | 0.1335 | 11798.5 | 50.00 | Sequence |
| IAd | 232 | PIPPSARHEGLSADL | RHEGLSADL | 0.1334 | 11808.5 | 50.00 | Sequence |
| IAd | 469 | TNPPANQTSAITNVV | ANQTSAITN | 0.1333 | 11821.5 | 50.00 | Sequence |
| IAd | 595 | GGSQHNRVVYQNPPA | QHNRVVYQN | 0.1324 | 11936.0 | 50.00 | Sequence |
| IAd | 89 | IVMEYVDGVTLRDIV | MEYVDGVTL | 0.1320 | 11983.9 | 50.00 | Sequence |
| IAd | 596 | GSQHNRVVYQNPPAG | QHNRVVYQN | 0.1309 | 12125.3 | 50.00 | Sequence |
| IAd | 574 | EPRLRALGWTGMLDK | PRLRALGWT | 0.1301 | 12231.9 | 50.00 | Sequence |
| IAd | 173 | AAVIGTAQYLSPEQA | AQYLSPEQA | 0.1296 | 12303.1 | 50.00 | Sequence |
| IAd | 410 | SAGDEITVNVSTGPE | DEITVNVST | 0.1289 | 12401.1 | 50.00 | Sequence |
| IAd | 500 | AGQTVDVAQKNLNVY | GQTVDVAQK | 0.1287 | 12422.5 | 50.00 | Sequence |
| IAd | 92 | EYVDGVTLRDIVHTE | VTLRDIVHT | 0.1285 | 12453.6 | 50.00 | Sequence |
| IAd | 480 | TNVVIIIVGSGPATK | NVVIIIVGS | 0.1283 | 12470.9 | 50.00 | Sequence |
| IAd | 93 | YVDGVTLRDIVHTEG | VTLRDIVHT | 0.1277 | 12551.8 | 50.00 | Sequence |
| IAd | 598 | QHNRVVYQNPPAGTG | QHNRVVYQN | 0.1275 | 12583.3 | 50.00 | Sequence |
| IAd | 225 | YQHVREDPIPPSARH | VREDPIPPS | 0.1267 | 12696.4 | 50.00 | Sequence |
| IAd | 129 | HQNGIIHRDVKPANI | IIHRDVKPA | 0.1266 | 12709.7 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAd | 217 | GDSPVSVAYQHVRED | PVSVAYQHV | 0.1262 | 12758.2 | 50.00 | Sequence |
| IAd | 294 | SLLSSAAGNLSGPRT | SSAAGNLSG | 0.1261 | 12774.1 | 50.00 | Sequence |
| IAd | 155 | DFGIARAIADSGNSV | IARAIADSG | 0.1257 | 12830.6 | 50.00 | Sequence |
| IAd | 202 | GCVLYEVLTGEPPFT | YEVLTGEPP | 0.1253 | 12893.5 | 50.00 | Sequence |
| IAd | 345 | VTIAINTFGGITRDV | INTFGGITR | 0.1253 | 12894.1 | 50.00 | Sequence |
| IAd | 157 | GIARAIADSGNSVTQ | IARAIADSG | 0.1251 | 12912.7 | 50.00 | Sequence |
| IAd | 579 | ALGWTGMLDKGADVD | WTGMLDKGA | 0.1248 | 12955.1 | 50.00 | Sequence |
| IAd | 593 | DAGGSQHNRVVYQNP | QHNRVVYQN | 0.1248 | 12962.2 | 50.00 | Sequence |
| IAd | 180 | QYLSPEQARGDSVDA | QARGDSVDA | 0.1247 | 12966.8 | 50.00 | Sequence |
| IAd | 601 | RVVYQNPPAGTGVNR | RVVYQNPPA | 0.1247 | 12967.7 | 50.00 | Sequence |
| IAd | 218 | DSPVSVAYQHVREDP | PVSVAYQHV | 0.1245 | 13005.3 | 50.00 | Sequence |
| IAd | 594 | AGGSQHNRVVYQNPP | QHNRVVYQN | 0.1243 | 13022.7 | 50.00 | Sequence |
| IAd | 156 | FGIARAIADSGNSVT | IARAIADSG | 0.1237 | 13108.3 | 50.00 | Sequence |
| IAd | 346 | TIAINTFGGITRDVQ | INTFGGITR | 0.1230 | 13211.0 | 50.00 | Sequence |
| IAd | 42 | RADLARDPSFYLRFR | RADLARDPS | 0.1216 | 13419.0 | 50.00 | Sequence |
| IAd | 198 | VYSLGCVLYEVLTGE | CVLYEVLTG | 0.1215 | 13433.5 | 50.00 | Sequence |
| IAd | 512 | NVYGFTKFSQASVDS | KFSQASVDS | 0.1212 | 13476.6 | 50.00 | Sequence |
| IAd | 548 | SVIELQVSKGNQFVM | VIELQVSKG | 0.1210 | 13495.2 | 50.00 | Sequence |
| IAd | 116 | EVIADACQALNFSHQ | ACQALNFSH | 0.1197 | 13695.5 | 50.00 | Sequence |
| IAd | 347 | IAINTFGGITRDVQV | INTFGGITR | 0.1194 | 13733.2 | 50.00 | Sequence |
| IAd | 77 | GEAETPAGPLPYIVM | EAETPAGPL | 0.1193 | 13745.4 | 50.00 | Sequence |
| IAd | 94 | VDGVTLRDIVHTEGP | VTLRDIVHT | 0.1193 | 13746.6 | 50.00 | Sequence |
| IAd | 78 | EAETPAGPLPYIVME | EAETPAGPL | 0.1187 | 13839.0 | 50.00 | Sequence |
| IAd | 481 | NVVIIIVGSGPATKD | NVVIIIVGS | 0.1186 | 13863.5 | 50.00 | Sequence |
| IAd | 115 | IEVIADACQALNFSH | EVIADACQA | 0.1177 | 13994.4 | 50.00 | Sequence |
| IAd | 199 | YSLGCVLYEVLTGEP | CVLYEVLTG | 0.1171 | 14082.9 | 50.00 | Sequence |
| IAd | 393 | IPPDHVIGTDPAANT | DHVIGTDPA | 0.1168 | 14122.6 | 50.00 | Sequence |
| IAd | 573 | AEPRLRALGWTGMLD | PRLRALGWT | 0.1166 | 14157.6 | 50.00 | Sequence |
| IAd | 394 | PPDHVIGTDPAANTS | DHVIGTDPA | 0.1163 | 14200.7 | 50.00 | Sequence |
| IAd | 607 | PPAGTGVNRDGIITL | VNRDGIITL | 0.1163 | 14205.5 | 50.00 | Sequence |
| IAd | 204 | VLYEVLTGEPPFTGD | YEVLTGEPP | 0.1158 | 14284.6 | 50.00 | Sequence |
| IAd | 213 | PPFTGDSPVSVAYQH | FTGDSPVSV | 0.1152 | 14375.0 | 50.00 | Sequence |
| IAd | 90 | VMEYVDGVTLRDIVH | MEYVDGVTL | 0.1145 | 14485.2 | 50.00 | Sequence |
| IAd | 396 | DHVIGTDPAANTSVS | DHVIGTDPA | 0.1144 | 14493.8 | 50.00 | Sequence |
| IAd | 226 | QHVREDPIPPSARHE | VREDPIPPS | 0.1142 | 14534.6 | 50.00 | Sequence |
| IAd | 74 | YDTGEAETPAGPLPY | EAETPAGPL | 0.1142 | 14535.6 | 50.00 | Sequence |
| IAd | 295 | LLSSAAGNLSGPRTD | SSAAGNLSG | 0.1140 | 14562.5 | 50.00 | Sequence |
| IAd | 219 | SPVSVAYQHVREDPI | PVSVAYQHV | 0.1119 | 14893.5 | 50.00 | Sequence |
| IAd | 205 | LYEVLTGEPPFTGDS | YEVLTGEPP | 0.1111 | 15023.6 | 50.00 | Sequence |
| IAd | 300 | AGNLSGPRTDPLPRQ | GPRTDPLPR | 0.1110 | 15050.1 | 50.00 | Sequence |
| IAd | 293 | TSLLSSAAGNLSGPR | LSSAAGNLS | 0.1107 | 15088.1 | 50.00 | Sequence |
| IAd | 501 | GQTVDVAQKNLNVYG | GQTVDVAQK | 0.1107 | 15093.0 | 50.00 | Sequence |
| IAd | 3 | PSHLSDRYELGEILG | RYELGEILG | 0.1107 | 15099.7 | 50.00 | Sequence |
| IAd | 178 | TAQYLSPEQARGDSV | AQYLSPEQA | 0.1084 | 15466.4 | 50.00 | Sequence |
| IAd | 468 | GTNPPANQTSAITNV | ANQTSAITN | 0.1084 | 15469.6 | 50.00 | Sequence |
| IAd | 220 | PVSVAYQHVREDPIP | PVSVAYQHV | 0.1078 | 15572.2 | 50.00 | Sequence |
| IAd | 247 | DAVVLKALAKNPENR | LKALAKNPE | 0.1075 | 15623.0 | 50.00 | Sequence |
| IAd | 296 | LSSAAGNLSGPRTDP | SSAAGNLSG | 0.1068 | 15747.4 | 50.00 | Sequence |
| IAd | 395 | PDHVIGTDPAANTSV | DHVIGTDPA | 0.1066 | 15784.6 | 50.00 | Sequence |
| IAd | 50 | SFYLRFRREAQNAAA | RREAQNAAA | 0.1058 | 15909.8 | 50.00 | Sequence |
| IAd | 507 | AQKNLNVYGFTKFSQ | QKNLNVYGF | 0.1053 | 16009.2 | 50.00 | Sequence |
| IAd | 370 | ADAIATLQNRGFKIR | DAIATLQNR | 0.1048 | 16091.4 | 50.00 | Sequence |
| IAd | 114 | AIEVIADACQALNFS | EVIADACQA | 0.1045 | 16135.5 | 50.00 | Sequence |
| IAd | 10 | YELGEILGFGGMSEV | YELGEILGF | 0.1040 | 16226.7 | 50.00 | Sequence |
| IAd | 8 | DRYELGEILGFGGMS | YELGEILGF | 0.1030 | 16400.7 | 50.00 | Sequence |
| IAd | 532 | EVTGTNPPAGTTVPV | PPAGTTVPV | 0.1030 | 16413.7 | 50.00 | Sequence |
| IAd | 130 | QNGIIHRDVKPANIM | IIHRDVKPA | 0.1027 | 16458.3 | 50.00 | Sequence |
| IAd | 419 | VSTGPEQREIPDVST | QREIPDVST | 0.1017 | 16631.6 | 50.00 | Sequence |
| IAd | 458 | STPELVGKVIGTNPP | STPELVGKV | 0.1012 | 16725.8 | 50.00 | Sequence |
| IAd | 527 | PRPAGEVTGTNPPAG | RPAGEVTGT | 0.1004 | 16879.8 | 50.00 | Sequence |
| IAd | 12 | LGEILGFGGMSEVHL | FGGMSEVHL | 0.1004 | 16880.2 | 50.00 | Sequence |
| IAd | 494 | KDIPDVAGQTVDVAQ | IPDVAGQTV | 0.1002 | 16917.1 | 50.00 | Sequence |
| IAd | 1 | TTPSHLSDRYELGEI | SHLSDRYEL | 0.0999 | 16964.2 | 50.00 | Sequence |
| IAd | 9 | RYELGEILGFGGMSE | YELGEILGF | 0.0996 | 17010.9 | 50.00 | Sequence |
| IAd | 95 | DGVTLRDIVHTEGPM | VTLRDIVHT | 0.0996 | 17015.3 | 50.00 | Sequence |
| IAd | 441 | KKLTAAGFGRFKQAN | KLTAAGFGR | 0.0995 | 17033.2 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAd | 179 | AQYLSPEQARGDSVD | AQYLSPEQA | 0.0994 | 17054.2 | 50.00 | Sequence |
| IAd | 277 | NGEPPEAPKVLTDAE | EAPKVLTDA | 0.0991 | 17103.2 | 50.00 | Sequence |
| IAd | 457 | PSTPELVGKVIGTNP | PELVGKVIG | 0.0988 | 17168.2 | 50.00 | Sequence |
| IAd | 79 | AETPAGPLPYIVMEY | TPAGPLPYI | 0.0987 | 17187.9 | 50.00 | Sequence |
| IAd | 490 | GPATKDIPDVAGQTV | IPDVAGQTV | 0.0985 | 17221.6 | 50.00 | Sequence |
| IAd | 2 | TPSHLSDRYELGEIL | SHLSDRYEL | 0.0983 | 17270.0 | 50.00 | Sequence |
| IAd | 206 | YEVLTGEPPFTGDSP | YEVLTGEPP | 0.0982 | 17274.1 | 50.00 | Sequence |
| IAd | 491 | PATKDIPDVAGQTVD | IPDVAGQTV | 0.0979 | 17334.7 | 50.00 | Sequence |
| IAd | 158 | IARAIADSGNSVTQT | IARAIADSG | 0.0979 | 17340.2 | 50.00 | Sequence |
| IAd | 411 | AGDEITVNVSTGPEQ | GDEITVNVS | 0.0978 | 17361.8 | 50.00 | Sequence |
| IAd | 454 | ANSPSTPELVGKVIG | PELVGKVIG | 0.0974 | 17430.5 | 50.00 | Sequence |
| IAd | 212 | EPPFTGDSPVSVAYQ | FTGDSPVSV | 0.0971 | 17491.9 | 50.00 | Sequence |
| IAd | 456 | SPSTPELVGKVIGTN | PELVGKVIG | 0.0961 | 17671.3 | 50.00 | Sequence |
| IAd | 448 | FGRFKQANSPSTPEL | FKQANSPST | 0.0961 | 17671.8 | 50.00 | Sequence |
| IAd | 131 | NGIIHRDVKPANIMI | IIHRDVKPA | 0.0958 | 17735.6 | 50.00 | Sequence |
| IAd | 227 | HVREDPIPPSARHEG | VREDPIPPS | 0.0950 | 17892.9 | 50.00 | Sequence |
| IAd | 592 | VDAGGSQHNRVVYQN | QHNRVVYQN | 0.0947 | 17937.5 | 50.00 | Sequence |
| IAd | 549 | VIELQVSKGNQFVMP | VIELQVSKG | 0.0945 | 17990.7 | 50.00 | Sequence |
| IAd | 119 | ADACQALNFSHQNGI | ACQALNFSH | 0.0943 | 18028.7 | 50.00 | Sequence |
| IAd | 301 | GNLSGPRTDPLPRQD | GPRTDPLPR | 0.0935 | 18174.5 | 50.00 | Sequence |
| IAd | 412 | GDEITVNVSTGPEQR | GDEITVNVS | 0.0933 | 18223.3 | 50.00 | Sequence |
| IAd | 455 | NSPSTPELVGKVIGT | STPELVGKV | 0.0930 | 18284.3 | 50.00 | Sequence |
| IAd | 118 | IADACQALNFSHQNG | ACQALNFSH | 0.0925 | 18388.3 | 50.00 | Sequence |
| IAd | 117 | VIADACQALNFSHQN | ACQALNFSH | 0.0921 | 18461.0 | 50.00 | Sequence |
| IAd | 299 | AAGNLSGPRTDPLPR | AGNLSGPRT | 0.0904 | 18799.1 | 50.00 | Sequence |
| IAd | 228 | VREDPIPPSARHEGL | VREDPIPPS | 0.0902 | 18846.3 | 50.00 | Sequence |
| IAd | 603 | VYQNPPAGTGVNRDG | PPAGTGVNR | 0.0900 | 18881.2 | 50.00 | Sequence |
| IAd | 599 | HNRVVYQNPPAGTGV | HNRVVYQNP | 0.0900 | 18891.4 | 50.00 | Sequence |
| IAd | 297 | SSAAGNLSGPRTDPL | SSAAGNLSG | 0.0888 | 19123.6 | 50.00 | Sequence |
| IAd | 508 | QKNLNVYGFTKFSQA | QKNLNVYGF | 0.0888 | 19124.9 | 50.00 | Sequence |
| IAd | 449 | GRFKQANSPSTPELV | FKQANSPST | 0.0884 | 19202.8 | 50.00 | Sequence |
| IAd | 96 | GVTLRDIVHTEGPMT | VTLRDIVHT | 0.0880 | 19305.7 | 50.00 | Sequence |
| IAd | 172 | TAAVIGTAQYLSPEQ | TAAVIGTAQ | 0.0874 | 19411.7 | 50.00 | Sequence |
| IAd | 302 | NLSGPRTDPLPRQDL | GPRTDPLPR | 0.0866 | 19594.7 | 50.00 | Sequence |
| IAd | 493 | TKDIPDVAGQTVDVA | VAGQTVDVA | 0.0861 | 19700.1 | 50.00 | Sequence |
| IAd | 450 | RFKQANSPSTPELVG | FKQANSPST | 0.0856 | 19813.4 | 50.00 | Sequence |
| IAd | 467 | IGTNPPANQTSAITN | ANQTSAITN | 0.0853 | 19865.1 | 50.00 | Sequence |
| IAd | 602 | VVYQNPPAGTGVNRD | PPAGTGVNR | 0.0853 | 19877.2 | 50.00 | Sequence |
| IAd | 453 | QANSPSTPELVGKVI | STPELVGKV | 0.0852 | 19895.2 | 50.00 | Sequence |
| IAd | 482 | VVIIIVGSGPATKDI | VVIIIVGSG | 0.0850 | 19925.2 | 50.00 | Sequence |
| IAd | 377 | QNRGFKIRTLQKPDS | IRTLQKPDS | 0.0843 | 20091.7 | 50.00 | Sequence |
| IAd | 248 | AVVLKALAKNPENRY | AVVLKALAK | 0.0842 | 20103.6 | 50.00 | Sequence |
| IAd | 275 | VHNGEPPEAPKVLTD | VHNGEPPEA | 0.0841 | 20136.7 | 50.00 | Sequence |
| IAd | 159 | ARAIADSGNSVTQTA | ARAIADSGN | 0.0840 | 20147.0 | 50.00 | Sequence |
| IAd | 72 | AVYDTGEAETPAGPL | EAETPAGPL | 0.0839 | 20160.5 | 50.00 | Sequence |
| IAd | 305 | GPRTDPLPRQDLDDT | GPRTDPLPR | 0.0834 | 20272.0 | 50.00 | Sequence |
| IAd | 604 | YQNPPAGTGVNRDGI | PPAGTGVNR | 0.0822 | 20535.2 | 50.00 | Sequence |
| IAd | 442 | KLTAAGFGRFKQANS | KLTAAGFGR | 0.0812 | 20761.3 | 50.00 | Sequence |
| IAd | 452 | KQANSPSTPELVGKV | KQANSPSTP | 0.0812 | 20780.1 | 50.00 | Sequence |
| IAd | 378 | NRGFKIRTLQKPDST | IRTLQKPDS | 0.0811 | 20801.1 | 50.00 | Sequence |
| IAd | 381 | FKIRTLQKPDSTIPP | FKIRTLQKP | 0.0810 | 20807.1 | 50.00 | Sequence |
| IAd | 43 | ADLARDPSFYLRFRR | ARDPSFYLR | 0.0810 | 20818.6 | 50.00 | Sequence |
| IAd | 276 | HNGEPPEAPKVLTDA | EAPKVLTDA | 0.0804 | 20941.1 | 50.00 | Sequence |
| IAd | 391 | STIPPDHVIGTDPAA | DHVIGTDPA | 0.0802 | 21001.4 | 50.00 | Sequence |
| IAd | 588 | KGADVDAGGSQHNRV | GADVDAGGS | 0.0799 | 21069.7 | 50.00 | Sequence |
| IAd | 600 | NRVVYQNPPAGTGVN | RVVYQNPPA | 0.0797 | 21104.9 | 50.00 | Sequence |
| IAd | 392 | TIPPDHVIGTDPAAN | DHVIGTDPA | 0.0795 | 21160.2 | 50.00 | Sequence |
| IAd | 272 | LVRVHNGEPPEAPKV | VHNGEPPEA | 0.0793 | 21205.6 | 50.00 | Sequence |
| IAd | 73 | VYDTGEAETPAGPLP | EAETPAGPL | 0.0791 | 21249.7 | 50.00 | Sequence |
| IAd | 447 | GFGRFKQANSPSTPE | FKQANSPST | 0.0790 | 21272.7 | 50.00 | Sequence |
| IAd | 446 | AGFGRFKQANSPSTP | FKQANSPST | 0.0784 | 21414.0 | 50.00 | Sequence |
| IAd | 303 | LSGPRTDPLPRQDLD | GPRTDPLPR | 0.0774 | 21650.7 | 50.00 | Sequence |
| IAd | 298 | SAAGNLSGPRTDPLP | AGNLSGPRT | 0.0772 | 21687.0 | 50.00 | Sequence |
| IAd | 254 | LAKNPENRYQTAAEM | NRYQTAAEM | 0.0761 | 21946.7 | 50.00 | Sequence |
| IAd | 382 | KIRTLQKPDSTIPPD | IRTLQKPDS | 0.0759 | 21992.6 | 50.00 | Sequence |
| IAd | 445 | AAGFGRFKQANSPST | FKQANSPST | 0.0756 | 22058.6 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAd | 160 | RAIADSGNSVTQTAA | RAIADSGNS | 0.0748 | 22264.8 | 50.00 | Sequence |
| IAd | 71 | VAVYDTGEAETPAGP | VAVYDTGEA | 0.0745 | 22341.8 | 50.00 | Sequence |
| IAd | 221 | VSVAYQHVREDPIPP | HVREDPIPP | 0.0743 | 22382.4 | 50.00 | Sequence |
| IAd | 315 | DLDDTDRDRSIGSVG | DRDRSIGSV | 0.0742 | 22411.5 | 50.00 | Sequence |
| IAd | 492 | ATKDIPDVAGQTVDV | IPDVAGQTV | 0.0733 | 22625.7 | 50.00 | Sequence |
| IAd | 372 | AIATLQNRGFKIRTL | LQNRGFKIR | 0.0730 | 22698.7 | 50.00 | Sequence |
| IAd | 211 | GEPPFTGDSPVSVAY | FTGDSPVSV | 0.0730 | 22698.7 | 50.00 | Sequence |
| IAd | 489 | SGPATKDIPDVAGQT | PATKDIPDV | 0.0725 | 22808.8 | 50.00 | Sequence |
| IAd | 371 | DAIATLQNRGFKIRT | DAIATLQNR | 0.0725 | 22819.2 | 50.00 | Sequence |
| IAd | 606 | NPPAGTGVNRDGIIT | PPAGTGVNR | 0.0724 | 22832.0 | 50.00 | Sequence |
| IAd | 162 | IADSGNSVTQTAAVI | GNSVTQTAA | 0.0718 | 22980.2 | 50.00 | Sequence |
| IAd | 121 | ACQALNFSHQNGIIH | ACQALNFSH | 0.0708 | 23252.6 | 50.00 | Sequence |
| IAd | 273 | VRVHNGEPPEAPKVL | VHNGEPPEA | 0.0703 | 23376.9 | 50.00 | Sequence |
| IAd | 383 | IRTLQKPDSTIPPDH | IRTLQKPDS | 0.0695 | 23559.8 | 50.00 | Sequence |
| IAd | 459 | TPELVGKVIGTNPPA | ELVGKVIGT | 0.0695 | 23576.3 | 50.00 | Sequence |
| IAd | 314 | QDLDDTDRDRSIGSV | DRDRSIGSV | 0.0689 | 23737.1 | 50.00 | Sequence |
| IAd | 49 | PSFYLRFRREAQNAA | RFRREAQNA | 0.0688 | 23753.5 | 50.00 | Sequence |
| IAd | 486 | IVGSGPATKDIPDVA | PATKDIPDV | 0.0682 | 23899.7 | 50.00 | Sequence |
| IAd | 120 | DACQALNFSHQNGII | ACQALNFSH | 0.0678 | 24013.0 | 50.00 | Sequence |
| IAd | 375 | TLQNRGFKIRTLQKP | FKIRTLQKP | 0.0675 | 24085.5 | 50.00 | Sequence |
| IAd | 70 | IVAVYDTGEAETPAG | VAVYDTGEA | 0.0670 | 24211.2 | 50.00 | Sequence |
| IAd | 380 | GFKIRTLQKPDSTIP | IRTLQKPDS | 0.0669 | 24246.1 | 50.00 | Sequence |
| IAd | 488 | GSGPATKDIPDVAGQ | PATKDIPDV | 0.0667 | 24298.1 | 50.00 | Sequence |
| IAd | 451 | FKQANSPSTPELVGK | FKQANSPST | 0.0665 | 24339.4 | 50.00 | Sequence |
| IAd | 274 | RVHNGEPPEAPKVLT | VHNGEPPEA | 0.0662 | 24433.9 | 50.00 | Sequence |
| IAd | 589 | GADVDAGGSQHNRVV | GADVDAGGS | 0.0659 | 24503.0 | 50.00 | Sequence |
| IAd | 210 | TGEPPFTGDSPVSVA | FTGDSPVSV | 0.0659 | 24518.1 | 50.00 | Sequence |
| IAd | 69 | AIVAVYDTGEAETPA | VAVYDTGEA | 0.0656 | 24575.7 | 50.00 | Sequence |
| IAd | 413 | DEITVNVSTGPEQRE | EITVNVSTG | 0.0654 | 24647.1 | 50.00 | Sequence |
| IAd | 443 | LTAAGFGRFKQANSP | LTAAGFGRF | 0.0653 | 24667.4 | 50.00 | Sequence |
| IAd | 373 | IATLQNRGFKIRTLQ | LQNRGFKIR | 0.0650 | 24741.9 | 50.00 | Sequence |
| IAd | 379 | RGFKIRTLQKPDSTI | IRTLQKPDS | 0.0650 | 24750.2 | 50.00 | Sequence |
| IAd | 605 | QNPPAGTGVNRDGII | PPAGTGVNR | 0.0645 | 24869.4 | 50.00 | Sequence |
| IAd | 249 | VVLKALAKNPENRYQ | LKALAKNPE | 0.0642 | 24955.4 | 50.00 | Sequence |
| IAd | 231 | DPIPPSARHEGLSAD | SARHEGLSA | 0.0642 | 24957.6 | 50.00 | Sequence |
| IAd | 511 | LNVYGFTKFSQASVD | FTKFSQASV | 0.0638 | 25065.8 | 50.00 | Sequence |
| IAd | 304 | SGPRTDPLPRQDLDD | GPRTDPLPR | 0.0626 | 25407.9 | 50.00 | Sequence |
| IAd | 250 | VLKALAKNPENRYQT | LKALAKNPE | 0.0623 | 25481.2 | 50.00 | Sequence |
| IAd | 44 | DLARDPSFYLRFRRE | ARDPSFYLR | 0.0613 | 25748.1 | 50.00 | Sequence |
| IAd | 485 | IIVGSGPATKDIPDV | PATKDIPDV | 0.0609 | 25862.0 | 50.00 | Sequence |
| IAd | 487 | VGSGPATKDIPDVAG | PATKDIPDV | 0.0609 | 25863.9 | 50.00 | Sequence |
| IAd | 376 | LQNRGFKIRTLQKPD | FKIRTLQKP | 0.0595 | 26257.8 | 50.00 | Sequence |
| IAd | 484 | IIIVGSGPATKDIPD | IIIVGSGPA | 0.0593 | 26323.0 | 50.00 | Sequence |
| IAd | 271 | DLVRVHNGEPPEAPK | VHNGEPPEA | 0.0593 | 26328.7 | 50.00 | Sequence |
| IAd | 483 | VIIIVGSGPATKDIP | IIIVGSGPA | 0.0591 | 26377.7 | 50.00 | Sequence |
| IAd | 161 | AIADSGNSVTQTAAV | GNSVTQTAA | 0.0587 | 26486.4 | 50.00 | Sequence |
| IAd | 306 | PRTDPLPRQDLDDTD | LPRQDLDDT | 0.0580 | 26699.6 | 50.00 | Sequence |
| IAd | 357 | RDVQVPDVRGQSSAD | VPDVRGQSS | 0.0573 | 26889.5 | 50.00 | Sequence |
| IAd | 45 | LARDPSFYLRFRREA | ARDPSFYLR | 0.0570 | 26976.9 | 50.00 | Sequence |
| IAd | 591 | DVDAGGSQHNRVVYQ | VDAGGSQHN | 0.0568 | 27045.3 | 50.00 | Sequence |
| IAd | 384 | RTLQKPDSTIPPDHV | QKPDSTIPP | 0.0566 | 27115.3 | 50.00 | Sequence |
| IAd | 528 | RPAGEVTGTNPPAGT | RPAGEVTGT | 0.0560 | 27276.0 | 50.00 | Sequence |
| IAd | 461 | ELVGKVIGTNPPANQ | KVIGTNPPA | 0.0551 | 27549.5 | 50.00 | Sequence |
| IAd | 550 | IELQVSKGNQFVMPD | VSKGNQFVM | 0.0551 | 27555.7 | 50.00 | Sequence |
| IAd | 460 | PELVGKVIGTNPPAN | ELVGKVIGT | 0.0547 | 27658.8 | 50.00 | Sequence |
| IAd | 385 | TLQKPDSTIPPDHVI | QKPDSTIPP | 0.0547 | 27680.0 | 50.00 | Sequence |
| IAd | 590 | ADVDAGGSQHNRVVY | VDAGGSQHN | 0.0540 | 27873.9 | 50.00 | Sequence |
| IAd | 209 | LTGEPPFTGDSPVSV | FTGDSPVSV | 0.0538 | 27936.1 | 50.00 | Sequence |
| IAd | 46 | ARDPSFYLRFRREAQ | ARDPSFYLR | 0.0526 | 28303.3 | 50.00 | Sequence |
| IAd | 390 | DSTIPPDHVIGTDPA | DHVIGTDPA | 0.0522 | 28431.0 | 50.00 | Sequence |
| IAd | 374 | ATLQNRGFKIRTLQK | QNRGFKIRT | 0.0522 | 28432.5 | 50.00 | Sequence |
| IAd | 387 | QKPDSTIPPDHVIGT | QKPDSTIPP | 0.0521 | 28454.1 | 50.00 | Sequence |
| IAd | 251 | LKALAKNPENRYQTA | LKALAKNPE | 0.0511 | 28756.8 | 50.00 | Sequence |
| IAd | 462 | LVGKVIGTNPPANQT | KVIGTNPPA | 0.0510 | 28803.5 | 50.00 | Sequence |
| IAd | 386 | LQKPDSTIPPDHVIG | QKPDSTIPP | 0.0487 | 29521.3 | 50.00 | Sequence |
| IAd | 418 | NVSTGPEQREIPDVS | PEQREIPDV | 0.0480 | 29743.4 | 50.00 | Sequence |

```
         IAd  417  VNVSTGPEQREIPDV  PEQREIPDV        0.0476      29860.8               50.00     Sequence
         IAd  313  RQDLDDTDRDRSIGS  RQDLDDTDR        0.0473      29983.8               50.00     Sequence
         IAd   11  ELGEILGFGGMSEVH  LGEILGFGG        0.0453      30642.1               50.00     Sequence
         IAd  414  EITVNVSTGPEQREI  EITVNVSTG        0.0450      30732.7               50.00     Sequence
         IAd  463  VGKVIGTNPPANQTS  GKVIGTNPP        0.0449      30765.6               50.00     Sequence
         IAd  253  ALAKNPENRYQTAAE  NPENRYQTA        0.0426      31534.4               50.00     Sequence
         IAd  464  GKVIGTNPPANQTSA  GKVIGTNPP        0.0413      31985.9               50.00     Sequence
         IAd  307  RTDPLPRQDLDDTDR  LPRQDLDDT        0.0413      31994.6               50.00     Sequence
         IAd  465  KVIGTNPPANQTSAI  KVIGTNPPA        0.0411      32056.3               50.00     Sequence
         IAd  510  NLNVYGFTKFSQASV  FTKFSQASV        0.0400      32430.2               50.00     Sequence
         IAd  310  PLPRQDLDDTDRDRS  LPRQDLDDT        0.0396      32573.4               50.00     Sequence
         IAd   47  RDPSFYLRFRREAQN  RDPSFYLRF        0.0396      32579.4               50.00     Sequence
         IAd  308  TDPLPRQDLDDTDRD  LPRQDLDDT        0.0390      32774.9               50.00     Sequence
         IAd  311  LPRQDLDDTDRDRSI  LPRQDLDDT        0.0387      32889.6               50.00     Sequence
         IAd  444  TAAGFGRFKQANSPS  RFKQANSPS        0.0380      33154.4               50.00     Sequence
         IAd  309  DPLPRQDLDDTDRDR  LPRQDLDDT        0.0379      33190.6               50.00     Sequence
         IAd  509  KNLNVYGFTKFSQAS  YGFTKFSQA        0.0374      33369.9               50.00     Sequence
         IAd  388  KPDSTIPPDHVIGTD  IPPDHVIGT        0.0374      33373.9               50.00     Sequence
         IAd  416  TVNVSTGPEQREIPD  GPEQREIPD        0.0372      33419.8               50.00     Sequence
         IAd   48  DPSFYLRFRREAQNA  RFRREAQNA        0.0366      33654.2               50.00     Sequence
         IAd  531  GEVTGTNPPAGTTVP  EVTGTNPPA        0.0354      34107.7               50.00     Sequence
         IAd  415  ITVNVSTGPEQREIP  TVNVSTGPE        0.0351      34207.1               50.00     Sequence
         IAd    0  MTTPSHLSDRYELGE  SHLSDRYEL        0.0346      34380.4               50.00     Sequence
         IAd  207  EVLTGEPPFTGDSPV  LTGEPPFTG        0.0340      34620.8               50.00     Sequence
         IAd  208  VLTGEPPFTGDSPVS  LTGEPPFTG        0.0339      34641.4               50.00     Sequence
         IAd  466  VIGTNPPANQTSAIT  PANQTSAIT        0.0320      35378.5               50.00     Sequence
         IAd  229  REDPIPPSARHEGLS  REDPIPPSA        0.0317      35464.3               50.00     Sequence
         IAd  230  EDPIPPSARHEGLSA  SARHEGLSA        0.0312      35664.8               50.00     Sequence
         IAd  389  PDSTIPPDHVIGTDP  IPPDHVIGT        0.0295      36317.9               50.00     Sequence
         IAd  529  PAGEVTGTNPPAGTT  PAGEVTGTN        0.0279      36960.9               50.00     Sequence
         IAd  252  KALAKNPENRYQTAA  KALAKNPEN        0.0273      37194.7               50.00     Sequence
         IAd  312  PRQDLDDTDRDRSIG  RQDLDDTDR        0.0223      39276.8               50.00     Sequence
         IAd  530  AGEVTGTNPPAGTTV  EVTGTNPPA        0.0219      39438.2               50.00     Sequence
-----------------------------------------------------------------------------------------------

Allele: IAd. Number of high binders 0. Number of weak binders 23. Number of peptides 612

-----------------------------------------------------------------------------------------------
-----------------------------------------------------------------------------------------------
      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
-----------------------------------------------------------------------------------------------
         IAs  351  TFGGITRDVQVPDVR  RDVQVPDVR        0.5490        131.5         WB      0.10     Sequence
         IAs  352  FGGITRDVQVPDVRG  RDVQVPDVR        0.5351        153.0         WB      0.10     Sequence
         IAs  353  GGITRDVQVPDVRGQ  RDVQVPDVR        0.5220        176.2         WB      0.10     Sequence
         IAs  354  GITRDVQVPDVRGQS  RDVQVPDVR        0.5126        195.1         WB      0.15     Sequence
         IAs  356  TRDVQVPDVRGQSSA  RDVQVPDVR        0.4984        227.5         WB      0.15     Sequence
         IAs  355  ITRDVQVPDVRGQSS  RDVQVPDVR        0.4955        234.8         WB      0.15     Sequence
         IAs  516  FTKFSQASVDSPRPA  ASVDSPRPA        0.4124        577.2                 0.80     Sequence
         IAs  517  TKFSQASVDSPRPAG  ASVDSPRPA        0.3975        677.9                 0.80     Sequence
         IAs  378  NRGFKIRTLQKPDST  RTLQKPDST        0.3877        754.0                 0.80     Sequence
         IAs  518  KFSQASVDSPRPAGE  ASVDSPRPA        0.3844        781.1                 0.80     Sequence
         IAs  519  FSQASVDSPRPAGEV  ASVDSPRPA        0.3762        854.0                 1.00     Sequence
         IAs  379  RGFKIRTLQKPDSTI  RTLQKPDST        0.3747        867.5                 1.00     Sequence
         IAs  357  RDVQVPDVRGQSSAD  RDVQVPDVR        0.3680        932.9                 1.00     Sequence
         IAs  382  KIRTLQKPDSTIPPD  RTLQKPDST        0.3623        992.5                 2.00     Sequence
         IAs  380  GFKIRTLQKPDSTIP  RTLQKPDST        0.3616       1000.1                 2.00     Sequence
         IAs  381  FKIRTLQKPDSTIPP  RTLQKPDST        0.3536       1089.5                 2.00     Sequence
         IAs  383  IRTLQKPDSTIPPDH  RTLQKPDST        0.3500       1133.6                 2.00     Sequence
         IAs  384  RTLQKPDSTIPPDHV  RTLQKPDST        0.3485       1152.0                 2.00     Sequence
         IAs   57  REAQNAAALNHPAIV  AALNHPAIV        0.3199       1569.3                 2.00     Sequence
         IAs  520  SQASVDSPRPAGEVT  ASVDSPRPA        0.3141       1671.5                 4.00     Sequence
         IAs   58  EAQNAAALNHPAIVA  AALNHPAIV        0.3125       1700.6                 4.00     Sequence
         IAs  521  QASVDSPRPAGEVTG  ASVDSPRPA        0.3102       1742.6                 4.00     Sequence
         IAs   60  QNAAALNHPAIVAVY  QNAAALNHP        0.3080       1784.8                 4.00     Sequence
         IAs   59  AQNAAALNHPAIVAV  AALNHPAIV        0.3069       1807.5                 4.00     Sequence
         IAs  130  QNGIIHRDVKPANIM  RDVKPANIM        0.2988       1972.5                 4.00     Sequence
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAs | 515 | GFTKFSQASVDSPRP | QASVDSPRP | 0.2855 | 2277.9 | 4.00 | Sequence |
| IAs | 446 | AGFGRFKQANSPSTP | KQANSPSTP | 0.2834 | 2330.8 | 4.00 | Sequence |
| IAs | 596 | GSQHNRVVYQNPPAG | RVVYQNPPA | 0.2828 | 2344.8 | 4.00 | Sequence |
| IAs | 131 | NGIIHRDVKPANIMI | RDVKPANIM | 0.2821 | 2363.6 | 4.00 | Sequence |
| IAs | 595 | GGSQHNRVVYQNPPA | RVVYQNPPA | 0.2793 | 2435.0 | 4.00 | Sequence |
| IAs | 448 | FGRFKQANSPSTPEL | KQANSPSTP | 0.2746 | 2561.4 | 4.00 | Sequence |
| IAs | 447 | GFGRFKQANSPSTPE | KQANSPSTP | 0.2740 | 2580.0 | 4.00 | Sequence |
| IAs | 449 | GRFKQANSPSTPELV | KQANSPSTP | 0.2731 | 2604.3 | 4.00 | Sequence |
| IAs | 597 | SQHNRVVYQNPPAGT | RVVYQNPPA | 0.2723 | 2626.9 | 4.00 | Sequence |
| IAs | 273 | VRVHNGEPPEAPKVL | EPPEAPKVL | 0.2696 | 2703.5 | 4.00 | Sequence |
| IAs | 599 | HNRVVYQNPPAGTGV | RVVYQNPPA | 0.2685 | 2737.8 | 4.00 | Sequence |
| IAs | 132 | GIIHRDVKPANIMIS | RDVKPANIM | 0.2683 | 2743.0 | 4.00 | Sequence |
| IAs | 598 | QHNRVVYQNPPAGTG | RVVYQNPPA | 0.2639 | 2875.4 | 8.00 | Sequence |
| IAs | 56 | RREAQNAAALNHPAI | QNAAALNHP | 0.2624 | 2923.5 | 8.00 | Sequence |
| IAs | 459 | TPELVGKVIGTNPPA | KVIGTNPPA | 0.2616 | 2948.0 | 8.00 | Sequence |
| IAs | 460 | PELVGKVIGTNPPAN | KVIGTNPPA | 0.2594 | 3019.7 | 8.00 | Sequence |
| IAs | 133 | IIHRDVKPANIMISA | RDVKPANIM | 0.2590 | 3032.3 | 8.00 | Sequence |
| IAs | 451 | FKQANSPSTPELVGK | KQANSPSTP | 0.2578 | 3071.5 | 8.00 | Sequence |
| IAs | 452 | KQANSPSTPELVGKV | KQANSPSTP | 0.2555 | 3149.5 | 8.00 | Sequence |
| IAs | 461 | ELVGKVIGTNPPANQ | KVIGTNPPA | 0.2551 | 3163.2 | 8.00 | Sequence |
| IAs | 450 | RFKQANSPSTPELVG | KQANSPSTP | 0.2516 | 3286.9 | 8.00 | Sequence |
| IAs | 274 | RVHNGEPPEAPKVLT | EPPEAPKVL | 0.2497 | 3355.5 | 8.00 | Sequence |
| IAs | 462 | LVGKVIGTNPPANQT | KVIGTNPPA | 0.2471 | 3451.7 | 8.00 | Sequence |
| IAs | 463 | VGKVIGTNPPANQTS | KVIGTNPPA | 0.2436 | 3581.7 | 8.00 | Sequence |
| IAs | 464 | GKVIGTNPPANQTSA | KVIGTNPPA | 0.2391 | 3762.8 | 8.00 | Sequence |
| IAs | 61 | NAAALNHPAIVAVYD | AALNHPAIV | 0.2382 | 3797.7 | 8.00 | Sequence |
| IAs | 600 | NRVVYQNPPAGTGVN | RVVYQNPPA | 0.2345 | 3952.2 | 8.00 | Sequence |
| IAs | 135 | HRDVKPANIMISATN | RDVKPANIM | 0.2266 | 4308.8 | 8.00 | Sequence |
| IAs | 275 | VHNGEPPEAPKVLTD | EPPEAPKVL | 0.2257 | 4348.9 | 8.00 | Sequence |
| IAs | 276 | HNGEPPEAPKVLTDA | EPPEAPKVL | 0.2194 | 4654.1 | 8.00 | Sequence |
| IAs | 134 | IHRDVKPANIMISAT | RDVKPANIM | 0.2176 | 4749.1 | 8.00 | Sequence |
| IAs | 324 | SIGSVGRWVAVVAVL | RWVAVVAVL | 0.2163 | 4815.9 | 8.00 | Sequence |
| IAs | 62 | AAALNHPAIVAVYDT | AALNHPAIV | 0.2141 | 4933.4 | 8.00 | Sequence |
| IAs | 496 | IPDVAGQTVDVAQKN | QTVDVAQKN | 0.2061 | 5373.9 | 16.00 | Sequence |
| IAs | 247 | DAVVLKALAKNPENR | KALAKNPEN | 0.2059 | 5385.9 | 16.00 | Sequence |
| IAs | 386 | LQKPDSTIPPDHVIG | KPDSTIPPD | 0.2048 | 5454.0 | 16.00 | Sequence |
| IAs | 498 | DVAGQTVDVAQKNLN | QTVDVAQKN | 0.2037 | 5517.3 | 16.00 | Sequence |
| IAs | 377 | QNRGFKIRTLQKPDS | FKIRTLQKP | 0.2016 | 5646.7 | 16.00 | Sequence |
| IAs | 552 | LQVSKGNQFVMPDLS | NQFVMPDLS | 0.2015 | 5650.3 | 16.00 | Sequence |
| IAs | 136 | RDVKPANIMISATNA | RDVKPANIM | 0.2015 | 5653.0 | 16.00 | Sequence |
| IAs | 298 | SAAGNLSGPRTDPLP | SAAGNLSGP | 0.2010 | 5679.8 | 16.00 | Sequence |
| IAs | 385 | TLQKPDSTIPPDHVI | KPDSTIPPD | 0.2004 | 5720.2 | 16.00 | Sequence |
| IAs | 497 | PDVAGQTVDVAQKNL | QTVDVAQKN | 0.2000 | 5742.1 | 16.00 | Sequence |
| IAs | 499 | VAGQTVDVAQKNLNV | QTVDVAQKN | 0.1985 | 5835.8 | 16.00 | Sequence |
| IAs | 458 | STPELVGKVIGTNPP | GKVIGTNPP | 0.1983 | 5852.4 | 16.00 | Sequence |
| IAs | 246 | LDAVVLKALAKNPEN | KALAKNPEN | 0.1970 | 5935.4 | 16.00 | Sequence |
| IAs | 248 | AVVLKALAKNPENRY | KALAKNPEN | 0.1959 | 6005.8 | 16.00 | Sequence |
| IAs | 387 | QKPDSTIPPDHVIGT | KPDSTIPPD | 0.1958 | 6011.9 | 16.00 | Sequence |
| IAs | 250 | VLKALAKNPENRYQT | KALAKNPEN | 0.1931 | 6188.6 | 16.00 | Sequence |
| IAs | 388 | KPDSTIPPDHVIGTD | KPDSTIPPD | 0.1914 | 6301.6 | 16.00 | Sequence |
| IAs | 325 | IGSVGRWVAVVAVLA | RWVAVVAVL | 0.1913 | 6307.9 | 16.00 | Sequence |
| IAs | 249 | VVLKALAKNPENRYQ | KALAKNPEN | 0.1903 | 6381.2 | 16.00 | Sequence |
| IAs | 350 | NTFGGITRDVQVPDV | GITRDVQVP | 0.1887 | 6493.8 | 16.00 | Sequence |
| IAs | 171 | QTAAVIGTAQYLSPE | AVIGTAQYL | 0.1885 | 6502.2 | 16.00 | Sequence |
| IAs | 555 | SKGNQFVMPDLSGMF | NQFVMPDLS | 0.1879 | 6550.3 | 16.00 | Sequence |
| IAs | 297 | SSAAGNLSGPRTDPL | GNLSGPRTD | 0.1855 | 6719.8 | 16.00 | Sequence |
| IAs | 272 | LVRVHNGEPPEAPKV | VRVHNGEPP | 0.1854 | 6724.2 | 16.00 | Sequence |
| IAs | 220 | PVSVAYQHVREDPIP | QHVREDPIP | 0.1851 | 6747.7 | 16.00 | Sequence |
| IAs | 55 | FRREAQNAAALNHPA | QNAAALNHP | 0.1834 | 6876.4 | 16.00 | Sequence |
| IAs | 553 | QVSKGNQFVMPDLSG | NQFVMPDLS | 0.1831 | 6897.1 | 16.00 | Sequence |
| IAs | 435 | TYAEAVKKLTAAGFG | KKLTAAGFG | 0.1816 | 7010.7 | 16.00 | Sequence |
| IAs | 33 | HRDVAVKVLRADLAR | VKVLRADLA | 0.1812 | 7039.4 | 16.00 | Sequence |
| IAs | 279 | EPPEAPKVLTDAERT | EPPEAPKVL | 0.1805 | 7095.4 | 16.00 | Sequence |
| IAs | 36 | VAVKVLRADLARDPS | VKVLRADLA | 0.1801 | 7121.1 | 16.00 | Sequence |
| IAs | 326 | GSVGRWVAVVAVLAV | RWVAVVAVL | 0.1794 | 7175.0 | 16.00 | Sequence |
| IAs | 522 | ASVDSPRPAGEVTGT | ASVDSPRPA | 0.1788 | 7225.6 | 16.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAs | 75 | DTGEAETPAGPLPYI | TPAGPLPYI | 0.1778 | 7305.2 | 16.00 | Sequence |
| IAs | 415 | ITVNVSTGPEQREIP | VNVSTGPEQ | 0.1774 | 7334.3 | 16.00 | Sequence |
| IAs | 295 | LLSSAAGNLSGPRTD | AAGNLSGPR | 0.1772 | 7347.5 | 16.00 | Sequence |
| IAs | 554 | VSKGNQFVMPDLSGM | NQFVMPDLS | 0.1772 | 7350.5 | 16.00 | Sequence |
| IAs | 168 | SVTQTAAVIGTAQYL | AVIGTAQYL | 0.1772 | 7350.8 | 16.00 | Sequence |
| IAs | 32 | LHRDVAVKVLRADLA | VKVLRADLA | 0.1770 | 7369.5 | 16.00 | Sequence |
| IAs | 601 | RVVYQNPPAGTGVNR | RVVYQNPPA | 0.1765 | 7405.3 | 16.00 | Sequence |
| IAs | 488 | GSGPATKDIPDVAGQ | SGPATKDIP | 0.1765 | 7406.1 | 16.00 | Sequence |
| IAs | 278 | GEPPEAPKVLTDAER | EPPEAPKVL | 0.1764 | 7417.2 | 16.00 | Sequence |
| IAs | 221 | VSVAYQHVREDPIPP | QHVREDPIP | 0.1757 | 7474.5 | 16.00 | Sequence |
| IAs | 514 | YGFTKFSQASVDSPR | FSQASVDSP | 0.1751 | 7516.3 | 16.00 | Sequence |
| IAs | 35 | DVAVKVLRADLARDP | VKVLRADLA | 0.1750 | 7528.3 | 16.00 | Sequence |
| IAs | 34 | RDVAVKVLRADLARD | VKVLRADLA | 0.1745 | 7571.7 | 16.00 | Sequence |
| IAs | 327 | SVGRWVAVVAVLAVL | RWVAVVAVL | 0.1733 | 7667.1 | 16.00 | Sequence |
| IAs | 416 | TVNVSTGPEQREIPD | TVNVSTGPE | 0.1733 | 7669.6 | 16.00 | Sequence |
| IAs | 169 | VTQTAAVIGTAQYLS | AVIGTAQYL | 0.1732 | 7674.1 | 16.00 | Sequence |
| IAs | 296 | LSSAAGNLSGPRTDP | AAGNLSGPR | 0.1727 | 7719.4 | 16.00 | Sequence |
| IAs | 170 | TQTAAVIGTAQYLSP | AVIGTAQYL | 0.1727 | 7719.9 | 16.00 | Sequence |
| IAs | 594 | AGGSQHNRVVYQNPP | NRVVYQNPP | 0.1726 | 7721.9 | 16.00 | Sequence |
| IAs | 489 | SGPATKDIPDVAGQT | SGPATKDIP | 0.1716 | 7811.5 | 16.00 | Sequence |
| IAs | 271 | DLVRVHNGEPPEAPK | HNGEPPEAP | 0.1716 | 7813.7 | 16.00 | Sequence |
| IAs | 270 | ADLVRVHNGEPPEAP | HNGEPPEAP | 0.1699 | 7952.2 | 16.00 | Sequence |
| IAs | 486 | IVGSGPATKDIPDVA | SGPATKDIP | 0.1697 | 7968.9 | 16.00 | Sequence |
| IAs | 487 | VGSGPATKDIPDVAG | SGPATKDIP | 0.1696 | 7981.5 | 16.00 | Sequence |
| IAs | 401 | TDPAANTSVSAGDEI | TSVSAGDEI | 0.1692 | 8017.2 | 16.00 | Sequence |
| IAs | 556 | KGNQFVMPDLSGMFW | NQFVMPDLS | 0.1689 | 8036.8 | 16.00 | Sequence |
| IAs | 376 | LQNRGFKIRTLQKPD | FKIRTLQKP | 0.1675 | 8161.9 | 16.00 | Sequence |
| IAs | 37 | AVKVLRADLARDPSF | VKVLRADLA | 0.1672 | 8194.4 | 16.00 | Sequence |
| IAs | 74 | YDTGEAETPAGPLPY | AETPAGPLP | 0.1662 | 8282.7 | 16.00 | Sequence |
| IAs | 277 | NGEPPEAPKVLTDAE | EPPEAPKVL | 0.1650 | 8387.3 | 16.00 | Sequence |
| IAs | 605 | QNPPAGTGVNRDGII | TGVNRDGII | 0.1647 | 8414.8 | 16.00 | Sequence |
| IAs | 76 | TGEAETPAGPLPYIV | TPAGPLPYI | 0.1635 | 8524.3 | 16.00 | Sequence |
| IAs | 411 | AGDEITVNVSTGPEQ | VNVSTGPEQ | 0.1621 | 8655.0 | 16.00 | Sequence |
| IAs | 77 | GEAETPAGPLPYIVM | TPAGPLPYI | 0.1604 | 8820.0 | 16.00 | Sequence |
| IAs | 206 | YEVLTGEPPFTGDSP | YEVLTGEPP | 0.1601 | 8840.8 | 16.00 | Sequence |
| IAs | 100 | RDIVHTEGPMTPKRA | EGPMTPKRA | 0.1599 | 8864.7 | 32.00 | Sequence |
| IAs | 54 | RFRREAQNAAALNHP | QNAAALNHP | 0.1595 | 8898.5 | 32.00 | Sequence |
| IAs | 222 | SVAYQHVREDPIPPS | QHVREDPIP | 0.1595 | 8906.7 | 32.00 | Sequence |
| IAs | 551 | ELQVSKGNQFVMPDL | LQVSKGNQF | 0.1584 | 9009.9 | 32.00 | Sequence |
| IAs | 402 | DPAANTSVSAGDEIT | TSVSAGDEI | 0.1579 | 9061.6 | 32.00 | Sequence |
| IAs | 329 | GRWVAVVAVLAVLTV | RWVAVVAVL | 0.1578 | 9063.0 | 32.00 | Sequence |
| IAs | 436 | YAEAVKKLTAAGFGR | KKLTAAGFG | 0.1578 | 9068.5 | 32.00 | Sequence |
| IAs | 606 | NPPAGTGVNRDGIIT | TGVNRDGII | 0.1578 | 9070.8 | 32.00 | Sequence |
| IAs | 255 | AKNPENRYQTAAEMR | RYQTAAEMR | 0.1577 | 9079.3 | 32.00 | Sequence |
| IAs | 485 | IIVGSGPATKDIPDV | SGPATKDIP | 0.1568 | 9169.1 | 32.00 | Sequence |
| IAs | 412 | GDEITVNVSTGPEQR | VNVSTGPEQ | 0.1563 | 9220.3 | 32.00 | Sequence |
| IAs | 79 | AETPAGPLPYIVMEY | AETPAGPLP | 0.1560 | 9250.3 | 32.00 | Sequence |
| IAs | 268 | MRADLVRVHNGEPPE | VRVHNGEPP | 0.1559 | 9252.1 | 32.00 | Sequence |
| IAs | 328 | VGRWVAVVAVLAVLT | RWVAVVAVL | 0.1559 | 9255.1 | 32.00 | Sequence |
| IAs | 483 | VIIIVGSGPATKDIP | SGPATKDIP | 0.1551 | 9338.2 | 32.00 | Sequence |
| IAs | 537 | NPPAGTTVPVDSVIE | NPPAGTTVP | 0.1550 | 9346.0 | 32.00 | Sequence |
| IAs | 63 | AALNHPAIVAVYDTG | AALNHPAIV | 0.1547 | 9372.2 | 32.00 | Sequence |
| IAs | 213 | PPFTGDSPVSVAYQH | SPVSVAYQH | 0.1542 | 9430.9 | 32.00 | Sequence |
| IAs | 223 | VAYQHVREDPIPPSA | QHVREDPIP | 0.1530 | 9550.1 | 32.00 | Sequence |
| IAs | 375 | TLQNRGFKIRTLQKP | RGFKIRTLQ | 0.1523 | 9620.4 | 32.00 | Sequence |
| IAs | 536 | TNPPAGTTVPVDSVI | NPPAGTTVP | 0.1523 | 9627.1 | 32.00 | Sequence |
| IAs | 225 | YQHVREDPIPPSARH | QHVREDPIP | 0.1522 | 9630.7 | 32.00 | Sequence |
| IAs | 484 | IIIVGSGPATKDIPD | SGPATKDIP | 0.1518 | 9675.9 | 32.00 | Sequence |
| IAs | 260 | NRYQTAAEMRADLVR | RYQTAAEMR | 0.1517 | 9682.8 | 32.00 | Sequence |
| IAs | 202 | GCVLYEVLTGEPPFT | YEVLTGEPP | 0.1517 | 9690.7 | 32.00 | Sequence |
| IAs | 413 | DEITVNVSTGPEQRE | TVNVSTGPE | 0.1498 | 9883.8 | 32.00 | Sequence |
| IAs | 78 | EAETPAGPLPYIVME | AETPAGPLP | 0.1492 | 9955.9 | 32.00 | Sequence |
| IAs | 205 | LYEVLTGEPPFTGDS | YEVLTGEPP | 0.1491 | 9962.9 | 32.00 | Sequence |
| IAs | 101 | DIVHTEGPMTPKRAI | VHTEGPMTP | 0.1490 | 9971.3 | 32.00 | Sequence |
| IAs | 414 | EITVNVSTGPEQREI | TVNVSTGPE | 0.1488 | 9989.9 | 32.00 | Sequence |
| IAs | 261 | RYQTAAEMRADLVRV | RYQTAAEMR | 0.1481 | 10068.7 | 32.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAs | 294 | SLLSSAAGNLSGPRT | AAGNLSGPR | 0.1474 | 10142.4 | 32.00 | Sequence |
| IAs | 81 | TPAGPLPYIVMEYVD | LPYIVMEYV | 0.1474 | 10149.8 | 32.00 | Sequence |
| IAs | 214 | PFTGDSPVSVAYQHV | SPVSVAYQH | 0.1473 | 10154.0 | 32.00 | Sequence |
| IAs | 224 | AYQHVREDPIPPSAR | QHVREDPIP | 0.1472 | 10171.4 | 32.00 | Sequence |
| IAs | 219 | SPVSVAYQHVREDPI | SPVSVAYQH | 0.1472 | 10172.8 | 32.00 | Sequence |
| IAs | 80 | ETPAGPLPYIVMEYV | LPYIVMEYV | 0.1470 | 10190.2 | 32.00 | Sequence |
| IAs | 201 | LGCVLYEVLTGEPPF | YEVLTGEPP | 0.1463 | 10270.8 | 32.00 | Sequence |
| IAs | 501 | GQTVDVAQKNLNVYG | QTVDVAQKN | 0.1461 | 10296.3 | 32.00 | Sequence |
| IAs | 31 | RLHRDVAVKVLRADL | RDVAVKVLR | 0.1459 | 10317.1 | 32.00 | Sequence |
| IAs | 607 | PPAGTGVNRDGIITL | TGVNRDGII | 0.1458 | 10322.3 | 32.00 | Sequence |
| IAs | 73 | VYDTGEAETPAGPLP | AETPAGPLP | 0.1453 | 10384.3 | 32.00 | Sequence |
| IAs | 174 | AVIGTAQYLSPEQAR | AVIGTAQYL | 0.1450 | 10418.6 | 32.00 | Sequence |
| IAs | 204 | VLYEVLTGEPPFTGD | YEVLTGEPP | 0.1448 | 10441.8 | 32.00 | Sequence |
| IAs | 256 | KNPENRYQTAAEMRA | RYQTAAEMR | 0.1444 | 10484.1 | 32.00 | Sequence |
| IAs | 534 | TGTNPPAGTTVPVDS | AGTTVPVDS | 0.1443 | 10493.8 | 32.00 | Sequence |
| IAs | 203 | CVLYEVLTGEPPFTG | YEVLTGEPP | 0.1442 | 10506.5 | 32.00 | Sequence |
| IAs | 531 | GEVTGTNPPAGTTVP | GEVTGTNPP | 0.1442 | 10507.6 | 32.00 | Sequence |
| IAs | 103 | VHTEGPMTPKRAIEV | VHTEGPMTP | 0.1442 | 10508.3 | 32.00 | Sequence |
| IAs | 500 | AGQTVDVAQKNLNVY | QTVDVAQKN | 0.1441 | 10512.3 | 32.00 | Sequence |
| IAs | 608 | PAGTGVNRDGIITLR | TGVNRDGII | 0.1441 | 10518.8 | 32.00 | Sequence |
| IAs | 403 | PAANTSVSAGDEITV | TSVSAGDEI | 0.1440 | 10532.2 | 32.00 | Sequence |
| IAs | 437 | AEAVKKLTAAGFGRF | KKLTAAGFG | 0.1434 | 10593.3 | 32.00 | Sequence |
| IAs | 102 | IVHTEGPMTPKRAIE | EGPMTPKRA | 0.1431 | 10632.0 | 32.00 | Sequence |
| IAs | 245 | DLDAVVLKALAKNPE | LKALAKNPE | 0.1428 | 10665.0 | 32.00 | Sequence |
| IAs | 293 | TSLLSSAAGNLSGPR | AAGNLSGPR | 0.1426 | 10684.8 | 32.00 | Sequence |
| IAs | 535 | GTNPPAGTTVPVDSV | AGTTVPVDS | 0.1425 | 10698.4 | 32.00 | Sequence |
| IAs | 200 | SLGCVLYEVLTGEPP | YEVLTGEPP | 0.1419 | 10763.9 | 32.00 | Sequence |
| IAs | 251 | LKALAKNPENRYQTA | LKALAKNPE | 0.1417 | 10797.9 | 32.00 | Sequence |
| IAs | 38 | VKVLRADLARDPSFY | VKVLRADLA | 0.1416 | 10807.7 | 32.00 | Sequence |
| IAs | 564 | DLSGMFWVDAEPRLR | MFWVDAEPR | 0.1408 | 10893.8 | 32.00 | Sequence |
| IAs | 173 | AAVIGTAQYLSPEQA | AQYLSPEQA | 0.1408 | 10898.9 | 32.00 | Sequence |
| IAs | 440 | VKKLTAAGFGRFKQA | KKLTAAGFG | 0.1408 | 10899.5 | 32.00 | Sequence |
| IAs | 330 | RWVAVVAVLAVLTVV | RWVAVVAVL | 0.1407 | 10913.2 | 32.00 | Sequence |
| IAs | 267 | EMRADLVRVHNGEPP | VRVHNGEPP | 0.1403 | 10953.2 | 32.00 | Sequence |
| IAs | 215 | FTGDSPVSVAYQHVR | SPVSVAYQH | 0.1400 | 10995.3 | 32.00 | Sequence |
| IAs | 269 | RADLVRVHNGEPPEA | VRVHNGEPP | 0.1397 | 11023.2 | 32.00 | Sequence |
| IAs | 257 | NPENRYQTAAEMRAD | RYQTAAEMR | 0.1396 | 11041.5 | 32.00 | Sequence |
| IAs | 557 | GNQFVMPDLSGMFWV | NQFVMPDLS | 0.1395 | 11046.7 | 32.00 | Sequence |
| IAs | 218 | DSPVSVAYQHVREDP | SPVSVAYQH | 0.1395 | 11053.1 | 32.00 | Sequence |
| IAs | 404 | AANTSVSAGDEITVN | TSVSAGDEI | 0.1393 | 11077.8 | 32.00 | Sequence |
| IAs | 439 | AVKKLTAAGFGRFKQ | KKLTAAGFG | 0.1392 | 11090.2 | 32.00 | Sequence |
| IAs | 259 | ENRYQTAAEMRADLV | RYQTAAEMR | 0.1384 | 11187.7 | 32.00 | Sequence |
| IAs | 441 | KKLTAAGFGRFKQAN | KKLTAAGFG | 0.1382 | 11212.3 | 32.00 | Sequence |
| IAs | 465 | KVIGTNPPANQTSAI | KVIGTNPPA | 0.1379 | 11251.2 | 32.00 | Sequence |
| IAs | 528 | RPAGEVTGTNPPAGT | GEVTGTNPP | 0.1367 | 11394.2 | 32.00 | Sequence |
| IAs | 563 | PDLSGMFWVDAEPRL | MFWVDAEPR | 0.1364 | 11429.0 | 32.00 | Sequence |
| IAs | 513 | VYGFTKFSQASVDSP | TKFSQASVD | 0.1361 | 11471.0 | 32.00 | Sequence |
| IAs | 527 | PRPAGEVTGTNPPAG | GEVTGTNPP | 0.1360 | 11485.1 | 32.00 | Sequence |
| IAs | 323 | RSIGSVGRWVAVVAV | RSIGSVGRW | 0.1346 | 11649.2 | 32.00 | Sequence |
| IAs | 610 | GTGVNRDGIITLRFG | TGVNRDGII | 0.1346 | 11658.1 | 32.00 | Sequence |
| IAs | 217 | GDSPVSVAYQHVRED | SPVSVAYQH | 0.1342 | 11703.3 | 32.00 | Sequence |
| IAs | 129 | HQNGIIHRDVKPANI | HRDVKPANI | 0.1333 | 11815.2 | 32.00 | Sequence |
| IAs | 226 | QHVREDPIPPSARHE | QHVREDPIP | 0.1329 | 11865.2 | 32.00 | Sequence |
| IAs | 280 | PPEAPKVLTDAERTS | KVLTDAERT | 0.1327 | 11893.6 | 32.00 | Sequence |
| IAs | 258 | PENRYQTAAEMRADL | RYQTAAEMR | 0.1324 | 11934.2 | 32.00 | Sequence |
| IAs | 72 | AVYDTGEAETPAGPL | GEAETPAGP | 0.1321 | 11968.0 | 32.00 | Sequence |
| IAs | 565 | LSGMFWVDAEPRLRA | MFWVDAEPR | 0.1314 | 12058.4 | 32.00 | Sequence |
| IAs | 216 | TGDSPVSVAYQHVRE | SPVSVAYQH | 0.1314 | 12060.2 | 32.00 | Sequence |
| IAs | 410 | SAGDEITVNVSTGPE | ITVNVSTGP | 0.1314 | 12070.6 | 32.00 | Sequence |
| IAs | 299 | AAGNLSGPRTDPLPR | AAGNLSGPR | 0.1311 | 12105.0 | 32.00 | Sequence |
| IAs | 604 | YQNPPAGTGVNRDGI | GTGVNRDGI | 0.1302 | 12220.0 | 32.00 | Sequence |
| IAs | 301 | GNLSGPRTDPLPRQD | RTDPLPRQD | 0.1298 | 12274.8 | 32.00 | Sequence |
| IAs | 65 | LNHPAIVAVYDTGEA | AIVAVYDTG | 0.1297 | 12286.3 | 32.00 | Sequence |
| IAs | 41 | LRADLARDPSFYLRF | LRADLARDP | 0.1295 | 12310.9 | 32.00 | Sequence |
| IAs | 495 | DIPDVAGQTVDVAQK | VAGQTVDVA | 0.1286 | 12434.2 | 32.00 | Sequence |
| IAs | 64 | ALNHPAIVAVYDTGE | AIVAVYDTG | 0.1286 | 12439.7 | 32.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAs | 609 | AGTGVNRDGIITLRF | TGVNRDGII | 0.1286 | 12440.2 | 32.00 | Sequence |
| IAs | 438 | EAVKKLTAAGFGRFK | KKLTAAGFG | 0.1285 | 12454.6 | 32.00 | Sequence |
| IAs | 530 | AGEVTGTNPPAGTTV | GEVTGTNPP | 0.1284 | 12467.3 | 32.00 | Sequence |
| IAs | 281 | PEAPKVLTDAERTSL | KVLTDAERT | 0.1276 | 12577.7 | 32.00 | Sequence |
| IAs | 176 | IGTAQYLSPEQARGD | GTAQYLSPE | 0.1273 | 12616.8 | 32.00 | Sequence |
| IAs | 562 | MPDLSGMFWVDAEPR | MFWVDAEPR | 0.1270 | 12659.1 | 32.00 | Sequence |
| IAs | 406 | NTSVSAGDEITVNVS | TSVSAGDEI | 0.1267 | 12690.2 | 32.00 | Sequence |
| IAs | 175 | VIGTAQYLSPEQARG | AQYLSPEQA | 0.1263 | 12756.2 | 32.00 | Sequence |
| IAs | 40 | VLRADLARDPSFYLR | LRADLARDP | 0.1258 | 12819.1 | 32.00 | Sequence |
| IAs | 405 | ANTSVSAGDEITVNV | TSVSAGDEI | 0.1254 | 12878.3 | 32.00 | Sequence |
| IAs | 172 | TAAVIGTAQYLSPEQ | AVIGTAQYL | 0.1252 | 12906.0 | 32.00 | Sequence |
| IAs | 529 | PAGEVTGTNPPAGTT | GEVTGTNPP | 0.1249 | 12941.2 | 32.00 | Sequence |
| IAs | 39 | KVLRADLARDPSFYL | LRADLARDP | 0.1245 | 13000.4 | 32.00 | Sequence |
| IAs | 282 | EAPKVLTDAERTSLL | KVLTDAERT | 0.1234 | 13159.5 | 32.00 | Sequence |
| IAs | 526 | SPRPAGEVTGTNPPA | GEVTGTNPP | 0.1219 | 13371.9 | 32.00 | Sequence |
| IAs | 99 | LRDIVHTEGPMTPKR | TEGPMTPKR | 0.1211 | 13480.6 | 32.00 | Sequence |
| IAs | 533 | VTGTNPPAGTTVPVD | VTGTNPPAG | 0.1207 | 13552.1 | 32.00 | Sequence |
| IAs | 94 | VDGVTLRDIVHTEGP | VDGVTLRDI | 0.1206 | 13556.8 | 32.00 | Sequence |
| IAs | 302 | NLSGPRTDPLPRQDL | RTDPLPRQD | 0.1196 | 13705.3 | 32.00 | Sequence |
| IAs | 86 | LPYIVMEYVDGVTLR | LPYIVMEYV | 0.1189 | 13814.0 | 32.00 | Sequence |
| IAs | 303 | LSGPRTDPLPRQDLD | LSGPRTDPL | 0.1182 | 13917.6 | 32.00 | Sequence |
| IAs | 110 | TPKRAIEVIADACQA | RAIEVIADA | 0.1175 | 14023.5 | 32.00 | Sequence |
| IAs | 550 | IELQVSKGNQFVMPD | SKGNQFVMP | 0.1174 | 14042.0 | 32.00 | Sequence |
| IAs | 112 | KRAIEVIADACQALN | RAIEVIADA | 0.1169 | 14113.0 | 32.00 | Sequence |
| IAs | 143 | IMISATNAVKVMDFG | NAVKVMDFG | 0.1168 | 14124.1 | 32.00 | Sequence |
| IAs | 104 | HTEGPMTPKRAIEVI | EGPMTPKRA | 0.1166 | 14165.6 | 32.00 | Sequence |
| IAs | 71 | VAVYDTGEAETPAGP | GEAETPAGP | 0.1161 | 14232.9 | 32.00 | Sequence |
| IAs | 503 | TVDVAQKNLNVYGFT | KNLNVYGFT | 0.1157 | 14291.1 | 32.00 | Sequence |
| IAs | 167 | NSVTQTAAVIGTAQY | AAVIGTAQY | 0.1154 | 14339.5 | 32.00 | Sequence |
| IAs | 300 | AGNLSGPRTDPLPRQ | LSGPRTDPL | 0.1149 | 14419.3 | 32.00 | Sequence |
| IAs | 263 | QTAAEMRADLVRVHN | QTAAEMRAD | 0.1148 | 14443.1 | 32.00 | Sequence |
| IAs | 262 | YQTAAEMRADLVRVH | QTAAEMRAD | 0.1147 | 14450.3 | 32.00 | Sequence |
| IAs | 111 | PKRAIEVIADACQAL | RAIEVIADA | 0.1123 | 14830.6 | 32.00 | Sequence |
| IAs | 532 | EVTGTNPPAGTTVPV | VTGTNPPAG | 0.1122 | 14847.8 | 32.00 | Sequence |
| IAs | 177 | GTAQYLSPEQARGDS | GTAQYLSPE | 0.1112 | 15009.0 | 32.00 | Sequence |
| IAs | 113 | RAIEVIADACQALNF | RAIEVIADA | 0.1112 | 15013.8 | 32.00 | Sequence |
| IAs | 445 | AAGFGRFKQANSPST | GRFKQANSP | 0.1105 | 15121.3 | 50.00 | Sequence |
| IAs | 567 | GMFWVDAEPRLRALG | MFWVDAEPR | 0.1096 | 15274.5 | 50.00 | Sequence |
| IAs | 453 | QANSPSTPELVGKVI | NSPSTPELV | 0.1093 | 15322.0 | 50.00 | Sequence |
| IAs | 568 | MFWVDAEPRLRALGW | MFWVDAEPR | 0.1090 | 15368.7 | 50.00 | Sequence |
| IAs | 252 | KALAKNPENRYQTAA | KALAKNPEN | 0.1090 | 15368.8 | 50.00 | Sequence |
| IAs | 566 | SGMFWVDAEPRLRAL | MFWVDAEPR | 0.1090 | 15371.2 | 50.00 | Sequence |
| IAs | 502 | QTVDVAQKNLNVYGF | QTVDVAQKN | 0.1085 | 15463.6 | 50.00 | Sequence |
| IAs | 144 | MISATNAVKVMDFGI | NAVKVMDFG | 0.1077 | 15587.4 | 50.00 | Sequence |
| IAs | 16 | LGFGGMSEVHLARDL | SEVHLARDL | 0.1067 | 15759.9 | 50.00 | Sequence |
| IAs | 97 | VTLRDIVHTEGPMTP | DIVHTEGPM | 0.1062 | 15844.5 | 50.00 | Sequence |
| IAs | 538 | PPAGTTVPVDSVIEL | PAGTTVPVD | 0.1061 | 15858.2 | 50.00 | Sequence |
| IAs | 373 | IATLQNRGFKIRTLQ | RGFKIRTLQ | 0.1060 | 15881.7 | 50.00 | Sequence |
| IAs | 98 | TLRDIVHTEGPMTPK | DIVHTEGPM | 0.1053 | 16008.9 | 50.00 | Sequence |
| IAs | 69 | AIVAVYDTGEAETPA | YDTGEAETP | 0.1048 | 16090.9 | 50.00 | Sequence |
| IAs | 28 | RDLRLHRDVAVKVLR | RDVAVKVLR | 0.1043 | 16167.8 | 50.00 | Sequence |
| IAs | 546 | VDSVIELQVSKGNQF | LQVSKGNQF | 0.1039 | 16241.8 | 50.00 | Sequence |
| IAs | 66 | NHPAIVAVYDTGEAE | HPAIVAVYD | 0.1039 | 16253.1 | 50.00 | Sequence |
| IAs | 490 | GPATKDIPDVAGQTV | PATKDIPDV | 0.1037 | 16272.4 | 50.00 | Sequence |
| IAs | 145 | ISATNAVKVMDFGIA | NAVKVMDFG | 0.1019 | 16607.9 | 50.00 | Sequence |
| IAs | 148 | TNAVKVMDFGIARAI | NAVKVMDFG | 0.1016 | 16658.3 | 50.00 | Sequence |
| IAs | 95 | DGVTLRDIVHTEGPM | DIVHTEGPM | 0.1013 | 16712.8 | 50.00 | Sequence |
| IAs | 539 | PAGTTVPVDSVIELQ | PAGTTVPVD | 0.1005 | 16851.7 | 50.00 | Sequence |
| IAs | 138 | VKPANIMISATNAVK | KPANIMISA | 0.1004 | 16882.0 | 50.00 | Sequence |
| IAs | 67 | HPAIVAVYDTGEAET | HPAIVAVYD | 0.0996 | 17016.4 | 50.00 | Sequence |
| IAs | 504 | VDVAQKNLNVYGFTK | KNLNVYGFT | 0.0990 | 17125.4 | 50.00 | Sequence |
| IAs | 418 | NVSTGPEQREIPDVS | STGPEQREI | 0.0989 | 17153.2 | 50.00 | Sequence |
| IAs | 420 | STGPEQREIPDVSTL | STGPEQREI | 0.0989 | 17153.6 | 50.00 | Sequence |
| IAs | 82 | PAGPLPYIVMEYVDG | LPYIVMEYV | 0.0985 | 17214.7 | 50.00 | Sequence |
| IAs | 107 | GPMTPKRAIEVIADA | RAIEVIADA | 0.0983 | 17254.3 | 50.00 | Sequence |
| IAs | 417 | VNVSTGPEQREIPDV | VNVSTGPEQ | 0.0982 | 17284.9 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAs | 165 | SGNSVTQTAAVIGTA | SVTQTAAVI | 0.0978 | 17363.6 | 50.00 | Sequence |
| IAs | 558 | NQFVMPDLSGMFWVD | NQFVMPDLS | 0.0974 | 17438.4 | 50.00 | Sequence |
| IAs | 85 | PLPYIVMEYVDGVTL | LPYIVMEYV | 0.0972 | 17461.4 | 50.00 | Sequence |
| IAs | 68 | PAIVAVYDTGEAETP | AIVAVYDTG | 0.0970 | 17499.1 | 50.00 | Sequence |
| IAs | 374 | ATLQNRGFKIRTLQK | RGFKIRTLQ | 0.0968 | 17540.6 | 50.00 | Sequence |
| IAs | 149 | NAVKVMDFGIARAIA | NAVKVMDFG | 0.0966 | 17576.5 | 50.00 | Sequence |
| IAs | 84 | GPLPYIVMEYVDGVT | LPYIVMEYV | 0.0965 | 17593.8 | 50.00 | Sequence |
| IAs | 30 | LRLHRDVAVKVLRAD | RDVAVKVLR | 0.0965 | 17603.1 | 50.00 | Sequence |
| IAs | 139 | KPANIMISATNAVKV | KPANIMISA | 0.0964 | 17618.4 | 50.00 | Sequence |
| IAs | 444 | TAAGFGRFKQANSPS | GRFKQANSP | 0.0960 | 17687.5 | 50.00 | Sequence |
| IAs | 525 | DSPRPAGEVTGTNPP | GEVTGTNPP | 0.0957 | 17762.1 | 50.00 | Sequence |
| IAs | 147 | ATNAVKVMDFGIARA | NAVKVMDFG | 0.0955 | 17790.8 | 50.00 | Sequence |
| IAs | 83 | AGPLPYIVMEYVDGV | LPYIVMEYV | 0.0951 | 17861.8 | 50.00 | Sequence |
| IAs | 317 | DDTDRDRSIGSVGRW | RSIGSVGRW | 0.0947 | 17943.7 | 50.00 | Sequence |
| IAs | 454 | ANSPSTPELVGKVIG | NSPSTPELV | 0.0943 | 18027.8 | 50.00 | Sequence |
| IAs | 491 | PATKDIPDVAGQTVD | ATKDIPDVA | 0.0942 | 18038.9 | 50.00 | Sequence |
| IAs | 199 | YSLGCVLYEVLTGEP | SLGCVLYEV | 0.0942 | 18043.0 | 50.00 | Sequence |
| IAs | 549 | VIELQVSKGNQFVMP | LQVSKGNQF | 0.0941 | 18069.6 | 50.00 | Sequence |
| IAs | 322 | DRSIGSVGRWVAVVA | RSIGSVGRW | 0.0937 | 18146.9 | 50.00 | Sequence |
| IAs | 137 | DVKPANIMISATNAV | IMISATNAV | 0.0933 | 18217.4 | 50.00 | Sequence |
| IAs | 29 | DLRLHRDVAVKVLRA | RDVAVKVLR | 0.0929 | 18289.8 | 50.00 | Sequence |
| IAs | 146 | SATNAVKVMDFGIAR | NAVKVMDFG | 0.0921 | 18449.3 | 50.00 | Sequence |
| IAs | 17 | GFGGMSEVHLARDLR | SEVHLARDL | 0.0920 | 18472.0 | 50.00 | Sequence |
| IAs | 547 | DSVIELQVSKGNQFV | LQVSKGNQF | 0.0917 | 18541.9 | 50.00 | Sequence |
| IAs | 419 | VSTGPEQREIPDVST | STGPEQREI | 0.0916 | 18550.7 | 50.00 | Sequence |
| IAs | 108 | PMTPKRAIEVIADAC | RAIEVIADA | 0.0915 | 18574.4 | 50.00 | Sequence |
| IAs | 207 | EVLTGEPPFTGDSPV | EVLTGEPPF | 0.0914 | 18605.2 | 50.00 | Sequence |
| IAs | 96 | GVTLRDIVHTEGPMT | RDIVHTEGP | 0.0912 | 18643.5 | 50.00 | Sequence |
| IAs | 321 | RDRSIGSVGRWVAVV | RSIGSVGRW | 0.0909 | 18691.2 | 50.00 | Sequence |
| IAs | 166 | GNSVTQTAAVIGTAQ | QTAAVIGTA | 0.0906 | 18753.0 | 50.00 | Sequence |
| IAs | 421 | TGPEQREIPDVSTLT | TGPEQREIP | 0.0904 | 18794.0 | 50.00 | Sequence |
| IAs | 194 | ARSDVYSLGCVLYEV | SLGCVLYEV | 0.0904 | 18805.2 | 50.00 | Sequence |
| IAs | 359 | VQVPDVRGQSSADAI | RGQSSADAI | 0.0900 | 18874.1 | 50.00 | Sequence |
| IAs | 511 | LNVYGFTKFSQASVD | TKFSQASVD | 0.0899 | 18902.3 | 50.00 | Sequence |
| IAs | 70 | IVAVYDTGEAETPAG | YDTGEAETP | 0.0891 | 19061.8 | 50.00 | Sequence |
| IAs | 318 | DTDRDRSIGSVGRWV | RSIGSVGRW | 0.0887 | 19156.5 | 50.00 | Sequence |
| IAs | 443 | LTAAGFGRFKQANSP | GRFKQANSP | 0.0885 | 19194.9 | 50.00 | Sequence |
| IAs | 128 | SHQNGIIHRDVKPAN | NGIIHRDVK | 0.0882 | 19248.4 | 50.00 | Sequence |
| IAs | 18 | FGGMSEVHLARDLRL | SEVHLARDL | 0.0879 | 19314.3 | 50.00 | Sequence |
| IAs | 198 | VYSLGCVLYEVLTGE | SLGCVLYEV | 0.0875 | 19397.2 | 50.00 | Sequence |
| IAs | 429 | PDVSTLTYAEAVKKL | TYAEAVKKL | 0.0875 | 19398.1 | 50.00 | Sequence |
| IAs | 474 | NQTSAITNVVIIIVG | SAITNVVII | 0.0875 | 19401.0 | 50.00 | Sequence |
| IAs | 195 | RSDVYSLGCVLYEVL | SLGCVLYEV | 0.0875 | 19405.8 | 50.00 | Sequence |
| IAs | 105 | TEGPMTPKRAIEVIA | EGPMTPKRA | 0.0875 | 19406.0 | 50.00 | Sequence |
| IAs | 304 | SGPRTDPLPRQDLDD | SGPRTDPLP | 0.0868 | 19552.7 | 50.00 | Sequence |
| IAs | 109 | MTPKRAIEVIADACQ | RAIEVIADA | 0.0864 | 19631.6 | 50.00 | Sequence |
| IAs | 431 | VSTLTYAEAVKKLTA | TYAEAVKKL | 0.0856 | 19806.3 | 50.00 | Sequence |
| IAs | 244 | ADLDAVVLKALAKNP | AVVLKALAK | 0.0855 | 19815.1 | 50.00 | Sequence |
| IAs | 292 | RTSLLSSAAGNLSGP | SAAGNLSGP | 0.0849 | 19949.3 | 50.00 | Sequence |
| IAs | 197 | DVYSLGCVLYEVLTG | SLGCVLYEV | 0.0848 | 19978.7 | 50.00 | Sequence |
| IAs | 196 | SDVYSLGCVLYEVLT | SLGCVLYEV | 0.0845 | 20041.3 | 50.00 | Sequence |
| IAs | 127 | FSHQNGIIHRDVKPA | NGIIHRDVK | 0.0843 | 20078.6 | 50.00 | Sequence |
| IAs | 92 | EYVDGVTLRDIVHTE | VDGVTLRDI | 0.0843 | 20079.3 | 50.00 | Sequence |
| IAs | 320 | DRDRSIGSVGRWVAV | RSIGSVGRW | 0.0842 | 20104.3 | 50.00 | Sequence |
| IAs | 283 | APKVLTDAERTSLLS | KVLTDAERT | 0.0841 | 20117.1 | 50.00 | Sequence |
| IAs | 93 | YVDGVTLRDIVHTEG | DGVTLRDIV | 0.0840 | 20158.5 | 50.00 | Sequence |
| IAs | 587 | DKGADVDAGGSQHNR | ADVDAGGSQ | 0.0839 | 20174.4 | 50.00 | Sequence |
| IAs | 512 | NVYGFTKFSQASVDS | TKFSQASVD | 0.0836 | 20233.2 | 50.00 | Sequence |
| IAs | 364 | VRGQSSADAIATLQN | RGQSSADAI | 0.0833 | 20312.6 | 50.00 | Sequence |
| IAs | 91 | MEYVDGVTLRDIVHT | VDGVTLRDI | 0.0832 | 20322.1 | 50.00 | Sequence |
| IAs | 482 | VVIIIVGSGPATKDI | VIIIVGSGP | 0.0829 | 20390.2 | 50.00 | Sequence |
| IAs | 505 | DVAQKNLNVYGFTKF | KNLNVYGFT | 0.0823 | 20516.8 | 50.00 | Sequence |
| IAs | 319 | TDRDRSIGSVGRWVA | RSIGSVGRW | 0.0823 | 20529.6 | 50.00 | Sequence |
| IAs | 89 | IVMEYVDGVTLRDIV | DGVTLRDIV | 0.0822 | 20541.4 | 50.00 | Sequence |
| IAs | 548 | SVIELQVSKGNQFVM | LQVSKGNQF | 0.0820 | 20591.9 | 50.00 | Sequence |
| IAs | 243 | SADLDAVVLKALAKN | AVVLKALAK | 0.0817 | 20660.2 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAs | 494 | KDIPDVAGQTVDVAQ | VAGQTVDVA | 0.0816 | 20683.5 | 50.00 | Sequence |
| IAs | 285 | KVLTDAERTSLLSSA | KVLTDAERT | 0.0814 | 20726.2 | 50.00 | Sequence |
| IAs | 475 | QTSAITNVVIIIVGS | SAITNVVII | 0.0813 | 20744.9 | 50.00 | Sequence |
| IAs | 164 | DSGNSVTQTAAVIGT | SVTQTAAVI | 0.0813 | 20747.8 | 50.00 | Sequence |
| IAs | 90 | VMEYVDGVTLRDIVH | DGVTLRDIV | 0.0812 | 20759.5 | 50.00 | Sequence |
| IAs | 116 | EVIADACQALNFSHQ | EVIADACQA | 0.0812 | 20779.7 | 50.00 | Sequence |
| IAs | 593 | DAGGSQHNRVVYQNP | AGGSQHNRV | 0.0811 | 20787.6 | 50.00 | Sequence |
| IAs | 479 | ITNVVIIIVGSGPAT | IIIVGSGPA | 0.0807 | 20879.8 | 50.00 | Sequence |
| IAs | 242 | LSADLDAVVLKALAK | AVVLKALAK | 0.0807 | 20885.6 | 50.00 | Sequence |
| IAs | 22 | SEVHLARDLRLHRDV | RDLRLHRDV | 0.0807 | 20890.6 | 50.00 | Sequence |
| IAs | 434 | LTYAEAVKKLTAAGF | TYAEAVKKL | 0.0807 | 20892.4 | 50.00 | Sequence |
| IAs | 162 | IADSGNSVTQTAAVI | SVTQTAAVI | 0.0806 | 20901.2 | 50.00 | Sequence |
| IAs | 584 | GMLDKGADVDAGGSQ | ADVDAGGSQ | 0.0802 | 20984.4 | 50.00 | Sequence |
| IAs | 493 | TKDIPDVAGQTVDVA | VAGQTVDVA | 0.0802 | 20988.0 | 50.00 | Sequence |
| IAs | 126 | NFSHQNGIIHRDVKP | NGIIHRDVK | 0.0802 | 20989.6 | 50.00 | Sequence |
| IAs | 395 | PDHVIGTDPAANTSV | HVIGTDPAA | 0.0801 | 21013.7 | 50.00 | Sequence |
| IAs | 430 | DVSTLTYAEAVKKLT | TYAEAVKKL | 0.0800 | 21047.2 | 50.00 | Sequence |
| IAs | 586 | LDKGADVDAGGSQHN | ADVDAGGSQ | 0.0799 | 21053.5 | 50.00 | Sequence |
| IAs | 508 | QKNLNVYGFTKFSQA | KNLNVYGFT | 0.0798 | 21079.7 | 50.00 | Sequence |
| IAs | 585 | MLDKGADVDAGGSQH | ADVDAGGSQ | 0.0797 | 21112.6 | 50.00 | Sequence |
| IAs | 163 | ADSGNSVTQTAAVIG | SVTQTAAVI | 0.0797 | 21115.3 | 50.00 | Sequence |
| IAs | 284 | PKVLTDAERTSLLSS | KVLTDAERT | 0.0795 | 21152.9 | 50.00 | Sequence |
| IAs | 561 | VMPDLSGMFWVDAEP | SGMFWVDAE | 0.0795 | 21164.3 | 50.00 | Sequence |
| IAs | 407 | TSVSAGDEITVNVST | TSVSAGDEI | 0.0793 | 21205.8 | 50.00 | Sequence |
| IAs | 363 | DVRGQSSADAIATLQ | RGQSSADAI | 0.0785 | 21395.5 | 50.00 | Sequence |
| IAs | 472 | PANQTSAITNVVIII | SAITNVVII | 0.0782 | 21456.2 | 50.00 | Sequence |
| IAs | 473 | ANQTSAITNVVIIIV | SAITNVVII | 0.0781 | 21482.4 | 50.00 | Sequence |
| IAs | 21 | MSEVHLARDLRLHRD | SEVHLARDL | 0.0780 | 21499.0 | 50.00 | Sequence |
| IAs | 140 | PANIMISATNAVKVM | SATNAVKVM | 0.0773 | 21652.8 | 50.00 | Sequence |
| IAs | 106 | EGPMTPKRAIEVIAD | EGPMTPKRA | 0.0771 | 21712.6 | 50.00 | Sequence |
| IAs | 239 | HEGLSADLDAVVLKA | HEGLSADLD | 0.0768 | 21789.4 | 50.00 | Sequence |
| IAs | 238 | RHEGLSADLDAVVLK | HEGLSADLD | 0.0766 | 21840.1 | 50.00 | Sequence |
| IAs | 155 | DFGIARAIADSGNSV | RAIADSGNS | 0.0763 | 21904.5 | 50.00 | Sequence |
| IAs | 360 | QVPDVRGQSSADAIA | RGQSSADAI | 0.0762 | 21921.3 | 50.00 | Sequence |
| IAs | 400 | GTDPAANTSVSAGDE | NTSVSAGDE | 0.0761 | 21939.8 | 50.00 | Sequence |
| IAs | 506 | VAQKNLNVYGFTKFS | KNLNVYGFT | 0.0760 | 21959.8 | 50.00 | Sequence |
| IAs | 13 | GEILGFGGMSEVHLA | GGMSEVHLA | 0.0757 | 22031.6 | 50.00 | Sequence |
| IAs | 394 | PPDHVIGTDPAANTS | HVIGTDPAA | 0.0757 | 22037.6 | 50.00 | Sequence |
| IAs | 432 | STLTYAEAVKKLTAA | TYAEAVKKL | 0.0757 | 22041.4 | 50.00 | Sequence |
| IAs | 114 | AIEVIADACQALNFS | EVIADACQA | 0.0757 | 22044.0 | 50.00 | Sequence |
| IAs | 478 | AITNVVIIIVGSGPA | VIIIVGSGP | 0.0755 | 22088.9 | 50.00 | Sequence |
| IAs | 142 | NIMISATNAVKVMDF | SATNAVKVM | 0.0752 | 22172.0 | 50.00 | Sequence |
| IAs | 305 | GPRTDPLPRQDLDDT | RTDPLPRQD | 0.0751 | 22175.6 | 50.00 | Sequence |
| IAs | 471 | PPANQTSAITNVVII | SAITNVVII | 0.0749 | 22223.9 | 50.00 | Sequence |
| IAs | 392 | TIPPDHVIGTDPAAN | HVIGTDPAA | 0.0747 | 22282.9 | 50.00 | Sequence |
| IAs | 361 | VPDVRGQSSADAIAT | RGQSSADAI | 0.0747 | 22289.4 | 50.00 | Sequence |
| IAs | 480 | TNVVIIIVGSGPATK | TNVVIIIVG | 0.0747 | 22290.3 | 50.00 | Sequence |
| IAs | 237 | ARHEGLSADLDAVVL | HEGLSADLD | 0.0744 | 22355.3 | 50.00 | Sequence |
| IAs | 19 | GGMSEVHLARDLRLH | MSEVHLARD | 0.0742 | 22393.3 | 50.00 | Sequence |
| IAs | 154 | MDFGIARAIADSGNS | RAIADSGNS | 0.0741 | 22427.0 | 50.00 | Sequence |
| IAs | 156 | FGIARAIADSGNSVT | RAIADSGNS | 0.0739 | 22474.6 | 50.00 | Sequence |
| IAs | 393 | IPPDHVIGTDPAANT | HVIGTDPAA | 0.0738 | 22489.7 | 50.00 | Sequence |
| IAs | 362 | PDVRGQSSADAIATL | RGQSSADAI | 0.0736 | 22548.4 | 50.00 | Sequence |
| IAs | 340 | VLTVVVTIAINTFGG | TVVVTIAIN | 0.0735 | 22581.4 | 50.00 | Sequence |
| IAs | 572 | DAEPRLRALGWTGML | RALGWTGML | 0.0729 | 22709.5 | 50.00 | Sequence |
| IAs | 208 | VLTGEPPFTGDSPVS | PPFTGDSPV | 0.0726 | 22786.1 | 50.00 | Sequence |
| IAs | 507 | AQKNLNVYGFTKFSQ | KNLNVYGFT | 0.0722 | 22884.2 | 50.00 | Sequence |
| IAs | 602 | VVYQNPPAGTGVNRD | VVYQNPPAG | 0.0720 | 22939.7 | 50.00 | Sequence |
| IAs | 560 | FVMPDLSGMFWVDAE | SGMFWVDAE | 0.0719 | 22960.8 | 50.00 | Sequence |
| IAs | 339 | AVLTVVVTIAINTFG | TVVVTIAIN | 0.0716 | 23036.7 | 50.00 | Sequence |
| IAs | 264 | TAAEMRADLVRVHNG | MRADLVRVH | 0.0716 | 23053.2 | 50.00 | Sequence |
| IAs | 433 | TLTYAEAVKKLTAAG | TYAEAVKKL | 0.0715 | 23077.1 | 50.00 | Sequence |
| IAs | 20 | GMSEVHLARDLRLHR | MSEVHLARD | 0.0713 | 23111.4 | 50.00 | Sequence |
| IAs | 125 | LNFSHQNGIIHRDVK | NGIIHRDVK | 0.0708 | 23235.0 | 50.00 | Sequence |
| IAs | 115 | IEVIADACQALNFSH | EVIADACQA | 0.0707 | 23264.7 | 50.00 | Sequence |
| IAs | 509 | KNLNVYGFTKFSQAS | KNLNVYGFT | 0.0706 | 23297.4 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAs | 158 | IARAIADSGNSVTQT | RAIADSGNS | 0.0703 | 23369.3 | 50.00 | Sequence |
| IAs | 477 | SAITNVVIIIVGSGP | SAITNVVII | 0.0701 | 23419.2 | 50.00 | Sequence |
| IAs | 291 | ERTSLLSSAAGNLSG | TSLLSSAAG | 0.0698 | 23493.6 | 50.00 | Sequence |
| IAs | 178 | TAQYLSPEQARGDSV | AQYLSPEQA | 0.0694 | 23588.3 | 50.00 | Sequence |
| IAs | 391 | STIPPDHVIGTDPAA | HVIGTDPAA | 0.0691 | 23684.7 | 50.00 | Sequence |
| IAs | 141 | ANIMISATNAVKVMD | SATNAVKVM | 0.0690 | 23705.8 | 50.00 | Sequence |
| IAs | 253 | ALAKNPENRYQTAAE | ALAKNPENR | 0.0681 | 23943.9 | 50.00 | Sequence |
| IAs | 290 | AERTSLLSSAAGNLS | TSLLSSAAG | 0.0677 | 24037.9 | 50.00 | Sequence |
| IAs | 23 | EVHLARDLRLHRDVA | RDLRLHRDV | 0.0676 | 24055.6 | 50.00 | Sequence |
| IAs | 540 | AGTTVPVDSVIELQV | GTTVPVDSV | 0.0670 | 24219.9 | 50.00 | Sequence |
| IAs | 573 | AEPRLRALGWTGMLD | RALGWTGML | 0.0669 | 24254.2 | 50.00 | Sequence |
| IAs | 338 | LAVLTVVVTIAINTF | TVVVTIAIN | 0.0668 | 24262.9 | 50.00 | Sequence |
| IAs | 157 | GIARAIADSGNSVTQ | RAIADSGNS | 0.0665 | 24349.9 | 50.00 | Sequence |
| IAs | 422 | GPEQREIPDVSTLTY | REIPDVSTL | 0.0662 | 24429.6 | 50.00 | Sequence |
| IAs | 337 | VLAVLTVVVTIAINT | TVVVTIAIN | 0.0654 | 24640.4 | 50.00 | Sequence |
| IAs | 14 | EILGFGGMSEVHLAR | GGMSEVHLA | 0.0654 | 24648.1 | 50.00 | Sequence |
| IAs | 455 | NSPSTPELVGKVIGT | NSPSTPELV | 0.0653 | 24655.9 | 50.00 | Sequence |
| IAs | 12 | LGEILGFGGMSEVHL | LGFGGMSEV | 0.0651 | 24713.8 | 50.00 | Sequence |
| IAs | 212 | EPPFTGDSPVSVAYQ | EPPFTGDSP | 0.0650 | 24752.1 | 50.00 | Sequence |
| IAs | 390 | DSTIPPDHVIGTDPA | DHVIGTDPA | 0.0650 | 24755.1 | 50.00 | Sequence |
| IAs | 583 | TGMLDKGADVDAGGS | KGADVDAGG | 0.0643 | 24937.8 | 50.00 | Sequence |
| IAs | 426 | REIPDVSTLTYAEAV | STLTYAEAV | 0.0643 | 24947.8 | 50.00 | Sequence |
| IAs | 15 | ILGFGGMSEVHLARD | GGMSEVHLA | 0.0642 | 24960.3 | 50.00 | Sequence |
| IAs | 372 | AIATLQNRGFKIRTL | NRGFKIRTL | 0.0641 | 24994.8 | 50.00 | Sequence |
| IAs | 88 | YIVMEYVDGVTLRDI | EYVDGVTLR | 0.0638 | 25084.0 | 50.00 | Sequence |
| IAs | 236 | SARHEGLSADLDAVV | HEGLSADLD | 0.0633 | 25194.4 | 50.00 | Sequence |
| IAs | 27 | ARDLRLHRDVAVKVL | RDLRLHRDV | 0.0632 | 25220.9 | 50.00 | Sequence |
| IAs | 336 | AVLAVLTVVVTIAIN | TVVVTIAIN | 0.0631 | 25263.5 | 50.00 | Sequence |
| IAs | 227 | HVREDPIPPSARHEG | HVREDPIPP | 0.0626 | 25403.6 | 50.00 | Sequence |
| IAs | 289 | DAERTSLLSSAAGNL | TSLLSSAAG | 0.0625 | 25426.4 | 50.00 | Sequence |
| IAs | 42 | RADLARDPSFYLRFR | RADLARDPS | 0.0622 | 25518.4 | 50.00 | Sequence |
| IAs | 574 | EPRLRALGWTGMLDK | RALGWTGML | 0.0621 | 25533.3 | 50.00 | Sequence |
| IAs | 331 | WVAVVAVLAVLTVVV | AVVAVLAVL | 0.0620 | 25561.8 | 50.00 | Sequence |
| IAs | 481 | NVVIIIVGSGPATKD | IIIVGSGPA | 0.0620 | 25568.4 | 50.00 | Sequence |
| IAs | 332 | VAVVAVLAVLTVVVT | AVVAVLAVL | 0.0620 | 25571.2 | 50.00 | Sequence |
| IAs | 333 | AVVAVLAVLTVVVTI | AVVAVLAVL | 0.0620 | 25571.8 | 50.00 | Sequence |
| IAs | 266 | AEMRADLVRVHNGEP | MRADLVRVH | 0.0615 | 25709.7 | 50.00 | Sequence |
| IAs | 577 | LRALGWTGMLDKGAD | RALGWTGML | 0.0611 | 25823.7 | 50.00 | Sequence |
| IAs | 24 | VHLARDLRLHRDVAV | RDLRLHRDV | 0.0611 | 25824.5 | 50.00 | Sequence |
| IAs | 235 | PSARHEGLSADLDAV | HEGLSADLD | 0.0607 | 25922.5 | 50.00 | Sequence |
| IAs | 611 | TGVNRDGIITLRFGQ | TGVNRDGII | 0.0603 | 26039.4 | 50.00 | Sequence |
| IAs | 476 | TSAITNVVIIIVGSG | SAITNVVII | 0.0603 | 26047.3 | 50.00 | Sequence |
| IAs | 365 | RGQSSADAIATLQNR | RGQSSADAI | 0.0600 | 26133.1 | 50.00 | Sequence |
| IAs | 254 | LAKNPENRYQTAAEM | NRYQTAAEM | 0.0596 | 26235.7 | 50.00 | Sequence |
| IAs | 87 | PYIVMEYVDGVTLRD | EYVDGVTLR | 0.0596 | 26249.6 | 50.00 | Sequence |
| IAs | 588 | KGADVDAGGSQHNRV | AGGSQHNRV | 0.0593 | 26307.9 | 50.00 | Sequence |
| IAs | 576 | RLRALGWTGMLDKGA | RALGWTGML | 0.0593 | 26312.2 | 50.00 | Sequence |
| IAs | 51 | FYLRFRREAQNAAAL | REAQNAAAL | 0.0591 | 26372.0 | 50.00 | Sequence |
| IAs | 423 | PEQREIPDVSTLTYA | EQREIPDVS | 0.0591 | 26389.2 | 50.00 | Sequence |
| IAs | 466 | VIGTNPPANQTSAIT | VIGTNPPAN | 0.0587 | 26494.4 | 50.00 | Sequence |
| IAs | 265 | AAEMRADLVRVHNGE | MRADLVRVH | 0.0586 | 26514.8 | 50.00 | Sequence |
| IAs | 470 | NPPANQTSAITNVVI | QTSAITNVV | 0.0584 | 26589.2 | 50.00 | Sequence |
| IAs | 366 | GQSSADAIATLQNRG | AIATLQNRG | 0.0579 | 26712.3 | 50.00 | Sequence |
| IAs | 11 | ELGEILGFGGMSEVH | GFGGMSEVH | 0.0577 | 26787.9 | 50.00 | Sequence |
| IAs | 117 | VIADACQALNFSHQN | QALNFSHQN | 0.0572 | 26925.0 | 50.00 | Sequence |
| IAs | 492 | ATKDIPDVAGQTVDV | ATKDIPDVA | 0.0571 | 26967.9 | 50.00 | Sequence |
| IAs | 160 | RAIADSGNSVTQTAA | RAIADSGNS | 0.0571 | 26969.9 | 50.00 | Sequence |
| IAs | 442 | KLTAAGFGRFKQANS | AGFGRFKQA | 0.0570 | 26979.0 | 50.00 | Sequence |
| IAs | 341 | LTVVVTIAINTFGGI | TVVVTIAIN | 0.0569 | 27007.9 | 50.00 | Sequence |
| IAs | 25 | HLARDLRLHRDVAVK | RDLRLHRDV | 0.0566 | 27103.3 | 50.00 | Sequence |
| IAs | 559 | QFVMPDLSGMFWVDA | LSGMFWVDA | 0.0566 | 27108.9 | 50.00 | Sequence |
| IAs | 575 | PRLRALGWTGMLDKG | RALGWTGML | 0.0560 | 27281.9 | 50.00 | Sequence |
| IAs | 241 | GLSADLDAVVLKALA | LDAVVLKAL | 0.0559 | 27319.7 | 50.00 | Sequence |
| IAs | 179 | AQYLSPEQARGDSVD | AQYLSPEQA | 0.0558 | 27326.8 | 50.00 | Sequence |
| IAs | 118 | IADACQALNFSHQNG | QALNFSHQN | 0.0558 | 27344.5 | 50.00 | Sequence |
| IAs | 234 | PPSARHEGLSADLDA | HEGLSADLD | 0.0558 | 27347.8 | 50.00 | Sequence |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| IAs | 342 | TVVVTIAINTFGGIT | TVVVTIAIN | 0.0556 | 27384.2 | 50.00 | Sequence |
| IAs | 348 | AINTFGGITRDVQVP | GITRDVQVP | 0.0555 | 27421.3 | 50.00 | Sequence |
| IAs | 589 | GADVDAGGSQHNRVV | AGGSQHNRV | 0.0549 | 27608.6 | 50.00 | Sequence |
| IAs | 288 | TDAERTSLLSSAAGN | TSLLSSAAG | 0.0548 | 27621.7 | 50.00 | Sequence |
| IAs | 578 | RALGWTGMLDKGADV | RALGWTGML | 0.0548 | 27630.4 | 50.00 | Sequence |
| IAs | 424 | EQREIPDVSTLTYAE | REIPDVSTL | 0.0545 | 27719.9 | 50.00 | Sequence |
| IAs | 193 | DARSDVYSLGCVLYE | DVYSLGCVL | 0.0542 | 27803.4 | 50.00 | Sequence |
| IAs | 52 | YLRFRREAQNAAALN | REAQNAAAL | 0.0542 | 27826.0 | 50.00 | Sequence |
| IAs | 367 | QSSADAIATLQNRGF | AIATLQNRG | 0.0537 | 27959.4 | 50.00 | Sequence |
| IAs | 306 | PRTDPLPRQDLDDTD | RTDPLPRQD | 0.0537 | 27977.8 | 50.00 | Sequence |
| IAs | 349 | INTFGGITRDVQVPD | GITRDVQVP | 0.0537 | 27979.9 | 50.00 | Sequence |
| IAs | 240 | EGLSADLDAVVLKAL | ADLDAVVLK | 0.0536 | 28005.1 | 50.00 | Sequence |
| IAs | 396 | DHVIGTDPAANTSVS | HVIGTDPAA | 0.0535 | 28031.5 | 50.00 | Sequence |
| IAs | 124 | ALNFSHQNGIIHRDV | QNGIIHRDV | 0.0533 | 28090.7 | 50.00 | Sequence |
| IAs | 524 | VDSPRPAGEVTGTNP | RPAGEVTGT | 0.0532 | 28106.8 | 50.00 | Sequence |
| IAs | 467 | IGTNPPANQTSAITN | IGTNPPANQ | 0.0529 | 28207.6 | 50.00 | Sequence |
| IAs | 161 | AIADSGNSVTQTAAV | NSVTQTAAV | 0.0529 | 28212.2 | 50.00 | Sequence |
| IAs | 26 | LARDLRLHRDVAVKV | RDLRLHRDV | 0.0529 | 28216.5 | 50.00 | Sequence |
| IAs | 209 | LTGEPPFTGDSPVSV | PPFTGDSPV | 0.0529 | 28223.5 | 50.00 | Sequence |
| IAs | 53 | LRFRREAQNAAALNH | REAQNAAAL | 0.0527 | 28272.7 | 50.00 | Sequence |
| IAs | 211 | GEPPFTGDSPVSVAY | PPFTGDSPV | 0.0525 | 28318.9 | 50.00 | Sequence |
| IAs | 428 | IPDVSTLTYAEAVKK | STLTYAEAV | 0.0523 | 28396.9 | 50.00 | Sequence |
| IAs | 569 | FWVDAEPRLRALGWT | EPRLRALGW | 0.0523 | 28398.1 | 50.00 | Sequence |
| IAs | 307 | RTDPLPRQDLDDTDR | RTDPLPRQD | 0.0522 | 28429.4 | 50.00 | Sequence |
| IAs | 151 | VKVMDFGIARAIADS | VKVMDFGIA | 0.0521 | 28446.4 | 50.00 | Sequence |
| IAs | 541 | GTTVPVDSVIELQVS | GTTVPVDSV | 0.0521 | 28458.1 | 50.00 | Sequence |
| IAs | 389 | PDSTIPPDHVIGTDP | PDSTIPPDH | 0.0520 | 28479.3 | 50.00 | Sequence |
| IAs | 368 | SSADAIATLQNRGFK | ATLQNRGFK | 0.0519 | 28529.9 | 50.00 | Sequence |
| IAs | 427 | EIPDVSTLTYAEAVK | STLTYAEAV | 0.0517 | 28570.1 | 50.00 | Sequence |
| IAs | 469 | TNPPANQTSAITNVV | QTSAITNVV | 0.0516 | 28603.2 | 50.00 | Sequence |
| IAs | 233 | IPPSARHEGLSADLD | HEGLSADLD | 0.0515 | 28636.3 | 50.00 | Sequence |
| IAs | 153 | VMDFGIARAIADSGN | MDFGIARAI | 0.0509 | 28834.0 | 50.00 | Sequence |
| IAs | 210 | TGEPPFTGDSPVSVA | PPFTGDSPV | 0.0505 | 28938.1 | 50.00 | Sequence |
| IAs | 358 | DVQVPDVRGQSSADA | VRGQSSADA | 0.0505 | 28954.4 | 50.00 | Sequence |
| IAs | 347 | IAINTFGGITRDVQV | FGGITRDVQ | 0.0503 | 29005.2 | 50.00 | Sequence |
| IAs | 159 | ARAIADSGNSVTQTA | RAIADSGNS | 0.0503 | 29018.0 | 50.00 | Sequence |
| IAs | 523 | SVDSPRPAGEVTGTN | RPAGEVTGT | 0.0502 | 29049.8 | 50.00 | Sequence |
| IAs | 152 | KVMDFGIARAIADSG | GIARAIADS | 0.0499 | 29128.1 | 50.00 | Sequence |
| IAs | 425 | QREIPDVSTLTYAEA | REIPDVSTL | 0.0496 | 29247.5 | 50.00 | Sequence |
| IAs | 457 | PSTPELVGKVIGTNP | LVGKVIGTN | 0.0493 | 29319.1 | 50.00 | Sequence |
| IAs | 119 | ADACQALNFSHQNGI | QALNFSHQN | 0.0493 | 29324.2 | 50.00 | Sequence |
| IAs | 150 | AVKVMDFGIARAIAD | VKVMDFGIA | 0.0490 | 29413.8 | 50.00 | Sequence |
| IAs | 603 | VYQNPPAGTGVNRDG | NPPAGTGVN | 0.0490 | 29416.4 | 50.00 | Sequence |
| IAs | 287 | LTDAERTSLLSSAAG | TDAERTSLL | 0.0486 | 29544.0 | 50.00 | Sequence |
| IAs | 456 | SPSTPELVGKVIGTN | TPELVGKVI | 0.0482 | 29690.1 | 50.00 | Sequence |
| IAs | 228 | VREDPIPPSARHEGL | REDPIPPSA | 0.0480 | 29732.8 | 50.00 | Sequence |
| IAs | 8 | DRYELGEILGFGGMS | EILGFGGMS | 0.0478 | 29808.2 | 50.00 | Sequence |
| IAs | 582 | WTGMLDKGADVDAGG | DKGADVDAG | 0.0474 | 29926.5 | 50.00 | Sequence |
| IAs | 10 | YELGEILGFGGMSEV | ELGEILGFG | 0.0471 | 30030.6 | 50.00 | Sequence |
| IAs | 409 | VSAGDEITVNVSTGP | ITVNVSTGP | 0.0463 | 30291.7 | 50.00 | Sequence |
| IAs | 369 | SADAIATLQNRGFKI | ATLQNRGFK | 0.0451 | 30689.8 | 50.00 | Sequence |
| IAs | 510 | NLNVYGFTKFSQASV | YGFTKFSQA | 0.0445 | 30893.1 | 50.00 | Sequence |
| IAs | 120 | DACQALNFSHQNGII | QALNFSHQN | 0.0443 | 30963.7 | 50.00 | Sequence |
| IAs | 570 | WVDAEPRLRALGWTG | WVDAEPRLR | 0.0433 | 31288.0 | 50.00 | Sequence |
| IAs | 2 | TPSHLSDRYELGEIL | SDRYELGEI | 0.0433 | 31292.4 | 50.00 | Sequence |
| IAs | 123 | QALNFSHQNGIIHRD | QALNFSHQN | 0.0432 | 31339.8 | 50.00 | Sequence |
| IAs | 371 | DAIATLQNRGFKIRT | AIATLQNRG | 0.0425 | 31554.9 | 50.00 | Sequence |
| IAs | 191 | SVDARSDVYSLGCVL | SVDARSDVY | 0.0424 | 31609.2 | 50.00 | Sequence |
| IAs | 335 | VAVLAVLTVVVTIAI | AVLAVLTVV | 0.0423 | 31623.6 | 50.00 | Sequence |
| IAs | 370 | ADAIATLQNRGFKIR | ATLQNRGFK | 0.0422 | 31666.4 | 50.00 | Sequence |
| IAs | 181 | YLSPEQARGDSVDAR | ARGDSVDAR | 0.0418 | 31798.5 | 50.00 | Sequence |
| IAs | 121 | ACQALNFSHQNGIIH | QALNFSHQN | 0.0417 | 31853.0 | 50.00 | Sequence |
| IAs | 7 | SDRYELGEILGFGGM | DRYELGEIL | 0.0415 | 31925.4 | 50.00 | Sequence |
| IAs | 122 | CQALNFSHQNGIIHR | QALNFSHQN | 0.0412 | 32004.6 | 50.00 | Sequence |
| IAs | 542 | TTVPVDSVIELQVSK | SVIELQVSK | 0.0411 | 32064.6 | 50.00 | Sequence |
| IAs | 334 | VVAVLAVLTVVVTIA | AVLAVLTVV | 0.0410 | 32097.2 | 50.00 | Sequence |

```
         IAs  468  GTNPPANQTSAITNV  PPANQTSAI        0.0408      32172.3            50.00     Sequence
         IAs  346  TIAINTFGGITRDVQ  FGGITRDVQ        0.0403      32336.0            50.00     Sequence
         IAs  180  QYLSPEQARGDSVDA  QYLSPEQAR        0.0400      32423.6            50.00     Sequence
         IAs  185  EQARGDSVDARSDVY  ARGDSVDAR        0.0399      32462.2            50.00     Sequence
         IAs  308  TDPLPRQDLDDTDRD  DPLPRQDLD        0.0398      32503.3            50.00     Sequence
         IAs    9  RYELGEILGFGGMSE  EILGFGGMS        0.0398      32522.3            50.00     Sequence
         IAs  182  LSPEQARGDSVDARS  ARGDSVDAR        0.0395      32593.5            50.00     Sequence
         IAs  186  QARGDSVDARSDVYS  ARGDSVDAR        0.0390      32791.2            50.00     Sequence
         IAs  229  REDPIPPSARHEGLS  REDPIPPSA        0.0389      32829.2            50.00     Sequence
         IAs  545  PVDSVIELQVSKGNQ  PVDSVIELQ        0.0385      32951.2            50.00     Sequence
         IAs  286  VLTDAERTSLLSSAA  TDAERTSLL        0.0384      32985.1            50.00     Sequence
         IAs  187  ARGDSVDARSDVYSL  ARGDSVDAR        0.0381      33096.7            50.00     Sequence
         IAs  592  VDAGGSQHNRVVYQN  AGGSQHNRV        0.0377      33270.1            50.00     Sequence
         IAs  544  VPVDSVIELQVSKGN  VPVDSVIEL        0.0375      33315.8            50.00     Sequence
         IAs    1  TTPSHLSDRYELGEI  TPSHLSDRY        0.0374      33356.6            50.00     Sequence
         IAs  543  TVPVDSVIELQVSKG  SVIELQVSK        0.0373      33385.1            50.00     Sequence
         IAs   43  ADLARDPSFYLRFRR  ADLARDPSF        0.0372      33435.4            50.00     Sequence
         IAs  581  GWTGMLDKGADVDAG  DKGADVDAG        0.0371      33470.5            50.00     Sequence
         IAs  309  DPLPRQDLDDTDRDR  DPLPRQDLD        0.0360      33867.2            50.00     Sequence
         IAs  590  ADVDAGGSQHNRVVY  AGGSQHNRV        0.0358      33941.6            50.00     Sequence
         IAs    0  MTTPSHLSDRYELGE  TPSHLSDRY        0.0353      34143.5            50.00     Sequence
         IAs  192  VDARSDVYSLGCVLY  DVYSLGCVL        0.0350      34225.2            50.00     Sequence
         IAs  343  VVVTIAINTFGGITR  VVTIAINTF        0.0350      34240.8            50.00     Sequence
         IAs  344  VVTIAINTFGGITRD  VVTIAINTF        0.0350      34244.5            50.00     Sequence
         IAs   44  DLARDPSFYLRFRRE  SFYLRFRRE        0.0345      34439.9            50.00     Sequence
         IAs  184  PEQARGDSVDARSDV  ARGDSVDAR        0.0343      34479.8            50.00     Sequence
         IAs  183  SPEQARGDSVDARSD  ARGDSVDAR        0.0342      34538.1            50.00     Sequence
         IAs  397  HVIGTDPAANTSVSA  HVIGTDPAA        0.0334      34831.5            50.00     Sequence
         IAs    5  HLSDRYELGEILGFG  SDRYELGEI        0.0334      34833.1            50.00     Sequence
         IAs  571  VDAEPRLRALGWTGM  PRLRALGWT        0.0333      34870.0            50.00     Sequence
         IAs  579  ALGWTGMLDKGADVD  GMLDKGADV        0.0329      35037.2            50.00     Sequence
         IAs  345  VTIAINTFGGITRDV  TFGGITRDV        0.0328      35067.9            50.00     Sequence
         IAs  398  VIGTDPAANTSVSAG  VIGTDPAAN        0.0327      35112.3            50.00     Sequence
         IAs    3  PSHLSDRYELGEILG  DRYELGEIL        0.0324      35226.1            50.00     Sequence
         IAs    4  SHLSDRYELGEILGF  DRYELGEIL        0.0320      35385.4            50.00     Sequence
         IAs  580  LGWTGMLDKGADVDA  MLDKGADVD        0.0316      35511.9            50.00     Sequence
         IAs  231  DPIPPSARHEGLSAD  DPIPPSARH        0.0315      35548.1            50.00     Sequence
         IAs  232  PIPPSARHEGLSADL  PPSARHEGL        0.0313      35643.2            50.00     Sequence
         IAs    6  LSDRYELGEILGFGG  SDRYELGEI        0.0304      35992.0            50.00     Sequence
         IAs  230  EDPIPPSARHEGLSA  PPSARHEGL        0.0302      36061.0            50.00     Sequence
         IAs  189  GDSVDARSDVYSLGC  GDSVDARSD        0.0301      36087.9            50.00     Sequence
         IAs  188  RGDSVDARSDVYSLG  GDSVDARSD        0.0300      36160.6            50.00     Sequence
         IAs  591  DVDAGGSQHNRVVYQ  AGGSQHNRV        0.0297      36266.8            50.00     Sequence
         IAs  399  IGTDPAANTSVSAGD  AANTSVSAG        0.0295      36344.6            50.00     Sequence
         IAs   48  DPSFYLRFRREAQNA  RFRREAQNA        0.0286      36673.6            50.00     Sequence
         IAs   50  SFYLRFRREAQNAAA  RFRREAQNA        0.0286      36675.2            50.00     Sequence
         IAs   47  RDPSFYLRFRREAQN  LRFRREAQN        0.0286      36691.9            50.00     Sequence
         IAs  310  PLPRQDLDDTDRDRS  QDLDDTDRD        0.0269      37354.0            50.00     Sequence
         IAs  190  DSVDARSDVYSLGCV  SVDARSDVY        0.0267      37450.4            50.00     Sequence
         IAs   49  PSFYLRFRREAQNAA  RFRREAQNA        0.0266      37479.1            50.00     Sequence
         IAs   46  ARDPSFYLRFRREAQ  SFYLRFRRE        0.0262      37655.5            50.00     Sequence
         IAs  311  LPRQDLDDTDRDRSI  QDLDDTDRD        0.0262      37669.8            50.00     Sequence
         IAs  408  SVSAGDEITVNVSTG  SAGDEITVN        0.0244      38414.4            50.00     Sequence
         IAs  316  LDDTDRDRSIGSVGR  RDRSIGSVG        0.0235      38794.5            50.00     Sequence
         IAs   45  LARDPSFYLRFRREA  SFYLRFRRE        0.0232      38907.5            50.00     Sequence
         IAs  315  DLDDTDRDRSIGSVG  RDRSIGSVG        0.0216      39583.1            50.00     Sequence
         IAs  312  PRQDLDDTDRDRSIG  QDLDDTDRD        0.0204      40107.3            50.00     Sequence
         IAs  313  RQDLDDTDRDRSIGS  QDLDDTDRD        0.0202      40171.2            50.00     Sequence
         IAs  314  QDLDDTDRDRSIGSV  QDLDDTDRD        0.0180      41169.6            50.00     Sequence
-----------------------------------------------------------------------------------------------------

Allele: IAs. Number of high binders 0. Number of weak binders 6. Number of peptides 612

-----------------------------------------------------------------------------------------------------
```

**Explain** the output.  Go **back**.