NetMHCII 2.0 Server - prediction results

Technical University of Denmark

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# Input is in FSA format
        NetMHCII version 2.0.

Strong binder threshold  50.00. Weak binder threshold 500.00.

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0101  279  LLNYLALLGWSIADD  YLALLGWSI        0.8685          4.2         SB     1.00     Sequence
   DRB1_0101  278  GLLNYLALLGWSIAD  YLALLGWSI        0.8683          4.2         SB     1.00     Sequence
   DRB1_0101  277  EGLLNYLALLGWSIA  YLALLGWSI        0.8677          4.2         SB     1.00     Sequence
   DRB1_0101  276  PEGLLNYLALLGWSI  YLALLGWSI        0.8608          4.5         SB     2.00     Sequence
   DRB1_0101  473  DRSMQRLRAARQLVG  MQRLRAARQ        0.8524          4.9         SB     2.00     Sequence
   DRB1_0101  280  LNYLALLGWSIADDH  YLALLGWSI        0.8515          5.0         SB     2.00     Sequence
   DRB1_0101  474  RSMQRLRAARQLVGH  MQRLRAARQ        0.8490          5.1         SB     4.00     Sequence
   DRB1_0101  240  IPKFAHLPTVLGEGT  FAHLPTVLG        0.8486          5.1         SB     4.00     Sequence
   DRB1_0101  229  QALIRIGVAERIPKF  IRIGVAERI        0.8393          5.7         SB     4.00     Sequence
   DRB1_0101  472  RDRSMQRLRAARQLV  MQRLRAARQ        0.8321          6.2         SB     4.00     Sequence
   DRB1_0101  281  NYLALLGWSIADDHD  YLALLGWSI        0.8269          6.5         SB     4.00     Sequence
   DRB1_0101  239  RIPKFAHLPTVLGEG  FAHLPTVLG        0.8256          6.6         SB     4.00     Sequence
   DRB1_0101  444  RKAFSPIRVAATGTT  FSPIRVAAT        0.8233          6.8         SB     4.00     Sequence
   DRB1_0101  241  PKFAHLPTVLGEGTK  FAHLPTVLG        0.8218          6.9         SB     8.00     Sequence
   DRB1_0101  475  SMQRLRAARQLVGHA  MQRLRAARQ        0.8172          7.2         SB     8.00     Sequence
   DRB1_0101   98  ARLLAAGEAYHAFST  LAAGEAYHA        0.8156          7.4         SB     8.00     Sequence
   DRB1_0101  228  HQALIRIGVAERIPK  IRIGVAERI        0.8139          7.5         SB     8.00     Sequence
   DRB1_0101  406  AAVLDAALAALTSVT  LDAALAALT        0.8137          7.5         SB     8.00     Sequence
   DRB1_0101  443  PRKAFSPIRVAATGT  FSPIRVAAT        0.8077          8.0         SB     8.00     Sequence
   DRB1_0101  230  ALIRIGVAERIPKFA  IRIGVAERI        0.8063          8.1         SB     8.00     Sequence
   DRB1_0101  242  KFAHLPTVLGEGTKK  FAHLPTVLG        0.8022          8.5         SB     8.00     Sequence
   DRB1_0101  238  ERIPKFAHLPTVLGE  FAHLPTVLG        0.8002          8.7         SB     8.00     Sequence
   DRB1_0101  407  AVLDAALAALTSVTD  DAALAALTS        0.7986          8.8         SB     8.00     Sequence
   DRB1_0101   54  EESYLALLDALRWLG  YLALLDALR        0.7929          9.4         SB     8.00     Sequence
   DRB1_0101  442  KPRKAFSPIRVAATG  FSPIRVAAT        0.7914          9.6         SB     8.00     Sequence
   DRB1_0101  282  YLALLGWSIADDHDL  YLALLGWSI        0.7902          9.7         SB     8.00     Sequence
   DRB1_0101   25  TALFNWAYARHTGGT  FNWAYARHT        0.7852         10.2         SB     8.00     Sequence
   DRB1_0101  445  KAFSPIRVAATGTTV  FSPIRVAAT        0.7849         10.3         SB     8.00     Sequence
   DRB1_0101  405  GAAVLDAALAALTSV  LDAALAALT        0.7845         10.3         SB     8.00     Sequence
   DRB1_0101  441  LKPRKAFSPIRVAAT  FSPIRVAAT        0.7833         10.4         SB     8.00     Sequence
   DRB1_0101  237  AERIPKFAHLPTVLG  FAHLPTVLG        0.7814         10.6         SB     8.00     Sequence
   DRB1_0101   99  RLLAAGEAYHAFSTP  LAAGEAYHA        0.7799         10.8         SB    16.00     Sequence
   DRB1_0101  143  RAAYLAEGRQPVVRL  YLAEGRQPV        0.7787         11.0         SB    16.00     Sequence
   DRB1_0101  227  LHQALIRIGVAERIP  IRIGVAERI        0.7786         11.0         SB    16.00     Sequence
   DRB1_0101  226  ALHQALIRIGVAERI  IRIGVAERI        0.7768         11.2         SB    16.00     Sequence
   DRB1_0101   53  SEESYLALLDALRWL  YLALLDALR        0.7758         11.3         SB    16.00     Sequence
   DRB1_0101   97  LARLLAAGEAYHAFS  LAAGEAYHA        0.7739         11.5         SB    16.00     Sequence
   DRB1_0101   55  ESYLALLDALRWLGL  YLALLDALR        0.7734         11.6         SB    16.00     Sequence
   DRB1_0101   96  VLARLLAAGEAYHAF  LAAGEAYHA        0.7674         12.4         SB    16.00     Sequence
   DRB1_0101  471  GRDRSMQRLRAARQL  MQRLRAARQ        0.7668         12.5         SB    16.00     Sequence
   DRB1_0101  404  DGAAVLDAALAALTS  LDAALAALT        0.7631         13.0         SB    16.00     Sequence
   DRB1_0101  231  LIRIGVAERIPKFAH  IRIGVAERI        0.7628         13.0         SB    16.00     Sequence
   DRB1_0101  403  PDGAAVLDAALAALT  AAVLDAALA        0.7615         13.2         SB    16.00     Sequence
   DRB1_0101   26  ALFNWAYARHTGGTF  FNWAYARHT        0.7614         13.2         SB    16.00     Sequence
   DRB1_0101   89  RAEIYRDVLARLLAA  YRDVLARLL        0.7610         13.3         SB    16.00     Sequence
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DRB1_0101  434  ALIEGLALKPRKAFS  GLALKPRKA       0.7594         13.5         SB    16.00     Sequence
DRB1_0101   94  RDVLARLLAAGEAYH  LARLLAAGE       0.7582         13.7         SB    16.00     Sequence
DRB1_0101   95  DVLARLLAAGEAYHA  ARLLAAGEA       0.7576         13.8         SB    16.00     Sequence
DRB1_0101  435  LIEGLALKPRKAFSP  GLALKPRKA       0.7571         13.8         SB    16.00     Sequence
DRB1_0101  446  AFSPIRVAATGTTVS  FSPIRVAAT       0.7560         14.0         SB    16.00     Sequence
DRB1_0101   27  LFNWAYARHTGGTFV  FNWAYARHT       0.7558         14.0         SB    16.00     Sequence
DRB1_0101  408  VLDAALAALTSVTDW  DAALAALTS       0.7523         14.6         SB    16.00     Sequence
DRB1_0101   90  AEIYRDVLARLLAAG  YRDVLARLL       0.7522         14.6         SB    16.00     Sequence
DRB1_0101  315  PARFDQKKADALNAE  FDQKKADAL       0.7512         14.8         SB    16.00     Sequence
DRB1_0101   52  DSEESYLALLDALRW  YLALLDALR       0.7458         15.6         SB    16.00     Sequence
DRB1_0101  243  FAHLPTVLGEGTKKL  FAHLPTVLG       0.7457         15.7         SB    16.00     Sequence
DRB1_0101   56  SYLALLDALRWLGLD  YLALLDALR       0.7406         16.6         SB    16.00     Sequence
DRB1_0101   24  RTALFNWAYARHTGG  FNWAYARHT       0.7377         17.1         SB    16.00     Sequence
DRB1_0101  142  QRAAYLAEGRQPVVR  YLAEGRQPV       0.7368         17.2         SB    16.00     Sequence
DRB1_0101   88  QRAEIYRDVLARLLA  YRDVLARLL       0.7365         17.3         SB    16.00     Sequence
DRB1_0101  136  RHLTDAQRAAYLAEG  TDAQRAAYL       0.7364         17.3         SB    16.00     Sequence
DRB1_0101  133  NFDRHLTDAQRAAYL  RHLTDAQRA       0.7358         17.4         SB    16.00     Sequence
DRB1_0101  433  DALIEGLALKPRKAF  GLALKPRKA       0.7346         17.7         SB    16.00     Sequence
DRB1_0101  370  TRIVVLGDAWELLKF  VVLGDAWEL       0.7322         18.1         SB    16.00     Sequence
DRB1_0101  144  AAYLAEGRQPVVRLR  YLAEGRQPV       0.7293         18.7         SB    16.00     Sequence
DRB1_0101   91  EIYRDVLARLLAAGE  YRDVLARLL       0.7286         18.9         SB    16.00     Sequence
DRB1_0101  354  IALDEAAFAAAAELV  DEAAFAAAA       0.7250         19.6         SB    16.00     Sequence
DRB1_0101  206  MKITHVLRGEDLLPS  THVLRGEDL       0.7240         19.8         SB    16.00     Sequence
DRB1_0101  314  SPARFDQKKADALNA  FDQKKADAL       0.7220         20.3         SB    16.00     Sequence
DRB1_0101  134  FDRHLTDAQRAAYLA  RHLTDAQRA       0.7217         20.3         SB    16.00     Sequence
DRB1_0101  316  ARFDQKKADALNAEH  FDQKKADAL       0.7215         20.4         SB    16.00     Sequence
DRB1_0101   93  YRDVLARLLAAGEAY  YRDVLARLL       0.7198         20.7         SB    16.00     Sequence
DRB1_0101   23  VRTALFNWAYARHTG  FNWAYARHT       0.7173         21.3         SB    16.00     Sequence
DRB1_0101  183  DFALTRASGDPLYTL  LTRASGDPL       0.7169         21.4         SB    16.00     Sequence
DRB1_0101  436  IEGLALKPRKAFSPI  GLALKPRKA       0.7158         21.6         SB    16.00     Sequence
DRB1_0101   92  IYRDVLARLLAAGEA  YRDVLARLL       0.7157         21.7         SB    16.00     Sequence
DRB1_0101  369  QTRIVVLGDAWELLK  VVLGDAWEL       0.7154         21.7         SB    16.00     Sequence
DRB1_0101   87  SQRAEIYRDVLARLL  YRDVLARLL       0.7144         22.0         SB    16.00     Sequence
DRB1_0101   51  RDSEESYLALLDALR  YLALLDALR       0.7116         22.7         SB    16.00     Sequence
DRB1_0101  100  LLAAGEAYHAFSTPE  LAAGEAYHA       0.7108         22.8         SB    16.00     Sequence
DRB1_0101  135  DRHLTDAQRAAYLAE  TDAQRAAYL       0.7092         23.3         SB    32.00     Sequence
DRB1_0101  320  QKKADALNAEHIRML  ADALNAEHI       0.7071         23.8         SB    32.00     Sequence
DRB1_0101  432  KDALIEGLALKPRKA  GLALKPRKA       0.7052         24.3         SB    32.00     Sequence
DRB1_0101  409  LDAALAALTSVTDWT  LDAALAALT       0.7038         24.7         SB    32.00     Sequence
DRB1_0101  184  FALTRASGDPLYTLV  LTRASGDPL       0.7033         24.8         SB    32.00     Sequence
DRB1_0101  447  FSPIRVAATGTTVSP  FSPIRVAAT       0.6998         25.7         SB    32.00     Sequence
DRB1_0101  232  IRIGVAERIPKFAHL  IRIGVAERI       0.6972         26.5         SB    32.00     Sequence
DRB1_0101  371  RIVVLGDAWELLKFF  VVLGDAWEL       0.6923         27.9         SB    32.00     Sequence
DRB1_0101  358  EAAFAAAAELVQTRI  AFAAAAELV       0.6919         28.0         SB    32.00     Sequence
DRB1_0101  117  EARHVAAGRNPKLGY  VAAGRNPKL       0.6918         28.1         SB    32.00     Sequence
DRB1_0101   57  YLALLDALRWLGLDW  YLALLDALR       0.6913         28.2         SB    32.00     Sequence
DRB1_0101  118  ARHVAAGRNPKLGYD  VAAGRNPKL       0.6911         28.3         SB    32.00     Sequence
DRB1_0101   22  LVRTALFNWAYARHT  FNWAYARHT       0.6898         28.7         SB    32.00     Sequence
DRB1_0101  145  AYLAEGRQPVVRLRM  YLAEGRQPV       0.6863         29.8         SB    32.00     Sequence
DRB1_0101  368  VQTRIVVLGDAWELL  VVLGDAWEL       0.6832         30.8         SB    32.00     Sequence
DRB1_0101  166  WNDLVRGPVTFAAGS  LVRGPVTFA       0.6802         31.8         SB    32.00     Sequence
DRB1_0101  141  AQRAAYLAEGRQPVV  YLAEGRQPV       0.6798         31.9         SB    32.00     Sequence
DRB1_0101  438  GLALKPRKAFSPIRV  GLALKPRKA       0.6795         32.1         SB    32.00     Sequence
DRB1_0101   28  FNWAYARHTGGTFVF  FNWAYARHT       0.6782         32.5         SB    32.00     Sequence
DRB1_0101  357  DEAAFAAAAELVQTR  AFAAAAELV       0.6772         32.9         SB    32.00     Sequence
DRB1_0101  437  EGLALKPRKAFSPIR  GLALKPRKA       0.6732         34.3         SB    32.00     Sequence
DRB1_0101  410  DAALAALTSVTDWTA  LAALTSVTD       0.6708         35.2         SB    32.00     Sequence
DRB1_0101  205  LMKITHVLRGEDLLP  THVLRGEDL       0.6686         36.1         SB    32.00     Sequence
DRB1_0101  355  ALDEAAFAAAAELVQ  DEAAFAAAA       0.6681         36.3         SB    32.00     Sequence
DRB1_0101  470  LGRDRSMQRLRAARQ  MQRLRAARQ       0.6670         36.7         SB    32.00     Sequence
DRB1_0101  137  HLTDAQRAAYLAEGR  TDAQRAAYL       0.6660         37.1         SB    32.00     Sequence
DRB1_0101  356  LDEAAFAAAAELVQT  AFAAAAELV       0.6660         37.1         SB    32.00     Sequence
DRB1_0101  214  GEDLLPSTPRQLALH  LLPSTPRQL       0.6660         37.1         SB    32.00     Sequence
DRB1_0101  204  ALMKITHVLRGEDLL  THVLRGEDL       0.6658         37.2         SB    32.00     Sequence
DRB1_0101  402  GPDGAAVLDAALAAL  AAVLDAALA       0.6650         37.5         SB    32.00     Sequence
DRB1_0101  430  ALKDALIEGLALKPR  DALIEGLAL       0.6634         38.2         SB    32.00     Sequence
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DRB1_0101  440  ALKPRKAFSPIRVAA  RKAFSPIRV        0.6633        38.2        SB    32.00     Sequence
DRB1_0101  207  KITHVLRGEDLLPST  THVLRGEDL        0.6614        39.0        SB    32.00     Sequence
DRB1_0101  297  FGLDEMVAAFDVADV  DEMVAAFDV        0.6596        39.8        SB    32.00     Sequence
DRB1_0101  317  RFDQKKADALNAEHI  FDQKKADAL        0.6568        41.0        SB    32.00     Sequence
DRB1_0101  164  LAWNDLVRGPVTFAA  NDLVRGPVT        0.6536        42.4        SB    32.00     Sequence
DRB1_0101  223  RQLALHQALIRIGVA  LHQALIRIG        0.6488        44.7        SB    32.00     Sequence
DRB1_0101  181  VPDFALTRASGDPLY  FALTRASGD        0.6487        44.7        SB    32.00     Sequence
DRB1_0101  359  AAFAAAAELVQTRIV  AFAAAAELV        0.6458        46.2        SB    32.00     Sequence
DRB1_0101  273  GFIPEGLLNYLALLG  PEGLLNYLA        0.6436        47.3        SB    32.00     Sequence
DRB1_0101  321  KKADALNAEHIRMLD  ADALNAEHI        0.6408        48.8        SB    32.00     Sequence
DRB1_0101  411  AALAALTSVTDWTAP  LAALTSVTD        0.6393        49.5        SB    32.00     Sequence
DRB1_0101  224  QLALHQALIRIGVAE  LHQALIRIG        0.6385        50.0        SB    32.00     Sequence
DRB1_0101  272  RGFIPEGLLNYLALL  PEGLLNYLA        0.6378        50.4        WB    32.00     Sequence
DRB1_0101  330  HIRMLDVGDFTVRLR  MLDVGDFTV        0.6368        50.9        WB    32.00     Sequence
DRB1_0101  167  NDLVRGPVTFAAGSV  LVRGPVTFA        0.6363        51.2        WB    32.00     Sequence
DRB1_0101  182  PDFALTRASGDPLYT  LTRASGDPL        0.6351        51.8        WB    32.00     Sequence
DRB1_0101  165  AWNDLVRGPVTFAAG  LVRGPVTFA        0.6337        52.6        WB    32.00     Sequence
DRB1_0101  215  EDLLPSTPRQLALHQ  LLPSTPRQL        0.6337        52.7        WB    32.00     Sequence
DRB1_0101  313  SSPARFDQKKADALN  FDQKKADAL        0.6334        52.8        WB    32.00     Sequence
DRB1_0101  146  YLAEGRQPVVRLRMP  YLAEGRQPV        0.6323        53.5        WB    32.00     Sequence
DRB1_0101  213  RGEDLLPSTPRQLAL  LLPSTPRQL        0.6320        53.6        WB    32.00     Sequence
DRB1_0101  353  HIALDEAAFAAAAEL  DEAAFAAAA        0.6313        54.0        WB    32.00     Sequence
DRB1_0101  431  LKDALIEGLALKPRK  DALIEGLAL        0.6310        54.2        WB    32.00     Sequence
DRB1_0101  372  IVVLGDAWELLKFFN  VVLGDAWEL        0.6288        55.5        WB    32.00     Sequence
DRB1_0101  222  PRQLALHQALIRIGV  LHQALIRIG        0.6257        57.4        WB    32.00     Sequence
DRB1_0101  439  LALKPRKAFSPIRVA  RKAFSPIRV        0.6246        58.1        WB    32.00     Sequence
DRB1_0101  274  FIPEGLLNYLALLGW  PEGLLNYLA        0.6244        58.2        WB    32.00     Sequence
DRB1_0101  367  LVQTRIVVLGDAWEL  VVLGDAWEL        0.6186        62.0        WB    32.00     Sequence
DRB1_0101  271  DRGFIPEGLLNYLAL  PEGLLNYLA        0.6185        62.0        WB    32.00     Sequence
DRB1_0101  119  RHVAAGRNPKLGYDN  VAAGRNPKL        0.6163        63.5        WB    32.00     Sequence
DRB1_0101  295  DLFGLDEMVAAFDVA  DEMVAAFDV        0.6127        66.0        WB    32.00     Sequence
DRB1_0101  101  LAAGEAYHAFSTPEE  LAAGEAYHA        0.6089        68.8        WB    32.00     Sequence
DRB1_0101  428  EAALKDALIEGLALK  DALIEGLAL        0.6089        68.8        WB    32.00     Sequence
DRB1_0101  216  DLLPSTPRQLALHQA  LLPSTPRQL        0.6066        70.6        WB    32.00     Sequence
DRB1_0101  246  LPTVLGEGTKKLSKR  VLGEGTKKL        0.6061        70.9        WB    32.00     Sequence
DRB1_0101  429  AALKDALIEGLALKP  DALIEGLAL        0.6052        71.6        WB    32.00     Sequence
DRB1_0101  296  LFGLDEMVAAFDVAD  DEMVAAFDV        0.6042        72.4        WB    32.00     Sequence
DRB1_0101  132  DNFDRHLTDAQRAAY  RHLTDAQRA        0.6039        72.6        WB    32.00     Sequence
DRB1_0101  185  ALTRASGDPLYTLVN  LTRASGDPL        0.6009        75.0        WB    50.00     Sequence
DRB1_0101  275  IPEGLLNYLALLGWS  PEGLLNYLA        0.6004        75.5        WB    50.00     Sequence
DRB1_0101  319  DQKKADALNAEHIRM  ADALNAEHI        0.5996        76.1        WB    50.00     Sequence
DRB1_0101  225  LALHQALIRIGVAER  LHQALIRIG        0.5987        76.8        WB    50.00     Sequence
DRB1_0101  285  LLGWSIADDHDLFGL  WSIADDHDL        0.5947        80.3        WB    50.00     Sequence
DRB1_0101  294  HDLFGLDEMVAAFDV  LFGLDEMVA        0.5926        82.1        WB    50.00     Sequence
DRB1_0101  292  DDHDLFGLDEMVAAF  LFGLDEMVA        0.5925        82.2        WB    50.00     Sequence
DRB1_0101  140  DAQRAAYLAEGRQPV  YLAEGRQPV        0.5910        83.6        WB    50.00     Sequence
DRB1_0101  293  DHDLFGLDEMVAAFD  LFGLDEMVA        0.5909        83.6        WB    50.00     Sequence
DRB1_0101  217  LLPSTPRQLALHQAL  LLPSTPRQL        0.5903        84.2        WB    50.00     Sequence
DRB1_0101   58  LALLDALRWLGLDWD  LDALRWLGL        0.5902        84.2        WB    50.00     Sequence
DRB1_0101  362  AAAAELVQTRIVVLG  AELVQTRIV        0.5890        85.4        WB    50.00     Sequence
DRB1_0101  413  LAALTSVTDWTAPLI  LTSVTDWTA        0.5885        85.8        WB    50.00     Sequence
DRB1_0101  360  AFAAAAELVQTRIVV  AFAAAAELV        0.5879        86.3        WB    50.00     Sequence
DRB1_0101  138  LTDAQRAAYLAEGRQ  TDAQRAAYL        0.5865        87.7        WB    50.00     Sequence
DRB1_0101  351  GHHIALDEAAFAAAA  IALDEAAFA        0.5862        88.0        WB    50.00     Sequence
DRB1_0101  220  STPRQLALHQALIRI  RQLALHQAL        0.5859        88.3        WB    50.00     Sequence
DRB1_0101  221  TPRQLALHQALIRIG  QLALHQALI        0.5854        88.8        WB    50.00     Sequence
DRB1_0101  303  VAAFDVADVNSSPAR  FDVADVNSS        0.5849        89.2        WB    50.00     Sequence
DRB1_0101  219  PSTPRQLALHQALIR  PRQLALHQA        0.5848        89.4        WB    50.00     Sequence
DRB1_0101   21  GLVRTALFNWAYARH  RTALFNWAY        0.5845        89.6        WB    50.00     Sequence
DRB1_0101  208  ITHVLRGEDLLPSTP  THVLRGEDL        0.5844        89.7        WB    50.00     Sequence
DRB1_0101  298  GLDEMVAAFDVADVN  DEMVAAFDV        0.5843        89.8        WB    50.00     Sequence
DRB1_0101  328  AEHIRMLDVGDFTVR  IRMLDVGDF        0.5836        90.5        WB    50.00     Sequence
DRB1_0101  116  VEARHVAAGRNPKLG  VAAGRNPKL        0.5804        93.7        WB    50.00     Sequence
DRB1_0101  329  EHIRMLDVGDFTVRL  MLDVGDFTV        0.5797        94.4        WB    50.00     Sequence
DRB1_0101  373  VVLGDAWELLKFFND  VVLGDAWEL        0.5784        95.7        WB    50.00     Sequence
DRB1_0101  191  GDPLYTLVNPCDDAL  LYTLVNPCD        0.5783        95.9        WB    50.00     Sequence
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DRB1_0101  212  LRGEDLLPSTPRQLA  LLPSTPRQL        0.5776           96.5           WB    50.00     Sequence
DRB1_0101  163  DLAWNDLVRGPVTFA  NDLVRGPVT        0.5760           98.3           WB    50.00     Sequence
DRB1_0101  352  HHIALDEAAFAAAAE  ALDEAAFAA        0.5756           98.6           WB    50.00     Sequence
DRB1_0101   15  TGTPHVGLVRTALFN  PHVGLVRTA        0.5745           99.9           WB    50.00     Sequence
DRB1_0101  173  PVTFAAGSVPDFALT  FAAGSVPDF        0.5735          101.0           WB    50.00     Sequence
DRB1_0101  270  RDRGFIPEGLLNYLA  PEGLLNYLA        0.5729          101.7           WB    50.00     Sequence
DRB1_0101  192  DPLYTLVNPCDDALM  LYTLVNPCD        0.5721          102.5           WB    50.00     Sequence
DRB1_0101  168  DLVRGPVTFAAGSVP  LVRGPVTFA        0.5717          103.0           WB    50.00     Sequence
DRB1_0101  322  KADALNAEHIRMLDV  ADALNAEHI        0.5714          103.3           WB    50.00     Sequence
DRB1_0101  469  LLGRDRSMQRLRAAR  DRSMQRLRA        0.5694          105.6           WB    50.00     Sequence
DRB1_0101  203  DALMKITHVLRGEDL  THVLRGEDL        0.5688          106.2           WB    50.00     Sequence
DRB1_0101  412  ALAALTSVTDWTAPL  LAALTSVTD        0.5671          108.2           WB    50.00     Sequence
DRB1_0101  200  PCDDALMKITHVLRG  DALMKITHV        0.5670          108.3           WB    50.00     Sequence
DRB1_0101  364  AAELVQTRIVVLGDA  LVQTRIVVL        0.5657          109.9           WB    50.00     Sequence
DRB1_0101  331  IRMLDVGDFTVRLRD  MLDVGDFTV        0.5651          110.5           WB    50.00     Sequence
DRB1_0101   16  GTPHVGLVRTALFNW  HVGLVRTAL        0.5642          111.7           WB    50.00     Sequence
DRB1_0101  448  SPIRVAATGTTVSPP  RVAATGTTV        0.5633          112.7           WB    50.00     Sequence
DRB1_0101   30  WAYARHTGGTFVFRI  ARHTGGTFV        0.5633          112.8           WB    50.00     Sequence
DRB1_0101  361  FAAAAELVQTRIVVL  AELVQTRIV        0.5628          113.3           WB    50.00     Sequence
DRB1_0101  425  PLIEAALKDALIEGL  EAALKDALI        0.5623          114.0           WB    50.00     Sequence
DRB1_0101  363  AAAELVQTRIVVLGD  LVQTRIVVL        0.5621          114.2           WB    50.00     Sequence
DRB1_0101  401  LGPDGAAVLDAALAA  AAVLDAALA        0.5612          115.4           WB    50.00     Sequence
DRB1_0101   17  TPHVGLVRTALFNWA  HVGLVRTAL        0.5593          117.8           WB    50.00     Sequence
DRB1_0101   20  VGLVRTALFNWAYAR  VRTALFNWA        0.5588          118.4           WB    50.00     Sequence
DRB1_0101  318  FDQKKADALNAEHIR  FDQKKADAL        0.5582          119.2           WB    50.00     Sequence
DRB1_0101  312  NSSPARFDQKKADAL  FDQKKADAL        0.5557          122.4           WB    50.00     Sequence
DRB1_0101  172  GPVTFAAGSVPDFAL  FAAGSVPDF        0.5539          124.8           WB    50.00     Sequence
DRB1_0101  268  AHRDRGFIPEGLLNY  DRGFIPEGL        0.5526          126.6           WB    50.00     Sequence
DRB1_0101  427  IEAALKDALIEGLAL  DALIEGLAL        0.5519          127.5           WB    50.00     Sequence
DRB1_0101  171  RGPVTFAAGSVPDFA  VTFAAGSVP        0.5503          129.8           WB    50.00     Sequence
DRB1_0101  180  SVPDFALTRASGDPL  FALTRASGD        0.5486          132.1           WB    50.00     Sequence
DRB1_0101  201  CDDALMKITHVLRGE  ALMKITHVL        0.5469          134.6           WB    50.00     Sequence
DRB1_0101  218  LPSTPRQLALHQALI  PRQLALHQA        0.5458          136.2           WB    50.00     Sequence
DRB1_0101   14  PTGTPHVGLVRTALF  HVGLVRTAL        0.5455          136.6           WB    50.00     Sequence
DRB1_0101  169  LVRGPVTFAAGSVPD  LVRGPVTFA        0.5428          140.7           WB    50.00     Sequence
DRB1_0101  193  PLYTLVNPCDDALMK  LYTLVNPCD        0.5425          141.2           WB    50.00     Sequence
DRB1_0101  323  ADALNAEHIRMLDVG  LNAEHIRML        0.5400          145.1           WB    50.00     Sequence
DRB1_0101   18  PHVGLVRTALFNWAY  HVGLVRTAL        0.5375          149.0           WB    50.00     Sequence
DRB1_0101  186  LTRASGDPLYTLVNP  LTRASGDPL        0.5369          150.1           WB    50.00     Sequence
DRB1_0101  418  SVTDWTAPLIEAALK  WTAPLIEAA        0.5343          154.3           WB    50.00     Sequence
DRB1_0101  299  LDEMVAAFDVADVNS  DEMVAAFDV        0.5343          154.4           WB    50.00     Sequence
DRB1_0101   19  HVGLVRTALFNWAYA  HVGLVRTAL        0.5338          155.2           WB    50.00     Sequence
DRB1_0101  269  HRDRGFIPEGLLNYL  DRGFIPEGL        0.5317          158.6           WB    50.00     Sequence
DRB1_0101  199  NPCDDALMKITHVLR  DALMKITHV        0.5316          158.8           WB    50.00     Sequence
DRB1_0101  419  VTDWTAPLIEAALKD  WTAPLIEAA        0.5301          161.4           WB    50.00     Sequence
DRB1_0101  461  PPLFESLELLGRDRS  FESLELLGR        0.5300          161.6           WB    50.00     Sequence
DRB1_0101  174  VTFAAGSVPDFALTR  FAAGSVPDF        0.5288          163.7           WB    50.00     Sequence
DRB1_0101   29  NWAYARHTGGTFVFR  WAYARHTGG        0.5279          165.3           WB    50.00     Sequence
DRB1_0101  170  VRGPVTFAAGSVPDF  PVTFAAGSV        0.5275          166.1           WB    50.00     Sequence
DRB1_0101  245  HLPTVLGEGTKKLSK  VLGEGTKKL        0.5273          166.3           WB    50.00     Sequence
DRB1_0101  458  TVSPPLFESLELLGR  PLFESLELL        0.5265          167.8           WB    50.00     Sequence
DRB1_0101    5  TVRVRFCPSPTGTPH  VRFCPSPTG        0.5246          171.4           WB    50.00     Sequence
DRB1_0101  459  VSPPLFESLELLGRD  PLFESLELL        0.5243          172.0           WB    50.00     Sequence
DRB1_0101  365  AELVQTRIVVLGDAW  LVQTRIVVL        0.5222          175.8           WB    50.00     Sequence
DRB1_0101  115  EVEARHVAAGRNPKL  VAAGRNPKL        0.5193          181.5           WB    50.00     Sequence
DRB1_0101  209  THVLRGEDLLPSTPR  THVLRGEDL        0.5190          182.1           WB    50.00     Sequence
DRB1_0101  291  ADDHDLFGLDEMVAA  LFGLDEMVA        0.5184          183.2           WB    50.00     Sequence
DRB1_0101  202  DDALMKITHVLRGED  ALMKITHVL        0.5181          183.8           WB    50.00     Sequence
DRB1_0101  460  SPPLFESLELLGRDR  PLFESLELL        0.5176          184.9           WB    50.00     Sequence
DRB1_0101  247  PTVLGEGTKKLSKRD  VLGEGTKKL        0.5162          187.6           WB    50.00     Sequence
DRB1_0101  462  PLFESLELLGRDRSM  FESLELLGR        0.5162          187.7           WB    50.00     Sequence
DRB1_0101   31  AYARHTGGTFVFRIE  ARHTGGTFV        0.5161          187.9           WB    50.00     Sequence
DRB1_0101  426  LIEAALKDALIEGLA  EAALKDALI        0.5137          192.7           WB    50.00     Sequence
DRB1_0101  131  YDNFDRHLTDAQRAA  RHLTDAQRA        0.5128          194.7           WB    50.00     Sequence
DRB1_0101  350  HGHHIALDEAAFAAA  IALDEAAFA        0.5095          201.8           WB    50.00     Sequence
DRB1_0101  468  ELLGRDRSMQRLRAA  DRSMQRLRA        0.5092          202.4           WB    50.00     Sequence
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DRB1_0101   59  ALLDALRWLGLDWDE  LDALRWLGL        0.5080        205.1         WB    50.00     Sequence
DRB1_0101  463  LFESLELLGRDRSMQ  SLELLGRDR        0.5068        207.8         WB    50.00     Sequence
DRB1_0101  304  AAFDVADVNSSPARF  FDVADVNSS        0.5054        210.9         WB    50.00     Sequence
DRB1_0101  286  LGWSIADDHDLFGLD  WSIADDHDL        0.5048        212.4         WB    50.00     Sequence
DRB1_0101   13  SPTGTPHVGLVRTAL  HVGLVRTAL        0.5018        219.3         WB    50.00     Sequence
DRB1_0101  236  VAERIPKFAHLPTVL  KFAHLPTVL        0.5004        222.6         WB    50.00     Sequence
DRB1_0101  267  FAHRDRGFIPEGLLN  DRGFIPEGL        0.5002        223.0         WB    50.00     Sequence
DRB1_0101  465  ESLELLGRDRSMQRL  ELLGRDRSM        0.5000        223.5         WB    50.00     Sequence
DRB1_0101  194  LYTLVNPCDDALMKI  LYTLVNPCD        0.5000        223.7         WB    50.00     Sequence
DRB1_0101  422  WTAPLIEAALKDALI  PLIEAALKD        0.4990        226.1         WB    50.00     Sequence
DRB1_0101  211  VLRGEDLLPSTPRQL  LLPSTPRQL        0.4985        227.3         WB    50.00     Sequence
DRB1_0101  327  NAEHIRMLDVGDFTV  IRMLDVGDF        0.4985        227.3         WB    50.00     Sequence
DRB1_0101  120  HVAAGRNPKLGYDNF  VAAGRNPKL        0.4978        229.0         WB    50.00     Sequence
DRB1_0101  366  ELVQTRIVVLGDAWE  LVQTRIVVL        0.4973        230.1         WB    50.00     Sequence
DRB1_0101   80  PYGPYRQSQRAEIYR  YRQSQRAEI        0.4945        237.2         WB    50.00     Sequence
DRB1_0101   81  YGPYRQSQRAEIYRD  YRQSQRAEI        0.4920        243.7         WB    50.00     Sequence
DRB1_0101  332  RMLDVGDFTVRLRDH  MLDVGDFTV        0.4876        255.8         WB    50.00     Sequence
DRB1_0101  400  ELGPDGAAVLDAALA  AAVLDAALA        0.4830        268.8         WB    50.00     Sequence
DRB1_0101   32  YARHTGGTFVFRIED  ARHTGGTFV        0.4829        269.1         WB    50.00     Sequence
DRB1_0101  417  TSVTDWTAPLIEAAL  WTAPLIEAA        0.4823        270.9         WB    50.00     Sequence
DRB1_0101  457  TTVSPPLFESLELLG  PLFESLELL        0.4818        272.3         WB    50.00     Sequence
DRB1_0101  190  SGDPLYTLVNPCDDA  LYTLVNPCD        0.4815        273.2         WB    50.00     Sequence
DRB1_0101  464  FESLELLGRDRSMQR  LELLGRDRS        0.4812        274.0         WB    50.00     Sequence
DRB1_0101  302  MVAAFDVADVNSSPA  FDVADVNSS        0.4810        274.7         WB    50.00     Sequence
DRB1_0101   60  LLDALRWLGLDWDEG  LDALRWLGL        0.4802        277.1         WB    50.00     Sequence
DRB1_0101  349  THGHHIALDEAAFAA  HHIALDEAA        0.4800        277.6         WB    50.00     Sequence
DRB1_0101  414  AALTSVTDWTAPLIE  LTSVTDWTA        0.4784        282.4         WB    50.00     Sequence
DRB1_0101  423  TAPLIEAALKDALIE  PLIEAALKD        0.4784        282.5         WB    50.00     Sequence
DRB1_0101  453  AATGTTVSPPLFESL  GTTVSPPLF        0.4764        288.7         WB    50.00     Sequence
DRB1_0101  424  APLIEAALKDALIEG  EAALKDALI        0.4739        296.5         WB    50.00     Sequence
DRB1_0101  128  KLGYDNFDRHLTDAQ  YDNFDRHLT        0.4739        296.7         WB    50.00     Sequence
DRB1_0101  175  TFAAGSVPDFALTRA  FAAGSVPDF        0.4714        304.7         WB    50.00     Sequence
DRB1_0101  456  GTTVSPPLFESLELL  PLFESLELL        0.4709        306.3         WB    50.00     Sequence
DRB1_0101  420  TDWTAPLIEAALKDA  WTAPLIEAA        0.4696        310.7         WB    50.00     Sequence
DRB1_0101   33  ARHTGGTFVFRIEDT  TGGTFVFRI        0.4696        310.7         WB    50.00     Sequence
DRB1_0101  248  TVLGEGTKKLSKRDP  VLGEGTKKL        0.4687        313.8         WB    50.00     Sequence
DRB1_0101  449  PIRVAATGTTVSPPL  RVAATGTTV        0.4677        317.2         WB    50.00     Sequence
DRB1_0101  284  ALLGWSIADDHDLFG  WSIADDHDL        0.4670        319.7         WB    50.00     Sequence
DRB1_0101  466  SLELLGRDRSMQRLR  ELLGRDRSM        0.4661        322.6         WB    50.00     Sequence
DRB1_0101  324  DALNAEHIRMLDVGD  LNAEHIRML        0.4660        323.0         WB    50.00     Sequence
DRB1_0101    4  ETVRVRFCPSPTGTP  VRFCPSPTG        0.4655        324.7         WB    50.00     Sequence
DRB1_0101   86  QSQRAEIYRDVLARL  IYRDVLARL        0.4649        326.8         WB    50.00     Sequence
DRB1_0101  300  DEMVAAFDVADVNSS  DEMVAAFDV        0.4649        327.0         WB    50.00     Sequence
DRB1_0101  139  TDAQRAAYLAEGRQP  TDAQRAAYL        0.4640        330.2         WB    50.00     Sequence
DRB1_0101    6  VRVRFCPSPTGTPHV  VRFCPSPTG        0.4639        330.4         WB    50.00     Sequence
DRB1_0101  198  VNPCDDALMKITHVL  DALMKITHV        0.4636        331.5         WB    50.00     Sequence
DRB1_0101  162  DDLAWNDLVRGPVTF  NDLVRGPVT        0.4623        336.1         WB    50.00     Sequence
DRB1_0101    3  TETVRVRFCPSPTGT  VRFCPSPTG        0.4617        338.5         WB    50.00     Sequence
DRB1_0101  325  ALNAEHIRMLDVGDF  LNAEHIRML        0.4615        339.2         WB    50.00     Sequence
DRB1_0101  266  LFAHRDRGFIPEGLL  DRGFIPEGL        0.4590        348.3         WB    50.00     Sequence
DRB1_0101  104  GEAYHAFSTPEEVEA  YHAFSTPEE        0.4572        355.5         WB    50.00     Sequence
DRB1_0101  467  LELLGRDRSMQRLRA  DRSMQRLRA        0.4567        357.0         WB    50.00     Sequence
DRB1_0101   50  QRDSEESYLALLDAL  SYLALLDAL        0.4559        360.2         WB    50.00     Sequence
DRB1_0101    0  VTATETVRVRFCPSP  VTATETVRV        0.4525        373.8         WB    50.00     Sequence
DRB1_0101  244  AHLPTVLGEGTKKLS  VLGEGTKKL        0.4504        382.3         WB    50.00     Sequence
DRB1_0101  337  GDFTVRLRDHLDTHG  TVRLRDHLD        0.4492        387.5         WB    50.00     Sequence
DRB1_0101   49  AQRDSEESYLALLDA  DSEESYLAL        0.4489        388.5         WB    50.00     Sequence
DRB1_0101  387  DDQYVIDPKAAAKEL  YVIDPKAAA        0.4472        396.0         WB    50.00     Sequence
DRB1_0101  130  GYDNFDRHLTDAQRA  RHLTDAQRA        0.4458        402.1         WB    50.00     Sequence
DRB1_0101  416  LTSVTDWTAPLIEAA  VTDWTAPLI        0.4446        407.1         WB    50.00     Sequence
DRB1_0101  127  PKLGYDNFDRHLTDA  YDNFDRHLT        0.4430        414.4         WB    50.00     Sequence
DRB1_0101   85  RQSQRAEIYRDVLAR  QRAEIYRDV        0.4425        416.6         WB    50.00     Sequence
DRB1_0101  386  NDDQYVIDPKAAAKE  QYVIDPKAA        0.4423        417.3         WB    50.00     Sequence
DRB1_0101  290  IADDHDLFGLDEMVA  LFGLDEMVA        0.4404        426.0         WB    50.00     Sequence
DRB1_0101  421  DWTAPLIEAALKDAL  PLIEAALKD        0.4395        430.3         WB    50.00     Sequence
DRB1_0101  454  ATGTTVSPPLFESLE  GTTVSPPLF        0.4388        433.7         WB    50.00     Sequence
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DRB1_0101  333  MLDVGDFTVRLRDHL  VGDFTVRLR        0.4382        436.2        WB    50.00     Sequence
DRB1_0101   82  GPYRQSQRAEIYRDV  YRQSQRAEI        0.4367        443.4        WB    50.00     Sequence
DRB1_0101  452  VAATGTTVSPPLFES  TGTTVSPPL        0.4358        447.9        WB    50.00     Sequence
DRB1_0101  326  LNAEHIRMLDVGDFT  LNAEHIRML        0.4353        450.1        WB    50.00     Sequence
DRB1_0101  415  ALTSVTDWTAPLIEA  LTSVTDWTA        0.4349        452.4        WB    50.00     Sequence
DRB1_0101  305  AFDVADVNSSPARFD  FDVADVNSS        0.4346        453.6        WB    50.00     Sequence
DRB1_0101  376  GDAWELLKFFNDDQY  WELLKFFND        0.4340        456.9        WB    50.00     Sequence
DRB1_0101  195  YTLVNPCDDALMKIT  VNPCDDALM        0.4336        458.5        WB    50.00     Sequence
DRB1_0101  176  FAAGSVPDFALTRAS  FAAGSVPDF        0.4320        466.7        WB    50.00     Sequence
DRB1_0101  129  LGYDNFDRHLTDAQR  YDNFDRHLT        0.4310        471.7        WB    50.00     Sequence
DRB1_0101   48  DAQRDSEESYLALLD  RDSEESYLA        0.4300        477.0        WB    50.00     Sequence
DRB1_0101   47  TDAQRDSEESYLALL  RDSEESYLA        0.4293        480.6        WB    50.00     Sequence
DRB1_0101  147  LAEGRQPVVRLRMPD  GRQPVVRLR        0.4284        485.1        WB    50.00     Sequence
DRB1_0101   39  TFVFRIEDTDAQRDS  FRIEDTDAQ        0.4282        486.5        WB    50.00     Sequence
DRB1_0101  336  VGDFTVRLRDHLDTH  TVRLRDHLD        0.4271        492.3        WB    50.00     Sequence
DRB1_0101   34  RHTGGTFVFRIEDTD  TGGTFVFRI        0.4261        497.6        WB    50.00     Sequence
DRB1_0101  388  DQYVIDPKAAAKELG  YVIDPKAAA        0.4250        503.5              50.00     Sequence
DRB1_0101  450  IRVAATGTTVSPPLF  RVAATGTTV        0.4242        507.7              50.00     Sequence
DRB1_0101  283  LALLGWSIADDHDLF  WSIADDHDL        0.4242        507.7              50.00     Sequence
DRB1_0101  178  AGSVPDFALTRASGD  FALTRASGD        0.4230        514.7              50.00     Sequence
DRB1_0101  188  RASGDPLYTLVNPCD  LYTLVNPCD        0.4225        516.9              50.00     Sequence
DRB1_0101  179  GSVPDFALTRASGDP  FALTRASGD        0.4196        533.9              50.00     Sequence
DRB1_0101  189  ASGDPLYTLVNPCDD  LYTLVNPCD        0.4162        553.7              50.00     Sequence
DRB1_0101  287  GWSIADDHDLFGLDE  WSIADDHDL        0.4155        557.6              50.00     Sequence
DRB1_0101  455  TGTTVSPPLFESLEL  GTTVSPPLF        0.4123        577.7              50.00     Sequence
DRB1_0101  378  AWELLKFFNDDQYVI  WELLKFFND        0.4120        579.3              50.00     Sequence
DRB1_0101  398  AKELGPDGAAVLDAA  LGPDGAAVL        0.4117        581.5              50.00     Sequence
DRB1_0101    2  ATETVRVRFCPSPTG  VRFCPSPTG        0.4114        583.0              50.00     Sequence
DRB1_0101  395  KAAAKELGPDGAAVL  AKELGPDGA        0.4109        586.5              50.00     Sequence
DRB1_0101    7  RVRFCPSPTGTPHVG  VRFCPSPTG        0.4100        591.9              50.00     Sequence
DRB1_0101  121  VAAGRNPKLGYDNFD  VAAGRNPKL        0.4090        598.6              50.00     Sequence
DRB1_0101  397  AAKELGPDGAAVLDA  ELGPDGAAV        0.4089        599.0              50.00     Sequence
DRB1_0101   79  GPYGPYRQSQRAEIY  YRQSQRAEI        0.4080        605.0              50.00     Sequence
DRB1_0101  385  FNDDQYVIDPKAAAK  QYVIDPKAA        0.4074        608.7              50.00     Sequence
DRB1_0101  301  EMVAAFDVADVNSSP  FDVADVNSS        0.4050        624.8              50.00     Sequence
DRB1_0101   84  YRQSQRAEIYRDVLA  QRAEIYRDV        0.4044        628.9              50.00     Sequence
DRB1_0101  235  GVAERIPKFAHLPTV  RIPKFAHLP        0.4018        647.3              50.00     Sequence
DRB1_0101   61  LDALRWLGLDWDEGP  LDALRWLGL        0.4002        658.5              50.00     Sequence
DRB1_0101   83  PYRQSQRAEIYRDVL  YRQSQRAEI        0.3995        663.2              50.00     Sequence
DRB1_0101  389  QYVIDPKAAAKELGP  YVIDPKAAA        0.3970        681.7              50.00     Sequence
DRB1_0101  381  LLKFFNDDQYVIDPK  FFNDDQYVI        0.3967        683.5              50.00     Sequence
DRB1_0101  338  DFTVRLRDHLDTHGH  TVRLRDHLD        0.3967        683.7              50.00     Sequence
DRB1_0101  125  RNPKLGYDNFDRHLT  YDNFDRHLT        0.3931        711.3              50.00     Sequence
DRB1_0101  233  RIGVAERIPKFAHLP  GVAERIPKF        0.3930        711.8              50.00     Sequence
DRB1_0101   12  PSPTGTPHVGLVRTA  PTGTPHVGL        0.3929        712.6              50.00     Sequence
DRB1_0101  126  NPKLGYDNFDRHLTD  YDNFDRHLT        0.3919        719.9              50.00     Sequence
DRB1_0101  342  RLRDHLDTHGHHIAL  HLDTHGHHI        0.3918        720.9              50.00     Sequence
DRB1_0101  451  RVAATGTTVSPPLFE  GTTVSPPLF        0.3911        726.8              50.00     Sequence
DRB1_0101  105  EAYHAFSTPEEVEAR  YHAFSTPEE        0.3908        728.5              50.00     Sequence
DRB1_0101   35  HTGGTFVFRIEDTDA  TGGTFVFRI        0.3904        732.3              50.00     Sequence
DRB1_0101  343  LRDHLDTHGHHIALD  HLDTHGHHI        0.3892        741.3              50.00     Sequence
DRB1_0101  377  DAWELLKFFNDDQYV  WELLKFFND        0.3837        787.4              50.00     Sequence
DRB1_0101  249  VLGEGTKKLSKRDPQ  VLGEGTKKL        0.3834        789.3              50.00     Sequence
DRB1_0101   37  GGTFVFRIEDTDAQR  FRIEDTDAQ        0.3827        795.6              50.00     Sequence
DRB1_0101  256  KLSKRDPQSNLFAHR  RDPQSNLFA        0.3825        797.3              50.00     Sequence
DRB1_0101  334  LDVGDFTVRLRDHLD  VGDFTVRLR        0.3815        806.3              50.00     Sequence
DRB1_0101  148  AEGRQPVVRLRMPDD  GRQPVVRLR        0.3812        808.3              50.00     Sequence
DRB1_0101  348  DTHGHHIALDEAAFA  HHIALDEAA        0.3801        818.2              50.00     Sequence
DRB1_0101  379  WELLKFFNDDQYVID  WELLKFFND        0.3800        818.7              50.00     Sequence
DRB1_0101   11  CPSPTGTPHVGLVRT  PTGTPHVGL        0.3796        822.4              50.00     Sequence
DRB1_0101   36  TGGTFVFRIEDTDAQ  TGGTFVFRI        0.3774        842.6              50.00     Sequence
DRB1_0101   38  GTFVFRIEDTDAQRD  FRIEDTDAQ        0.3764        852.0              50.00     Sequence
DRB1_0101  399  KELGPDGAAVLDAAL  LGPDGAAVL        0.3741        873.3              50.00     Sequence
DRB1_0101  339  FTVRLRDHLDTHGHH  TVRLRDHLD        0.3737        876.6              50.00     Sequence
DRB1_0101   40  FVFRIEDTDAQRDSE  FRIEDTDAQ        0.3720        893.5              50.00     Sequence
DRB1_0101  265  NLFAHRDRGFIPEGL  DRGFIPEGL        0.3713        900.3              50.00     Sequence
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DRB1_0101  335  DVGDFTVRLRDHLDT  TVRLRDHLD         0.3706         906.9                 50.00     Sequence
DRB1_0101  374  VLGDAWELLKFFNDD  VLGDAWELL         0.3697         915.6                 50.00     Sequence
DRB1_0101  288  WSIADDHDLFGLDEM  WSIADDHDL         0.3693         919.5                 50.00     Sequence
DRB1_0101  257  LSKRDPQSNLFAHRD  RDPQSNLFA         0.3686         926.2                 50.00     Sequence
DRB1_0101  306  FDVADVNSSPARFDQ  FDVADVNSS         0.3672         941.0                 50.00     Sequence
DRB1_0101  187  TRASGDPLYTLVNPC  SGDPLYTLV         0.3645         968.3                 50.00     Sequence
DRB1_0101  396  AAAKELGPDGAAVLD  ELGPDGAAV         0.3642         971.7                 50.00     Sequence
DRB1_0101  344  RDHLDTHGHHIALDE  LDTHGHHIA         0.3639         975.3                 50.00     Sequence
DRB1_0101  375  LGDAWELLKFFNDDQ  WELLKFFND         0.3637         977.6                 50.00     Sequence
DRB1_0101  161  DDDLAWNDLVRGPVT  NDLVRGPVT         0.3605        1011.4                 50.00     Sequence
DRB1_0101  210  HVLRGEDLLPSTPRQ  LRGEDLLPS         0.3602        1014.9                 50.00     Sequence
DRB1_0101   10  FCPSPTGTPHVGLVR  SPTGTPHVG         0.3593        1024.8                 50.00     Sequence
DRB1_0101  234  IGVAERIPKFAHLPT  GVAERIPKF         0.3577        1043.2                 50.00     Sequence
DRB1_0101  103  AGEAYHAFSTPEEVE  YHAFSTPEE         0.3567        1054.4                 50.00     Sequence
DRB1_0101  177  AAGSVPDFALTRASG  PDFALTRAS         0.3555        1068.0                 50.00     Sequence
DRB1_0101  106  AYHAFSTPEEVEARH  YHAFSTPEE         0.3495        1138.9                 50.00     Sequence
DRB1_0101  197  LVNPCDDALMKITHV  DALMKITHV         0.3457        1187.5                 50.00     Sequence
DRB1_0101  107  YHAFSTPEEVEARHV  FSTPEEVEA         0.3423        1232.1                 50.00     Sequence
DRB1_0101  196  TLVNPCDDALMKITH  VNPCDDALM         0.3418        1238.9                 50.00     Sequence
DRB1_0101  153  PVVRLRMPDDDLAWN  LRMPDDDLA         0.3414        1243.9                 50.00     Sequence
DRB1_0101  254  TKKLSKRDPQSNLFA  LSKRDPQSN         0.3408        1252.4                 50.00     Sequence
DRB1_0101  384  FFNDDQYVIDPKAAA  QYVIDPKAA         0.3392        1273.7                 50.00     Sequence
DRB1_0101  380  ELLKFFNDDQYVIDP  FFNDDQYVI         0.3383        1285.6                 50.00     Sequence
DRB1_0101   46  DTDAQRDSEESYLAL  DSEESYLAL         0.3379        1292.4                 50.00     Sequence
DRB1_0101  149  EGRQPVVRLRMPDDD  GRQPVVRLR         0.3375        1297.4                 50.00     Sequence
DRB1_0101  255  KKLSKRDPQSNLFAH  LSKRDPQSN         0.3342        1344.2                 50.00     Sequence
DRB1_0101  154  VVRLRMPDDDLAWND  LRMPDDDLA         0.3310        1392.4                 50.00     Sequence
DRB1_0101  102  AAGEAYHAFSTPEEV  YHAFSTPEE         0.3304        1401.5                 50.00     Sequence
DRB1_0101    8  VRFCPSPTGTPHVGL  VRFCPSPTG         0.3303        1403.0                 50.00     Sequence
DRB1_0101  308  VADVNSSPARFDQKK  VNSSPARFD         0.3276        1443.9                 50.00     Sequence
DRB1_0101  151  RQPVVRLRMPDDDLA  VVRLRMPDD         0.3261        1468.2                 50.00     Sequence
DRB1_0101  341  VRLRDHLDTHGHHIA  HLDTHGHHI         0.3259        1470.5                 50.00     Sequence
DRB1_0101   78  GGPYGPYRQSQRAEI  YRQSQRAEI         0.3234        1511.1                 50.00     Sequence
DRB1_0101  150  GRQPVVRLRMPDDDL  RQPVVRLRM         0.3228        1520.8                 50.00     Sequence
DRB1_0101    1  TATETVRVRFCPSPT  TETVRVRFC         0.3227        1522.0                 50.00     Sequence
DRB1_0101  347  LDTHGHHIALDEAAF  HHIALDEAA         0.3186        1592.6                 50.00     Sequence
DRB1_0101   41  VFRIEDTDAQRDSEE  FRIEDTDAQ         0.3184        1594.8                 50.00     Sequence
DRB1_0101  260  RDPQSNLFAHRDRGF  QSNLFAHRD         0.3182        1599.3                 50.00     Sequence
DRB1_0101  110  FSTPEEVEARHVAAG  PEEVEARHV         0.3180        1602.4                 50.00     Sequence
DRB1_0101  346  HLDTHGHHIALDEAA  LDTHGHHIA         0.3147        1659.5                 50.00     Sequence
DRB1_0101  345  DHLDTHGHHIALDEA  LDTHGHHIA         0.3144        1665.9                 50.00     Sequence
DRB1_0101    9  RFCPSPTGTPHVGLV  SPTGTPHVG         0.3139        1674.6                 50.00     Sequence
DRB1_0101  340  TVRLRDHLDTHGHHI  TVRLRDHLD         0.3120        1709.3                 50.00     Sequence
DRB1_0101  152  QPVVRLRMPDDDLAW  LRMPDDDLA         0.3082        1782.2                 50.00     Sequence
DRB1_0101  394  PKAAAKELGPDGAAV  AKELGPDGA         0.3075        1794.0                 50.00     Sequence
DRB1_0101  382  LKFFNDDQYVIDPKA  FFNDDQYVI         0.3074        1796.8                 50.00     Sequence
DRB1_0101  112  TPEEVEARHVAAGRN  EVEARHVAA         0.3012        1922.2                 50.00     Sequence
DRB1_0101  307  DVADVNSSPARFDQK  VADVNSSPA         0.2960        2032.6                 50.00     Sequence
DRB1_0101   63  ALRWLGLDWDEGPEV  WLGLDWDEG         0.2960        2033.3                 50.00     Sequence
DRB1_0101  383  KFFNDDQYVIDPKAA  QYVIDPKAA         0.2949        2056.2                 50.00     Sequence
DRB1_0101  261  DPQSNLFAHRDRGFI  LFAHRDRGF         0.2947        2061.8                 50.00     Sequence
DRB1_0101  262  PQSNLFAHRDRGFIP  LFAHRDRGF         0.2878        2222.0                 50.00     Sequence
DRB1_0101  390  YVIDPKAAAKELGPD  YVIDPKAAA         0.2869        2242.0                 50.00     Sequence
DRB1_0101  109  AFSTPEEVEARHVAA  PEEVEARHV         0.2869        2244.2                 50.00     Sequence
DRB1_0101  258  SKRDPQSNLFAHRDR  RDPQSNLFA         0.2857        2273.2                 50.00     Sequence
DRB1_0101  263  QSNLFAHRDRGFIPE  LFAHRDRGF         0.2855        2276.4                 50.00     Sequence
DRB1_0101  253  GTKKLSKRDPQSNLF  LSKRDPQSN         0.2854        2280.6                 50.00     Sequence
DRB1_0101  114  EEVEARHVAAGRNPK  ARHVAAGRN         0.2848        2295.8                 50.00     Sequence
DRB1_0101  155  VRLRMPDDDLAWNDL  LRMPDDDLA         0.2834        2329.9                 50.00     Sequence
DRB1_0101  111  STPEEVEARHVAAGR  PEEVEARHV         0.2765        2509.3                 50.00     Sequence
DRB1_0101  108  HAFSTPEEVEARHVA  FSTPEEVEA         0.2765        2509.8                 50.00     Sequence
DRB1_0101  113  PEEVEARHVAAGRNP  EVEARHVAA         0.2723        2627.6                 50.00     Sequence
DRB1_0101   64  LRWLGLDWDEGPEVG  LGLDWDEGP         0.2675        2767.1                 50.00     Sequence
DRB1_0101  160  PDDDLAWNDLVRGPV  WNDLVRGPV         0.2651        2841.2                 50.00     Sequence
DRB1_0101  159  MPDDDLAWNDLVRGP  DDLAWNDLV         0.2607        2979.4                 50.00     Sequence
DRB1_0101  158  RMPDDDLAWNDLVRG  DDLAWNDLV         0.2604        2987.6                 50.00     Sequence
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   DRB1_0101  259  KRDPQSNLFAHRDRG  RDPQSNLFA        0.2595       3018.1               50.00    Sequence
   DRB1_0101   42  FRIEDTDAQRDSEES  FRIEDTDAQ        0.2576       3081.4               50.00    Sequence
   DRB1_0101   65  RWLGLDWDEGPEVGG  LDWDEGPEV        0.2560       3132.8               50.00    Sequence
   DRB1_0101  156  RLRMPDDDLAWNDLV  LRMPDDDLA        0.2550       3167.7               50.00    Sequence
   DRB1_0101   62  DALRWLGLDWDEGPE  LGLDWDEGP        0.2530       3237.8               50.00    Sequence
   DRB1_0101  252  EGTKKLSKRDPQSNL  LSKRDPQSN        0.2526       3251.0               50.00    Sequence
   DRB1_0101   66  WLGLDWDEGPEVGGP  LDWDEGPEV        0.2498       3352.5               50.00    Sequence
   DRB1_0101  309  ADVNSSPARFDQKKA  VNSSPARFD        0.2484       3402.2               50.00    Sequence
   DRB1_0101  264  SNLFAHRDRGFIPEG  LFAHRDRGF        0.2459       3494.5               50.00    Sequence
   DRB1_0101  393  DPKAAAKELGPDGAA  AKELGPDGA        0.2433       3595.6               50.00    Sequence
   DRB1_0101  157  LRMPDDDLAWNDLVR  DDLAWNDLV        0.2422       3639.6               50.00    Sequence
   DRB1_0101   67  LGLDWDEGPEVGGPY  WDEGPEVGG        0.2403       3711.9               50.00    Sequence
   DRB1_0101   45  EDTDAQRDSEESYLA  RDSEESYLA        0.2401       3720.7               50.00    Sequence
   DRB1_0101   68  GLDWDEGPEVGGPYG  WDEGPEVGG        0.2329       4024.1               50.00    Sequence
   DRB1_0101  251  GEGTKKLSKRDPQSN  LSKRDPQSN        0.2263       4323.0               50.00    Sequence
   DRB1_0101  289  SIADDHDLFGLDEMV  DLFGLDEMV        0.2225       4500.7               50.00    Sequence
   DRB1_0101   69  LDWDEGPEVGGPYGP  WDEGPEVGG        0.2188       4684.4               50.00    Sequence
   DRB1_0101  392  IDPKAAAKELGPDGA  AKELGPDGA        0.2155       4855.0               50.00    Sequence
   DRB1_0101   44  IEDTDAQRDSEESYL  TDAQRDSEE        0.2150       4882.9               50.00    Sequence
   DRB1_0101   43  RIEDTDAQRDSEESY  IEDTDAQRD        0.2136       4957.9               50.00    Sequence
   DRB1_0101  310  DVNSSPARFDQKKAD  VNSSPARFD        0.2005       5711.9               50.00    Sequence
   DRB1_0101   71  WDEGPEVGGPYGPYR  WDEGPEVGG        0.1992       5795.6               50.00    Sequence
   DRB1_0101   76  EVGGPYGPYRQSQRA  GPYGPYRQS        0.1987       5825.0               50.00    Sequence
   DRB1_0101   70  DWDEGPEVGGPYGPY  WDEGPEVGG        0.1977       5889.2               50.00    Sequence
   DRB1_0101  124  GRNPKLGYDNFDRHL  KLGYDNFDR        0.1967       5952.7               50.00    Sequence
   DRB1_0101   73  EGPEVGGPYGPYRQS  EVGGPYGPY        0.1885       6505.4               50.00    Sequence
   DRB1_0101   77  VGGPYGPYRQSQRAE  GPYRQSQRA        0.1873       6587.6               50.00    Sequence
   DRB1_0101  311  VNSSPARFDQKKADA  VNSSPARFD        0.1851       6746.1               50.00    Sequence
   DRB1_0101   74  GPEVGGPYGPYRQSQ  EVGGPYGPY        0.1841       6822.2               50.00    Sequence
   DRB1_0101  391  VIDPKAAAKELGPDG  VIDPKAAAK        0.1800       7129.0               50.00    Sequence
   DRB1_0101   75  PEVGGPYGPYRQSQR  EVGGPYGPY        0.1771       7360.9               50.00    Sequence
   DRB1_0101   72  DEGPEVGGPYGPYRQ  PEVGGPYGP        0.1670       8203.8               50.00    Sequence
   DRB1_0101  123  AGRNPKLGYDNFDRH  RNPKLGYDN        0.1565       9191.6               50.00    Sequence
   DRB1_0101  122  AAGRNPKLGYDNFDR  RNPKLGYDN        0.1521       9647.7               50.00    Sequence
   DRB1_0101  250  LGEGTKKLSKRDPQS  TKKLSKRDP        0.1413      10843.5               50.00    Sequence
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Allele: DRB1_0101. Number of high binders 123. Number of weak binders 202. Number of peptides 476

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random    Identity
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   DRB1_0301  466  SLELLGRDRSMQRLR  LELLGRDRS        0.8267          6.5         SB     0.05    Sequence
   DRB1_0301  465  ESLELLGRDRSMQRL  LELLGRDRS        0.8089          7.9         SB     0.10    Sequence
   DRB1_0301  467  LELLGRDRSMQRLRA  LELLGRDRS        0.8076          8.0         SB     0.10    Sequence
   DRB1_0301  464  FESLELLGRDRSMQR  LELLGRDRS        0.7819         10.6         SB     0.15    Sequence
   DRB1_0301  463  LFESLELLGRDRSMQ  LELLGRDRS        0.6513         43.5         SB     2.00    Sequence
   DRB1_0301  294  HDLFGLDEMVAAFDV  HDLFGLDEM        0.6128         66.0         WB     4.00    Sequence
   DRB1_0301  387  DDQYVIDPKAAAKEL  YVIDPKAAA        0.6084         69.2         WB     4.00    Sequence
   DRB1_0301   89  RAEIYRDVLARLLAA  RAEIYRDVL        0.6064         70.7         WB     4.00    Sequence
   DRB1_0301  468  ELLGRDRSMQRLRAA  LLGRDRSMQ        0.6012         74.8         WB     4.00    Sequence
   DRB1_0301  381  LLKFFNDDQYVIDPK  LLKFFNDDQ        0.5967         78.6         WB     4.00    Sequence
   DRB1_0301  292  DDHDLFGLDEMVAAF  HDLFGLDEM        0.5873         87.0         WB     4.00    Sequence
   DRB1_0301  293  DHDLFGLDEMVAAFD  HDLFGLDEM        0.5871         87.1         WB     4.00    Sequence
   DRB1_0301   88  QRAEIYRDVLARLLA  RAEIYRDVL        0.5711        103.6         WB     4.00    Sequence
   DRB1_0301  334  LDVGDFTVRLRDHLD  VGDFTVRLR        0.5704        104.4         WB     4.00    Sequence
   DRB1_0301  380  ELLKFFNDDQYVIDP  LLKFFNDDQ        0.5695        105.4         WB     4.00    Sequence
   DRB1_0301  386  NDDQYVIDPKAAAKE  YVIDPKAAA        0.5685        106.6         WB     4.00    Sequence
   DRB1_0301  332  RMLDVGDFTVRLRDH  RMLDVGDFT        0.5671        108.2         WB     4.00    Sequence
   DRB1_0301  462  PLFESLELLGRDRSM  LELLGRDRS        0.5668        108.5         WB     4.00    Sequence
   DRB1_0301  331  IRMLDVGDFTVRLRD  RMLDVGDFT        0.5649        110.8         WB     4.00    Sequence
   DRB1_0301  333  MLDVGDFTVRLRDHL  VGDFTVRLR        0.5617        114.6         WB     4.00    Sequence
   DRB1_0301  335  DVGDFTVRLRDHLDT  VGDFTVRLR        0.5579        119.5         WB     4.00    Sequence
   DRB1_0301  469  LLGRDRSMQRLRAAR  LLGRDRSMQ        0.5554        122.8         WB     4.00    Sequence
   DRB1_0301  336  VGDFTVRLRDHLDTH  VGDFTVRLR        0.5469        134.6         WB     8.00    Sequence
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DRB1_0301   56  SYLALLDALRWLGLD  YLALLDALR        0.5428        140.8         WB      8.00     Sequence
DRB1_0301  330  HIRMLDVGDFTVRLR  RMLDVGDFT        0.5387        147.2         WB      8.00     Sequence
DRB1_0301  291  ADDHDLFGLDEMVAA  HDLFGLDEM        0.5381        148.1         WB      8.00     Sequence
DRB1_0301   87  SQRAEIYRDVLARLL  RAEIYRDVL        0.5359        151.7         WB      8.00     Sequence
DRB1_0301  379  WELLKFFNDDQYVID  LLKFFNDDQ        0.5330        156.5         WB      8.00     Sequence
DRB1_0301  385  FNDDQYVIDPKAAAK  YVIDPKAAA        0.5325        157.2         WB      8.00     Sequence
DRB1_0301  388  DQYVIDPKAAAKELG  YVIDPKAAA        0.5215        177.2         WB      8.00     Sequence
DRB1_0301   55  ESYLALLDALRWLGL  YLALLDALR        0.5211        178.0         WB      8.00     Sequence
DRB1_0301  351  GHHIALDEAAFAAAA  GHHIALDEA        0.5120        196.3         WB      8.00     Sequence
DRB1_0301  382  LKFFNDDQYVIDPKA  LKFFNDDQY        0.5105        199.5         WB      8.00     Sequence
DRB1_0301   57  YLALLDALRWLGLDW  YLALLDALR        0.5088        203.3         WB      8.00     Sequence
DRB1_0301   66  WLGLDWDEGPEVGGP  WLGLDWDEG        0.4994        225.0         WB      8.00     Sequence
DRB1_0301   91  EIYRDVLARLLAAGE  IYRDVLARL        0.4972        230.6         WB      8.00     Sequence
DRB1_0301  384  FFNDDQYVIDPKAAA  DDQYVIDPK        0.4956        234.5         WB      8.00     Sequence
DRB1_0301  231  LIRIGVAERIPKFAH  LIRIGVAER        0.4952        235.4         WB      8.00     Sequence
DRB1_0301  350  HGHHIALDEAAFAAA  GHHIALDEA        0.4936        239.5         WB      8.00     Sequence
DRB1_0301   90  AEIYRDVLARLLAAG  IYRDVLARL        0.4905        247.9         WB      8.00     Sequence
DRB1_0301  329  EHIRMLDVGDFTVRL  RMLDVGDFT        0.4848        263.5         WB      8.00     Sequence
DRB1_0301  295  DLFGLDEMVAAFDVA  DLFGLDEMV        0.4843        265.0         WB      8.00     Sequence
DRB1_0301  378  AWELLKFFNDDQYVI  LLKFFNDDQ        0.4794        279.6         WB      8.00     Sequence
DRB1_0301   65  RWLGLDWDEGPEVGG  WLGLDWDEG        0.4757        290.9         WB     16.00     Sequence
DRB1_0301   86  QSQRAEIYRDVLARL  RAEIYRDVL        0.4751        292.8         WB     16.00     Sequence
DRB1_0301  135  DRHLTDAQRAAYLAE  RHLTDAQRA        0.4724        301.3         WB     16.00     Sequence
DRB1_0301  230  ALIRIGVAERIPKFA  LIRIGVAER        0.4708        306.5         WB     16.00     Sequence
DRB1_0301   54  EESYLALLDALRWLG  YLALLDALR        0.4690        312.6         WB     16.00     Sequence
DRB1_0301  134  FDRHLTDAQRAAYLA  RHLTDAQRA        0.4679        316.3         WB     16.00     Sequence
DRB1_0301   92  IYRDVLARLLAAGEA  IYRDVLARL        0.4663        321.8         WB     16.00     Sequence
DRB1_0301   64  LRWLGLDWDEGPEVG  WLGLDWDEG        0.4635        332.0         WB     16.00     Sequence
DRB1_0301  203  DALMKITHVLRGEDL  LMKITHVLR        0.4601        344.2         WB     16.00     Sequence
DRB1_0301  349  THGHHIALDEAAFAA  GHHIALDEA        0.4582        351.6         WB     16.00     Sequence
DRB1_0301  201  CDDALMKITHVLRGE  LMKITHVLR        0.4560        360.0         WB     16.00     Sequence
DRB1_0301  389  QYVIDPKAAAKELGP  QYVIDPKAA        0.4514        378.2         WB     16.00     Sequence
DRB1_0301  205  LMKITHVLRGEDLLP  LMKITHVLR        0.4487        389.6         WB     16.00     Sequence
DRB1_0301  199  NPCDDALMKITHVLR  LMKITHVLR        0.4462        400.2         WB     16.00     Sequence
DRB1_0301  371  RIVVLGDAWELLKFF  RIVVLGDAW        0.4442        409.0         WB     16.00     Sequence
DRB1_0301  204  ALMKITHVLRGEDLL  LMKITHVLR        0.4432        413.2         WB     16.00     Sequence
DRB1_0301  286  LGWSIADDHDLFGLD  SIADDHDLF        0.4428        415.2         WB     16.00     Sequence
DRB1_0301  200  PCDDALMKITHVLRG  LMKITHVLR        0.4421        418.5         WB     16.00     Sequence
DRB1_0301  461  PPLFESLELLGRDRS  LELLGRDRS        0.4417        420.3         WB     16.00     Sequence
DRB1_0301  285  LLGWSIADDHDLFGL  LGWSIADDH        0.4410        423.2         WB     16.00     Sequence
DRB1_0301  404  DGAAVLDAALAALTS  AVLDAALAA        0.4409        424.0         WB     16.00     Sequence
DRB1_0301  202  DDALMKITHVLRGED  LMKITHVLR        0.4379        437.8         WB     16.00     Sequence
DRB1_0301  229  QALIRIGVAERIPKF  LIRIGVAER        0.4362        445.9         WB     16.00     Sequence
DRB1_0301  133  NFDRHLTDAQRAAYL  RHLTDAQRA        0.4305        474.1         WB     16.00     Sequence
DRB1_0301   63  ALRWLGLDWDEGPEV  WLGLDWDEG        0.4304        475.0         WB     16.00     Sequence
DRB1_0301  323  ADALNAEHIRMLDVG  ADALNAEHI        0.4284        485.4         WB     16.00     Sequence
DRB1_0301  470  LGRDRSMQRLRAARQ  LGRDRSMQR        0.4246        505.5                16.00     Sequence
DRB1_0301  296  LFGLDEMVAAFDVAD  LFGLDEMVA        0.4233        512.7                16.00     Sequence
DRB1_0301  348  DTHGHHIALDEAAFA  GHHIALDEA        0.4231        513.6                16.00     Sequence
DRB1_0301  370  TRIVVLGDAWELLKF  RIVVLGDAW        0.4229        514.9                16.00     Sequence
DRB1_0301   97  LARLLAAGEAYHAFS  LLAAGEAYH        0.4227        516.3                16.00     Sequence
DRB1_0301  180  SVPDFALTRASGDPL  SVPDFALTR        0.4216        522.5                16.00     Sequence
DRB1_0301  337  GDFTVRLRDHLDTHG  FTVRLRDHL        0.4207        527.4                16.00     Sequence
DRB1_0301  161  DDDLAWNDLVRGPVT  LAWNDLVRG        0.4185        539.8                16.00     Sequence
DRB1_0301  322  KADALNAEHIRMLDV  ADALNAEHI        0.4185        540.1                16.00     Sequence
DRB1_0301  474  RSMQRLRAARQLVGH  SMQRLRAAR        0.4179        543.7                16.00     Sequence
DRB1_0301  475  SMQRLRAARQLVGHA  SMQRLRAAR        0.4169        549.4                16.00     Sequence
DRB1_0301  126  NPKLGYDNFDRHLTD  LGYDNFDRH        0.4160        555.0                16.00     Sequence
DRB1_0301  290  IADDHDLFGLDEMVA  HDLFGLDEM        0.4142        565.6                16.00     Sequence
DRB1_0301  214  GEDLLPSTPRQLALH  GEDLLPSTP        0.4124        576.8                16.00     Sequence
DRB1_0301  406  AAVLDAALAALTSVT  AVLDAALAA        0.4070        611.8                16.00     Sequence
DRB1_0301  403  PDGAAVLDAALAALT  AVLDAALAA        0.4066        614.4                16.00     Sequence
DRB1_0301  473  DRSMQRLRAARQLVG  SMQRLRAAR        0.4057        620.4                16.00     Sequence
DRB1_0301  289  SIADDHDLFGLDEMV  SIADDHDLF        0.4048        626.3                16.00     Sequence
DRB1_0301  162  DDLAWNDLVRGPVTF  DDLAWNDLV        0.4019        646.5                16.00     Sequence
DRB1_0301  136  RHLTDAQRAAYLAEG  RHLTDAQRA        0.4012        651.0                16.00     Sequence
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DRB1_0301   53  SEESYLALLDALRWL  YLALLDALR        0.4011        652.1                 16.00     Sequence
DRB1_0301  436  IEGLALKPRKAFSPI  LALKPRKAF        0.4003        657.7                 16.00     Sequence
DRB1_0301  383  KFFNDDQYVIDPKAA  FFNDDQYVI        0.3990        666.7                 16.00     Sequence
DRB1_0301  284  ALLGWSIADDHDLFG  LGWSIADDH        0.3990        666.8                 16.00     Sequence
DRB1_0301  125  RNPKLGYDNFDRHLT  LGYDNFDRH        0.3971        680.8                 16.00     Sequence
DRB1_0301  405  GAAVLDAALAALTSV  AVLDAALAA        0.3960        689.0                 32.00     Sequence
DRB1_0301  155  VRLRMPDDDLAWNDL  VRLRMPDDD        0.3948        697.7                 32.00     Sequence
DRB1_0301  179  GSVPDFALTRASGDP  SVPDFALTR        0.3934        709.0                 32.00     Sequence
DRB1_0301  160  PDDDLAWNDLVRGPV  LAWNDLVRG        0.3933        709.3                 32.00     Sequence
DRB1_0301   40  FVFRIEDTDAQRDSE  FVFRIEDTD        0.3920        719.7                 32.00     Sequence
DRB1_0301  228  HQALIRIGVAERIPK  LIRIGVAER        0.3897        737.4                 32.00     Sequence
DRB1_0301  321  KKADALNAEHIRMLD  ADALNAEHI        0.3886        746.6                 32.00     Sequence
DRB1_0301   39  TFVFRIEDTDAQRDS  RIEDTDAQR        0.3884        748.3                 32.00     Sequence
DRB1_0301  398  AKELGPDGAAVLDAA  AKELGPDGA        0.3882        749.9                 32.00     Sequence
DRB1_0301  152  QPVVRLRMPDDDLAW  QPVVRLRMP        0.3874        755.9                 32.00     Sequence
DRB1_0301  232  IRIGVAERIPKFAHL  IRIGVAERI        0.3867        761.7                 32.00     Sequence
DRB1_0301  339  FTVRLRDHLDTHGHH  FTVRLRDHL        0.3855        771.7                 32.00     Sequence
DRB1_0301  283  LALLGWSIADDHDLF  LGWSIADDH        0.3838        786.2                 32.00     Sequence
DRB1_0301  338  DFTVRLRDHLDTHGH  FTVRLRDHL        0.3821        801.1                 32.00     Sequence
DRB1_0301  128  KLGYDNFDRHLTDAQ  LGYDNFDRH        0.3816        805.1                 32.00     Sequence
DRB1_0301  328  AEHIRMLDVGDFTVR  LDVGDFTVR        0.3812        808.6                 32.00     Sequence
DRB1_0301  435  LIEGLALKPRKAFSP  IEGLALKPR        0.3803        816.8                 32.00     Sequence
DRB1_0301  222  PRQLALHQALIRIGV  LALHQALIR        0.3803        816.9                 32.00     Sequence
DRB1_0301  369  QTRIVVLGDAWELLK  RIVVLGDAW        0.3795        823.4                 32.00     Sequence
DRB1_0301  154  VVRLRMPDDDLAWND  VRLRMPDDD        0.3791        827.4                 32.00     Sequence
DRB1_0301  196  TLVNPCDDALMKITH  NPCDDALMK        0.3787        830.6                 32.00     Sequence
DRB1_0301  213  RGEDLLPSTPRQLAL  GEDLLPSTP        0.3783        834.5                 32.00     Sequence
DRB1_0301   17  TPHVGLVRTALFNWA  TPHVGLVRT        0.3781        836.5                 32.00     Sequence
DRB1_0301   96  VLARLLAAGEAYHAF  LARLLAAGE        0.3779        838.3                 32.00     Sequence
DRB1_0301  151  RQPVVRLRMPDDDLA  QPVVRLRMP        0.3777        840.2                 32.00     Sequence
DRB1_0301  193  PLYTLVNPCDDALMK  LVNPCDDAL        0.3768        848.3                 32.00     Sequence
DRB1_0301  153  PVVRLRMPDDDLAWN  VRLRMPDDD        0.3761        854.0                 32.00     Sequence
DRB1_0301  212  LRGEDLLPSTPRQLA  GEDLLPSTP        0.3728        885.8                 32.00     Sequence
DRB1_0301  472  RDRSMQRLRAARQLV  SMQRLRAAR        0.3724        889.2                 32.00     Sequence
DRB1_0301  127  PKLGYDNFDRHLTDA  LGYDNFDRH        0.3713        900.3                 32.00     Sequence
DRB1_0301  223  RQLALHQALIRIGVA  LALHQALIR        0.3705        907.9                 32.00     Sequence
DRB1_0301  178  AGSVPDFALTRASGD  VPDFALTRA        0.3677        935.3                 32.00     Sequence
DRB1_0301  208  ITHVLRGEDLLPSTP  HVLRGEDLL        0.3676        937.3                 32.00     Sequence
DRB1_0301  434  ALIEGLALKPRKAFS  IEGLALKPR        0.3675        937.6                 32.00     Sequence
DRB1_0301  407  AVLDAALAALTSVTD  AVLDAALAA        0.3658        954.7                 32.00     Sequence
DRB1_0301  194  LYTLVNPCDDALMKI  TLVNPCDDA        0.3647        966.2                 32.00     Sequence
DRB1_0301  181  VPDFALTRASGDPLY  VPDFALTRA        0.3645        968.6                 32.00     Sequence
DRB1_0301  288  WSIADDHDLFGLDEM  SIADDHDLF        0.3629        985.4                 32.00     Sequence
DRB1_0301  132  DNFDRHLTDAQRAAY  RHLTDAQRA        0.3622        993.2                 32.00     Sequence
DRB1_0301  437  EGLALKPRKAFSPIR  GLALKPRKA        0.3618        997.7                 32.00     Sequence
DRB1_0301  275  IPEGLLNYLALLGWS  IPEGLLNYL        0.3615       1000.9                 32.00     Sequence
DRB1_0301   98  ARLLAAGEAYHAFST  ARLLAAGEA        0.3612       1003.8                 32.00     Sequence
DRB1_0301  195  YTLVNPCDDALMKIT  TLVNPCDDA        0.3608       1008.0                 32.00     Sequence
DRB1_0301  197  LVNPCDDALMKITHV  NPCDDALMK        0.3607       1009.3                 32.00     Sequence
DRB1_0301  198  VNPCDDALMKITHVL  NPCDDALMK        0.3604       1012.4                 32.00     Sequence
DRB1_0301  287  GWSIADDHDLFGLDE  SIADDHDLF        0.3598       1019.6                 32.00     Sequence
DRB1_0301  274  FIPEGLLNYLALLGW  IPEGLLNYL        0.3594       1023.8                 32.00     Sequence
DRB1_0301  397  AAKELGPDGAAVLDA  AKELGPDGA        0.3579       1040.5                 32.00     Sequence
DRB1_0301   16  GTPHVGLVRTALFNW  TPHVGLVRT        0.3574       1046.0                 32.00     Sequence
DRB1_0301  320  QKKADALNAEHIRML  ADALNAEHI        0.3561       1060.6                 32.00     Sequence
DRB1_0301  129  LGYDNFDRHLTDAQR  LGYDNFDRH        0.3558       1064.1                 32.00     Sequence
DRB1_0301  209  THVLRGEDLLPSTPR  HVLRGEDLL        0.3553       1070.2                 32.00     Sequence
DRB1_0301  460  SPPLFESLELLGRDR  PLFESLELL        0.3536       1089.5                 32.00     Sequence
DRB1_0301  221  TPRQLALHQALIRIG  LALHQALIR        0.3533       1093.7                 32.00     Sequence
DRB1_0301  159  MPDDDLAWNDLVRGP  LAWNDLVRG        0.3514       1115.7                 32.00     Sequence
DRB1_0301  211  VLRGEDLLPSTPRQL  GEDLLPSTP        0.3508       1123.8                 32.00     Sequence
DRB1_0301  377  DAWELLKFFNDDQYV  LKFFNDDQY        0.3504       1128.0                 32.00     Sequence
DRB1_0301  443  PRKAFSPIRVAATGT  RKAFSPIRV        0.3492       1142.6                 32.00     Sequence
DRB1_0301  210  HVLRGEDLLPSTPRQ  HVLRGEDLL        0.3492       1143.3                 32.00     Sequence
DRB1_0301  438  GLALKPRKAFSPIRV  GLALKPRKA        0.3484       1152.9                 32.00     Sequence
DRB1_0301   41  VFRIEDTDAQRDSEE  FRIEDTDAQ        0.3471       1169.3                 32.00     Sequence
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DRB1_0301  207  KITHVLRGEDLLPST  HVLRGEDLL        0.3470       1170.5               32.00     Sequence
DRB1_0301  390  YVIDPKAAAKELGPD  YVIDPKAAA        0.3467       1173.8               32.00     Sequence
DRB1_0301  297  FGLDEMVAAFDVADV  FGLDEMVAA        0.3466       1175.4               32.00     Sequence
DRB1_0301  143  RAAYLAEGRQPVVRL  YLAEGRQPV        0.3465       1176.9               32.00     Sequence
DRB1_0301   95  DVLARLLAAGEAYHA  LARLLAAGE        0.3458       1186.3               32.00     Sequence
DRB1_0301  246  LPTVLGEGTKKLSKR  LPTVLGEGT        0.3450       1196.4               32.00     Sequence
DRB1_0301  263  QSNLFAHRDRGFIPE  LFAHRDRGF        0.3443       1205.9               32.00     Sequence
DRB1_0301  124  GRNPKLGYDNFDRHL  LGYDNFDRH        0.3429       1223.5               32.00     Sequence
DRB1_0301  433  DALIEGLALKPRKAF  IEGLALKPR        0.3429       1224.1               32.00     Sequence
DRB1_0301  306  FDVADVNSSPARFDQ  FDVADVNSS        0.3428       1225.7               32.00     Sequence
DRB1_0301  264  SNLFAHRDRGFIPEG  NLFAHRDRG        0.3420       1235.1               32.00     Sequence
DRB1_0301  402  GPDGAAVLDAALAAL  AVLDAALAA        0.3413       1244.7               32.00     Sequence
DRB1_0301   38  GTFVFRIEDTDAQRD  FVFRIEDTD        0.3410       1248.5               32.00     Sequence
DRB1_0301  442  KPRKAFSPIRVAATG  RKAFSPIRV        0.3410       1249.5               32.00     Sequence
DRB1_0301  363  AAAELVQTRIVVLGD  AAELVQTRI        0.3403       1258.0               32.00     Sequence
DRB1_0301  352  HHIALDEAAFAAAAE  IALDEAAFA        0.3392       1273.4               32.00     Sequence
DRB1_0301  158  RMPDDDLAWNDLVRG  RMPDDDLAW        0.3383       1285.5               32.00     Sequence
DRB1_0301  177  AAGSVPDFALTRASG  SVPDFALTR        0.3383       1285.8               32.00     Sequence
DRB1_0301  150  GRQPVVRLRMPDDDL  RQPVVRLRM        0.3381       1288.8               32.00     Sequence
DRB1_0301  368  VQTRIVVLGDAWELL  RIVVLGDAW        0.3375       1297.8               32.00     Sequence
DRB1_0301  364  AAELVQTRIVVLGDA  AAELVQTRI        0.3374       1298.4               32.00     Sequence
DRB1_0301   94  RDVLARLLAAGEAYH  RDVLARLLA        0.3350       1333.0               32.00     Sequence
DRB1_0301   58  LALLDALRWLGLDWD  LALLDALRW        0.3349       1333.8               32.00     Sequence
DRB1_0301  396  AAAKELGPDGAAVLD  AKELGPDGA        0.3339       1348.9               32.00     Sequence
DRB1_0301   25  TALFNWAYARHTGGT  TALFNWAYA        0.3325       1369.5               32.00     Sequence
DRB1_0301  441  LKPRKAFSPIRVAAT  RKAFSPIRV        0.3316       1383.4               32.00     Sequence
DRB1_0301  308  VADVNSSPARFDQKK  VADVNSSPA        0.3313       1387.4               32.00     Sequence
DRB1_0301  262  PQSNLFAHRDRGFIP  LFAHRDRGF        0.3308       1394.6               32.00     Sequence
DRB1_0301  372  IVVLGDAWELLKFFN  IVVLGDAWE        0.3301       1405.4               32.00     Sequence
DRB1_0301  424  APLIEAALKDALIEG  IEAALKDAL        0.3290       1422.7               32.00     Sequence
DRB1_0301   15  TGTPHVGLVRTALFN  TPHVGLVRT        0.3268       1457.3               32.00     Sequence
DRB1_0301   42  FRIEDTDAQRDSEES  RIEDTDAQR        0.3255       1477.5               32.00     Sequence
DRB1_0301  156  RLRMPDDDLAWNDLV  LRMPDDDLA        0.3253       1480.4               32.00     Sequence
DRB1_0301  163  DLAWNDLVRGPVTFA  DLAWNDLVR        0.3250       1484.8               32.00     Sequence
DRB1_0301  432  KDALIEGLALKPRKA  KDALIEGLA        0.3247       1489.4               32.00     Sequence
DRB1_0301  184  FALTRASGDPLYTLV  TRASGDPLY        0.3235       1508.8               32.00     Sequence
DRB1_0301  206  MKITHVLRGEDLLPS  MKITHVLRG        0.3234       1510.6               32.00     Sequence
DRB1_0301  273  GFIPEGLLNYLALLG  IPEGLLNYL        0.3216       1540.8               32.00     Sequence
DRB1_0301  347  LDTHGHHIALDEAAF  GHHIALDEA        0.3216       1541.6               32.00     Sequence
DRB1_0301  431  LKDALIEGLALKPRK  KDALIEGLA        0.3214       1544.0               32.00     Sequence
DRB1_0301   93  YRDVLARLLAAGEAY  RDVLARLLA        0.3212       1547.8               32.00     Sequence
DRB1_0301  220  STPRQLALHQALIRI  LALHQALIR        0.3209       1552.6               32.00     Sequence
DRB1_0301  227  LHQALIRIGVAERIP  LIRIGVAER        0.3198       1571.0               32.00     Sequence
DRB1_0301   67  LGLDWDEGPEVGGPY  LDWDEGPEV        0.3153       1649.6               32.00     Sequence
DRB1_0301  157  LRMPDDDLAWNDLVR  LRMPDDDLA        0.3136       1679.4               32.00     Sequence
DRB1_0301  272  RGFIPEGLLNYLALL  IPEGLLNYL        0.3127       1696.6               32.00     Sequence
DRB1_0301  192  DPLYTLVNPCDDALM  LVNPCDDAL        0.3124       1702.5               32.00     Sequence
DRB1_0301  183  DFALTRASGDPLYTL  TRASGDPLY        0.3124       1702.7               32.00     Sequence
DRB1_0301  225  LALHQALIRIGVAER  LALHQALIR        0.3120       1709.3               32.00     Sequence
DRB1_0301  215  EDLLPSTPRQLALHQ  LLPSTPRQL        0.3104       1740.2               32.00     Sequence
DRB1_0301  305  AFDVADVNSSPARFD  VADVNSSPA        0.3097       1753.5               32.00     Sequence
DRB1_0301  395  KAAAKELGPDGAAVL  AKELGPDGA        0.3094       1758.1               32.00     Sequence
DRB1_0301   24  RTALFNWAYARHTGG  TALFNWAYA        0.3081       1782.6               32.00     Sequence
DRB1_0301  142  QRAAYLAEGRQPVVR  YLAEGRQPV        0.3075       1795.4               32.00     Sequence
DRB1_0301  307  DVADVNSSPARFDQK  VADVNSSPA        0.3070       1804.3               32.00     Sequence
DRB1_0301  425  PLIEAALKDALIEGL  IEAALKDAL        0.3058       1828.3               32.00     Sequence
DRB1_0301  426  LIEAALKDALIEGLA  IEAALKDAL        0.3058       1828.9               32.00     Sequence
DRB1_0301   14  PTGTPHVGLVRTALF  TPHVGLVRT        0.3044       1857.1               32.00     Sequence
DRB1_0301  299  LDEMVAAFDVADVNS  EMVAAFDVA        0.3035       1874.8               32.00     Sequence
DRB1_0301  224  QLALHQALIRIGVAE  LALHQALIR        0.3032       1879.5               32.00     Sequence
DRB1_0301  444  RKAFSPIRVAATGTT  RKAFSPIRV        0.3027       1891.5               32.00     Sequence
DRB1_0301  459  VSPPLFESLELLGRD  PLFESLELL        0.3021       1901.9               32.00     Sequence
DRB1_0301  245  HLPTVLGEGTKKLSK  LPTVLGEGT        0.3015       1914.3               32.00     Sequence
DRB1_0301  362  AAAAELVQTRIVVLG  AAELVQTRI        0.3007       1932.2               32.00     Sequence
DRB1_0301   23  VRTALFNWAYARHTG  ALFNWAYAR        0.2998       1951.0               50.00     Sequence
DRB1_0301  427  IEAALKDALIEGLAL  IEAALKDAL        0.2996       1954.5               50.00     Sequence
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DRB1_0301  471  GRDRSMQRLRAARQL  SMQRLRAAR        0.2994       1959.9                 50.00     Sequence
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DRB1_0301  131  YDNFDRHLTDAQRAA  HLTDAQRAA        0.2982       1984.5                 50.00     Sequence
DRB1_0301  182  PDFALTRASGDPLYT  TRASGDPLY        0.2978       1992.5                 50.00     Sequence
DRB1_0301  186  LTRASGDPLYTLVNP  LTRASGDPL        0.2969       2012.3                 50.00     Sequence
DRB1_0301  353  HIALDEAAFAAAAEL  IALDEAAFA        0.2968       2014.8                 50.00     Sequence
DRB1_0301  301  EMVAAFDVADVNSSP  EMVAAFDVA        0.2958       2036.9                 50.00     Sequence
DRB1_0301  176  FAAGSVPDFALTRAS  SVPDFALTR        0.2956       2040.8                 50.00     Sequence
DRB1_0301    0  VTATETVRVRFCPSP  VTATETVRV        0.2907       2152.5                 50.00     Sequence
DRB1_0301  423  TAPLIEAALKDALIE  IEAALKDAL        0.2904       2160.4                 50.00     Sequence
DRB1_0301  430  ALKDALIEGLALKPR  KDALIEGLA        0.2900       2169.7                 50.00     Sequence
DRB1_0301  149  EGRQPVVRLRMPDDD  QPVVRLRMP        0.2896       2177.3                 50.00     Sequence
DRB1_0301  265  NLFAHRDRGFIPEGL  NLFAHRDRG        0.2896       2179.0                 50.00     Sequence
DRB1_0301  300  DEMVAAFDVADVNSS  EMVAAFDVA        0.2896       2179.4                 50.00     Sequence
DRB1_0301  261  DPQSNLFAHRDRGFI  LFAHRDRGF        0.2884       2207.0                 50.00     Sequence
DRB1_0301  123  AGRNPKLGYDNFDRH  LGYDNFDRH        0.2862       2259.5                 50.00     Sequence
DRB1_0301  271  DRGFIPEGLLNYLAL  FIPEGLLNY        0.2859       2266.4                 50.00     Sequence
DRB1_0301  216  DLLPSTPRQLALHQA  LLPSTPRQL        0.2859       2266.5                 50.00     Sequence
DRB1_0301  226  ALHQALIRIGVAERI  LIRIGVAER        0.2854       2280.6                 50.00     Sequence
DRB1_0301   85  RQSQRAEIYRDVLAR  RAEIYRDVL        0.2847       2297.3                 50.00     Sequence
DRB1_0301  401  LGPDGAAVLDAALAA  DGAAVLDAA        0.2834       2330.7                 50.00     Sequence
DRB1_0301  440  ALKPRKAFSPIRVAA  RKAFSPIRV        0.2830       2338.6                 50.00     Sequence
DRB1_0301   99  RLLAAGEAYHAFSTP  LLAAGEAYH        0.2817       2372.4                 50.00     Sequence
DRB1_0301  298  GLDEMVAAFDVADVN  EMVAAFDVA        0.2815       2377.9                 50.00     Sequence
DRB1_0301   26  ALFNWAYARHTGGTF  LFNWAYARH        0.2796       2427.9                 50.00     Sequence
DRB1_0301  175  TFAAGSVPDFALTRA  SVPDFALTR        0.2788       2449.3                 50.00     Sequence
DRB1_0301   18  PHVGLVRTALFNWAY  VGLVRTALF        0.2767       2505.5                 50.00     Sequence
DRB1_0301  185  ALTRASGDPLYTLVN  LTRASGDPL        0.2767       2505.7                 50.00     Sequence
DRB1_0301  282  YLALLGWSIADDHDL  LGWSIADDH        0.2761       2520.7                 50.00     Sequence
DRB1_0301   68  GLDWDEGPEVGGPYG  LDWDEGPEV        0.2757       2532.1                 50.00     Sequence
DRB1_0301   19  HVGLVRTALFNWAYA  VGLVRTALF        0.2737       2588.4                 50.00     Sequence
DRB1_0301  365  AELVQTRIVVLGDAW  LVQTRIVVL        0.2734       2595.3                 50.00     Sequence
DRB1_0301  361  FAAAAELVQTRIVVL  AAELVQTRI        0.2727       2615.2                 50.00     Sequence
DRB1_0301  340  TVRLRDHLDTHGHHI  VRLRDHLDT        0.2710       2662.9                 50.00     Sequence
DRB1_0301  341  VRLRDHLDTHGHHIA  RLRDHLDTH        0.2705       2677.6                 50.00     Sequence
DRB1_0301  141  AQRAAYLAEGRQPVV  YLAEGRQPV        0.2697       2700.8                 50.00     Sequence
DRB1_0301   52  DSEESYLALLDALRW  YLALLDALR        0.2692       2717.7                 50.00     Sequence
DRB1_0301  413  LAALTSVTDWTAPLI  LAALTSVTD        0.2666       2795.2                 50.00     Sequence
DRB1_0301  217  LLPSTPRQLALHQAL  LLPSTPRQL        0.2659       2814.1                 50.00     Sequence
DRB1_0301  327  NAEHIRMLDVGDFTV  RMLDVGDFT        0.2648       2847.6                 50.00     Sequence
DRB1_0301   22  LVRTALFNWAYARHT  ALFNWAYAR        0.2634       2891.0                 50.00     Sequence
DRB1_0301   62  DALRWLGLDWDEGPE  WLGLDWDEG        0.2634       2893.2                 50.00     Sequence
DRB1_0301  219  PSTPRQLALHQALIR  PRQLALHQA        0.2633       2896.4                 50.00     Sequence
DRB1_0301  458  TVSPPLFESLELLGR  PLFESLELL        0.2632       2898.0                 50.00     Sequence
DRB1_0301  304  AAFDVADVNSSPARF  FDVADVNSS        0.2630       2904.8                 50.00     Sequence
DRB1_0301  118  ARHVAAGRNPKLGYD  VAAGRNPKL        0.2621       2934.9                 50.00     Sequence
DRB1_0301  144  AAYLAEGRQPVVRLR  AAYLAEGRQ        0.2610       2968.0                 50.00     Sequence
DRB1_0301  439  LALKPRKAFSPIRVA  LALKPRKAF        0.2584       3052.6                 50.00     Sequence
DRB1_0301  324  DALNAEHIRMLDVGD  DALNAEHIR        0.2582       3061.4                 50.00     Sequence
DRB1_0301  422  WTAPLIEAALKDALI  APLIEAALK        0.2577       3076.6                 50.00     Sequence
DRB1_0301  412  ALAALTSVTDWTAPL  LAALTSVTD        0.2554       3153.0                 50.00     Sequence
DRB1_0301  408  VLDAALAALTSVTDW  LDAALAALT        0.2553       3156.8                 50.00     Sequence
DRB1_0301  325  ALNAEHIRMLDVGDF  ALNAEHIRM        0.2550       3166.4                 50.00     Sequence
DRB1_0301  148  AEGRQPVVRLRMPDD  RQPVVRLRM        0.2542       3193.9                 50.00     Sequence
DRB1_0301  302  MVAAFDVADVNSSPA  FDVADVNSS        0.2540       3200.9                 50.00     Sequence
DRB1_0301  373  VVLGDAWELLKFFND  VLGDAWELL        0.2538       3207.8                 50.00     Sequence
DRB1_0301  367  LVQTRIVVLGDAWEL  LVQTRIVVL        0.2527       3246.0                 50.00     Sequence
DRB1_0301  191  GDPLYTLVNPCDDAL  LVNPCDDAL        0.2518       3279.0                 50.00     Sequence
DRB1_0301  326  LNAEHIRMLDVGDFT  LNAEHIRML        0.2511       3304.8                 50.00     Sequence
DRB1_0301  429  AALKDALIEGLALKP  LKDALIEGL        0.2505       3324.1                 50.00     Sequence
DRB1_0301  244  AHLPTVLGEGTKKLS  LPTVLGEGT        0.2492       3372.7                 50.00     Sequence
DRB1_0301   43  RIEDTDAQRDSEESY  RIEDTDAQR        0.2467       3465.4                 50.00     Sequence
DRB1_0301  174  VTFAAGSVPDFALTR  SVPDFALTR        0.2449       3535.1                 50.00     Sequence
DRB1_0301  319  DQKKADALNAEHIRM  ADALNAEHI        0.2435       3588.0                 50.00     Sequence
DRB1_0301  164  LAWNDLVRGPVTFAA  LAWNDLVRG        0.2426       3621.4                 50.00     Sequence
DRB1_0301  346  HLDTHGHHIALDEAA  GHHIALDEA        0.2405       3705.3                 50.00     Sequence
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DRB1_0301  233  RIGVAERIPKFAHLP  RIGVAERIP        0.2392       3757.1                 50.00     Sequence
DRB1_0301   69  LDWDEGPEVGGPYGP  LDWDEGPEV        0.2377       3818.9                 50.00     Sequence
DRB1_0301  117  EARHVAAGRNPKLGY  VAAGRNPKL        0.2372       3841.7                 50.00     Sequence
DRB1_0301   13  SPTGTPHVGLVRTAL  TPHVGLVRT        0.2371       3842.5                 50.00     Sequence
DRB1_0301   81  YGPYRQSQRAEIYRD  GPYRQSQRA        0.2365       3871.4                 50.00     Sequence
DRB1_0301  146  YLAEGRQPVVRLRMP  YLAEGRQPV        0.2358       3901.1                 50.00     Sequence
DRB1_0301  303  VAAFDVADVNSSPAR  FDVADVNSS        0.2347       3945.6                 50.00     Sequence
DRB1_0301  137  HLTDAQRAAYLAEGR  HLTDAQRAA        0.2343       3962.2                 50.00     Sequence
DRB1_0301  376  GDAWELLKFFNDDQY  LKFFNDDQY        0.2339       3979.9                 50.00     Sequence
DRB1_0301  450  IRVAATGTTVSPPLF  IRVAATGTT        0.2310       4107.6                 50.00     Sequence
DRB1_0301  366  ELVQTRIVVLGDAWE  LVQTRIVVL        0.2307       4120.3                 50.00     Sequence
DRB1_0301  260  RDPQSNLFAHRDRGF  LFAHRDRGF        0.2295       4175.0                 50.00     Sequence
DRB1_0301   82  GPYRQSQRAEIYRDV  GPYRQSQRA        0.2288       4206.8                 50.00     Sequence
DRB1_0301  270  RDRGFIPEGLLNYLA  FIPEGLLNY        0.2281       4239.4                 50.00     Sequence
DRB1_0301   61  LDALRWLGLDWDEGP  WLGLDWDEG        0.2256       4351.6                 50.00     Sequence
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DRB1_0301   59  ALLDALRWLGLDWDE  LDALRWLGL        0.2246       4399.8                 50.00     Sequence
DRB1_0301   27  LFNWAYARHTGGTFV  FNWAYARHT        0.2231       4472.2                 50.00     Sequence
DRB1_0301  409  LDAALAALTSVTDWT  LDAALAALT        0.2231       4474.7                 50.00     Sequence
DRB1_0301  147  LAEGRQPVVRLRMPD  RQPVVRLRM        0.2217       4539.4                 50.00     Sequence
DRB1_0301   20  VGLVRTALFNWAYAR  VGLVRTALF        0.2217       4542.1                 50.00     Sequence
DRB1_0301  281  NYLALLGWSIADDHD  LALLGWSIA        0.2175       4752.4                 50.00     Sequence
DRB1_0301  428  EAALKDALIEGLALK  LKDALIEGL        0.2173       4761.4                 50.00     Sequence
DRB1_0301  276  PEGLLNYLALLGWSI  GLLNYLALL        0.2167       4791.9                 50.00     Sequence
DRB1_0301  344  RDHLDTHGHHIALDE  RDHLDTHGH        0.2155       4854.3                 50.00     Sequence
DRB1_0301  140  DAQRAAYLAEGRQPV  RAAYLAEGR        0.2138       4944.4                 50.00     Sequence
DRB1_0301  449  PIRVAATGTTVSPPL  VAATGTTVS        0.2136       4955.9                 50.00     Sequence
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DRB1_0301  277  EGLLNYLALLGWSIA  GLLNYLALL        0.2117       5061.2                 50.00     Sequence
DRB1_0301  313  SSPARFDQKKADALN  SSPARFDQK        0.2107       5114.6                 50.00     Sequence
DRB1_0301  145  AYLAEGRQPVVRLRM  YLAEGRQPV        0.2107       5115.9                 50.00     Sequence
DRB1_0301   84  YRQSQRAEIYRDVLA  RAEIYRDVL        0.2103       5136.6                 50.00     Sequence
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DRB1_0301   51  RDSEESYLALLDALR  YLALLDALR        0.2063       5365.7                 50.00     Sequence
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DRB1_0301  310  DVNSSPARFDQKKAD  DVNSSPARF        0.1963       5979.6                 50.00     Sequence
DRB1_0301  457  TTVSPPLFESLELLG  PLFESLELL        0.1956       6020.5                 50.00     Sequence
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DRB1_0301  234  IGVAERIPKFAHLPT  IGVAERIPK        0.1933       6178.2                 50.00     Sequence
DRB1_0301  318  FDQKKADALNAEHIR  FDQKKADAL        0.1932       6180.5                 50.00     Sequence
DRB1_0301  120  HVAAGRNPKLGYDNF  VAAGRNPKL        0.1932       6181.0                 50.00     Sequence
DRB1_0301  269  HRDRGFIPEGLLNYL  FIPEGLLNY        0.1918       6278.4                 50.00     Sequence
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DRB1_0301  445  KAFSPIRVAATGTTV  FSPIRVAAT        0.1865       6646.1                 50.00     Sequence
DRB1_0301   60  LLDALRWLGLDWDEG  LLDALRWLG        0.1858       6693.8                 50.00     Sequence
DRB1_0301  100  LLAAGEAYHAFSTPE  LLAAGEAYH        0.1855       6715.9                 50.00     Sequence
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DRB1_0301  255  KKLSKRDPQSNLFAH  KKLSKRDPQ        0.1828       6917.2                 50.00     Sequence
DRB1_0301   21  GLVRTALFNWAYARH  ALFNWAYAR        0.1825       6942.7                 50.00     Sequence
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DRB1_0301  107  YHAFSTPEEVEARHV  HAFSTPEEV        0.1813       7027.7                 50.00     Sequence
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DRB1_0301  446  AFSPIRVAATGTTVS  FSPIRVAAT        0.1800       7131.0                 50.00     Sequence
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DRB1_0301    1  TATETVRVRFCPSPT  TATETVRVR        0.1792       7193.6                 50.00     Sequence
DRB1_0301  266  LFAHRDRGFIPEGLL  LFAHRDRGF        0.1790       7210.4                 50.00     Sequence
DRB1_0301  190  SGDPLYTLVNPCDDA  PLYTLVNPC        0.1787       7229.2                 50.00     Sequence
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DRB1_0301  447  FSPIRVAATGTTVSP  IRVAATGTT        0.1777       7313.7                 50.00     Sequence
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DRB1_0301  417  TSVTDWTAPLIEAAL  SVTDWTAPL        0.1766       7399.3                 50.00     Sequence
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DRB1_0301  452  VAATGTTVSPPLFES  VAATGTTVS        0.1746       7560.8                 50.00     Sequence
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DRB1_0301  105  EAYHAFSTPEEVEAR  HAFSTPEEV        0.1706       7895.1                 50.00     Sequence
DRB1_0301  108  HAFSTPEEVEARHVA  HAFSTPEEV        0.1683       8093.2                 50.00     Sequence
DRB1_0301  374  VLGDAWELLKFFNDD  VLGDAWELL        0.1683       8094.5                 50.00     Sequence
DRB1_0301  238  ERIPKFAHLPTVLGE  PKFAHLPTV        0.1666       8239.5                 50.00     Sequence
DRB1_0301  448  SPIRVAATGTTVSPP  IRVAATGTT        0.1664       8257.9                 50.00     Sequence
DRB1_0301  311  VNSSPARFDQKKADA  SSPARFDQK        0.1660       8295.9                 50.00     Sequence
DRB1_0301  278  GLLNYLALLGWSIAD  GLLNYLALL        0.1635       8528.6                 50.00     Sequence
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DRB1_0301    3  TETVRVRFCPSPTGT  TVRVRFCPS        0.1629       8582.5                 50.00     Sequence
DRB1_0301    2  ATETVRVRFCPSPTG  ATETVRVRF        0.1569       9151.5                 50.00     Sequence
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DRB1_0301  189  ASGDPLYTLVNPCDD  SGDPLYTLV        0.1462      10278.7                 50.00     Sequence
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DRB1_0301  268  AHRDRGFIPEGLLNY  FIPEGLLNY        0.1427      10681.7                 50.00     Sequence
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DRB1_0301  235  GVAERIPKFAHLPTV  VAERIPKFA        0.1407      10905.3                 50.00     Sequence
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DRB1_0301  241  PKFAHLPTVLGEGTK  PKFAHLPTV        0.1339      11737.6                 50.00     Sequence
DRB1_0301  359  AAFAAAAELVQTRIV  FAAAAELVQ        0.1326      11907.8                 50.00     Sequence
DRB1_0301   28  FNWAYARHTGGTFVF  FNWAYARHT        0.1325      11924.9                 50.00     Sequence
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DRB1_0301  250  LGEGTKKLSKRDPQS  LGEGTKKLS        0.1319      12006.2                 50.00     Sequence
DRB1_0301   47  TDAQRDSEESYLALL  AQRDSEESY        0.1312      12090.6                 50.00     Sequence
DRB1_0301  315  PARFDQKKADALNAE  FDQKKADAL        0.1310      12117.5                 50.00     Sequence
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DRB1_0301  173  PVTFAAGSVPDFALT  FAAGSVPDF        0.1292      12358.4                 50.00     Sequence
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DRB1_0301  456  GTTVSPPLFESLELL  PLFESLELL        0.1288      12407.0                 50.00     Sequence
DRB1_0301   34  RHTGGTFVFRIEDTD  FVFRIEDTD        0.1286      12436.6                 50.00     Sequence
DRB1_0301   48  DAQRDSEESYLALLD  DAQRDSEES        0.1285      12445.6                 50.00     Sequence
DRB1_0301  242  KFAHLPTVLGEGTKK  LPTVLGEGT        0.1284      12464.1                 50.00     Sequence
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   DRB1_0301  166  WNDLVRGPVTFAAGS  NDLVRGPVT        0.1283      12470.5                   50.00     Sequence
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   DRB1_0301   46  DTDAQRDSEESYLAL  AQRDSEESY        0.1257      12830.6                   50.00     Sequence
   DRB1_0301  420  TDWTAPLIEAALKDA  APLIEAALK        0.1230      13207.4                   50.00     Sequence
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   DRB1_0301   45  EDTDAQRDSEESYLA  DAQRDSEES        0.1142      14537.3                   50.00     Sequence
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   DRB1_0301  454  ATGTTVSPPLFESLE  TGTTVSPPL        0.0934      18206.7                   50.00     Sequence
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   DRB1_0301  392  IDPKAAAKELGPDGA  AKELGPDGA        0.0763      21899.7                   50.00     Sequence
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   DRB1_0301  169  LVRGPVTFAAGSVPD  LVRGPVTFA        0.0636      25121.7                   50.00     Sequence
   DRB1_0301   71  WDEGPEVGGPYGPYR  GPEVGGPYG        0.0615      25696.9                   50.00     Sequence
   DRB1_0301   70  DWDEGPEVGGPYGPY  DWDEGPEVG        0.0381      33091.7                   50.00     Sequence
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Allele: DRB1_0301. Number of high binders 5. Number of weak binders 64. Number of peptides 476

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0401  473  DRSMQRLRAARQLVG  RSMQRLRAA        0.7138         22.1          SB     2.00     Sequence
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DRB1_0401  474  RSMQRLRAARQLVGH  RSMQRLRAA         0.6914          28.2          SB     2.00     Sequence
DRB1_0401    5  TVRVRFCPSPTGTPH  VRFCPSPTG         0.6897          28.7          SB     2.00     Sequence
DRB1_0401  470  LGRDRSMQRLRAARQ  RSMQRLRAA         0.6660          37.1          SB     4.00     Sequence
DRB1_0401  295  DLFGLDEMVAAFDVA  LFGLDEMVA         0.6641          37.9          SB     4.00     Sequence
DRB1_0401    7  RVRFCPSPTGTPHVG  VRFCPSPTG         0.6626          38.5          SB     4.00     Sequence
DRB1_0401  294  HDLFGLDEMVAAFDV  LFGLDEMVA         0.6607          39.3          SB     4.00     Sequence
DRB1_0401  471  GRDRSMQRLRAARQL  RSMQRLRAA         0.6588          40.1          SB     4.00     Sequence
DRB1_0401    4  ETVRVRFCPSPTGTP  VRFCPSPTG         0.6554          41.6          SB     4.00     Sequence
DRB1_0401  296  LFGLDEMVAAFDVAD  LFGLDEMVA         0.6536          42.5          SB     4.00     Sequence
DRB1_0401  240  IPKFAHLPTVLGEGT  FAHLPTVLG         0.6424          47.9          SB     4.00     Sequence
DRB1_0401  293  DHDLFGLDEMVAAFD  LFGLDEMVA         0.6325          53.3          WB     4.00     Sequence
DRB1_0401  239  RIPKFAHLPTVLGEG  FAHLPTVLG         0.6266          56.8          WB     8.00     Sequence
DRB1_0401  241  PKFAHLPTVLGEGTK  FAHLPTVLG         0.6200          61.0          WB     8.00     Sequence
DRB1_0401   39  TFVFRIEDTDAQRDS  FRIEDTDAQ         0.6183          62.2          WB     8.00     Sequence
DRB1_0401   38  GTFVFRIEDTDAQRD  FRIEDTDAQ         0.6071          70.2          WB     8.00     Sequence
DRB1_0401  238  ERIPKFAHLPTVLGE  FAHLPTVLG         0.5990          76.6          WB     8.00     Sequence
DRB1_0401  469  LLGRDRSMQRLRAAR  LGRDRSMQR         0.5954          79.6          WB     8.00     Sequence
DRB1_0401  468  ELLGRDRSMQRLRAA  LGRDRSMQR         0.5804          93.7          WB     8.00     Sequence
DRB1_0401    3  TETVRVRFCPSPTGT  VRFCPSPTG         0.5775          96.7          WB     8.00     Sequence
DRB1_0401   37  GGTFVFRIEDTDAQR  FVFRIEDTD         0.5760          98.2          WB     8.00     Sequence
DRB1_0401   40  FVFRIEDTDAQRDSE  FRIEDTDAQ         0.5757          98.5          WB     8.00     Sequence
DRB1_0401  292  DDHDLFGLDEMVAAF  LFGLDEMVA         0.5740         100.4          WB     8.00     Sequence
DRB1_0401  475  SMQRLRAARQLVGHA  MQRLRAARQ         0.5727         101.9          WB     8.00     Sequence
DRB1_0401  444  RKAFSPIRVAATGTT  RKAFSPIRV         0.5635         112.5          WB    16.00     Sequence
DRB1_0401  237  AERIPKFAHLPTVLG  FAHLPTVLG         0.5562         121.7          WB    16.00     Sequence
DRB1_0401   90  AEIYRDVLARLLAAG  EIYRDVLAR         0.5410         143.5          WB    16.00     Sequence
DRB1_0401    8  VRFCPSPTGTPHVGL  VRFCPSPTG         0.5410         143.5          WB    16.00     Sequence
DRB1_0401   91  EIYRDVLARLLAAGE  EIYRDVLAR         0.5406         144.1          WB    16.00     Sequence
DRB1_0401   55  ESYLALLDALRWLGL  SYLALLDAL         0.5393         146.2          WB    16.00     Sequence
DRB1_0401  351  GHHIALDEAAFAAAA  HIALDEAAF         0.5300         161.7          WB    16.00     Sequence
DRB1_0401  467  LELLGRDRSMQRLRA  LGRDRSMQR         0.5292         163.0          WB    16.00     Sequence
DRB1_0401  443  PRKAFSPIRVAATGT  RKAFSPIRV         0.5279         165.4          WB    16.00     Sequence
DRB1_0401   54  EESYLALLDALRWLG  ESYLALLDA         0.5241         172.4          WB    16.00     Sequence
DRB1_0401  350  HGHHIALDEAAFAAA  HHIALDEAA         0.5210         178.2          WB    16.00     Sequence
DRB1_0401   36  TGGTFVFRIEDTDAQ  TFVFRIEDT         0.5200         180.0          WB    16.00     Sequence
DRB1_0401  210  HVLRGEDLLPSTPRQ  LRGEDLLPS         0.5184         183.2          WB    16.00     Sequence
DRB1_0401   41  VFRIEDTDAQRDSEE  FRIEDTDAQ         0.5131         194.0          WB    16.00     Sequence
DRB1_0401  442  KPRKAFSPIRVAATG  RKAFSPIRV         0.5128         194.6          WB    16.00     Sequence
DRB1_0401   89  RAEIYRDVLARLLAA  EIYRDVLAR         0.5124         195.6          WB    16.00     Sequence
DRB1_0401  209  THVLRGEDLLPSTPR  LRGEDLLPS         0.5114         197.6          WB    16.00     Sequence
DRB1_0401  352  HHIALDEAAFAAAAE  HHIALDEAA         0.5099         200.8          WB    16.00     Sequence
DRB1_0401  329  EHIRMLDVGDFTVRL  RMLDVGDFT         0.5097         201.3          WB    16.00     Sequence
DRB1_0401  441  LKPRKAFSPIRVAAT  RKAFSPIRV         0.5093         202.3          WB    16.00     Sequence
DRB1_0401  297  FGLDEMVAAFDVADV  FGLDEMVAA         0.5092         202.4          WB    16.00     Sequence
DRB1_0401  447  FSPIRVAATGTTVSP  IRVAATGTT         0.5056         210.4          WB    16.00     Sequence
DRB1_0401  449  PIRVAATGTTVSPPL  IRVAATGTT         0.5020         218.8          WB    16.00     Sequence
DRB1_0401  291  ADDHDLFGLDEMVAA  LFGLDEMVA         0.5017         219.6          WB    16.00     Sequence
DRB1_0401   53  SEESYLALLDALRWL  ESYLALLDA         0.4988         226.6          WB    16.00     Sequence
DRB1_0401  446  AFSPIRVAATGTTVS  IRVAATGTT         0.4973         230.2          WB    16.00     Sequence
DRB1_0401  211  VLRGEDLLPSTPRQL  LRGEDLLPS         0.4972         230.5          WB    16.00     Sequence
DRB1_0401  445  KAFSPIRVAATGTTV  FSPIRVAAT         0.4954         235.1          WB    16.00     Sequence
DRB1_0401  450  IRVAATGTTVSPPLF  IRVAATGTT         0.4946         237.1          WB    16.00     Sequence
DRB1_0401  330  HIRMLDVGDFTVRLR  RMLDVGDFT         0.4944         237.6          WB    16.00     Sequence
DRB1_0401  448  SPIRVAATGTTVSPP  IRVAATGTT         0.4929         241.4          WB    16.00     Sequence
DRB1_0401    2  ATETVRVRFCPSPTG  VRFCPSPTG         0.4890         251.8          WB    16.00     Sequence
DRB1_0401  466  SLELLGRDRSMQRLR  LGRDRSMQR         0.4876         255.8          WB    32.00     Sequence
DRB1_0401  328  AEHIRMLDVGDFTVR  RMLDVGDFT         0.4845         264.4          WB    32.00     Sequence
DRB1_0401   94  RDVLARLLAAGEAYH  DVLARLLAA         0.4842         265.3          WB    32.00     Sequence
DRB1_0401  242  KFAHLPTVLGEGTKK  FAHLPTVLG         0.4823         271.0          WB    32.00     Sequence
DRB1_0401   92  IYRDVLARLLAAGEA  DVLARLLAA         0.4781         283.3          WB    32.00     Sequence
DRB1_0401   88  QRAEIYRDVLARLLA  EIYRDVLAR         0.4742         295.6          WB    32.00     Sequence
DRB1_0401  331  IRMLDVGDFTVRLRD  RMLDVGDFT         0.4724         301.3          WB    32.00     Sequence
DRB1_0401  349  THGHHIALDEAAFAA  HHIALDEAA         0.4720         302.7          WB    32.00     Sequence
DRB1_0401   95  DVLARLLAAGEAYHA  DVLARLLAA         0.4706         307.2          WB    32.00     Sequence
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DRB1_0401   25  TALFNWAYARHTGGT  LFNWAYARH        0.4627        334.8         WB    32.00     Sequence
DRB1_0401  208  ITHVLRGEDLLPSTP  LRGEDLLPS        0.4620        337.3         WB    32.00     Sequence
DRB1_0401  379  WELLKFFNDDQYVID  WELLKFFND        0.4607        342.0         WB    32.00     Sequence
DRB1_0401  332  RMLDVGDFTVRLRDH  RMLDVGDFT        0.4577        353.3         WB    32.00     Sequence
DRB1_0401   93  YRDVLARLLAAGEAY  DVLARLLAA        0.4569        356.6         WB    32.00     Sequence
DRB1_0401  378  AWELLKFFNDDQYVI  WELLKFFND        0.4541        367.3         WB    32.00     Sequence
DRB1_0401   24  RTALFNWAYARHTGG  LFNWAYARH        0.4530        371.7         WB    32.00     Sequence
DRB1_0401   52  DSEESYLALLDALRW  SYLALLDAL        0.4515        377.9         WB    32.00     Sequence
DRB1_0401  167  NDLVRGPVTFAAGSV  DLVRGPVTF        0.4384        435.5         WB    32.00     Sequence
DRB1_0401   56  SYLALLDALRWLGLD  SYLALLDAL        0.4357        448.3         WB    32.00     Sequence
DRB1_0401  301  EMVAAFDVADVNSSP  EMVAAFDVA        0.4353        450.5         WB    32.00     Sequence
DRB1_0401  128  KLGYDNFDRHLTDAQ  KLGYDNFDR        0.4352        450.7         WB    32.00     Sequence
DRB1_0401  465  ESLELLGRDRSMQRL  LGRDRSMQR        0.4341        456.3         WB    32.00     Sequence
DRB1_0401  327  NAEHIRMLDVGDFTV  RMLDVGDFT        0.4333        460.2         WB    32.00     Sequence
DRB1_0401  440  ALKPRKAFSPIRVAA  RKAFSPIRV        0.4319        467.0         WB    32.00     Sequence
DRB1_0401  410  DAALAALTSVTDWTA  LAALTSVTD        0.4307        473.2         WB    32.00     Sequence
DRB1_0401  192  DPLYTLVNPCDDALM  LYTLVNPCD        0.4287        483.9         WB    32.00     Sequence
DRB1_0401   42  FRIEDTDAQRDSEES  FRIEDTDAQ        0.4281        486.8         WB    32.00     Sequence
DRB1_0401   26  ALFNWAYARHTGGTF  LFNWAYARH        0.4271        492.1         WB    32.00     Sequence
DRB1_0401  381  LLKFFNDDQYVIDPK  KFFNDDQYV        0.4270        492.8         WB    32.00     Sequence
DRB1_0401  377  DAWELLKFFNDDQYV  WELLKFFND        0.4220        520.1               32.00     Sequence
DRB1_0401   18  PHVGLVRTALFNWAY  GLVRTALFN        0.4211        525.3               32.00     Sequence
DRB1_0401  168  DLVRGPVTFAAGSVP  DLVRGPVTF        0.4204        529.3               32.00     Sequence
DRB1_0401   87  SQRAEIYRDVLARLL  EIYRDVLAR        0.4202        530.1               32.00     Sequence
DRB1_0401   23  VRTALFNWAYARHTG  LFNWAYARH        0.4201        530.9               32.00     Sequence
DRB1_0401  380  ELLKFFNDDQYVIDP  LKFFNDDQY        0.4186        539.7               32.00     Sequence
DRB1_0401  126  NPKLGYDNFDRHLTD  KLGYDNFDR        0.4180        542.8               32.00     Sequence
DRB1_0401  191  GDPLYTLVNPCDDAL  LYTLVNPCD        0.4177        544.6               32.00     Sequence
DRB1_0401  127  PKLGYDNFDRHLTDA  KLGYDNFDR        0.4176        545.1               32.00     Sequence
DRB1_0401   20  VGLVRTALFNWAYAR  GLVRTALFN        0.4172        547.6               32.00     Sequence
DRB1_0401   21  GLVRTALFNWAYARH  GLVRTALFN        0.4171        548.6               32.00     Sequence
DRB1_0401  212  LRGEDLLPSTPRQLA  LRGEDLLPS        0.4166        551.1               32.00     Sequence
DRB1_0401  353  HIALDEAAFAAAAEL  HIALDEAAF        0.4164        552.3               32.00     Sequence
DRB1_0401   19  HVGLVRTALFNWAYA  GLVRTALFN        0.4159        555.4               32.00     Sequence
DRB1_0401  223  RQLALHQALIRIGVA  LALHQALIR        0.4141        566.2               32.00     Sequence
DRB1_0401  300  DEMVAAFDVADVNSS  EMVAAFDVA        0.4123        577.4               32.00     Sequence
DRB1_0401  382  LKFFNDDQYVIDPKA  KFFNDDQYV        0.4117        581.4               32.00     Sequence
DRB1_0401  207  KITHVLRGEDLLPST  LRGEDLLPS        0.4115        582.6               32.00     Sequence
DRB1_0401  225  LALHQALIRIGVAER  LALHQALIR        0.4103        590.5               32.00     Sequence
DRB1_0401  125  RNPKLGYDNFDRHLT  KLGYDNFDR        0.4096        594.4               32.00     Sequence
DRB1_0401  302  MVAAFDVADVNSSPA  AFDVADVNS        0.4091        597.9               32.00     Sequence
DRB1_0401  407  AVLDAALAALTSVTD  AVLDAALAA        0.4088        600.1               32.00     Sequence
DRB1_0401  409  LDAALAALTSVTDWT  LAALTSVTD        0.4084        602.3               32.00     Sequence
DRB1_0401  229  QALIRIGVAERIPKF  LIRIGVAER        0.4080        605.2               32.00     Sequence
DRB1_0401  412  ALAALTSVTDWTAPL  LAALTSVTD        0.4078        606.6               32.00     Sequence
DRB1_0401  388  DQYVIDPKAAAKELG  QYVIDPKAA        0.4064        615.3               32.00     Sequence
DRB1_0401  413  LAALTSVTDWTAPLI  LAALTSVTD        0.4055        621.3               32.00     Sequence
DRB1_0401   27  LFNWAYARHTGGTFV  LFNWAYARH        0.4047        626.7               32.00     Sequence
DRB1_0401   34  RHTGGTFVFRIEDTD  RHTGGTFVF        0.4045        628.7               32.00     Sequence
DRB1_0401  387  DDQYVIDPKAAAKEL  QYVIDPKAA        0.4040        632.1               32.00     Sequence
DRB1_0401  166  WNDLVRGPVTFAAGS  DLVRGPVTF        0.4038        633.1               32.00     Sequence
DRB1_0401  411  AALAALTSVTDWTAP  LAALTSVTD        0.4038        633.4               32.00     Sequence
DRB1_0401  203  DALMKITHVLRGEDL  LMKITHVLR        0.4035        635.4               32.00     Sequence
DRB1_0401  304  AAFDVADVNSSPARF  FDVADVNSS        0.4024        642.9               32.00     Sequence
DRB1_0401  222  PRQLALHQALIRIGV  LALHQALIR        0.4020        645.3               32.00     Sequence
DRB1_0401  461  PPLFESLELLGRDRS  LFESLELLG        0.4008        654.4               32.00     Sequence
DRB1_0401  464  FESLELLGRDRSMQR  LGRDRSMQR        0.3988        668.5               32.00     Sequence
DRB1_0401  383  KFFNDDQYVIDPKAA  KFFNDDQYV        0.3985        670.5               32.00     Sequence
DRB1_0401  228  HQALIRIGVAERIPK  LIRIGVAER        0.3967        684.0               32.00     Sequence
DRB1_0401   96  VLARLLAAGEAYHAF  RLLAAGEAY        0.3964        685.8               32.00     Sequence
DRB1_0401  134  FDRHLTDAQRAAYLA  RHLTDAQRA        0.3961        687.8               32.00     Sequence
DRB1_0401   35  HTGGTFVFRIEDTDA  TFVFRIEDT        0.3948        697.7               32.00     Sequence
DRB1_0401  348  DTHGHHIALDEAAFA  HHIALDEAA        0.3944        701.3               32.00     Sequence
DRB1_0401  104  GEAYHAFSTPEEVEA  YHAFSTPEE        0.3939        705.0               32.00     Sequence
DRB1_0401  133  NFDRHLTDAQRAAYL  RHLTDAQRA        0.3930        712.0               32.00     Sequence
DRB1_0401  190  SGDPLYTLVNPCDDA  LYTLVNPCD        0.3927        714.3               32.00     Sequence
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DRB1_0401	163	DLAWNDLVRGPVTFA	DLAWNDLVR	0.3924	715.9	32.00	Sequence
DRB1_0401	376	GDAWELLKFFNDDQY	WELLKFFND	0.3923	717.1	32.00	Sequence
DRB1_0401	299	LDEMVAAFDVADVNS	EMVAAFDVA	0.3920	719.7	32.00	Sequence
DRB1_0401	389	QYVIDPKAAAKELGP	YVIDPKAAA	0.3911	726.5	32.00	Sequence
DRB1_0401	462	PLFESLELLGRDRSM	LFESLELLG	0.3893	740.4	32.00	Sequence
DRB1_0401	408	VLDAALAALTSVTDW	DAALAALTS	0.3890	743.4	32.00	Sequence
DRB1_0401	105	EAYHAFSTPEEVEAR	YHAFSTPEE	0.3876	754.8	32.00	Sequence
DRB1_0401	384	FFNDDQYVIDPKAAA	FFNDDQYVI	0.3874	755.8	32.00	Sequence
DRB1_0401	151	RQPVVRLRMPDDDLA	VVRLRMPDD	0.3864	764.4	50.00	Sequence
DRB1_0401	22	LVRTALFNWAYARHT	LFNWAYARH	0.3863	764.8	50.00	Sequence
DRB1_0401	386	NDDQYVIDPKAAAKE	QYVIDPKAA	0.3859	768.5	50.00	Sequence
DRB1_0401	366	ELVQTRIVVLGDAWE	ELVQTRIVV	0.3855	771.5	50.00	Sequence
DRB1_0401	439	LALKPRKAFSPIRVA	RKAFSPIRV	0.3852	774.5	50.00	Sequence
DRB1_0401	155	VRLRMPDDDLAWNDL	RLRMPDDDL	0.3834	789.9	50.00	Sequence
DRB1_0401	303	VAAFDVADVNSSPAR	FDVADVNSS	0.3832	791.6	50.00	Sequence
DRB1_0401	132	DNFDRHLTDAQRAAY	RHLTDAQRA	0.3825	797.2	50.00	Sequence
DRB1_0401	224	QLALHQALIRIGVAE	LALHQALIR	0.3823	799.1	50.00	Sequence
DRB1_0401	156	RLRMPDDDLAWNDLV	RLRMPDDDL	0.3815	805.7	50.00	Sequence
DRB1_0401	298	GLDEMVAAFDVADVN	EMVAAFDVA	0.3803	816.3	50.00	Sequence
DRB1_0401	154	VVRLRMPDDDLAWND	RLRMPDDDL	0.3799	820.1	50.00	Sequence
DRB1_0401	17	TPHVGLVRTALFNWA	VGLVRTALF	0.3787	830.9	50.00	Sequence
DRB1_0401	438	GLALKPRKAFSPIRV	LKPRKAFSP	0.3778	838.9	50.00	Sequence
DRB1_0401	205	LMKITHVLRGEDLLP	LMKITHVLR	0.3765	851.1	50.00	Sequence
DRB1_0401	365	AELVQTRIVVLGDAW	ELVQTRIVV	0.3747	867.6	50.00	Sequence
DRB1_0401	193	PLYTLVNPCDDALMK	LYTLVNPCD	0.3731	882.2	50.00	Sequence
DRB1_0401	435	LIEGLALKPRKAFSP	LIEGLALKP	0.3730	883.4	50.00	Sequence
DRB1_0401	221	TPRQLALHQALIRIG	LALHQALIR	0.3728	885.5	50.00	Sequence
DRB1_0401	202	DDALMKITHVLRGED	LMKITHVLR	0.3725	888.4	50.00	Sequence
DRB1_0401	326	LNAEHIRMLDVGDFT	RMLDVGDFT	0.3715	898.3	50.00	Sequence
DRB1_0401	135	DRHLTDAQRAAYLAE	RHLTDAQRA	0.3705	908.0	50.00	Sequence
DRB1_0401	460	SPPLFESLELLGRDR	PLFESLELL	0.3701	911.5	50.00	Sequence
DRB1_0401	99	RLLAAGEAYHAFSTP	RLLAAGEAY	0.3699	913.5	50.00	Sequence
DRB1_0401	433	DALIEGLALKPRKAF	LIEGLALKP	0.3695	917.8	50.00	Sequence
DRB1_0401	124	GRNPKLGYDNFDRHL	KLGYDNFDR	0.3695	917.8	50.00	Sequence
DRB1_0401	276	PEGLLNYLALLGWSI	PEGLLNYLA	0.3694	918.7	50.00	Sequence
DRB1_0401	188	RASGDPLYTLVNPCD	RASGDPLYT	0.3691	921.4	50.00	Sequence
DRB1_0401	206	MKITHVLRGEDLLPS	LRGEDLLPS	0.3688	925.2	50.00	Sequence
DRB1_0401	243	FAHLPTVLGEGTKKL	FAHLPTVLG	0.3681	931.7	50.00	Sequence
DRB1_0401	153	PVVRLRMPDDDLAWN	RLRMPDDDL	0.3676	936.4	50.00	Sequence
DRB1_0401	98	ARLLAAGEAYHAFST	RLLAAGEAY	0.3676	936.9	50.00	Sequence
DRB1_0401	305	AFDVADVNSSPARFD	FDVADVNSS	0.3669	944.2	50.00	Sequence
DRB1_0401	290	IADDHDLFGLDEMVA	LFGLDEMVA	0.3654	959.8	50.00	Sequence
DRB1_0401	406	AAVLDAALAALTSVT	AVLDAALAA	0.3648	965.1	50.00	Sequence
DRB1_0401	1	TATETVRVRFCPSPT	RVRFCPSPT	0.3635	979.0	50.00	Sequence
DRB1_0401	97	LARLLAAGEAYHAFS	RLLAAGEAY	0.3630	984.7	50.00	Sequence
DRB1_0401	385	FNDDQYVIDPKAAAK	QYVIDPKAA	0.3621	994.0	50.00	Sequence
DRB1_0401	152	QPVVRLRMPDDDLAW	RLRMPDDDL	0.3617	998.6	50.00	Sequence
DRB1_0401	434	ALIEGLALKPRKAFS	LIEGLALKP	0.3615	1000.2	50.00	Sequence
DRB1_0401	51	RDSEESYLALLDALR	SYLALLDAL	0.3613	1003.3	50.00	Sequence
DRB1_0401	165	AWNDLVRGPVTFAAG	DLVRGPVTF	0.3612	1004.0	50.00	Sequence
DRB1_0401	86	QSQRAEIYRDVLARL	EIYRDVLAR	0.3598	1019.4	50.00	Sequence
DRB1_0401	236	VAERIPKFAHLPTVL	PKFAHLPTV	0.3576	1044.0	50.00	Sequence
DRB1_0401	63	ALRWLGLDWDEGPEV	LRWLGLDWD	0.3558	1063.8	50.00	Sequence
DRB1_0401	204	ALMKITHVLRGEDLL	LMKITHVLR	0.3553	1069.9	50.00	Sequence
DRB1_0401	273	GFIPEGLLNYLALLG	PEGLLNYLA	0.3543	1082.3	50.00	Sequence
DRB1_0401	282	YLALLGWSIADDHDL	YLALLGWSI	0.3517	1113.2	50.00	Sequence
DRB1_0401	432	KDALIEGLALKPRKA	LIEGLALKP	0.3503	1130.1	50.00	Sequence
DRB1_0401	162	DDLAWNDLVRGPVTF	DLAWNDLVR	0.3499	1134.6	50.00	Sequence
DRB1_0401	230	ALIRIGVAERIPKFA	LIRIGVAER	0.3485	1151.8	50.00	Sequence
DRB1_0401	103	AGEAYHAFSTPEEVE	YHAFSTPEE	0.3485	1152.1	50.00	Sequence
DRB1_0401	281	NYLALLGWSIADDHD	YLALLGWSI	0.3483	1154.5	50.00	Sequence
DRB1_0401	364	AAELVQTRIVVLGDA	ELVQTRIVV	0.3474	1165.2	50.00	Sequence
DRB1_0401	150	GRQPVVRLRMPDDDL	VVRLRMPDD	0.3471	1169.0	50.00	Sequence
DRB1_0401	220	STPRQLALHQALIRI	LALHQALIR	0.3456	1188.2	50.00	Sequence
DRB1_0401	189	ASGDPLYTLVNPCDD	DPLYTLVNP	0.3456	1188.6	50.00	Sequence
DRB1_0401	227	LHQALIRIGVAERIP	LIRIGVAER	0.3456	1188.9	50.00	Sequence

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DRB1_0401  279  LLNYLALLGWSIADD  YLALLGWSI        0.3446       1201.9                 50.00     Sequence
DRB1_0401  272  RGFIPEGLLNYLALL  GFIPEGLLN        0.3440       1209.6                 50.00     Sequence
DRB1_0401  463  LFESLELLGRDRSMQ  LFESLELLG        0.3435       1215.6                 50.00     Sequence
DRB1_0401  136  RHLTDAQRAAYLAEG  RHLTDAQRA        0.3405       1255.8                 50.00     Sequence
DRB1_0401  280  LNYLALLGWSIADDH  YLALLGWSI        0.3400       1262.7                 50.00     Sequence
DRB1_0401   64  LRWLGLDWDEGPEVG  LRWLGLDWD        0.3385       1284.1                 50.00     Sequence
DRB1_0401   62  DALRWLGLDWDEGPE  LRWLGLDWD        0.3383       1286.4                 50.00     Sequence
DRB1_0401  106  AYHAFSTPEEVEARH  YHAFSTPEE        0.3361       1317.8                 50.00     Sequence
DRB1_0401  164  LAWNDLVRGPVTFAA  DLVRGPVTF        0.3351       1331.8                 50.00     Sequence
DRB1_0401  275  IPEGLLNYLALLGWS  PEGLLNYLA        0.3350       1333.4                 50.00     Sequence
DRB1_0401   57  YLALLDALRWLGLDW  YLALLDALR        0.3336       1353.7                 50.00     Sequence
DRB1_0401  201  CDDALMKITHVLRGE  LMKITHVLR        0.3334       1356.8                 50.00     Sequence
DRB1_0401   16  GTPHVGLVRTALFNW  VGLVRTALF        0.3330       1361.9                 50.00     Sequence
DRB1_0401  131  YDNFDRHLTDAQRAA  RHLTDAQRA        0.3328       1365.4                 50.00     Sequence
DRB1_0401   28  FNWAYARHTGGTFVF  FNWAYARHT        0.3297       1411.9                 50.00     Sequence
DRB1_0401  161  DDDLAWNDLVRGPVT  DLAWNDLVR        0.3283       1433.1                 50.00     Sequence
DRB1_0401   33  ARHTGGTFVFRIEDT  RHTGGTFVF        0.3282       1434.1                 50.00     Sequence
DRB1_0401  271  DRGFIPEGLLNYLAL  GFIPEGLLN        0.3265       1461.7                 50.00     Sequence
DRB1_0401  459  VSPPLFESLELLGRD  PLFESLELL        0.3257       1473.4                 50.00     Sequence
DRB1_0401   85  RQSQRAEIYRDVLAR  EIYRDVLAR        0.3246       1492.0                 50.00     Sequence
DRB1_0401  123  AGRNPKLGYDNFDRH  KLGYDNFDR        0.3240       1500.7                 50.00     Sequence
DRB1_0401  277  EGLLNYLALLGWSIA  LLNYLALLG        0.3240       1501.4                 50.00     Sequence
DRB1_0401  278  GLLNYLALLGWSIAD  YLALLGWSI        0.3236       1508.5                 50.00     Sequence
DRB1_0401  182  PDFALTRASGDPLYT  FALTRASGD        0.3226       1525.1                 50.00     Sequence
DRB1_0401  405  GAAVLDAALAALTSV  AVLDAALAA        0.3225       1525.5                 50.00     Sequence
DRB1_0401  451  RVAATGTTVSPPLFE  RVAATGTTV        0.3218       1537.0                 50.00     Sequence
DRB1_0401  416  LTSVTDWTAPLIEAA  LTSVTDWTA        0.3212       1547.1                 50.00     Sequence
DRB1_0401  415  ALTSVTDWTAPLIEA  LTSVTDWTA        0.3204       1561.8                 50.00     Sequence
DRB1_0401  226  ALHQALIRIGVAERI  QALIRIGVA        0.3192       1581.0                 50.00     Sequence
DRB1_0401   61  LDALRWLGLDWDEGP  LRWLGLDWD        0.3189       1585.9                 50.00     Sequence
DRB1_0401  181  VPDFALTRASGDPLY  FALTRASGD        0.3159       1639.2                 50.00     Sequence
DRB1_0401  274  FIPEGLLNYLALLGW  PEGLLNYLA        0.3152       1651.3                 50.00     Sequence
DRB1_0401  363  AAAELVQTRIVVLGD  ELVQTRIVV        0.3138       1676.7                 50.00     Sequence
DRB1_0401  283  LALLGWSIADDHDLF  LLGWSIADD        0.3120       1709.3                 50.00     Sequence
DRB1_0401  102  AAGEAYHAFSTPEEV  YHAFSTPEE        0.3084       1777.7                 50.00     Sequence
DRB1_0401  284  ALLGWSIADDHDLFG  LLGWSIADD        0.3083       1779.7                 50.00     Sequence
DRB1_0401  187  TRASGDPLYTLVNPC  RASGDPLYT        0.3064       1817.1                 50.00     Sequence
DRB1_0401  231  LIRIGVAERIPKFAH  LIRIGVAER        0.3037       1870.8                 50.00     Sequence
DRB1_0401  200  PCDDALMKITHVLRG  DALMKITHV        0.3034       1877.1                 50.00     Sequence
DRB1_0401  333  MLDVGDFTVRLRDHL  MLDVGDFTV        0.3032       1879.7                 50.00     Sequence
DRB1_0401  160  PDDDLAWNDLVRGPV  DLAWNDLVR        0.3029       1886.9                 50.00     Sequence
DRB1_0401    9  RFCPSPTGTPHVGLV  RFCPSPTGT        0.3025       1894.5                 50.00     Sequence
DRB1_0401  306  FDVADVNSSPARFDQ  FDVADVNSS        0.3022       1901.0                 50.00     Sequence
DRB1_0401  180  SVPDFALTRASGDPL  FALTRASGD        0.3018       1910.1                 50.00     Sequence
DRB1_0401  375  LGDAWELLKFFNDDQ  WELLKFFND        0.3008       1930.4                 50.00     Sequence
DRB1_0401  436  IEGLALKPRKAFSPI  IEGLALKPR        0.3004       1937.7                 50.00     Sequence
DRB1_0401  107  YHAFSTPEEVEARHV  YHAFSTPEE        0.2995       1958.1                 50.00     Sequence
DRB1_0401  325  ALNAEHIRMLDVGDF  EHIRMLDVG        0.2987       1974.9                 50.00     Sequence
DRB1_0401  339  FTVRLRDHLDTHGHH  RLRDHLDTH        0.2957       2039.9                 50.00     Sequence
DRB1_0401  219  PSTPRQLALHQALIR  LALHQALIR        0.2947       2062.3                 50.00     Sequence
DRB1_0401  361  FAAAAELVQTRIVVL  FAAAAELVQ        0.2945       2067.0                 50.00     Sequence
DRB1_0401  169  LVRGPVTFAAGSVPD  VRGPVTFAA        0.2935       2087.8                 50.00     Sequence
DRB1_0401  179  GSVPDFALTRASGDP  FALTRASGD        0.2931       2098.3                 50.00     Sequence
DRB1_0401  404  DGAAVLDAALAALTS  AVLDAALAA        0.2917       2128.6                 50.00     Sequence
DRB1_0401  414  AALTSVTDWTAPLIE  LTSVTDWTA        0.2912       2140.0                 50.00     Sequence
DRB1_0401  341  VRLRDHLDTHGHHIA  RLRDHLDTH        0.2911       2143.9                 50.00     Sequence
DRB1_0401  437  EGLALKPRKAFSPIR  GLALKPRKA        0.2891       2190.4                 50.00     Sequence
DRB1_0401  194  LYTLVNPCDDALMKI  LYTLVNPCD        0.2877       2223.8                 50.00     Sequence
DRB1_0401  340  TVRLRDHLDTHGHHI  RLRDHLDTH        0.2858       2268.7                 50.00     Sequence
DRB1_0401  338  DFTVRLRDHLDTHGH  VRLRDHLDT        0.2857       2273.3                 50.00     Sequence
DRB1_0401  148  AEGRQPVVRLRMPDD  AEGRQPVVR        0.2838       2320.3                 50.00     Sequence
DRB1_0401  101  LAAGEAYHAFSTPEE  YHAFSTPEE        0.2819       2367.2                 50.00     Sequence
DRB1_0401  270  RDRGFIPEGLLNYLA  RGFIPEGLL        0.2818       2370.9                 50.00     Sequence
DRB1_0401  130  GYDNFDRHLTDAQRA  RHLTDAQRA        0.2818       2371.2                 50.00     Sequence
DRB1_0401   32  YARHTGGTFVFRIED  RHTGGTFVF        0.2807       2397.6                 50.00     Sequence
DRB1_0401  149  EGRQPVVRLRMPDDD  VVRLRMPDD        0.2796       2427.3                 50.00     Sequence
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DRB1_0401   15  TGTPHVGLVRTALFN  VGLVRTALF        0.2795       2430.2               50.00     Sequence
DRB1_0401  431  LKDALIEGLALKPRK  LIEGLALKP        0.2784       2460.4               50.00     Sequence
DRB1_0401  362  AAAAELVQTRIVVLG  ELVQTRIVV        0.2772       2490.1               50.00     Sequence
DRB1_0401  186  LTRASGDPLYTLVNP  RASGDPLYT        0.2761       2520.5               50.00     Sequence
DRB1_0401  458  TVSPPLFESLELLGR  PLFESLELL        0.2761       2522.3               50.00     Sequence
DRB1_0401    0  VTATETVRVRFCPSP  VTATETVRV        0.2730       2608.1               50.00     Sequence
DRB1_0401  285  LLGWSIADDHDLFGL  LLGWSIADD        0.2728       2611.9               50.00     Sequence
DRB1_0401   60  LLDALRWLGLDWDEG  LRWLGLDWD        0.2724       2622.6               50.00     Sequence
DRB1_0401  360  AFAAAAELVQTRIVV  FAAAAELVQ        0.2719       2636.9               50.00     Sequence
DRB1_0401  199  NPCDDALMKITHVLR  DALMKITHV        0.2714       2652.1               50.00     Sequence
DRB1_0401   58  LALLDALRWLGLDWD  LALLDALRW        0.2701       2690.7               50.00     Sequence
DRB1_0401  183  DFALTRASGDPLYTL  FALTRASGD        0.2695       2707.5               50.00     Sequence
DRB1_0401  347  LDTHGHHIALDEAAF  HHIALDEAA        0.2672       2776.2               50.00     Sequence
DRB1_0401  266  LFAHRDRGFIPEGLL  LFAHRDRGF        0.2671       2778.2               50.00     Sequence
DRB1_0401  268  AHRDRGFIPEGLLNY  AHRDRGFIP        0.2667       2790.2               50.00     Sequence
DRB1_0401   82  GPYRQSQRAEIYRDV  YRQSQRAEI        0.2625       2921.0               50.00     Sequence
DRB1_0401  369  QTRIVVLGDAWELLK  TRIVVLGDA        0.2617       2945.3               50.00     Sequence
DRB1_0401  170  VRGPVTFAAGSVPDF  VRGPVTFAA        0.2616       2950.7               50.00     Sequence
DRB1_0401   81  YGPYRQSQRAEIYRD  PYRQSQRAE        0.2611       2963.7               50.00     Sequence
DRB1_0401   50  QRDSEESYLALLDAL  RDSEESYLA        0.2606       2981.3               50.00     Sequence
DRB1_0401  370  TRIVVLGDAWELLKF  TRIVVLGDA        0.2595       3018.2               50.00     Sequence
DRB1_0401  147  LAEGRQPVVRLRMPD  AEGRQPVVR        0.2571       3097.7               50.00     Sequence
DRB1_0401   65  RWLGLDWDEGPEVGG  WLGLDWDEG        0.2568       3105.8               50.00     Sequence
DRB1_0401  173  PVTFAAGSVPDFALT  TFAAGSVPD        0.2560       3135.2               50.00     Sequence
DRB1_0401  368  VQTRIVVLGDAWELL  TRIVVLGDA        0.2557       3142.9               50.00     Sequence
DRB1_0401  232  IRIGVAERIPKFAHL  IRIGVAERI        0.2557       3144.6               50.00     Sequence
DRB1_0401   83  PYRQSQRAEIYRDVL  PYRQSQRAE        0.2550       3167.8               50.00     Sequence
DRB1_0401   31  AYARHTGGTFVFRIE  RHTGGTFVF        0.2547       3177.0               50.00     Sequence
DRB1_0401  367  LVQTRIVVLGDAWEL  TRIVVLGDA        0.2547       3178.0               50.00     Sequence
DRB1_0401  359  AAFAAAAELVQTRIV  FAAAAELVQ        0.2510       3308.4               50.00     Sequence
DRB1_0401  354  IALDEAAFAAAAELV  IALDEAAFA        0.2506       3320.6               50.00     Sequence
DRB1_0401  265  NLFAHRDRGFIPEGL  LFAHRDRGF        0.2498       3352.2               50.00     Sequence
DRB1_0401  178  AGSVPDFALTRASGD  PDFALTRAS        0.2493       3369.9               50.00     Sequence
DRB1_0401  235  GVAERIPKFAHLPTV  AERIPKFAH        0.2488       3386.2               50.00     Sequence
DRB1_0401  159  MPDDDLAWNDLVRGP  DLAWNDLVR        0.2486       3393.9               50.00     Sequence
DRB1_0401  403  PDGAAVLDAALAALT  AVLDAALAA        0.2483       3404.3               50.00     Sequence
DRB1_0401  320  QKKADALNAEHIRML  QKKADALNA        0.2482       3409.7               50.00     Sequence
DRB1_0401  430  ALKDALIEGLALKPR  DALIEGLAL        0.2480       3415.3               50.00     Sequence
DRB1_0401  158  RMPDDDLAWNDLVRG  RMPDDDLAW        0.2477       3428.7               50.00     Sequence
DRB1_0401  122  AAGRNPKLGYDNFDR  KLGYDNFDR        0.2473       3441.1               50.00     Sequence
DRB1_0401  172  GPVTFAAGSVPDFAL  TFAAGSVPD        0.2458       3497.9               50.00     Sequence
DRB1_0401  317  RFDQKKADALNAEHI  QKKADALNA        0.2452       3522.2               50.00     Sequence
DRB1_0401  337  GDFTVRLRDHLDTHG  FTVRLRDHL        0.2450       3531.1               50.00     Sequence
DRB1_0401   30  WAYARHTGGTFVFRI  WAYARHTGG        0.2444       3551.7               50.00     Sequence
DRB1_0401   80  PYGPYRQSQRAEIYR  PYRQSQRAE        0.2438       3574.3               50.00     Sequence
DRB1_0401  374  VLGDAWELLKFFNDD  WELLKFFND        0.2435       3587.4               50.00     Sequence
DRB1_0401  100  LLAAGEAYHAFSTPE  LAAGEAYHA        0.2419       3650.1               50.00     Sequence
DRB1_0401   29  NWAYARHTGGTFVFR  WAYARHTGG        0.2407       3698.7               50.00     Sequence
DRB1_0401  319  DQKKADALNAEHIRM  QKKADALNA        0.2405       3707.1               50.00     Sequence
DRB1_0401  267  FAHRDRGFIPEGLLN  AHRDRGFIP        0.2388       3775.8               50.00     Sequence
DRB1_0401  157  LRMPDDDLAWNDLVR  LRMPDDDLA        0.2383       3793.1               50.00     Sequence
DRB1_0401  269  HRDRGFIPEGLLNYL  RGFIPEGLL        0.2375       3829.1               50.00     Sequence
DRB1_0401   84  YRQSQRAEIYRDVLA  RQSQRAEIY        0.2375       3829.5               50.00     Sequence
DRB1_0401  334  LDVGDFTVRLRDHLD  LDVGDFTVR        0.2371       3846.0               50.00     Sequence
DRB1_0401  184  FALTRASGDPLYTLV  FALTRASGD        0.2366       3867.4               50.00     Sequence
DRB1_0401  417  TSVTDWTAPLIEAAL  VTDWTAPLI        0.2362       3881.5               50.00     Sequence
DRB1_0401  324  DALNAEHIRMLDVGD  HIRMLDVGD        0.2359       3892.8               50.00     Sequence
DRB1_0401  390  YVIDPKAAAKELGPD  YVIDPKAAA        0.2346       3949.8               50.00     Sequence
DRB1_0401  233  RIGVAERIPKFAHLP  IGVAERIPK        0.2344       3959.5               50.00     Sequence
DRB1_0401  358  EAAFAAAAELVQTRI  FAAAAELVQ        0.2339       3980.8               50.00     Sequence
DRB1_0401  174  VTFAAGSVPDFALTR  TFAAGSVPD        0.2330       4019.3               50.00     Sequence
DRB1_0401  257  LSKRDPQSNLFAHRD  LSKRDPQSN        0.2294       4179.1               50.00     Sequence
DRB1_0401  256  KLSKRDPQSNLFAHR  LSKRDPQSN        0.2291       4194.2               50.00     Sequence
DRB1_0401  264  SNLFAHRDRGFIPEG  LFAHRDRGF        0.2276       4261.4               50.00     Sequence
DRB1_0401  373  VVLGDAWELLKFFND  WELLKFFND        0.2268       4298.5               50.00     Sequence
DRB1_0401  146  YLAEGRQPVVRLRMP  AEGRQPVVR        0.2253       4367.6               50.00     Sequence
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DRB1_0401   14  PTGTPHVGLVRTALF  VGLVRTALF        0.2250        4383.1                  50.00     Sequence
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DRB1_0401  318  FDQKKADALNAEHIR  QKKADALNA        0.2245        4405.5                  50.00     Sequence
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DRB1_0401  286  LGWSIADDHDLFGLD  WSIADDHDL        0.2223        4511.0                  50.00     Sequence
DRB1_0401   59  ALLDALRWLGLDWDE  LRWLGLDWD        0.2197        4641.0                  50.00     Sequence
DRB1_0401  175  TFAAGSVPDFALTRA  TFAAGSVPD        0.2179        4731.0                  50.00     Sequence
DRB1_0401  342  RLRDHLDTHGHHIAL  RLRDHLDTH        0.2167        4794.2                  50.00     Sequence
DRB1_0401  335  DVGDFTVRLRDHLDT  FTVRLRDHL        0.2143        4921.5                  50.00     Sequence
DRB1_0401  117  EARHVAAGRNPKLGY  RHVAAGRNP        0.2137        4952.3                  50.00     Sequence
DRB1_0401  371  RIVVLGDAWELLKFF  RIVVLGDAW        0.2121        5038.8                  50.00     Sequence
DRB1_0401  452  VAATGTTVSPPLFES  VAATGTTVS        0.2120        5046.8                  50.00     Sequence
DRB1_0401  116  VEARHVAAGRNPKLG  RHVAAGRNP        0.2111        5091.3                  50.00     Sequence
DRB1_0401  315  PARFDQKKADALNAE  RFDQKKADA        0.2111        5095.1                  50.00     Sequence
DRB1_0401  198  VNPCDDALMKITHVL  DALMKITHV        0.2107        5115.3                  50.00     Sequence
DRB1_0401  316  ARFDQKKADALNAEH  QKKADALNA        0.2090        5211.6                  50.00     Sequence
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DRB1_0401  263  QSNLFAHRDRGFIPE  LFAHRDRGF        0.2079        5272.0                  50.00     Sequence
DRB1_0401  234  IGVAERIPKFAHLPT  IGVAERIPK        0.2054        5415.5                  50.00     Sequence
DRB1_0401  255  KKLSKRDPQSNLFAH  LSKRDPQSN        0.2052        5427.8                  50.00     Sequence
DRB1_0401  185  ALTRASGDPLYTLVN  RASGDPLYT        0.2015        5652.3                  50.00     Sequence
DRB1_0401  115  EVEARHVAAGRNPKL  RHVAAGRNP        0.2013        5664.6                  50.00     Sequence
DRB1_0401  140  DAQRAAYLAEGRQPV  RAAYLAEGR        0.2006        5708.5                  50.00     Sequence
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DRB1_0401   79  GPYGPYRQSQRAEIY  RQSQRAEIY        0.1982        5856.8                  50.00     Sequence
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DRB1_0401  429  AALKDALIEGLALKP  DALIEGLAL        0.1971        5924.7                  50.00     Sequence
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DRB1_0401  142  QRAAYLAEGRQPVVR  RAAYLAEGR        0.1935        6161.3                  50.00     Sequence
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DRB1_0401  314  SPARFDQKKADALNA  RFDQKKADA        0.1901        6393.8                  50.00     Sequence
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DRB1_0401  287  GWSIADDHDLFGLDE  WSIADDHDL        0.1852        6739.6                  50.00     Sequence
DRB1_0401  423  TAPLIEAALKDALIE  PLIEAALKD        0.1848        6772.3                  50.00     Sequence
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DRB1_0401  260  RDPQSNLFAHRDRGF  RDPQSNLFA        0.1840        6828.2                  50.00     Sequence
DRB1_0401  258  SKRDPQSNLFAHRDR  RDPQSNLFA        0.1839        6837.0                  50.00     Sequence
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DRB1_0401  145  AYLAEGRQPVVRLRM  YLAEGRQPV        0.1803        7110.8                  50.00     Sequence
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DRB1_0401  259  KRDPQSNLFAHRDRG  RDPQSNLFA        0.1755        7485.9                  50.00     Sequence
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DRB1_0401  139  TDAQRAAYLAEGRQP  RAAYLAEGR        0.1744        7575.7                  50.00     Sequence
DRB1_0401  248  TVLGEGTKKLSKRDP  VLGEGTKKL        0.1739        7614.3                  50.00     Sequence
DRB1_0401  176  FAAGSVPDFALTRAS  SVPDFALTR        0.1719        7780.9                  50.00     Sequence
DRB1_0401  372  IVVLGDAWELLKFFN  VVLGDAWEL        0.1718        7794.4                  50.00     Sequence
DRB1_0401  424  APLIEAALKDALIEG  PLIEAALKD        0.1716        7807.3                  50.00     Sequence
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DRB1_0401  346  HLDTHGHHIALDEAA  HHIALDEAA        0.1705       7902.3                 50.00     Sequence
DRB1_0401  401  LGPDGAAVLDAALAA  AAVLDAALA        0.1700       7944.0                 50.00     Sequence
DRB1_0401  420  TDWTAPLIEAALKDA  PLIEAALKD        0.1669       8217.1                 50.00     Sequence
DRB1_0401  245  HLPTVLGEGTKKLSK  TVLGEGTKK        0.1609       8765.1                 50.00     Sequence
DRB1_0401  113  PEEVEARHVAAGRNP  EVEARHVAA        0.1595       8897.4                 50.00     Sequence
DRB1_0401  307  DVADVNSSPARFDQK  DVADVNSSP        0.1595       8904.0                 50.00     Sequence
DRB1_0401  313  SSPARFDQKKADALN  RFDQKKADA        0.1585       8998.1                 50.00     Sequence
DRB1_0401  400  ELGPDGAAVLDAALA  AAVLDAALA        0.1560       9246.3                 50.00     Sequence
DRB1_0401  356  LDEAAFAAAAELVQT  FAAAAELVQ        0.1527       9578.9                 50.00     Sequence
DRB1_0401  289  SIADDHDLFGLDEMV  SIADDHDLF        0.1521       9648.4                 50.00     Sequence
DRB1_0401  138  LTDAQRAAYLAEGRQ  RAAYLAEGR        0.1515       9708.8                 50.00     Sequence
DRB1_0401  244  AHLPTVLGEGTKKLS  TVLGEGTKK        0.1498       9889.0                 50.00     Sequence
DRB1_0401  355  ALDEAAFAAAAELVQ  ALDEAAFAA        0.1491       9965.0                 50.00     Sequence
DRB1_0401  321  KKADALNAEHIRMLD  KKADALNAE        0.1467      10229.7                 50.00     Sequence
DRB1_0401  144  AAYLAEGRQPVVRLR  YLAEGRQPV        0.1450      10416.1                 50.00     Sequence
DRB1_0401  312  NSSPARFDQKKADAL  PARFDQKKA        0.1446      10464.5                 50.00     Sequence
DRB1_0401  322  KADALNAEHIRMLDV  ALNAEHIRM        0.1436      10572.1                 50.00     Sequence
DRB1_0401  253  GTKKLSKRDPQSNLF  LSKRDPQSN        0.1433      10608.5                 50.00     Sequence
DRB1_0401  217  LLPSTPRQLALHQAL  PRQLALHQA        0.1423      10721.8                 50.00     Sequence
DRB1_0401  399  KELGPDGAAVLDAAL  KELGPDGAA        0.1418      10785.0                 50.00     Sequence
DRB1_0401  428  EAALKDALIEGLALK  DALIEGLAL        0.1416      10809.8                 50.00     Sequence
DRB1_0401  108  HAFSTPEEVEARHVA  HAFSTPEEV        0.1401      10975.5                 50.00     Sequence
DRB1_0401  261  DPQSNLFAHRDRGFI  LFAHRDRGF        0.1398      11022.5                 50.00     Sequence
DRB1_0401   13  SPTGTPHVGLVRTAL  PHVGLVRTA        0.1375      11294.0                 50.00     Sequence
DRB1_0401  249  VLGEGTKKLSKRDPQ  VLGEGTKKL        0.1369      11365.0                 50.00     Sequence
DRB1_0401  214  GEDLLPSTPRQLALH  EDLLPSTPR        0.1357      11520.1                 50.00     Sequence
DRB1_0401  120  HVAAGRNPKLGYDNF  VAAGRNPKL        0.1349      11614.2                 50.00     Sequence
DRB1_0401  215  EDLLPSTPRQLALHQ  EDLLPSTPR        0.1341      11716.6                 50.00     Sequence
DRB1_0401  343  LRDHLDTHGHHIALD  RDHLDTHGH        0.1324      11934.3                 50.00     Sequence
DRB1_0401   48  DAQRDSEESYLALLD  RDSEESYLA        0.1324      11937.4                 50.00     Sequence
DRB1_0401  398  AKELGPDGAAVLDAA  KELGPDGAA        0.1303      12203.3                 50.00     Sequence
DRB1_0401  112  TPEEVEARHVAAGRN  EVEARHVAA        0.1303      12208.7                 50.00     Sequence
DRB1_0401  427  IEAALKDALIEGLAL  EAALKDALI        0.1299      12266.5                 50.00     Sequence
DRB1_0401  121  VAAGRNPKLGYDNFD  VAAGRNPKL        0.1285      12450.6                 50.00     Sequence
DRB1_0401  453  AATGTTVSPPLFESL  AATGTTVSP        0.1240      13070.0                 50.00     Sequence
DRB1_0401  251  GEGTKKLSKRDPQSN  LSKRDPQSN        0.1238      13096.7                 50.00     Sequence
DRB1_0401  216  DLLPSTPRQLALHQA  DLLPSTPRQ        0.1233      13171.5                 50.00     Sequence
DRB1_0401  344  RDHLDTHGHHIALDE  DHLDTHGHH        0.1232      13180.9                 50.00     Sequence
DRB1_0401  426  LIEAALKDALIEGLA  EAALKDALI        0.1219      13378.0                 50.00     Sequence
DRB1_0401   43  RIEDTDAQRDSEESY  RIEDTDAQR        0.1214      13438.6                 50.00     Sequence
DRB1_0401  397  AAKELGPDGAAVLDA  KELGPDGAA        0.1208      13530.9                 50.00     Sequence
DRB1_0401  395  KAAAKELGPDGAAVL  KAAAKELGP        0.1177      13987.8                 50.00     Sequence
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DRB1_0401   47  TDAQRDSEESYLALL  RDSEESYLA        0.1157      14296.9                 50.00     Sequence
DRB1_0401   12  PSPTGTPHVGLVRTA  GTPHVGLVR        0.1147      14447.3                 50.00     Sequence
DRB1_0401   10  FCPSPTGTPHVGLVR  FCPSPTGTP        0.1135      14641.2                 50.00     Sequence
DRB1_0401  252  EGTKKLSKRDPQSNL  LSKRDPQSN        0.1107      15086.3                 50.00     Sequence
DRB1_0401  394  PKAAAKELGPDGAAV  KAAAKELGP        0.1080      15543.1                 50.00     Sequence
DRB1_0401  311  VNSSPARFDQKKADA  RFDQKKADA        0.1077      15583.3                 50.00     Sequence
DRB1_0401  110  FSTPEEVEARHVAAG  FSTPEEVEA        0.1075      15631.5                 50.00     Sequence
DRB1_0401  456  GTTVSPPLFESLELL  PLFESLELL        0.1067      15752.9                 50.00     Sequence
DRB1_0401  396  AAAKELGPDGAAVLD  KELGPDGAA        0.1047      16105.8                 50.00     Sequence
DRB1_0401  109  AFSTPEEVEARHVAA  FSTPEEVEA        0.1043      16180.4                 50.00     Sequence
DRB1_0401  250  LGEGTKKLSKRDPQS  GEGTKKLSK        0.1030      16410.7                 50.00     Sequence
DRB1_0401   46  DTDAQRDSEESYLAL  AQRDSEESY        0.1005      16854.4                 50.00     Sequence
DRB1_0401  111  STPEEVEARHVAAGR  EVEARHVAA        0.0994      17065.5                 50.00     Sequence
DRB1_0401   67  LGLDWDEGPEVGGPY  LGLDWDEGP        0.0977      17371.9                 50.00     Sequence
DRB1_0401  345  DHLDTHGHHIALDEA  GHHIALDEA        0.0945      17985.3                 50.00     Sequence
DRB1_0401  308  VADVNSSPARFDQKK  VADVNSSPA        0.0925      18378.1                 50.00     Sequence
DRB1_0401  393  DPKAAAKELGPDGAA  KAAAKELGP        0.0922      18428.9                 50.00     Sequence
DRB1_0401  310  DVNSSPARFDQKKAD  PARFDQKKA        0.0898      18929.9                 50.00     Sequence
DRB1_0401  309  ADVNSSPARFDQKKA  ADVNSSPAR        0.0857      19778.3                 50.00     Sequence
DRB1_0401   45  EDTDAQRDSEESYLA  DAQRDSEES        0.0838      20198.3                 50.00     Sequence
DRB1_0401   11  CPSPTGTPHVGLVRT  PTGTPHVGL        0.0833      20296.2                 50.00     Sequence
DRB1_0401  454  ATGTTVSPPLFESLE  ATGTTVSPP        0.0815      20708.5                 50.00     Sequence
DRB1_0401  455  TGTTVSPPLFESLEL  GTTVSPPLF        0.0799      21052.9                 50.00     Sequence
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   DRB1_0401   68  GLDWDEGPEVGGPYG  LDWDEGPEV        0.0797   21101.9               50.00     Sequence
   DRB1_0401   77  VGGPYGPYRQSQRAE  YGPYRQSQR        0.0779   21521.1               50.00     Sequence
   DRB1_0401  392  IDPKAAAKELGPDGA  KAAAKELGP        0.0754   22121.9               50.00     Sequence
   DRB1_0401   75  PEVGGPYGPYRQSQR  PEVGGPYGP        0.0698   23506.8               50.00     Sequence
   DRB1_0401   69  LDWDEGPEVGGPYGP  LDWDEGPEV        0.0694   23593.2               50.00     Sequence
   DRB1_0401  391  VIDPKAAAKELGPDG  VIDPKAAAK        0.0639   25055.0               50.00     Sequence
   DRB1_0401   74  GPEVGGPYGPYRQSQ  PEVGGPYGP        0.0636   25131.0               50.00     Sequence
   DRB1_0401   76  EVGGPYGPYRQSQRA  YGPYRQSQR        0.0633   25212.4               50.00     Sequence
   DRB1_0401   73  EGPEVGGPYGPYRQS  PEVGGPYGP        0.0599   26165.7               50.00     Sequence
   DRB1_0401   71  WDEGPEVGGPYGPYR  WDEGPEVGG        0.0585   26553.6               50.00     Sequence
   DRB1_0401   70  DWDEGPEVGGPYGPY  WDEGPEVGG        0.0543   27786.3               50.00     Sequence
   DRB1_0401   44  IEDTDAQRDSEESYL  DAQRDSEES        0.0522   28409.5               50.00     Sequence
   DRB1_0401   72  DEGPEVGGPYGPYRQ  PEVGGPYGP        0.0511   28750.8               50.00     Sequence
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Allele: DRB1_0401. Number of high binders 13. Number of weak binders 74. Number of peptides 476

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0404  410  DAALAALTSVTDWTA  AALAALTSV        0.7077      23.6         SB     4.00     Sequence
   DRB1_0404  409  LDAALAALTSVTDWT  AALAALTSV        0.6988      26.0         SB     4.00     Sequence
   DRB1_0404  411  AALAALTSVTDWTAP  AALAALTSV        0.6865      29.7         SB     4.00     Sequence
   DRB1_0404  408  VLDAALAALTSVTDW  AALAALTSV        0.6745      33.8         SB     4.00     Sequence
   DRB1_0404    5  TVRVRFCPSPTGTPH  RVRFCPSPT        0.6566      41.1         SB     8.00     Sequence
   DRB1_0404    4  ETVRVRFCPSPTGTP  RVRFCPSPT        0.6437      47.2         SB     8.00     Sequence
   DRB1_0404   55  ESYLALLDALRWLGL  SYLALLDAL        0.6416      48.3         SB     8.00     Sequence
   DRB1_0404   54  EESYLALLDALRWLG  SYLALLDAL        0.6312      54.1         WB     8.00     Sequence
   DRB1_0404  407  AVLDAALAALTSVTD  AALAALTSV        0.6306      54.4         WB     8.00     Sequence
   DRB1_0404   56  SYLALLDALRWLGLD  SYLALLDAL        0.6293      55.2         WB     8.00     Sequence
   DRB1_0404  328  AEHIRMLDVGDFTVR  HIRMLDVGD        0.6281      55.9         WB     8.00     Sequence
   DRB1_0404  327  NAEHIRMLDVGDFTV  HIRMLDVGD        0.6273      56.4         WB     8.00     Sequence
   DRB1_0404  281  NYLALLGWSIADDHD  ALLGWSIAD        0.6237      58.6         WB     8.00     Sequence
   DRB1_0404  282  YLALLGWSIADDHDL  ALLGWSIAD        0.6234      58.8         WB     8.00     Sequence
   DRB1_0404  277  EGLLNYLALLGWSIA  GLLNYLALL        0.6115      66.9         WB     8.00     Sequence
   DRB1_0404  191  GDPLYTLVNPCDDAL  PLYTLVNPC        0.6089      68.8         WB     8.00     Sequence
   DRB1_0404    6  VRVRFCPSPTGTPHV  RVRFCPSPT        0.6051      71.7         WB    16.00     Sequence
   DRB1_0404   53  SEESYLALLDALRWL  SYLALLDAL        0.6047      72.0         WB    16.00     Sequence
   DRB1_0404    3  TETVRVRFCPSPTGT  RVRFCPSPT        0.6035      73.0         WB    16.00     Sequence
   DRB1_0404  192  DPLYTLVNPCDDALM  PLYTLVNPC        0.6032      73.2         WB    16.00     Sequence
   DRB1_0404  329  EHIRMLDVGDFTVRL  HIRMLDVGD        0.6013      74.7         WB    16.00     Sequence
   DRB1_0404  278  GLLNYLALLGWSIAD  GLLNYLALL        0.5972      78.1         WB    16.00     Sequence
   DRB1_0404  190  SGDPLYTLVNPCDDA  PLYTLVNPC        0.5943      80.6         WB    16.00     Sequence
   DRB1_0404  300  DEMVAAFDVADVNSS  MVAAFDVAD        0.5937      81.1         WB    16.00     Sequence
   DRB1_0404  280  LNYLALLGWSIADDH  LALLGWSIA        0.5937      81.1         WB    16.00     Sequence
   DRB1_0404   94  RDVLARLLAAGEAYH  DVLARLLAA        0.5876      86.6         WB    16.00     Sequence
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   DRB1_0404  301  EMVAAFDVADVNSSP  MVAAFDVAD        0.5791      95.0         WB    16.00     Sequence
   DRB1_0404  202  DDALMKITHVLRGED  ALMKITHVL        0.5767      97.5         WB    16.00     Sequence
   DRB1_0404  203  DALMKITHVLRGEDL  ALMKITHVL        0.5751      99.2         WB    16.00     Sequence
   DRB1_0404  330  HIRMLDVGDFTVRLR  HIRMLDVGD        0.5737     100.7         WB    16.00     Sequence
   DRB1_0404  239  RIPKFAHLPTVLGEG  PKFAHLPTV        0.5736     100.8         WB    16.00     Sequence
   DRB1_0404  283  LALLGWSIADDHDLF  LALLGWSIA        0.5730     101.5         WB    16.00     Sequence
   DRB1_0404  299  LDEMVAAFDVADVNS  MVAAFDVAD        0.5725     102.0         WB    16.00     Sequence
   DRB1_0404  279  LLNYLALLGWSIADD  LALLGWSIA        0.5725     102.1         WB    16.00     Sequence
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   DRB1_0404  240  IPKFAHLPTVLGEGT  KFAHLPTVL        0.5685     106.6         WB    16.00     Sequence
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   DRB1_0404   93  YRDVLARLLAAGEAY  DVLARLLAA        0.5642     111.6         WB    16.00     Sequence
   DRB1_0404  241  PKFAHLPTVLGEGTK  KFAHLPTVL        0.5615     114.9         WB    16.00     Sequence
   DRB1_0404   52  DSEESYLALLDALRW  SYLALLDAL        0.5576     120.0         WB    16.00     Sequence
   DRB1_0404  193  PLYTLVNPCDDALMK  PLYTLVNPC        0.5572     120.4         WB    16.00     Sequence
   DRB1_0404  201  CDDALMKITHVLRGE  ALMKITHVL        0.5563     121.6         WB    16.00     Sequence
   DRB1_0404  275  IPEGLLNYLALLGWS  EGLLNYLAL        0.5541     124.5         WB    16.00     Sequence
   DRB1_0404  238  ERIPKFAHLPTVLGE  PKFAHLPTV        0.5512     128.5         WB    16.00     Sequence
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DRB1_0404  298  GLDEMVAAFDVADVN  MVAAFDVAD        0.5506        129.3         WB    16.00      Sequence
DRB1_0404  448  SPIRVAATGTTVSPP  RVAATGTTV        0.5500        130.2         WB    16.00      Sequence
DRB1_0404    2  ATETVRVRFCPSPTG  TVRVRFCPS        0.5476        133.6         WB    16.00      Sequence
DRB1_0404  378  AWELLKFFNDDQYVI  ELLKFFNDD        0.5474        133.9         WB    16.00      Sequence
DRB1_0404  449  PIRVAATGTTVSPPL  RVAATGTTV        0.5471        134.4         WB    16.00      Sequence
DRB1_0404  379  WELLKFFNDDQYVID  ELLKFFNDD        0.5470        134.5         WB    16.00      Sequence
DRB1_0404  406  AAVLDAALAALTSVT  AALAALTSV        0.5453        137.0         WB    16.00      Sequence
DRB1_0404  447  FSPIRVAATGTTVSP  IRVAATGTT        0.5443        138.5         WB    16.00      Sequence
DRB1_0404  274  FIPEGLLNYLALLGW  EGLLNYLAL        0.5377        148.8         WB    16.00      Sequence
DRB1_0404   92  IYRDVLARLLAAGEA  DVLARLLAA        0.5364        150.9         WB    16.00      Sequence
DRB1_0404  377  DAWELLKFFNDDQYV  ELLKFFNDD        0.5362        151.1         WB    16.00      Sequence
DRB1_0404  189  ASGDPLYTLVNPCDD  PLYTLVNPC        0.5356        152.2         WB    16.00      Sequence
DRB1_0404  370  TRIVVLGDAWELLKF  RIVVLGDAW        0.5347        153.6         WB    16.00      Sequence
DRB1_0404   19  HVGLVRTALFNWAYA  HVGLVRTAL        0.5300        161.6         WB    16.00      Sequence
DRB1_0404  369  QTRIVVLGDAWELLK  RIVVLGDAW        0.5291        163.2         WB    16.00      Sequence
DRB1_0404  366  ELVQTRIVVLGDAWE  ELVQTRIVV        0.5263        168.3         WB    16.00      Sequence
DRB1_0404   18  PHVGLVRTALFNWAY  HVGLVRTAL        0.5251        170.4         WB    16.00      Sequence
DRB1_0404    7  RVRFCPSPTGTPHVG  RVRFCPSPT        0.5244        171.6         WB    32.00      Sequence
DRB1_0404   38  GTFVFRIEDTDAQRD  FVFRIEDTD        0.5229        174.5         WB    32.00      Sequence
DRB1_0404  325  ALNAEHIRMLDVGDF  HIRMLDVGD        0.5215        177.2         WB    32.00      Sequence
DRB1_0404   17  TPHVGLVRTALFNWA  HVGLVRTAL        0.5211        178.0         WB    32.00      Sequence
DRB1_0404   39  TFVFRIEDTDAQRDS  FVFRIEDTD        0.5201        179.9         WB    32.00      Sequence
DRB1_0404  368  VQTRIVVLGDAWELL  RIVVLGDAW        0.5182        183.6         WB    32.00      Sequence
DRB1_0404   37  GGTFVFRIEDTDAQR  FVFRIEDTD        0.5163        187.5         WB    32.00      Sequence
DRB1_0404  297  FGLDEMVAAFDVADV  MVAAFDVAD        0.5157        188.6         WB    32.00      Sequence
DRB1_0404  412  ALAALTSVTDWTAPL  ALAALTSVT        0.5141        191.9         WB    32.00      Sequence
DRB1_0404  273  GFIPEGLLNYLALLG  EGLLNYLAL        0.5128        194.7         WB    32.00      Sequence
DRB1_0404  367  LVQTRIVVLGDAWEL  RIVVLGDAW        0.5119        196.6         WB    32.00      Sequence
DRB1_0404  200  PCDDALMKITHVLRG  DALMKITHV        0.5117        197.0         WB    32.00      Sequence
DRB1_0404   22  LVRTALFNWAYARHT  LVRTALFNW        0.5116        197.3         WB    32.00      Sequence
DRB1_0404  380  ELLKFFNDDQYVIDP  ELLKFFNDD        0.5108        199.0         WB    32.00      Sequence
DRB1_0404  446  AFSPIRVAATGTTVS  IRVAATGTT        0.5088        203.4         WB    32.00      Sequence
DRB1_0404   16  GTPHVGLVRTALFNW  HVGLVRTAL        0.5085        203.9         WB    32.00      Sequence
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DRB1_0404  450  IRVAATGTTVSPPLF  RVAATGTTV        0.5054        211.0         WB    32.00      Sequence
DRB1_0404   24  RTALFNWAYARHTGG  ALFNWAYAR        0.5042        213.7         WB    32.00      Sequence
DRB1_0404  302  MVAAFDVADVNSSPA  MVAAFDVAD        0.5012        220.7         WB    32.00      Sequence
DRB1_0404  204  ALMKITHVLRGEDLL  ALMKITHVL        0.4960        233.5         WB    32.00      Sequence
DRB1_0404  376  GDAWELLKFFNDDQY  ELLKFFNDD        0.4952        235.6         WB    32.00      Sequence
DRB1_0404   23  VRTALFNWAYARHTG  ALFNWAYAR        0.4943        237.7         WB    32.00      Sequence
DRB1_0404   25  TALFNWAYARHTGGT  ALFNWAYAR        0.4907        247.4         WB    32.00      Sequence
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DRB1_0404  365  AELVQTRIVVLGDAW  ELVQTRIVV        0.4880        254.7         WB    32.00      Sequence
DRB1_0404  371  RIVVLGDAWELLKFF  RIVVLGDAW        0.4823        270.7         WB    32.00      Sequence
DRB1_0404  223  RQLALHQALIRIGVA  RQLALHQAL        0.4822        271.1         WB    32.00      Sequence
DRB1_0404  152  QPVVRLRMPDDDLAW  RLRMPDDDL        0.4796        278.8         WB    32.00      Sequence
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DRB1_0404   51  RDSEESYLALLDALR  SYLALLDAL        0.4762        289.1         WB    32.00      Sequence
DRB1_0404  222  PRQLALHQALIRIGV  RQLALHQAL        0.4731        299.2         WB    32.00      Sequence
DRB1_0404   21  GLVRTALFNWAYARH  LVRTALFNW        0.4720        302.7         WB    32.00      Sequence
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DRB1_0404   36  TGGTFVFRIEDTDAQ  FVFRIEDTD        0.4679        316.3         WB    32.00      Sequence
DRB1_0404  445  KAFSPIRVAATGTTV  FSPIRVAAT        0.4669        320.1         WB    32.00      Sequence
DRB1_0404   40  FVFRIEDTDAQRDSE  FVFRIEDTD        0.4659        323.4         WB    32.00      Sequence
DRB1_0404  474  RSMQRLRAARQLVGH  RLRAARQLV        0.4650        326.6         WB    32.00      Sequence
DRB1_0404  364  AAELVQTRIVVLGDA  ELVQTRIVV        0.4617        338.6         WB    32.00      Sequence
DRB1_0404   15  TGTPHVGLVRTALFN  HVGLVRTAL        0.4598        345.3         WB    32.00      Sequence
DRB1_0404  284  ALLGWSIADDHDLFG  ALLGWSIAD        0.4593        347.2         WB    32.00      Sequence
DRB1_0404  151  RQPVVRLRMPDDDLA  RLRMPDDDL        0.4580        352.4         WB    32.00      Sequence
DRB1_0404  221  TPRQLALHQALIRIG  RQLALHQAL        0.4563        358.7         WB    32.00      Sequence
DRB1_0404  296  LFGLDEMVAAFDVAD  MVAAFDVAD        0.4560        360.1         WB    32.00      Sequence
DRB1_0404  242  KFAHLPTVLGEGTKK  KFAHLPTVL        0.4547        365.1         WB    32.00      Sequence
DRB1_0404    1  TATETVRVRFCPSPT  TVRVRFCPS        0.4544        366.1         WB    32.00      Sequence
DRB1_0404  475  SMQRLRAARQLVGHA  RLRAARQLV        0.4531        371.5         WB    32.00      Sequence
DRB1_0404   20  VGLVRTALFNWAYAR  LVRTALFNW        0.4514        378.2         WB    32.00      Sequence
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DRB1_0404  228  HQALIRIGVAERIPK  ALIRIGVAE        0.4492        387.5         WB    32.00     Sequence
DRB1_0404  229  QALIRIGVAERIPKF  ALIRIGVAE        0.4475        394.8         WB    32.00     Sequence
DRB1_0404  363  AAAELVQTRIVVLGD  ELVQTRIVV        0.4458        402.2         WB    32.00     Sequence
DRB1_0404  352  HHIALDEAAFAAAAE  HIALDEAAF        0.4456        402.8         WB    32.00     Sequence
DRB1_0404  473  DRSMQRLRAARQLVG  SMQRLRAAR        0.4453        404.1         WB    32.00     Sequence
DRB1_0404  207  KITHVLRGEDLLPST  HVLRGEDLL        0.4451        405.0         WB    32.00     Sequence
DRB1_0404  154  VVRLRMPDDDLAWND  RLRMPDDDL        0.4450        405.6         WB    32.00     Sequence
DRB1_0404   89  RAEIYRDVLARLLAA  DVLARLLAA        0.4420        418.8         WB    32.00     Sequence
DRB1_0404  351  GHHIALDEAAFAAAA  HIALDEAAF        0.4416        420.6         WB    32.00     Sequence
DRB1_0404  199  NPCDDALMKITHVLR  DALMKITHV        0.4410        423.2         WB    32.00     Sequence
DRB1_0404  205  LMKITHVLRGEDLLP  LMKITHVLR        0.4392        431.9         WB    32.00     Sequence
DRB1_0404  405  GAAVLDAALAALTSV  AAVLDAALA        0.4376        439.4         WB    32.00     Sequence
DRB1_0404  324  DALNAEHIRMLDVGD  HIRMLDVGD        0.4375        439.8         WB    32.00     Sequence
DRB1_0404  413  LAALTSVTDWTAPLI  LAALTSVTD        0.4370        441.9         WB    32.00     Sequence
DRB1_0404   26  ALFNWAYARHTGGTF  ALFNWAYAR        0.4360        446.9         WB    32.00     Sequence
DRB1_0404  209  THVLRGEDLLPSTPR  HVLRGEDLL        0.4352        450.7         WB    32.00     Sequence
DRB1_0404  208  ITHVLRGEDLLPSTP  HVLRGEDLL        0.4324        464.8         WB    32.00     Sequence
DRB1_0404   62  DALRWLGLDWDEGPE  RWLGLDWDE        0.4292        481.0         WB    32.00     Sequence
DRB1_0404  295  DLFGLDEMVAAFDVA  DLFGLDEMV        0.4292        481.1         WB    32.00     Sequence
DRB1_0404  220  STPRQLALHQALIRI  RQLALHQAL        0.4290        482.3         WB    32.00     Sequence
DRB1_0404  227  LHQALIRIGVAERIP  ALIRIGVAE        0.4284        485.0         WB    32.00     Sequence
DRB1_0404  272  RGFIPEGLLNYLALL  FIPEGLLNY        0.4283        485.5         WB    32.00     Sequence
DRB1_0404  444  RKAFSPIRVAATGTT  FSPIRVAAT        0.4279        487.8         WB    32.00     Sequence
DRB1_0404  155  VRLRMPDDDLAWNDL  RLRMPDDDL        0.4278        488.4         WB    32.00     Sequence
DRB1_0404   57  YLALLDALRWLGLDW  YLALLDALR        0.4277        488.7         WB    32.00     Sequence
DRB1_0404   61  LDALRWLGLDWDEGP  DALRWLGLD        0.4271        492.1         WB    32.00     Sequence
DRB1_0404   96  VLARLLAAGEAYHAF  VLARLLAAG        0.4264        495.6         WB    32.00     Sequence
DRB1_0404  375  LGDAWELLKFFNDDQ  ELLKFFNDD        0.4250        503.5               32.00     Sequence
DRB1_0404  156  RLRMPDDDLAWNDLV  RLRMPDDDL        0.4248        504.4               32.00     Sequence
DRB1_0404  350  HGHHIALDEAAFAAA  HIALDEAAF        0.4235        511.8               32.00     Sequence
DRB1_0404  226  ALHQALIRIGVAERI  ALIRIGVAE        0.4227        515.9               32.00     Sequence
DRB1_0404  150  GRQPVVRLRMPDDDL  PVVRLRMPD        0.4212        524.7               32.00     Sequence
DRB1_0404  210  HVLRGEDLLPSTPRQ  HVLRGEDLL        0.4207        527.5               32.00     Sequence
DRB1_0404  294  HDLFGLDEMVAAFDV  DLFGLDEMV        0.4197        532.9               32.00     Sequence
DRB1_0404  451  RVAATGTTVSPPLFE  RVAATGTTV        0.4177        544.7               32.00     Sequence
DRB1_0404  206  MKITHVLRGEDLLPS  HVLRGEDLL        0.4170        549.0               32.00     Sequence
DRB1_0404  167  NDLVRGPVTFAAGSV  DLVRGPVTF        0.4137        568.9               32.00     Sequence
DRB1_0404  166  WNDLVRGPVTFAAGS  DLVRGPVTF        0.4136        569.4               32.00     Sequence
DRB1_0404  230  ALIRIGVAERIPKFA  ALIRIGVAE        0.4117        581.5               32.00     Sequence
DRB1_0404   60  LLDALRWLGLDWDEG  ALRWLGLDW        0.4090        598.6               32.00     Sequence
DRB1_0404  293  DHDLFGLDEMVAAFD  DLFGLDEMV        0.4084        602.5               32.00     Sequence
DRB1_0404  225  LALHQALIRIGVAER  ALIRIGVAE        0.4083        603.0               32.00     Sequence
DRB1_0404  362  AAAAELVQTRIVVLG  ELVQTRIVV        0.4079        605.7               32.00     Sequence
DRB1_0404  459  VSPPLFESLELLGRD  PLFESLELL        0.4058        619.7               50.00     Sequence
DRB1_0404  443  PRKAFSPIRVAATGT  AFSPIRVAA        0.4051        624.0               50.00     Sequence
DRB1_0404   35  HTGGTFVFRIEDTDA  FVFRIEDTD        0.4031        637.8               50.00     Sequence
DRB1_0404  442  KPRKAFSPIRVAATG  FSPIRVAAT        0.4018        647.2               50.00     Sequence
DRB1_0404  168  DLVRGPVTFAAGSVP  DLVRGPVTF        0.4007        655.1               50.00     Sequence
DRB1_0404  165  AWNDLVRGPVTFAAG  DLVRGPVTF        0.3992        665.6               50.00     Sequence
DRB1_0404   63  ALRWLGLDWDEGPEV  RWLGLDWDE        0.3982        672.7               50.00     Sequence
DRB1_0404  472  RDRSMQRLRAARQLV  SMQRLRAAR        0.3943        701.6               50.00     Sequence
DRB1_0404   14  PTGTPHVGLVRTALF  HVGLVRTAL        0.3942        702.3               50.00     Sequence
DRB1_0404  466  SLELLGRDRSMQRLR  ELLGRDRSM        0.3932        710.3               50.00     Sequence
DRB1_0404  460  SPPLFESLELLGRDR  PLFESLELL        0.3899        736.1               50.00     Sequence
DRB1_0404    8  VRFCPSPTGTPHVGL  VRFCPSPTG        0.3888        744.6               50.00     Sequence
DRB1_0404  338  DFTVRLRDHLDTHGH  FTVRLRDHL        0.3872        757.6               50.00     Sequence
DRB1_0404  339  FTVRLRDHLDTHGHH  FTVRLRDHL        0.3847        778.9               50.00     Sequence
DRB1_0404  303  VAAFDVADVNSSPAR  FDVADVNSS        0.3846        779.8               50.00     Sequence
DRB1_0404  462  PLFESLELLGRDRSM  PLFESLELL        0.3827        795.5               50.00     Sequence
DRB1_0404  458  TVSPPLFESLELLGR  PLFESLELL        0.3821        800.6               50.00     Sequence
DRB1_0404  292  DDHDLFGLDEMVAAF  DLFGLDEMV        0.3813        807.6               50.00     Sequence
DRB1_0404  224  QLALHQALIRIGVAE  LALHQALIR        0.3807        812.6               50.00     Sequence
DRB1_0404  349  THGHHIALDEAAFAA  HHIALDEAA        0.3806        813.6               50.00     Sequence
DRB1_0404  415  ALTSVTDWTAPLIEA  SVTDWTAPL        0.3805        815.1               50.00     Sequence
DRB1_0404  236  VAERIPKFAHLPTVL  PKFAHLPTV        0.3796        822.7               50.00     Sequence
DRB1_0404  194  LYTLVNPCDDALMKI  TLVNPCDDA        0.3793        825.0               50.00     Sequence
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DRB1_0404  461  PPLFESLELLGRDRS  PLFESLELL        0.3770       846.5                 50.00     Sequence
DRB1_0404  441  LKPRKAFSPIRVAAT  KPRKAFSPI        0.3767       849.2                 50.00     Sequence
DRB1_0404  187  TRASGDPLYTLVNPC  PLYTLVNPC        0.3758       857.2                 50.00     Sequence
DRB1_0404  197  LVNPCDDALMKITHV  LVNPCDDAL        0.3751       863.4                 50.00     Sequence
DRB1_0404   59  ALLDALRWLGLDWDE  DALRWLGLD        0.3751       863.5                 50.00     Sequence
DRB1_0404  467  LELLGRDRSMQRLRA  ELLGRDRSM        0.3747       867.4                 50.00     Sequence
DRB1_0404  465  ESLELLGRDRSMQRL  ELLGRDRSM        0.3730       883.8                 50.00     Sequence
DRB1_0404   88  QRAEIYRDVLARLLA  EIYRDVLAR        0.3730       883.9                 50.00     Sequence
DRB1_0404   97  LARLLAAGEAYHAFS  RLLAAGEAY        0.3729       884.1                 50.00     Sequence
DRB1_0404  305  AFDVADVNSSPARFD  FDVADVNSS        0.3713       899.5                 50.00     Sequence
DRB1_0404  337  GDFTVRLRDHLDTHG  FTVRLRDHL        0.3699       913.4                 50.00     Sequence
DRB1_0404  271  DRGFIPEGLLNYLAL  FIPEGLLNY        0.3678       934.7                 50.00     Sequence
DRB1_0404  304  AAFDVADVNSSPARF  FDVADVNSS        0.3676       936.3                 50.00     Sequence
DRB1_0404  219  PSTPRQLALHQALIR  RQLALHQAL        0.3661       952.1                 50.00     Sequence
DRB1_0404  414  AALTSVTDWTAPLIE  SVTDWTAPL        0.3661       952.6                 50.00     Sequence
DRB1_0404  416  LTSVTDWTAPLIEAA  SVTDWTAPL        0.3659       953.7                 50.00     Sequence
DRB1_0404  404  DGAAVLDAALAALTS  VLDAALAAL        0.3641       972.7                 50.00     Sequence
DRB1_0404  463  LFESLELLGRDRSMQ  ELLGRDRSM        0.3639       975.1                 50.00     Sequence
DRB1_0404  468  ELLGRDRSMQRLRAA  ELLGRDRSM        0.3631       983.3                 50.00     Sequence
DRB1_0404  464  FESLELLGRDRSMQR  ELLGRDRSM        0.3617       998.8                 50.00     Sequence
DRB1_0404  198  VNPCDDALMKITHVL  DALMKITHV        0.3611      1004.5                 50.00     Sequence
DRB1_0404  195  YTLVNPCDDALMKIT  LVNPCDDAL        0.3609      1006.8                 50.00     Sequence
DRB1_0404  104  GEAYHAFSTPEEVEA  AYHAFSTPE        0.3601      1016.4                 50.00     Sequence
DRB1_0404  164  LAWNDLVRGPVTFAA  DLVRGPVTF        0.3592      1026.4                 50.00     Sequence
DRB1_0404  417  TSVTDWTAPLIEAAL  SVTDWTAPL        0.3573      1047.2                 50.00     Sequence
DRB1_0404  306  FDVADVNSSPARFDQ  FDVADVNSS        0.3564      1057.9                 50.00     Sequence
DRB1_0404  103  AGEAYHAFSTPEEVE  AYHAFSTPE        0.3560      1062.4                 50.00     Sequence
DRB1_0404   34  RHTGGTFVFRIEDTD  FVFRIEDTD        0.3559      1062.7                 50.00     Sequence
DRB1_0404  353  HIALDEAAFAAAAEL  HIALDEAAF        0.3559      1063.2                 50.00     Sequence
DRB1_0404  374  VLGDAWELLKFFNDD  ELLKFFNDD        0.3537      1088.9                 50.00     Sequence
DRB1_0404  361  FAAAAELVQTRIVVL  ELVQTRIVV        0.3531      1095.7                 50.00     Sequence
DRB1_0404   64  LRWLGLDWDEGPEVG  WLGLDWDEG        0.3517      1112.1                 50.00     Sequence
DRB1_0404  196  TLVNPCDDALMKITH  LVNPCDDAL        0.3505      1127.0                 50.00     Sequence
DRB1_0404  336  VGDFTVRLRDHLDTH  FTVRLRDHL        0.3471      1169.9                 50.00     Sequence
DRB1_0404  105  EAYHAFSTPEEVEAR  AYHAFSTPE        0.3469      1171.5                 50.00     Sequence
DRB1_0404  372  IVVLGDAWELLKFFN  IVVLGDAWE        0.3435      1216.5                 50.00     Sequence
DRB1_0404   99  RLLAAGEAYHAFSTP  RLLAAGEAY        0.3431      1220.5                 50.00     Sequence
DRB1_0404   87  SQRAEIYRDVLARLL  EIYRDVLAR        0.3394      1270.8                 50.00     Sequence
DRB1_0404  403  PDGAAVLDAALAALT  AAVLDAALA        0.3368      1307.9                 50.00     Sequence
DRB1_0404    0  VTATETVRVRFCPSP  TVRVRFCPS        0.3341      1346.3                 50.00     Sequence
DRB1_0404  471  GRDRSMQRLRAARQL  SMQRLRAAR        0.3333      1357.3                 50.00     Sequence
DRB1_0404  149  EGRQPVVRLRMPDDD  PVVRLRMPD        0.3330      1361.5                 50.00     Sequence
DRB1_0404  291  ADDHDLFGLDEMVAA  DLFGLDEMV        0.3324      1370.6                 50.00     Sequence
DRB1_0404   27  LFNWAYARHTGGTFV  LFNWAYARH        0.3275      1445.5                 50.00     Sequence
DRB1_0404  439  LALKPRKAFSPIRVA  LALKPRKAF        0.3274      1446.8                 50.00     Sequence
DRB1_0404  173  PVTFAAGSVPDFALT  TFAAGSVPD        0.3273      1449.2                 50.00     Sequence
DRB1_0404   58  LALLDALRWLGLDWD  DALRWLGLD        0.3269      1455.0                 50.00     Sequence
DRB1_0404  331  IRMLDVGDFTVRLRD  IRMLDVGDF        0.3265      1461.5                 50.00     Sequence
DRB1_0404   98  ARLLAAGEAYHAFST  RLLAAGEAY        0.3264      1463.0                 50.00     Sequence
DRB1_0404   50  QRDSEESYLALLDAL  SYLALLDAL        0.3236      1507.8                 50.00     Sequence
DRB1_0404  102  AAGEAYHAFSTPEEV  AYHAFSTPE        0.3197      1572.8                 50.00     Sequence
DRB1_0404  425  PLIEAALKDALIEGL  LIEAALKDA        0.3195      1576.9                 50.00     Sequence
DRB1_0404  163  DLAWNDLVRGPVTFA  DLVRGPVTF        0.3181      1600.0                 50.00     Sequence
DRB1_0404  433  DALIEGLALKPRKAF  LIEGLALKP        0.3168      1623.1                 50.00     Sequence
DRB1_0404    9  RFCPSPTGTPHVGLV  RFCPSPTGT        0.3137      1677.6                 50.00     Sequence
DRB1_0404  235  GVAERIPKFAHLPTV  PKFAHLPTV        0.3134      1683.0                 50.00     Sequence
DRB1_0404  423  TAPLIEAALKDALIE  IEAALKDAL        0.3128      1695.1                 50.00     Sequence
DRB1_0404  348  DTHGHHIALDEAAFA  HHIALDEAA        0.3123      1704.0                 50.00     Sequence
DRB1_0404  426  LIEAALKDALIEGLA  LIEAALKDA        0.3120      1710.2                 50.00     Sequence
DRB1_0404  180  SVPDFALTRASGDPL  DFALTRASG        0.3117      1714.3                 50.00     Sequence
DRB1_0404  172  GPVTFAAGSVPDFAL  TFAAGSVPD        0.3108      1731.2                 50.00     Sequence
DRB1_0404   65  RWLGLDWDEGPEVGG  WLGLDWDEG        0.3108      1731.9                 50.00     Sequence
DRB1_0404   86  QSQRAEIYRDVLARL  RAEIYRDVL        0.3087      1772.4                 50.00     Sequence
DRB1_0404  182  PDFALTRASGDPLYT  FALTRASGD        0.3085      1775.7                 50.00     Sequence
DRB1_0404  183  DFALTRASGDPLYTL  FALTRASGD        0.3085      1775.8                 50.00     Sequence
DRB1_0404  438  GLALKPRKAFSPIRV  LALKPRKAF        0.3059      1826.1                 50.00     Sequence
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DRB1_0404  424  APLIEAALKDALIEG  LIEAALKDA        0.3050       1844.6              50.00     Sequence
DRB1_0404  457  TTVSPPLFESLELLG  PLFESLELL        0.3042       1860.5              50.00     Sequence
DRB1_0404  418  SVTDWTAPLIEAALK  SVTDWTAPL        0.3039       1866.7              50.00     Sequence
DRB1_0404  360  AFAAAAELVQTRIVV  ELVQTRIVV        0.3032       1879.9              50.00     Sequence
DRB1_0404  181  VPDFALTRASGDPLY  FALTRASGD        0.3032       1880.4              50.00     Sequence
DRB1_0404  440  ALKPRKAFSPIRVAA  KPRKAFSPI        0.3031       1882.7              50.00     Sequence
DRB1_0404  174  VTFAAGSVPDFALTR  TFAAGSVPD        0.3030       1884.2              50.00     Sequence
DRB1_0404  381  LLKFFNDDQYVIDPK  LLKFFNDDQ        0.3027       1890.4              50.00     Sequence
DRB1_0404   13  SPTGTPHVGLVRTAL  HVGLVRTAL        0.3013       1919.0              50.00     Sequence
DRB1_0404  171  RGPVTFAAGSVPDFA  TFAAGSVPD        0.3011       1923.8              50.00     Sequence
DRB1_0404  335  DVGDFTVRLRDHLDT  FTVRLRDHL        0.3004       1937.9              50.00     Sequence
DRB1_0404  243  FAHLPTVLGEGTKKL  FAHLPTVLG        0.2972       2006.1              50.00     Sequence
DRB1_0404  179  GSVPDFALTRASGDP  DFALTRASG        0.2960       2033.5              50.00     Sequence
DRB1_0404  452  VAATGTTVSPPLFES  VAATGTTVS        0.2955       2043.5              50.00     Sequence
DRB1_0404  211  VLRGEDLLPSTPRQL  VLRGEDLLP        0.2936       2086.2              50.00     Sequence
DRB1_0404  270  RDRGFIPEGLLNYLA  FIPEGLLNY        0.2936       2087.0              50.00     Sequence
DRB1_0404  231  LIRIGVAERIPKFAH  LIRIGVAER        0.2931       2097.0              50.00     Sequence
DRB1_0404  402  GPDGAAVLDAALAAL  AAVLDAALA        0.2916       2131.6              50.00     Sequence
DRB1_0404   41  VFRIEDTDAQRDSEE  FRIEDTDAQ        0.2914       2136.5              50.00     Sequence
DRB1_0404  431  LKDALIEGLALKPRK  DALIEGLAL        0.2882       2212.4              50.00     Sequence
DRB1_0404  432  KDALIEGLALKPRKA  DALIEGLAL        0.2878       2221.7              50.00     Sequence
DRB1_0404  217  LLPSTPRQLALHQAL  LLPSTPRQL        0.2871       2238.7              50.00     Sequence
DRB1_0404  470  LGRDRSMQRLRAARQ  SMQRLRAAR        0.2846       2299.1              50.00     Sequence
DRB1_0404  148  AEGRQPVVRLRMPDD  PVVRLRMPD        0.2839       2317.8              50.00     Sequence
DRB1_0404  184  FALTRASGDPLYTLV  FALTRASGD        0.2827       2347.1              50.00     Sequence
DRB1_0404  218  LPSTPRQLALHQALI  RQLALHQAL        0.2826       2350.6              50.00     Sequence
DRB1_0404  422  WTAPLIEAALKDALI  TAPLIEAAL        0.2822       2360.2              50.00     Sequence
DRB1_0404  106  AYHAFSTPEEVEARH  AYHAFSTPE        0.2793       2435.6              50.00     Sequence
DRB1_0404  469  LLGRDRSMQRLRAAR  RSMQRLRAA        0.2768       2502.2              50.00     Sequence
DRB1_0404  334  LDVGDFTVRLRDHLD  FTVRLRDHL        0.2739       2580.6              50.00     Sequence
DRB1_0404  101  LAAGEAYHAFSTPEE  AYHAFSTPE        0.2736       2590.2              50.00     Sequence
DRB1_0404  212  LRGEDLLPSTPRQLA  LLPSTPRQL        0.2733       2598.3              50.00     Sequence
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DRB1_0404  175  TFAAGSVPDFALTRA  TFAAGSVPD        0.2731       2604.6              50.00     Sequence
DRB1_0404  178  AGSVPDFALTRASGD  SVPDFALTR        0.2726       2618.6              50.00     Sequence
DRB1_0404  169  LVRGPVTFAAGSVPD  LVRGPVTFA        0.2697       2701.8              50.00     Sequence
DRB1_0404  290  IADDHDLFGLDEMVA  DLFGLDEMV        0.2693       2714.8              50.00     Sequence
DRB1_0404  332  RMLDVGDFTVRLRDH  RMLDVGDFT        0.2690       2721.0              50.00     Sequence
DRB1_0404  434  ALIEGLALKPRKAFS  LIEGLALKP        0.2678       2756.9              50.00     Sequence
DRB1_0404  435  LIEGLALKPRKAFSP  LIEGLALKP        0.2665       2795.7              50.00     Sequence
DRB1_0404  427  IEAALKDALIEGLAL  IEAALKDAL        0.2664       2798.5              50.00     Sequence
DRB1_0404  430  ALKDALIEGLALKPR  DALIEGLAL        0.2662       2807.0              50.00     Sequence
DRB1_0404  186  LTRASGDPLYTLVNP  LTRASGDPL        0.2661       2809.9              50.00     Sequence
DRB1_0404  437  EGLALKPRKAFSPIR  LALKPRKAF        0.2646       2855.6              50.00     Sequence
DRB1_0404  373  VVLGDAWELLKFFND  VVLGDAWEL        0.2644       2861.0              50.00     Sequence
DRB1_0404  100  LLAAGEAYHAFSTPE  AYHAFSTPE        0.2639       2878.0              50.00     Sequence
DRB1_0404   85  RQSQRAEIYRDVLAR  RAEIYRDVL        0.2626       2918.0              50.00     Sequence
DRB1_0404  118  ARHVAAGRNPKLGYD  HVAAGRNPK        0.2612       2961.1              50.00     Sequence
DRB1_0404  119  RHVAAGRNPKLGYDN  HVAAGRNPK        0.2610       2969.6              50.00     Sequence
DRB1_0404  340  TVRLRDHLDTHGHHI  RLRDHLDTH        0.2593       3023.6              50.00     Sequence
DRB1_0404  170  VRGPVTFAAGSVPDF  PVTFAAGSV        0.2591       3030.0              50.00     Sequence
DRB1_0404  333  MLDVGDFTVRLRDHL  FTVRLRDHL        0.2578       3072.0              50.00     Sequence
DRB1_0404  269  HRDRGFIPEGLLNYL  FIPEGLLNY        0.2571       3098.0              50.00     Sequence
DRB1_0404  382  LKFFNDDQYVIDPKA  LKFFNDDQY        0.2546       3181.9              50.00     Sequence
DRB1_0404  285  LLGWSIADDHDLFGL  LLGWSIADD        0.2535       3219.9              50.00     Sequence
DRB1_0404  117  EARHVAAGRNPKLGY  HVAAGRNPK        0.2531       3233.3              50.00     Sequence
DRB1_0404   28  FNWAYARHTGGTFVF  FNWAYARHT        0.2513       3297.4              50.00     Sequence
DRB1_0404   42  FRIEDTDAQRDSEES  FRIEDTDAQ        0.2503       3334.2              50.00     Sequence
DRB1_0404  421  DWTAPLIEAALKDAL  TAPLIEAAL        0.2488       3387.8              50.00     Sequence
DRB1_0404  234  IGVAERIPKFAHLPT  RIPKFAHLP        0.2472       3446.7              50.00     Sequence
DRB1_0404  214  GEDLLPSTPRQLALH  LLPSTPRQL        0.2428       3614.1              50.00     Sequence
DRB1_0404  120  HVAAGRNPKLGYDNF  HVAAGRNPK        0.2425       3625.2              50.00     Sequence
DRB1_0404  213  RGEDLLPSTPRQLAL  LLPSTPRQL        0.2413       3675.3              50.00     Sequence
DRB1_0404  341  VRLRDHLDTHGHHIA  RLRDHLDTH        0.2394       3750.2              50.00     Sequence
DRB1_0404  436  IEGLALKPRKAFSPI  LALKPRKAF        0.2374       3831.0              50.00     Sequence
DRB1_0404  429  AALKDALIEGLALKP  LKDALIEGL        0.2367       3860.7              50.00     Sequence
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DRB1_0404  455  TGTTVSPPLFESLEL  TGTTVSPPL        0.2360       3888.5                 50.00     Sequence
DRB1_0404  347  LDTHGHHIALDEAAF  HIALDEAAF        0.2360       3892.0                 50.00     Sequence
DRB1_0404  215  EDLLPSTPRQLALHQ  LLPSTPRQL        0.2334       4003.0                 50.00     Sequence
DRB1_0404  456  GTTVSPPLFESLELL  PLFESLELL        0.2333       4006.5                 50.00     Sequence
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DRB1_0404  233  RIGVAERIPKFAHLP  IGVAERIPK        0.2287       4210.6                 50.00     Sequence
DRB1_0404  147  LAEGRQPVVRLRMPD  PVVRLRMPD        0.2275       4263.7                 50.00     Sequence
DRB1_0404  126  NPKLGYDNFDRHLTD  NPKLGYDNF        0.2273       4273.9                 50.00     Sequence
DRB1_0404  428  EAALKDALIEGLALK  LKDALIEGL        0.2250       4381.1                 50.00     Sequence
DRB1_0404  185  ALTRASGDPLYTLVN  LTRASGDPL        0.2242       4419.6                 50.00     Sequence
DRB1_0404  216  DLLPSTPRQLALHQA  LLPSTPRQL        0.2211       4571.1                 50.00     Sequence
DRB1_0404  124  GRNPKLGYDNFDRHL  NPKLGYDNF        0.2184       4707.7                 50.00     Sequence
DRB1_0404  116  VEARHVAAGRNPKLG  HVAAGRNPK        0.2181       4723.7                 50.00     Sequence
DRB1_0404   66  WLGLDWDEGPEVGGP  WLGLDWDEG        0.2169       4782.0                 50.00     Sequence
DRB1_0404  453  AATGTTVSPPLFESL  TGTTVSPPL        0.2158       4840.4                 50.00     Sequence
DRB1_0404  420  TDWTAPLIEAALKDA  TAPLIEAAL        0.2157       4844.5                 50.00     Sequence
DRB1_0404  286  LGWSIADDHDLFGLD  WSIADDHDL        0.2128       5002.4                 50.00     Sequence
DRB1_0404  323  ADALNAEHIRMLDVG  EHIRMLDVG        0.2122       5034.7                 50.00     Sequence
DRB1_0404  388  DQYVIDPKAAAKELG  QYVIDPKAA        0.2118       5055.5                 50.00     Sequence
DRB1_0404  401  LGPDGAAVLDAALAA  AAVLDAALA        0.2116       5066.6                 50.00     Sequence
DRB1_0404  146  YLAEGRQPVVRLRMP  YLAEGRQPV        0.2116       5066.7                 50.00     Sequence
DRB1_0404  389  QYVIDPKAAAKELGP  QYVIDPKAA        0.2111       5094.7                 50.00     Sequence
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DRB1_0404  419  VTDWTAPLIEAALKD  TAPLIEAAL        0.1965       5967.7                 50.00     Sequence
DRB1_0404  342  RLRDHLDTHGHHIAL  RLRDHLDTH        0.1960       5999.7                 50.00     Sequence
DRB1_0404  143  RAAYLAEGRQPVVRL  YLAEGRQPV        0.1946       6087.0                 50.00     Sequence
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DRB1_0404  142  QRAAYLAEGRQPVVR  YLAEGRQPV        0.1862       6668.5                 50.00     Sequence
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DRB1_0404   30  WAYARHTGGTFVFRI  YARHTGGTF        0.1741       7602.1                 50.00     Sequence
DRB1_0404  357  DEAAFAAAAELVQTR  AAFAAAAEL        0.1712       7843.4                 50.00     Sequence
DRB1_0404  121  VAAGRNPKLGYDNFD  NPKLGYDNF        0.1707       7889.6                 50.00     Sequence
DRB1_0404   33  ARHTGGTFVFRIEDT  TFVFRIEDT        0.1702       7927.2                 50.00     Sequence
DRB1_0404  245  HLPTVLGEGTKKLSK  HLPTVLGEG        0.1701       7934.9                 50.00     Sequence
DRB1_0404  134  FDRHLTDAQRAAYLA  FDRHLTDAQ        0.1699       7952.2                 50.00     Sequence
DRB1_0404  160  PDDDLAWNDLVRGPV  DDLAWNDLV        0.1699       7957.6                 50.00     Sequence
DRB1_0404  256  KLSKRDPQSNLFAHR  KRDPQSNLF        0.1693       8006.3                 50.00     Sequence
DRB1_0404  244  AHLPTVLGEGTKKLS  HLPTVLGEG        0.1686       8064.7                 50.00     Sequence
DRB1_0404  140  DAQRAAYLAEGRQPV  QRAAYLAEG        0.1682       8106.2                 50.00     Sequence
DRB1_0404   32  YARHTGGTFVFRIED  YARHTGGTF        0.1674       8175.6                 50.00     Sequence
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DRB1_0404  383  KFFNDDQYVIDPKAA  KFFNDDQYV        0.1674       8176.7                 50.00     Sequence
DRB1_0404  127  PKLGYDNFDRHLTDA  PKLGYDNFD        0.1662       8276.7                 50.00     Sequence
DRB1_0404  385  FNDDQYVIDPKAAAK  QYVIDPKAA        0.1654       8348.3                 50.00     Sequence
DRB1_0404  122  AAGRNPKLGYDNFDR  NPKLGYDNF        0.1638       8497.3                 50.00     Sequence
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DRB1_0404  257  LSKRDPQSNLFAHRD  KRDPQSNLF        0.1638      8500.0              50.00     Sequence
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DRB1_0404  354  IALDEAAFAAAAELV  IALDEAAFA        0.1636      8518.5              50.00     Sequence
DRB1_0404   31  AYARHTGGTFVFRIE  YARHTGGTF        0.1622      8643.9              50.00     Sequence
DRB1_0404  254  TKKLSKRDPQSNLFA  KKLSKRDPQ        0.1597      8883.8              50.00     Sequence
DRB1_0404  131  YDNFDRHLTDAQRAA  FDRHLTDAQ        0.1579      9053.7              50.00     Sequence
DRB1_0404   49  AQRDSEESYLALLDA  SEESYLALL        0.1566      9186.3              50.00     Sequence
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DRB1_0404  356  LDEAAFAAAAELVQT  AAFAAAAEL        0.1545      9398.9              50.00     Sequence
DRB1_0404  346  HLDTHGHHIALDEAA  HHIALDEAA        0.1526      9595.2              50.00     Sequence
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DRB1_0404  107  YHAFSTPEEVEARHV  HAFSTPEEV        0.1472     10163.7              50.00     Sequence
DRB1_0404  322  KADALNAEHIRMLDV  KADALNAEH        0.1436     10575.9              50.00     Sequence
DRB1_0404  159  MPDDDLAWNDLVRGP  DDLAWNDLV        0.1434     10593.1              50.00     Sequence
DRB1_0404  253  GTKKLSKRDPQSNLF  KLSKRDPQS        0.1431     10631.7              50.00     Sequence
DRB1_0404  128  KLGYDNFDRHLTDAQ  KLGYDNFDR        0.1428     10663.5              50.00     Sequence
DRB1_0404  390  YVIDPKAAAKELGPD  YVIDPKAAA        0.1424     10713.8              50.00     Sequence
DRB1_0404  139  TDAQRAAYLAEGRQP  RAAYLAEGR        0.1399     11001.8              50.00     Sequence
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DRB1_0404  135  DRHLTDAQRAAYLAE  RHLTDAQRA        0.1337     11764.6              50.00     Sequence
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DRB1_0404  158  RMPDDDLAWNDLVRG  RMPDDDLAW        0.1320     11982.3              50.00     Sequence
DRB1_0404   83  PYRQSQRAEIYRDVL  RAEIYRDVL        0.1319     12002.7              50.00     Sequence
DRB1_0404  108  HAFSTPEEVEARHVA  HAFSTPEEV        0.1310     12115.0              50.00     Sequence
DRB1_0404  138  LTDAQRAAYLAEGRQ  RAAYLAEGR        0.1268     12677.9              50.00     Sequence
DRB1_0404  265  NLFAHRDRGFIPEGL  LFAHRDRGF        0.1259     12808.9              50.00     Sequence
DRB1_0404  264  SNLFAHRDRGFIPEG  LFAHRDRGF        0.1252     12903.0              50.00     Sequence
DRB1_0404  136  RHLTDAQRAAYLAEG  RHLTDAQRA        0.1250     12934.9              50.00     Sequence
DRB1_0404  246  LPTVLGEGTKKLSKR  TVLGEGTKK        0.1239     13082.1              50.00     Sequence
DRB1_0404  317  RFDQKKADALNAEHI  QKKADALNA        0.1231     13200.1              50.00     Sequence
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DRB1_0404  307  DVADVNSSPARFDQK  VADVNSSPA        0.1228     13247.8              50.00     Sequence
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DRB1_0404  137  HLTDAQRAAYLAEGR  HLTDAQRAA        0.1204     13596.0              50.00     Sequence
DRB1_0404  247  PTVLGEGTKKLSKRD  TVLGEGTKK        0.1177     13989.7              50.00     Sequence
DRB1_0404  129  LGYDNFDRHLTDAQR  NFDRHLTDA        0.1165     14180.0              50.00     Sequence
DRB1_0404  248  TVLGEGTKKLSKRDP  TVLGEGTKK        0.1161     14239.3              50.00     Sequence
DRB1_0404  319  DQKKADALNAEHIRM  QKKADALNA        0.1133     14676.5              50.00     Sequence
DRB1_0404  263  QSNLFAHRDRGFIPE  NLFAHRDRG        0.1118     14914.7              50.00     Sequence
DRB1_0404  321  KKADALNAEHIRMLD  KADALNAEH        0.1076     15601.2              50.00     Sequence
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DRB1_0404  397  AAKELGPDGAAVLDA  ELGPDGAAV        0.1029     16426.5              50.00     Sequence
DRB1_0404   81  YGPYRQSQRAEIYRD  YGPYRQSQR        0.1015     16672.2              50.00     Sequence
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DRB1_0404   80  PYGPYRQSQRAEIYR  YGPYRQSQR        0.1003     16899.3              50.00     Sequence
DRB1_0404   79  GPYGPYRQSQRAEIY  YGPYRQSQR        0.0997     17008.3              50.00     Sequence
DRB1_0404  308  VADVNSSPARFDQKK  VADVNSSPA        0.0992     17099.7              50.00     Sequence
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DRB1_0404  262  PQSNLFAHRDRGFIP  NLFAHRDRG        0.0965     17605.2              50.00     Sequence
DRB1_0404  396  AAAKELGPDGAAVLD  KELGPDGAA        0.0958     17737.3              50.00     Sequence
DRB1_0404   47  TDAQRDSEESYLALL  SEESYLALL        0.0949     17902.0              50.00     Sequence
DRB1_0404   78  GGPYGPYRQSQRAEI  YGPYRQSQR        0.0947     17946.2              50.00     Sequence
DRB1_0404   43  RIEDTDAQRDSEESY  RIEDTDAQR        0.0941     18054.3              50.00     Sequence
DRB1_0404  315  PARFDQKKADALNAE  FDQKKADAL        0.0936     18167.0              50.00     Sequence
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   DRB1_0404   11  CPSPTGTPHVGLVRT  CPSPTGTPH        0.0910      18673.4                 50.00     Sequence
   DRB1_0404  112  TPEEVEARHVAAGRN  EVEARHVAA        0.0895      18979.9                 50.00     Sequence
   DRB1_0404   82  GPYRQSQRAEIYRDV  YRQSQRAEI        0.0888      19135.8                 50.00     Sequence
   DRB1_0404  250  LGEGTKKLSKRDPQS  KLSKRDPQS        0.0880      19292.8                 50.00     Sequence
   DRB1_0404   76  EVGGPYGPYRQSQRA  EVGGPYGPY        0.0879      19314.1                 50.00     Sequence
   DRB1_0404  314  SPARFDQKKADALNA  RFDQKKADA        0.0879      19323.5                 50.00     Sequence
   DRB1_0404   75  PEVGGPYGPYRQSQR  EVGGPYGPY        0.0865      19608.9                 50.00     Sequence
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   DRB1_0404  261  DPQSNLFAHRDRGFI  NLFAHRDRG        0.0839      20171.2                 50.00     Sequence
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   DRB1_0404  392  IDPKAAAKELGPDGA  KAAAKELGP        0.0644      24918.2                 50.00     Sequence
   DRB1_0404   68  GLDWDEGPEVGGPYG  GLDWDEGPE        0.0637      25102.7                 50.00     Sequence
   DRB1_0404   69  LDWDEGPEVGGPYGP  LDWDEGPEV        0.0620      25551.6                 50.00     Sequence
   DRB1_0404   71  WDEGPEVGGPYGPYR  EVGGPYGPY        0.0607      25933.4                 50.00     Sequence
   DRB1_0404   70  DWDEGPEVGGPYGPY  EGPEVGGPY        0.0578      26745.3                 50.00     Sequence
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Allele: DRB1_0404. Number of high binders 7. Number of weak binders 131. Number of peptides 476

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0405  239  RIPKFAHLPTVLGEG  KFAHLPTVL        0.7580         13.7         SB     0.80     Sequence
   DRB1_0405  238  ERIPKFAHLPTVLGE  KFAHLPTVL        0.7536         14.4         SB     0.80     Sequence
   DRB1_0405  240  IPKFAHLPTVLGEGT  KFAHLPTVL        0.7506         14.9         SB     0.80     Sequence
   DRB1_0405  241  PKFAHLPTVLGEGTK  FAHLPTVLG        0.7330         18.0         SB     2.00     Sequence
   DRB1_0405  237  AERIPKFAHLPTVLG  KFAHLPTVL        0.7233         20.0         SB     2.00     Sequence
   DRB1_0405  190  SGDPLYTLVNPCDDA  DPLYTLVNP        0.6855         30.1         SB     4.00     Sequence
   DRB1_0405  189  ASGDPLYTLVNPCDD  DPLYTLVNP        0.6820         31.2         SB     4.00     Sequence
   DRB1_0405  379  WELLKFFNDDQYVID  LLKFFNDDQ        0.6650         37.5         SB     8.00     Sequence
   DRB1_0405  191  GDPLYTLVNPCDDAL  DPLYTLVNP        0.6581         40.4         SB     8.00     Sequence
   DRB1_0405  188  RASGDPLYTLVNPCD  DPLYTLVNP        0.6500         44.1         SB     8.00     Sequence
   DRB1_0405  378  AWELLKFFNDDQYVI  WELLKFFND        0.6445         46.8         SB     8.00     Sequence
   DRB1_0405  192  DPLYTLVNPCDDALM  DPLYTLVNP        0.6398         49.3         SB     8.00     Sequence
   DRB1_0405    4  ETVRVRFCPSPTGTP  RVRFCPSPT        0.6277         56.2         WB     8.00     Sequence
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   DRB1_0405    5  TVRVRFCPSPTGTPH  RVRFCPSPT        0.6163         63.6         WB    16.00     Sequence
   DRB1_0405  377  DAWELLKFFNDDQYV  WELLKFFND        0.6146         64.7         WB    16.00     Sequence
   DRB1_0405    3  TETVRVRFCPSPTGT  RVRFCPSPT        0.6145         64.8         WB    16.00     Sequence
   DRB1_0405   61  LDALRWLGLDWDEGP  ALRWLGLDW        0.6136         65.4         WB    16.00     Sequence
   DRB1_0405   62  DALRWLGLDWDEGPE  ALRWLGLDW        0.6119         66.6         WB    16.00     Sequence
   DRB1_0405  381  LLKFFNDDQYVIDPK  LKFFNDDQY        0.6076         69.8         WB    16.00     Sequence
   DRB1_0405  277  EGLLNYLALLGWSIA  LLNYLALLG        0.6050         71.8         WB    16.00     Sequence
   DRB1_0405   60  LLDALRWLGLDWDEG  ALRWLGLDW        0.6022         74.0         WB    16.00     Sequence
   DRB1_0405  327  NAEHIRMLDVGDFTV  IRMLDVGDF        0.5997         76.1         WB    16.00     Sequence
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DRB1_0405    6  VRVRFCPSPTGTPHV  RVRFCPSPT         0.5993          76.3          WB    16.00     Sequence
DRB1_0405   38  GTFVFRIEDTDAQRD  FVFRIEDTD         0.5928          81.9          WB    16.00     Sequence
DRB1_0405  276  PEGLLNYLALLGWSI  GLLNYLALL         0.5910          83.5          WB    16.00     Sequence
DRB1_0405  326  LNAEHIRMLDVGDFT  NAEHIRMLD         0.5892          85.2          WB    16.00     Sequence
DRB1_0405    2  ATETVRVRFCPSPTG  RVRFCPSPT         0.5862          88.0          WB    16.00     Sequence
DRB1_0405  187  TRASGDPLYTLVNPC  DPLYTLVNP         0.5857          88.4          WB    16.00     Sequence
DRB1_0405  363  AAAELVQTRIVVLGD  LVQTRIVVL         0.5818          92.3          WB    16.00     Sequence
DRB1_0405  278  GLLNYLALLGWSIAD  LLNYLALLG         0.5817          92.4          WB    16.00     Sequence
DRB1_0405  364  AAELVQTRIVVLGDA  LVQTRIVVL         0.5815          92.6          WB    16.00     Sequence
DRB1_0405  376  GDAWELLKFFNDDQY  WELLKFFND         0.5810          93.1          WB    16.00     Sequence
DRB1_0405   37  GGTFVFRIEDTDAQR  FVFRIEDTD         0.5809          93.2          WB    16.00     Sequence
DRB1_0405  242  KFAHLPTVLGEGTKK  FAHLPTVLG         0.5772          96.9          WB    16.00     Sequence
DRB1_0405   59  ALLDALRWLGLDWDE  ALRWLGLDW         0.5761          98.1          WB    16.00     Sequence
DRB1_0405   39  TFVFRIEDTDAQRDS  FVFRIEDTD         0.5749          99.4          WB    16.00     Sequence
DRB1_0405  328  AEHIRMLDVGDFTVR  IRMLDVGDF         0.5724         102.2          WB    16.00     Sequence
DRB1_0405  362  AAAAELVQTRIVVLG  LVQTRIVVL         0.5701         104.7          WB    16.00     Sequence
DRB1_0405  274  FIPEGLLNYLALLGW  GLLNYLALL         0.5700         104.9          WB    16.00     Sequence
DRB1_0405  329  EHIRMLDVGDFTVRL  RMLDVGDFT         0.5686         106.5          WB    16.00     Sequence
DRB1_0405  382  LKFFNDDQYVIDPKA  LKFFNDDQY         0.5633         112.7          WB    32.00     Sequence
DRB1_0405  275  IPEGLLNYLALLGWS  GLLNYLALL         0.5614         115.0          WB    32.00     Sequence
DRB1_0405  325  ALNAEHIRMLDVGDF  IRMLDVGDF         0.5610         115.5          WB    32.00     Sequence
DRB1_0405  279  LLNYLALLGWSIADD  LLNYLALLG         0.5609         115.8          WB    32.00     Sequence
DRB1_0405  409  LDAALAALTSVTDWT  AALAALTSV         0.5602         116.6          WB    32.00     Sequence
DRB1_0405  361  FAAAAELVQTRIVVL  AELVQTRIV         0.5593         117.8          WB    32.00     Sequence
DRB1_0405   40  FVFRIEDTDAQRDSE  FVFRIEDTD         0.5585         118.8          WB    32.00     Sequence
DRB1_0405  236  VAERIPKFAHLPTVL  PKFAHLPTV         0.5584         118.9          WB    32.00     Sequence
DRB1_0405  410  DAALAALTSVTDWTA  LAALTSVTD         0.5564         121.5          WB    32.00     Sequence
DRB1_0405  104  GEAYHAFSTPEEVEA  YHAFSTPEE         0.5536         125.2          WB    32.00     Sequence
DRB1_0405  223  RQLALHQALIRIGVA  QLALHQALI         0.5529         126.2          WB    32.00     Sequence
DRB1_0405  103  AGEAYHAFSTPEEVE  YHAFSTPEE         0.5521         127.2          WB    32.00     Sequence
DRB1_0405  210  HVLRGEDLLPSTPRQ  VLRGEDLLP         0.5491         131.5          WB    32.00     Sequence
DRB1_0405  408  VLDAALAALTSVTDW  LAALTSVTD         0.5481         132.9          WB    32.00     Sequence
DRB1_0405   36  TGGTFVFRIEDTDAQ  FVFRIEDTD         0.5478         133.3          WB    32.00     Sequence
DRB1_0405   63  ALRWLGLDWDEGPEV  LRWLGLDWD         0.5441         138.8          WB    32.00     Sequence
DRB1_0405  365  AELVQTRIVVLGDAW  LVQTRIVVL         0.5437         139.4          WB    32.00     Sequence
DRB1_0405  186  LTRASGDPLYTLVNP  DPLYTLVNP         0.5405         144.3          WB    32.00     Sequence
DRB1_0405  222  PRQLALHQALIRIGV  QLALHQALI         0.5403         144.6          WB    32.00     Sequence
DRB1_0405  366  ELVQTRIVVLGDAWE  ELVQTRIVV         0.5396         145.6          WB    32.00     Sequence
DRB1_0405   58  LALLDALRWLGLDWD  ALRWLGLDW         0.5389         146.8          WB    32.00     Sequence
DRB1_0405  105  EAYHAFSTPEEVEAR  YHAFSTPEE         0.5360         151.6          WB    32.00     Sequence
DRB1_0405  273  GFIPEGLLNYLALLG  GLLNYLALL         0.5355         152.4          WB    32.00     Sequence
DRB1_0405  460  SPPLFESLELLGRDR  LFESLELLG         0.5348         153.4          WB    32.00     Sequence
DRB1_0405  272  RGFIPEGLLNYLALL  FIPEGLLNY         0.5342         154.4          WB    32.00     Sequence
DRB1_0405  375  LGDAWELLKFFNDDQ  WELLKFFND         0.5326         157.2          WB    32.00     Sequence
DRB1_0405   53  SEESYLALLDALRWL  SYLALLDAL         0.5321         157.9          WB    32.00     Sequence
DRB1_0405  330  HIRMLDVGDFTVRLR  IRMLDVGDF         0.5315         158.9          WB    32.00     Sequence
DRB1_0405    1  TATETVRVRFCPSPT  RVRFCPSPT         0.5307         160.4          WB    32.00     Sequence
DRB1_0405  102  AAGEAYHAFSTPEEV  EAYHAFSTP         0.5307         160.5          WB    32.00     Sequence
DRB1_0405  151  RQPVVRLRMPDDDLA  VVRLRMPDD         0.5305         160.7          WB    32.00     Sequence
DRB1_0405  411  AALAALTSVTDWTAP  LAALTSVTD         0.5300         161.6          WB    32.00     Sequence
DRB1_0405  209  THVLRGEDLLPSTPR  VLRGEDLLP         0.5294         162.7          WB    32.00     Sequence
DRB1_0405   54  EESYLALLDALRWLG  SYLALLDAL         0.5288         163.8          WB    32.00     Sequence
DRB1_0405  461  PPLFESLELLGRDRS  LFESLELLG         0.5286         164.2          WB    32.00     Sequence
DRB1_0405  182  PDFALTRASGDPLYT  FALTRASGD         0.5250         170.5          WB    32.00     Sequence
DRB1_0405   89  RAEIYRDVLARLLAA  IYRDVLARL         0.5248         170.9          WB    32.00     Sequence
DRB1_0405  181  VPDFALTRASGDPLY  FALTRASGD         0.5234         173.6          WB    32.00     Sequence
DRB1_0405  221  TPRQLALHQALIRIG  QLALHQALI         0.5212         177.7          WB    32.00     Sequence
DRB1_0405   88  QRAEIYRDVLARLLA  IYRDVLARL         0.5211         178.1          WB    32.00     Sequence
DRB1_0405  294  HDLFGLDEMVAAFDV  DLFGLDEMV         0.5209         178.3          WB    32.00     Sequence
DRB1_0405  152  QPVVRLRMPDDDLAW  VVRLRMPDD         0.5206         179.0          WB    32.00     Sequence
DRB1_0405   52  DSEESYLALLDALRW  YLALLDALR         0.5197         180.6          WB    32.00     Sequence
DRB1_0405  459  VSPPLFESLELLGRD  LFESLELLG         0.5196         180.9          WB    32.00     Sequence
DRB1_0405    7  RVRFCPSPTGTPHVG  RVRFCPSPT         0.5186         182.8          WB    32.00     Sequence
DRB1_0405  295  DLFGLDEMVAAFDVA  DLFGLDEMV         0.5181         183.9          WB    32.00     Sequence
DRB1_0405   91  EIYRDVLARLLAAGE  IYRDVLARL         0.5119         196.6          WB    32.00     Sequence
DRB1_0405  150  GRQPVVRLRMPDDDL  VVRLRMPDD         0.5100         200.8          WB    32.00     Sequence
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DRB1_0405  180  SVPDFALTRASGDPL  FALTRASGD         0.5089         203.1          WB    32.00      Sequence
DRB1_0405  462  PLFESLELLGRDRSM  LFESLELLG         0.5087         203.6          WB    32.00      Sequence
DRB1_0405   55  ESYLALLDALRWLGL  SYLALLDAL         0.5087         203.6          WB    32.00      Sequence
DRB1_0405  282  YLALLGWSIADDHDL  LLGWSIADD         0.5081         204.8          WB    32.00      Sequence
DRB1_0405  208  ITHVLRGEDLLPSTP  VLRGEDLLP         0.5057         210.3          WB    32.00      Sequence
DRB1_0405  296  LFGLDEMVAAFDVAD  FGLDEMVAA         0.5036         215.1          WB    32.00      Sequence
DRB1_0405  407  AVLDAALAALTSVTD  LAALTSVTD         0.5020         218.7          WB    32.00      Sequence
DRB1_0405  153  PVVRLRMPDDDLAWN  VVRLRMPDD         0.5013         220.5          WB    32.00      Sequence
DRB1_0405   90  AEIYRDVLARLLAAG  IYRDVLARL         0.5006         222.1          WB    32.00      Sequence
DRB1_0405   87  SQRAEIYRDVLARLL  EIYRDVLAR         0.5005         222.3          WB    32.00      Sequence
DRB1_0405  474  RSMQRLRAARQLVGH  QRLRAARQL         0.4990         225.9          WB    32.00      Sequence
DRB1_0405  271  DRGFIPEGLLNYLAL  FIPEGLLNY         0.4984         227.4          WB    32.00      Sequence
DRB1_0405   35  HTGGTFVFRIEDTDA  FVFRIEDTD         0.4984         227.6          WB    32.00      Sequence
DRB1_0405  224  QLALHQALIRIGVAE  QLALHQALI         0.4983         227.8          WB    32.00      Sequence
DRB1_0405  101  LAAGEAYHAFSTPEE  EAYHAFSTP         0.4982         227.9          WB    32.00      Sequence
DRB1_0405  297  FGLDEMVAAFDVADV  FGLDEMVAA         0.4975         229.6          WB    32.00      Sequence
DRB1_0405  211  VLRGEDLLPSTPRQL  VLRGEDLLP         0.4973         230.2          WB    32.00      Sequence
DRB1_0405   56  SYLALLDALRWLGLD  YLALLDALR         0.4973         230.3          WB    32.00      Sequence
DRB1_0405  324  DALNAEHIRMLDVGD  NAEHIRMLD         0.4959         233.7          WB    32.00      Sequence
DRB1_0405   25  TALFNWAYARHTGGT  FNWAYARHT         0.4958         234.1          WB    32.00      Sequence
DRB1_0405   51  RDSEESYLALLDALR  YLALLDALR         0.4956         234.5          WB    32.00      Sequence
DRB1_0405  337  GDFTVRLRDHLDTHG  FTVRLRDHL         0.4935         239.8          WB    32.00      Sequence
DRB1_0405  183  DFALTRASGDPLYTL  FALTRASGD         0.4935         239.9          WB    32.00      Sequence
DRB1_0405  283  LALLGWSIADDHDLF  LLGWSIADD         0.4915         245.1          WB    32.00      Sequence
DRB1_0405  179  GSVPDFALTRASGDP  FALTRASGD         0.4911         246.2          WB    32.00      Sequence
DRB1_0405  444  RKAFSPIRVAATGTT  RKAFSPIRV         0.4906         247.6          WB    32.00      Sequence
DRB1_0405  475  SMQRLRAARQLVGHA  QRLRAARQL         0.4896         250.3          WB    32.00      Sequence
DRB1_0405  338  DFTVRLRDHLDTHGH  FTVRLRDHL         0.4891         251.7          WB    32.00      Sequence
DRB1_0405  281  NYLALLGWSIADDHD  LLGWSIADD         0.4890         251.9          WB    32.00      Sequence
DRB1_0405  331  IRMLDVGDFTVRLRD  IRMLDVGDF         0.4878         255.2          WB    32.00      Sequence
DRB1_0405  442  KPRKAFSPIRVAATG  KAFSPIRVA         0.4875         255.9          WB    32.00      Sequence
DRB1_0405   24  RTALFNWAYARHTGG  FNWAYARHT         0.4861         259.8          WB    32.00      Sequence
DRB1_0405  383  KFFNDDQYVIDPKAA  KFFNDDQYV         0.4852         262.6          WB    32.00      Sequence
DRB1_0405  184  FALTRASGDPLYTLV  FALTRASGD         0.4847         264.0          WB    32.00      Sequence
DRB1_0405  336  VGDFTVRLRDHLDTH  FTVRLRDHL         0.4819         272.1          WB    32.00      Sequence
DRB1_0405   57  YLALLDALRWLGLDW  DALRWLGLD         0.4803         276.7          WB    32.00      Sequence
DRB1_0405  339  FTVRLRDHLDTHGHH  FTVRLRDHL         0.4801         277.3          WB    32.00      Sequence
DRB1_0405  473  DRSMQRLRAARQLVG  QRLRAARQL         0.4797         278.7          WB    32.00      Sequence
DRB1_0405  220  STPRQLALHQALIRI  QLALHQALI         0.4782         283.2          WB    32.00      Sequence
DRB1_0405  293  DHDLFGLDEMVAAFD  DLFGLDEMV         0.4768         287.5          WB    32.00      Sequence
DRB1_0405  458  TVSPPLFESLELLGR  LFESLELLG         0.4710         305.9          WB    50.00      Sequence
DRB1_0405  360  AFAAAAELVQTRIVV  AELVQTRIV         0.4710         306.1          WB    50.00      Sequence
DRB1_0405  412  ALAALTSVTDWTAPL  LAALTSVTD         0.4705         307.6          WB    50.00      Sequence
DRB1_0405  154  VVRLRMPDDDLAWND  VVRLRMPDD         0.4683         315.2          WB    50.00      Sequence
DRB1_0405  463  LFESLELLGRDRSMQ  LFESLELLG         0.4662         322.4          WB    50.00      Sequence
DRB1_0405  443  PRKAFSPIRVAATGT  KAFSPIRVA         0.4661         322.8          WB    50.00      Sequence
DRB1_0405  270  RDRGFIPEGLLNYLA  GFIPEGLLN         0.4658         323.6          WB    50.00      Sequence
DRB1_0405  284  ALLGWSIADDHDLFG  LLGWSIADD         0.4652         326.0          WB    50.00      Sequence
DRB1_0405  445  KAFSPIRVAATGTTV  FSPIRVAAT         0.4645         328.2          WB    50.00      Sequence
DRB1_0405   23  VRTALFNWAYARHTG  FNWAYARHT         0.4638         330.7          WB    50.00      Sequence
DRB1_0405  149  EGRQPVVRLRMPDDD  VVRLRMPDD         0.4634         332.4          WB    50.00      Sequence
DRB1_0405   92  IYRDVLARLLAAGEA  IYRDVLARL         0.4627         334.6          WB    50.00      Sequence
DRB1_0405   86  QSQRAEIYRDVLARL  EIYRDVLAR         0.4610         341.0          WB    50.00      Sequence
DRB1_0405  441  LKPRKAFSPIRVAAT  RKAFSPIRV         0.4610         341.1          WB    50.00      Sequence
DRB1_0405  178  AGSVPDFALTRASGD  FALTRASGD         0.4604         343.4          WB    50.00      Sequence
DRB1_0405  207  KITHVLRGEDLLPST  HVLRGEDLL         0.4603         343.5          WB    50.00      Sequence
DRB1_0405  280  LNYLALLGWSIADDH  LLGWSIADD         0.4601         344.2          WB    50.00      Sequence
DRB1_0405  446  AFSPIRVAATGTTVS  IRVAATGTT         0.4592         347.6          WB    50.00      Sequence
DRB1_0405  335  DVGDFTVRLRDHLDT  FTVRLRDHL         0.4582         351.5          WB    50.00      Sequence
DRB1_0405  298  GLDEMVAAFDVADVN  DEMVAAFDV         0.4581         351.7          WB    50.00      Sequence
DRB1_0405   26  ALFNWAYARHTGGTF  FNWAYARHT         0.4573         354.9          WB    50.00      Sequence
DRB1_0405  367  LVQTRIVVLGDAWEL  LVQTRIVVL         0.4558         360.6          WB    50.00      Sequence
DRB1_0405  447  FSPIRVAATGTTVSP  IRVAATGTT         0.4541         367.4          WB    50.00      Sequence
DRB1_0405  292  DDHDLFGLDEMVAAF  DLFGLDEMV         0.4509         380.3          WB    50.00      Sequence
DRB1_0405  472  RDRSMQRLRAARQLV  QRLRAARQL         0.4482         391.4          WB    50.00      Sequence
DRB1_0405   34  RHTGGTFVFRIEDTD  FVFRIEDTD         0.4473         395.4          WB    50.00      Sequence
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DRB1_0405  202  DDALMKITHVLRGED  LMKITHVLR        0.4468        397.7         WB    50.00     Sequence
DRB1_0405  193  PLYTLVNPCDDALMK  PLYTLVNPC        0.4431        413.7         WB    50.00     Sequence
DRB1_0405  300  DEMVAAFDVADVNSS  MVAAFDVAD        0.4416        420.9         WB    50.00     Sequence
DRB1_0405  299  LDEMVAAFDVADVNS  MVAAFDVAD        0.4413        421.9         WB    50.00     Sequence
DRB1_0405  467  LELLGRDRSMQRLRA  LGRDRSMQR        0.4411        423.1         WB    50.00     Sequence
DRB1_0405  203  DALMKITHVLRGEDL  LMKITHVLR        0.4406        425.2         WB    50.00     Sequence
DRB1_0405  466  SLELLGRDRSMQRLR  LGRDRSMQR        0.4385        435.1         WB    50.00     Sequence
DRB1_0405  468  ELLGRDRSMQRLRAA  LGRDRSMQR        0.4366        444.0         WB    50.00     Sequence
DRB1_0405   22  LVRTALFNWAYARHT  FNWAYARHT        0.4338        457.9         WB    50.00     Sequence
DRB1_0405  374  VLGDAWELLKFFNDD  WELLKFFND        0.4325        464.0         WB    50.00     Sequence
DRB1_0405  465  ESLELLGRDRSMQRL  LGRDRSMQR        0.4318        467.7         WB    50.00     Sequence
DRB1_0405  167  NDLVRGPVTFAAGSV  LVRGPVTFA        0.4306        473.9         WB    50.00     Sequence
DRB1_0405   41  VFRIEDTDAQRDSEE  FRIEDTDAQ        0.4304        474.7         WB    50.00     Sequence
DRB1_0405  166  WNDLVRGPVTFAAGS  LVRGPVTFA        0.4301        476.5         WB    50.00     Sequence
DRB1_0405  212  LRGEDLLPSTPRQLA  LRGEDLLPS        0.4293        480.2         WB    50.00     Sequence
DRB1_0405  384  FFNDDQYVIDPKAAA  FNDDQYVID        0.4287        483.6         WB    50.00     Sequence
DRB1_0405  106  AYHAFSTPEEVEARH  YHAFSTPEE        0.4281        487.0         WB    50.00     Sequence
DRB1_0405   64  LRWLGLDWDEGPEVG  LRWLGLDWD        0.4271        492.3         WB    50.00     Sequence
DRB1_0405  269  HRDRGFIPEGLLNYL  FIPEGLLNY        0.4264        496.0         WB    50.00     Sequence
DRB1_0405   27  LFNWAYARHTGGTFV  FNWAYARHT        0.4258        498.9         WB    50.00     Sequence
DRB1_0405  448  SPIRVAATGTTVSPP  IRVAATGTT        0.4246        505.5               50.00     Sequence
DRB1_0405  206  MKITHVLRGEDLLPS  HVLRGEDLL        0.4245        506.0               50.00     Sequence
DRB1_0405  413  LAALTSVTDWTAPLI  LAALTSVTD        0.4227        516.1               50.00     Sequence
DRB1_0405  225  LALHQALIRIGVAER  ALHQALIRI        0.4221        519.3               50.00     Sequence
DRB1_0405  334  LDVGDFTVRLRDHLD  FTVRLRDHL        0.4200        531.2               50.00     Sequence
DRB1_0405  449  PIRVAATGTTVSPPL  IRVAATGTT        0.4187        538.8               50.00     Sequence
DRB1_0405  291  ADDHDLFGLDEMVAA  DLFGLDEMV        0.4179        543.8               50.00     Sequence
DRB1_0405  204  ALMKITHVLRGEDLL  LMKITHVLR        0.4165        552.0               50.00     Sequence
DRB1_0405  359  AAFAAAAELVQTRIV  AELVQTRIV        0.4151        560.3               50.00     Sequence
DRB1_0405   94  RDVLARLLAAGEAYH  LARLLAAGE        0.4142        565.9               50.00     Sequence
DRB1_0405   85  RQSQRAEIYRDVLAR  RAEIYRDVL        0.4141        566.5               50.00     Sequence
DRB1_0405  434  ALIEGLALKPRKAFS  LIEGLALKP        0.4139        567.4               50.00     Sequence
DRB1_0405  165  AWNDLVRGPVTFAAG  LVRGPVTFA        0.4134        571.0               50.00     Sequence
DRB1_0405  201  CDDALMKITHVLRGE  DALMKITHV        0.4129        573.6               50.00     Sequence
DRB1_0405  148  AEGRQPVVRLRMPDD  VVRLRMPDD        0.4128        574.1               50.00     Sequence
DRB1_0405  470  LGRDRSMQRLRAARQ  LGRDRSMQR        0.4123        577.7               50.00     Sequence
DRB1_0405   21  GLVRTALFNWAYARH  GLVRTALFN        0.4117        581.3               50.00     Sequence
DRB1_0405  433  DALIEGLALKPRKAF  LIEGLALKP        0.4115        582.5               50.00     Sequence
DRB1_0405   93  YRDVLARLLAAGEAY  LARLLAAGE        0.4112        584.5               50.00     Sequence
DRB1_0405  243  FAHLPTVLGEGTKKL  FAHLPTVLG        0.4110        585.9               50.00     Sequence
DRB1_0405  432  KDALIEGLALKPRKA  LIEGLALKP        0.4104        589.7               50.00     Sequence
DRB1_0405  235  GVAERIPKFAHLPTV  PKFAHLPTV        0.4090        598.7               50.00     Sequence
DRB1_0405  469  LLGRDRSMQRLRAAR  LGRDRSMQR        0.4078        606.4               50.00     Sequence
DRB1_0405  219  PSTPRQLALHQALIR  QLALHQALI        0.4070        611.9               50.00     Sequence
DRB1_0405  205  LMKITHVLRGEDLLP  LMKITHVLR        0.4059        618.7               50.00     Sequence
DRB1_0405  450  IRVAATGTTVSPPLF  IRVAATGTT        0.4053        623.3               50.00     Sequence
DRB1_0405   50  QRDSEESYLALLDAL  SYLALLDAL        0.4038        633.2               50.00     Sequence
DRB1_0405  464  FESLELLGRDRSMQR  ELLGRDRSM        0.4026        641.2               50.00     Sequence
DRB1_0405   18  PHVGLVRTALFNWAY  GLVRTALFN        0.4005        656.4               50.00     Sequence
DRB1_0405  457  TTVSPPLFESLELLG  LFESLELLG        0.3978        675.4               50.00     Sequence
DRB1_0405  164  LAWNDLVRGPVTFAA  LVRGPVTFA        0.3972        680.3               50.00     Sequence
DRB1_0405  332  RMLDVGDFTVRLRDH  RMLDVGDFT        0.3963        686.5               50.00     Sequence
DRB1_0405  168  DLVRGPVTFAAGSVP  LVRGPVTFA        0.3956        692.3               50.00     Sequence
DRB1_0405   95  DVLARLLAAGEAYHA  LARLLAAGE        0.3953        694.4               50.00     Sequence
DRB1_0405   42  FRIEDTDAQRDSEES  FRIEDTDAQ        0.3912        725.5               50.00     Sequence
DRB1_0405  226  ALHQALIRIGVAERI  ALHQALIRI        0.3908        728.6               50.00     Sequence
DRB1_0405   20  VGLVRTALFNWAYAR  GLVRTALFN        0.3899        736.0               50.00     Sequence
DRB1_0405  301  EMVAAFDVADVNSSP  MVAAFDVAD        0.3899        736.1               50.00     Sequence
DRB1_0405  200  PCDDALMKITHVLRG  DALMKITHV        0.3894        740.2               50.00     Sequence
DRB1_0405  214  GEDLLPSTPRQLALH  LLPSTPRQL        0.3892        741.3               50.00     Sequence
DRB1_0405  285  LLGWSIADDHDLFGL  LLGWSIADD        0.3890        743.2               50.00     Sequence
DRB1_0405  368  VQTRIVVLGDAWELL  TRIVVLGDA        0.3875        755.1               50.00     Sequence
DRB1_0405  213  RGEDLLPSTPRQLAL  LLPSTPRQL        0.3842        782.7               50.00     Sequence
DRB1_0405   19  HVGLVRTALFNWAYA  GLVRTALFN        0.3840        784.6               50.00     Sequence
DRB1_0405  385  FNDDQYVIDPKAAAK  DQYVIDPKA        0.3821        800.8               50.00     Sequence
DRB1_0405  369  QTRIVVLGDAWELLK  TRIVVLGDA        0.3813        807.6               50.00     Sequence
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DRB1_0405  323  ADALNAEHIRMLDVG  LNAEHIRML        0.3807        812.7                 50.00     Sequence
DRB1_0405  163  DLAWNDLVRGPVTFA  LVRGPVTFA        0.3807        813.4                 50.00     Sequence
DRB1_0405  435  LIEGLALKPRKAFSP  LIEGLALKP        0.3771        845.0                 50.00     Sequence
DRB1_0405  130  GYDNFDRHLTDAQRA  FDRHLTDAQ        0.3770        846.6                 50.00     Sequence
DRB1_0405  340  TVRLRDHLDTHGHHI  TVRLRDHLD        0.3763        852.2                 50.00     Sequence
DRB1_0405   17  TPHVGLVRTALFNWA  GLVRTALFN        0.3738        876.2                 50.00     Sequence
DRB1_0405    0  VTATETVRVRFCPSP  VRVRFCPSP        0.3720        893.1                 50.00     Sequence
DRB1_0405  155  VRLRMPDDDLAWNDL  LRMPDDDLA        0.3719        894.2                 50.00     Sequence
DRB1_0405  471  GRDRSMQRLRAARQL  MQRLRAARQ        0.3711        901.5                 50.00     Sequence
DRB1_0405  215  EDLLPSTPRQLALHQ  LLPSTPRQL        0.3705        907.7                 50.00     Sequence
DRB1_0405  185  ALTRASGDPLYTLVN  LTRASGDPL        0.3689        923.3                 50.00     Sequence
DRB1_0405  431  LKDALIEGLALKPRK  LIEGLALKP        0.3674        938.6                 50.00     Sequence
DRB1_0405  440  ALKPRKAFSPIRVAA  RKAFSPIRV        0.3672        941.0                 50.00     Sequence
DRB1_0405  268  AHRDRGFIPEGLLNY  FIPEGLLNY        0.3662        951.4                 50.00     Sequence
DRB1_0405  302  MVAAFDVADVNSSPA  FDVADVNSS        0.3654        959.2                 50.00     Sequence
DRB1_0405  387  DDQYVIDPKAAAKEL  DQYVIDPKA        0.3652        961.2                 50.00     Sequence
DRB1_0405  129  LGYDNFDRHLTDAQR  GYDNFDRHL        0.3649        964.6                 50.00     Sequence
DRB1_0405  216  DLLPSTPRQLALHQA  LLPSTPRQL        0.3647        966.2                 50.00     Sequence
DRB1_0405   16  GTPHVGLVRTALFNW  HVGLVRTAL        0.3647        966.5                 50.00     Sequence
DRB1_0405  306  FDVADVNSSPARFDQ  FDVADVNSS        0.3640        973.8                 50.00     Sequence
DRB1_0405  228  HQALIRIGVAERIPK  LIRIGVAER        0.3625        990.1                 50.00     Sequence
DRB1_0405  438  GLALKPRKAFSPIRV  GLALKPRKA        0.3619        996.7                 50.00     Sequence
DRB1_0405  370  TRIVVLGDAWELLKF  TRIVVLGDA        0.3616        999.8                 50.00     Sequence
DRB1_0405  386  NDDQYVIDPKAAAKE  DQYVIDPKA        0.3613       1003.1                 50.00     Sequence
DRB1_0405  333  MLDVGDFTVRLRDHL  MLDVGDFTV        0.3609       1006.9                 50.00     Sequence
DRB1_0405  227  LHQALIRIGVAERIP  ALIRIGVAE        0.3606       1009.9                 50.00     Sequence
DRB1_0405  229  QALIRIGVAERIPKF  LIRIGVAER        0.3597       1020.3                 50.00     Sequence
DRB1_0405  439  LALKPRKAFSPIRVA  RKAFSPIRV        0.3592       1026.0                 50.00     Sequence
DRB1_0405  305  AFDVADVNSSPARFD  FDVADVNSS        0.3563       1058.2                 50.00     Sequence
DRB1_0405   84  YRQSQRAEIYRDVLA  YRQSQRAEI        0.3546       1078.4                 50.00     Sequence
DRB1_0405   15  TGTPHVGLVRTALFN  HVGLVRTAL        0.3539       1086.1                 50.00     Sequence
DRB1_0405  218  LPSTPRQLALHQALI  QLALHQALI        0.3521       1107.3                 50.00     Sequence
DRB1_0405  131  YDNFDRHLTDAQRAA  FDRHLTDAQ        0.3515       1114.5                 50.00     Sequence
DRB1_0405  199  NPCDDALMKITHVLR  DALMKITHV        0.3486       1150.3                 50.00     Sequence
DRB1_0405  373  VVLGDAWELLKFFND  WELLKFFND        0.3468       1173.2                 50.00     Sequence
DRB1_0405  132  DNFDRHLTDAQRAAY  FDRHLTDAQ        0.3464       1177.9                 50.00     Sequence
DRB1_0405   49  AQRDSEESYLALLDA  SEESYLALL        0.3462       1181.5                 50.00     Sequence
DRB1_0405  290  IADDHDLFGLDEMVA  DLFGLDEMV        0.3460       1183.4                 50.00     Sequence
DRB1_0405  414  AALTSVTDWTAPLIE  SVTDWTAPL        0.3446       1201.2                 50.00     Sequence
DRB1_0405  100  LLAAGEAYHAFSTPE  EAYHAFSTP        0.3428       1225.5                 50.00     Sequence
DRB1_0405  416  LTSVTDWTAPLIEAA  VTDWTAPLI        0.3419       1237.6                 50.00     Sequence
DRB1_0405  418  SVTDWTAPLIEAALK  VTDWTAPLI        0.3416       1241.7                 50.00     Sequence
DRB1_0405  169  LVRGPVTFAAGSVPD  LVRGPVTFA        0.3414       1243.2                 50.00     Sequence
DRB1_0405  217  LLPSTPRQLALHQAL  LLPSTPRQL        0.3413       1244.8                 50.00     Sequence
DRB1_0405  156  RLRMPDDDLAWNDLV  RLRMPDDDL        0.3399       1263.7                 50.00     Sequence
DRB1_0405  415  ALTSVTDWTAPLIEA  VTDWTAPLI        0.3397       1267.0                 50.00     Sequence
DRB1_0405  406  AAVLDAALAALTSVT  ALAALTSVT        0.3383       1285.6                 50.00     Sequence
DRB1_0405  128  KLGYDNFDRHLTDAQ  LGYDNFDRH        0.3370       1304.0                 50.00     Sequence
DRB1_0405  417  TSVTDWTAPLIEAAL  VTDWTAPLI        0.3366       1309.4                 50.00     Sequence
DRB1_0405   96  VLARLLAAGEAYHAF  VLARLLAAG        0.3364       1313.4                 50.00     Sequence
DRB1_0405  388  DQYVIDPKAAAKELG  YVIDPKAAA        0.3356       1323.7                 50.00     Sequence
DRB1_0405  107  YHAFSTPEEVEARHV  YHAFSTPEE        0.3317       1382.0                 50.00     Sequence
DRB1_0405  430  ALKDALIEGLALKPR  LIEGLALKP        0.3306       1398.6                 50.00     Sequence
DRB1_0405  230  ALIRIGVAERIPKFA  LIRIGVAER        0.3293       1418.2                 50.00     Sequence
DRB1_0405  322  KADALNAEHIRMLDV  LNAEHIRML        0.3285       1429.5                 50.00     Sequence
DRB1_0405  162  DDLAWNDLVRGPVTF  LAWNDLVRG        0.3285       1429.9                 50.00     Sequence
DRB1_0405    8  VRFCPSPTGTPHVGL  VRFCPSPTG        0.3272       1450.5                 50.00     Sequence
DRB1_0405  437  EGLALKPRKAFSPIR  GLALKPRKA        0.3267       1458.4                 50.00     Sequence
DRB1_0405  127  PKLGYDNFDRHLTDA  LGYDNFDRH        0.3264       1462.2                 50.00     Sequence
DRB1_0405  425  PLIEAALKDALIEGL  PLIEAALKD        0.3261       1467.5                 50.00     Sequence
DRB1_0405  304  AAFDVADVNSSPARF  FDVADVNSS        0.3258       1473.2                 50.00     Sequence
DRB1_0405   28  FNWAYARHTGGTFVF  FNWAYARHT        0.3245       1493.2                 50.00     Sequence
DRB1_0405  126  NPKLGYDNFDRHLTD  LGYDNFDRH        0.3244       1495.0                 50.00     Sequence
DRB1_0405  133  NFDRHLTDAQRAAYL  FDRHLTDAQ        0.3242       1498.3                 50.00     Sequence
DRB1_0405  194  LYTLVNPCDDALMKI  LYTLVNPCD        0.3232       1513.7                 50.00     Sequence
DRB1_0405  405  GAAVLDAALAALTSV  GAAVLDAAL        0.3232       1514.7                 50.00     Sequence
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DRB1_0405	303	VAAFDVADVNSSPAR	FDVADVNSS	0.3221	1532.4	50.00	Sequence
DRB1_0405	81	YGPYRQSQRAEIYRD	YRQSQRAEI	0.3219	1536.6	50.00	Sequence
DRB1_0405	429	AALKDALIEGLALKP	LIEGLALKP	0.3194	1578.2	50.00	Sequence
DRB1_0405	307	DVADVNSSPARFDQK	ADVNSSPAR	0.3180	1601.5	50.00	Sequence
DRB1_0405	161	DDDLAWNDLVRGPVT	DLAWNDLVR	0.3160	1637.3	50.00	Sequence
DRB1_0405	14	PTGTPHVGLVRTALF	HVGLVRTAL	0.3155	1646.3	50.00	Sequence
DRB1_0405	173	PVTFAAGSVPDFALT	FAAGSVPDF	0.3123	1703.4	50.00	Sequence
DRB1_0405	426	LIEAALKDALIEGLA	LIEAALKDA	0.3122	1706.8	50.00	Sequence
DRB1_0405	82	GPYRQSQRAEIYRDV	YRQSQRAEI	0.3111	1725.9	50.00	Sequence
DRB1_0405	308	VADVNSSPARFDQKK	ADVNSSPAR	0.3105	1737.7	50.00	Sequence
DRB1_0405	83	PYRQSQRAEIYRDVL	YRQSQRAEI	0.3102	1742.9	50.00	Sequence
DRB1_0405	423	TAPLIEAALKDALIE	PLIEAALKD	0.3075	1794.6	50.00	Sequence
DRB1_0405	424	APLIEAALKDALIEG	PLIEAALKD	0.3059	1826.9	50.00	Sequence
DRB1_0405	80	PYGPYRQSQRAEIYR	YRQSQRAEI	0.3036	1872.2	50.00	Sequence
DRB1_0405	436	IEGLALKPRKAFSPI	GLALKPRKA	0.3019	1906.2	50.00	Sequence
DRB1_0405	174	VTFAAGSVPDFALTR	FAAGSVPDF	0.3012	1921.3	50.00	Sequence
DRB1_0405	451	RVAATGTTVSPPLFE	RVAATGTTV	0.2990	1967.0	50.00	Sequence
DRB1_0405	147	LAEGRQPVVRLRMPD	QPVVRLRMP	0.2990	1967.9	50.00	Sequence
DRB1_0405	404	DGAAVLDAALAALTS	GAAVLDAAL	0.2990	1968.2	50.00	Sequence
DRB1_0405	267	FAHRDRGFIPEGLLN	FAHRDRGFI	0.2974	2002.9	50.00	Sequence
DRB1_0405	79	GPYGPYRQSQRAEIY	GPYRQSQRA	0.2969	2013.8	50.00	Sequence
DRB1_0405	419	VTDWTAPLIEAALKD	VTDWTAPLI	0.2957	2039.6	50.00	Sequence
DRB1_0405	172	GPVTFAAGSVPDFAL	PVTFAAGSV	0.2948	2060.0	50.00	Sequence
DRB1_0405	428	EAALKDALIEGLALK	AALKDALIE	0.2936	2087.1	50.00	Sequence
DRB1_0405	157	LRMPDDDLAWNDLVR	LRMPDDDLA	0.2916	2132.1	50.00	Sequence
DRB1_0405	403	PDGAAVLDAALAALT	GAAVLDAAL	0.2904	2160.7	50.00	Sequence
DRB1_0405	422	WTAPLIEAALKDALI	PLIEAALKD	0.2899	2171.5	50.00	Sequence
DRB1_0405	171	RGPVTFAAGSVPDFA	PVTFAAGSV	0.2899	2171.7	50.00	Sequence
DRB1_0405	427	IEAALKDALIEGLAL	AALKDALIE	0.2892	2188.8	50.00	Sequence
DRB1_0405	176	FAAGSVPDFALTRAS	FAAGSVPDF	0.2888	2198.3	50.00	Sequence
DRB1_0405	371	RIVVLGDAWELLKFF	IVVLGDAWE	0.2888	2198.4	50.00	Sequence
DRB1_0405	134	FDRHLTDAQRAAYLA	FDRHLTDAQ	0.2876	2225.8	50.00	Sequence
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DRB1_0405	175	TFAAGSVPDFALTRA	FAAGSVPDF	0.2875	2229.4	50.00	Sequence
DRB1_0405	65	RWLGLDWDEGPEVGG	GLDWDEGPE	0.2863	2258.6	50.00	Sequence
DRB1_0405	258	SKRDPQSNLFAHRDR	DPQSNLFAH	0.2851	2287.3	50.00	Sequence
DRB1_0405	125	RNPKLGYDNFDRHLT	PKLGYDNFD	0.2850	2288.8	50.00	Sequence
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DRB1_0405	358	EAAFAAAAELVQTRI	FAAAAELVQ	0.2826	2349.2	50.00	Sequence
DRB1_0405	402	GPDGAAVLDAALAAL	GAAVLDAAL	0.2817	2372.0	50.00	Sequence
DRB1_0405	231	LIRIGVAERIPKFAH	LIRIGVAER	0.2817	2373.4	50.00	Sequence
DRB1_0405	198	VNPCDDALMKITHVL	DALMKITHV	0.2813	2383.7	50.00	Sequence
DRB1_0405	66	WLGLDWDEGPEVGGP	LDWDEGPEV	0.2807	2398.7	50.00	Sequence
DRB1_0405	259	KRDPQSNLFAHRDRG	DPQSNLFAH	0.2769	2500.6	50.00	Sequence
DRB1_0405	67	LGLDWDEGPEVGGPY	LDWDEGPEV	0.2759	2525.4	50.00	Sequence
DRB1_0405	48	DAQRDSEESYLALLD	SEESYLALL	0.2745	2564.5	50.00	Sequence
DRB1_0405	78	GGPYGPYRQSQRAEI	YRQSQRAEI	0.2740	2578.0	50.00	Sequence
DRB1_0405	170	VRGPVTFAAGSVPDF	PVTFAAGSV	0.2739	2581.8	50.00	Sequence
DRB1_0405	257	LSKRDPQSNLFAHRD	DPQSNLFAH	0.2738	2585.6	50.00	Sequence
DRB1_0405	177	AAGSVPDFALTRASG	AGSVPDFAL	0.2718	2641.6	50.00	Sequence
DRB1_0405	256	KLSKRDPQSNLFAHR	KLSKRDPQS	0.2713	2655.1	50.00	Sequence
DRB1_0405	234	IGVAERIPKFAHLPT	ERIPKFAHL	0.2711	2660.3	50.00	Sequence
DRB1_0405	248	TVLGEGTKKLSKRDP	VLGEGTKKL	0.2710	2663.1	50.00	Sequence
DRB1_0405	146	YLAEGRQPVVRLRMP	QPVVRLRMP	0.2707	2673.5	50.00	Sequence
DRB1_0405	315	PARFDQKKADALNAE	ARFDQKKAD	0.2702	2687.8	50.00	Sequence
DRB1_0405	456	GTTVSPPLFESLELL	PLFESLELL	0.2693	2713.5	50.00	Sequence
DRB1_0405	249	VLGEGTKKLSKRDPQ	LGEGTKKLS	0.2683	2743.5	50.00	Sequence
DRB1_0405	33	ARHTGGTFVFRIEDT	GTFVFRIED	0.2679	2755.4	50.00	Sequence
DRB1_0405	314	SPARFDQKKADALNA	PARFDQKKA	0.2674	2771.0	50.00	Sequence
DRB1_0405	401	LGPDGAAVLDAALAA	GAAVLDAAL	0.2670	2780.9	50.00	Sequence
DRB1_0405	341	VRLRDHLDTHGHHIA	VRLRDHLDT	0.2666	2793.0	50.00	Sequence
DRB1_0405	421	DWTAPLIEAALKDAL	PLIEAALKD	0.2663	2801.7	50.00	Sequence
DRB1_0405	13	SPTGTPHVGLVRTAL	TPHVGLVRT	0.2663	2801.8	50.00	Sequence
DRB1_0405	124	GRNPKLGYDNFDRHL	PKLGYDNFD	0.2663	2802.4	50.00	Sequence
DRB1_0405	255	KKLSKRDPQSNLFAH	SKRDPQSNL	0.2663	2803.1	50.00	Sequence
DRB1_0405	313	SSPARFDQKKADALN	PARFDQKKA	0.2660	2812.9	50.00	Sequence

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DRB1_0405	260	RDPQSNLFAHRDRGF	DPQSNLFAH	0.2603	2990.4	50.00	Sequence
DRB1_0405	261	DPQSNLFAHRDRGFI	DPQSNLFAH	0.2592	3026.9	50.00	Sequence
DRB1_0405	289	SIADDHDLFGLDEMV	DLFGLDEMV	0.2588	3038.5	50.00	Sequence
DRB1_0405	347	LDTHGHHIALDEAAF	HGHHIALDE	0.2578	3073.1	50.00	Sequence
DRB1_0405	420	TDWTAPLIEAALKDA	TAPLIEAAL	0.2565	3116.3	50.00	Sequence
DRB1_0405	159	MPDDDLAWNDLVRGP	DLAWNDLVR	0.2563	3122.0	50.00	Sequence
DRB1_0405	309	ADVNSSPARFDQKKA	ADVNSSPAR	0.2559	3135.4	50.00	Sequence
DRB1_0405	9	RFCPSPTGTPHVGLV	FCPSPTGTP	0.2545	3185.3	50.00	Sequence
DRB1_0405	400	ELGPDGAAVLDAALA	GAAVLDAAL	0.2529	3240.6	50.00	Sequence
DRB1_0405	312	NSSPARFDQKKADAL	PARFDQKKA	0.2518	3279.1	50.00	Sequence
DRB1_0405	349	THGHHIALDEAAFAA	IALDEAAFA	0.2516	3284.9	50.00	Sequence
DRB1_0405	233	RIGVAERIPKFAHLP	ERIPKFAHL	0.2507	3317.1	50.00	Sequence
DRB1_0405	97	LARLLAAGEAYHAFS	LARLLAAGE	0.2503	3334.3	50.00	Sequence
DRB1_0405	452	VAATGTTVSPPLFES	VAATGTTVS	0.2493	3367.7	50.00	Sequence
DRB1_0405	32	YARHTGGTFVFRIED	YARHTGGTF	0.2493	3368.2	50.00	Sequence
DRB1_0405	310	DVNSSPARFDQKKAD	ARFDQKKAD	0.2492	3374.2	50.00	Sequence
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DRB1_0405	99	RLLAAGEAYHAFSTP	LLAAGEAYH	0.2470	3452.2	50.00	Sequence
DRB1_0405	232	IRIGVAERIPKFAHL	GVAERIPKF	0.2457	3504.1	50.00	Sequence
DRB1_0405	311	VNSSPARFDQKKADA	PARFDQKKA	0.2442	3558.8	50.00	Sequence
DRB1_0405	158	RMPDDDLAWNDLVRG	DDLAWNDLV	0.2437	3578.6	50.00	Sequence
DRB1_0405	389	QYVIDPKAAAKELGP	YVIDPKAAA	0.2435	3587.2	50.00	Sequence
DRB1_0405	350	HGHHIALDEAAFAAA	IALDEAAFA	0.2433	3595.1	50.00	Sequence
DRB1_0405	372	IVVLGDAWELLKFFN	IVVLGDAWE	0.2431	3603.5	50.00	Sequence
DRB1_0405	246	LPTVLGEGTKKLSKR	LGEGTKKLS	0.2420	3645.5	50.00	Sequence
DRB1_0405	197	LVNPCDDALMKITHV	DALMKITHV	0.2415	3664.5	50.00	Sequence
DRB1_0405	43	RIEDTDAQRDSEESY	RIEDTDAQR	0.2415	3667.7	50.00	Sequence
DRB1_0405	455	TGTTVSPPLFESLEL	TGTTVSPPL	0.2403	3711.8	50.00	Sequence
DRB1_0405	145	AYLAEGRQPVVRLRM	YLAEGRQPV	0.2368	3858.8	50.00	Sequence
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DRB1_0405	321	KKADALNAEHIRMLD	LNAEHIRML	0.2324	4045.2	50.00	Sequence
DRB1_0405	254	TKKLSKRDPQSNLFA	KLSKRDPQS	0.2320	4061.2	50.00	Sequence
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DRB1_0405	12	PSPTGTPHVGLVRTA	TPHVGLVRT	0.2300	4152.8	50.00	Sequence
DRB1_0405	244	AHLPTVLGEGTKKLS	AHLPTVLGE	0.2297	4165.0	50.00	Sequence
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DRB1_0405	399	KELGPDGAAVLDAAL	GAAVLDAAL	0.2287	4212.2	50.00	Sequence
DRB1_0405	453	AATGTTVSPPLFESL	TGTTVSPPL	0.2267	4301.4	50.00	Sequence
DRB1_0405	454	ATGTTVSPPLFESLE	TGTTVSPPL	0.2262	4324.5	50.00	Sequence
DRB1_0405	123	AGRNPKLGYDNFDRH	PKLGYDNFD	0.2236	4448.8	50.00	Sequence
DRB1_0405	115	EVEARHVAAGRNPKL	VEARHVAAG	0.2233	4463.6	50.00	Sequence
DRB1_0405	265	NLFAHRDRGFIPEGL	FAHRDRGFI	0.2227	4491.5	50.00	Sequence
DRB1_0405	10	FCPSPTGTPHVGLVR	FCPSPTGTP	0.2215	4550.9	50.00	Sequence
DRB1_0405	357	DEAAFAAAAELVQTR	FAAAAELVQ	0.2210	4575.5	50.00	Sequence
DRB1_0405	11	CPSPTGTPHVGLVRT	TPHVGLVRT	0.2207	4589.4	50.00	Sequence
DRB1_0405	245	HLPTVLGEGTKKLSK	VLGEGTKKL	0.2199	4630.8	50.00	Sequence
DRB1_0405	345	DHLDTHGHHIALDEA	DTHGHHIAL	0.2179	4731.9	50.00	Sequence
DRB1_0405	68	GLDWDEGPEVGGPYG	LDWDEGPEV	0.2153	4868.4	50.00	Sequence
DRB1_0405	114	EEVEARHVAAGRNPK	VEARHVAAG	0.2142	4925.7	50.00	Sequence
DRB1_0405	351	GHHIALDEAAFAAAA	IALDEAAFA	0.2136	4958.8	50.00	Sequence
DRB1_0405	262	PQSNLFAHRDRGFIP	FAHRDRGFI	0.2128	4999.8	50.00	Sequence
DRB1_0405	143	RAAYLAEGRQPVVRL	YLAEGRQPV	0.2122	5034.0	50.00	Sequence
DRB1_0405	252	EGTKKLSKRDPQSNL	GTKKLSKRD	0.2104	5132.0	50.00	Sequence
DRB1_0405	264	SNLFAHRDRGFIPEG	FAHRDRGFI	0.2088	5222.6	50.00	Sequence
DRB1_0405	135	DRHLTDAQRAAYLAE	DRHLTDAQR	0.2082	5254.7	50.00	Sequence
DRB1_0405	356	LDEAAFAAAAELVQT	FAAAAELVQ	0.2059	5390.8	50.00	Sequence
DRB1_0405	316	ARFDQKKADALNAEH	ARFDQKKAD	0.2040	5499.8	50.00	Sequence
DRB1_0405	263	QSNLFAHRDRGFIPE	FAHRDRGFI	0.2024	5594.9	50.00	Sequence
DRB1_0405	113	PEEVEARHVAAGRNP	EVEARHVAA	0.2021	5611.5	50.00	Sequence
DRB1_0405	288	WSIADDHDLFGLDEM	HDLFGLDEM	0.2017	5639.1	50.00	Sequence
DRB1_0405	142	QRAAYLAEGRQPVVR	YLAEGRQPV	0.2017	5641.4	50.00	Sequence
DRB1_0405	342	RLRDHLDTHGHHIAL	RLRDHLDTH	0.2012	5667.7	50.00	Sequence

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   DRB1_0405   77  VGGPYGPYRQSQRAE  GPYRQSQRA        0.2008       5692.1                 50.00     Sequence
   DRB1_0405  141  AQRAAYLAEGRQPVV  YLAEGRQPV        0.1982       5858.4                 50.00     Sequence
   DRB1_0405  116  VEARHVAAGRNPKLG  VEARHVAAG        0.1962       5984.3                 50.00     Sequence
   DRB1_0405  122  AAGRNPKLGYDNFDR  PKLGYDNFD        0.1959       6000.9                 50.00     Sequence
   DRB1_0405  286  LGWSIADDHDLFGLD  LGWSIADDH        0.1925       6232.0                 50.00     Sequence
   DRB1_0405   46  DTDAQRDSEESYLAL  QRDSEESYL        0.1907       6352.4                 50.00     Sequence
   DRB1_0405  352  HHIALDEAAFAAAAE  IALDEAAFA        0.1903       6376.4                 50.00     Sequence
   DRB1_0405  390  YVIDPKAAAKELGPD  YVIDPKAAA        0.1885       6504.1                 50.00     Sequence
   DRB1_0405  251  GEGTKKLSKRDPQSN  GTKKLSKRD        0.1883       6516.9                 50.00     Sequence
   DRB1_0405   31  AYARHTGGTFVFRIE  YARHTGGTF        0.1876       6570.1                 50.00     Sequence
   DRB1_0405  196  TLVNPCDDALMKITH  LVNPCDDAL        0.1871       6602.8                 50.00     Sequence
   DRB1_0405   98  ARLLAAGEAYHAFST  LLAAGEAYH        0.1828       6921.7                 50.00     Sequence
   DRB1_0405  108  HAFSTPEEVEARHVA  HAFSTPEEV        0.1815       7016.7                 50.00     Sequence
   DRB1_0405   30  WAYARHTGGTFVFRI  YARHTGGTF        0.1810       7056.9                 50.00     Sequence
   DRB1_0405  344  RDHLDTHGHHIALDE  HGHHIALDE        0.1804       7100.4                 50.00     Sequence
   DRB1_0405  140  DAQRAAYLAEGRQPV  YLAEGRQPV        0.1790       7208.7                 50.00     Sequence
   DRB1_0405  355  ALDEAAFAAAAELVQ  FAAAAELVQ        0.1781       7281.4                 50.00     Sequence
   DRB1_0405   76  EVGGPYGPYRQSQRA  GPYGPYRQS        0.1761       7437.3                 50.00     Sequence
   DRB1_0405  112  TPEEVEARHVAAGRN  EVEARHVAA        0.1749       7539.7                 50.00     Sequence
   DRB1_0405  353  HIALDEAAFAAAAEL  IALDEAAFA        0.1725       7730.8                 50.00     Sequence
   DRB1_0405  287  GWSIADDHDLFGLDE  WSIADDHDL        0.1691       8027.5                 50.00     Sequence
   DRB1_0405  121  VAAGRNPKLGYDNFD  GRNPKLGYD        0.1680       8117.6                 50.00     Sequence
   DRB1_0405  117  EARHVAAGRNPKLGY  ARHVAAGRN        0.1654       8348.3                 50.00     Sequence
   DRB1_0405  343  LRDHLDTHGHHIALD  LRDHLDTHG        0.1646       8421.4                 50.00     Sequence
   DRB1_0405   29  NWAYARHTGGTFVFR  YARHTGGTF        0.1645       8436.5                 50.00     Sequence
   DRB1_0405  136  RHLTDAQRAAYLAEG  RHLTDAQRA        0.1628       8586.2                 50.00     Sequence
   DRB1_0405   45  EDTDAQRDSEESYLA  QRDSEESYL        0.1611       8750.7                 50.00     Sequence
   DRB1_0405  320  QKKADALNAEHIRML  LNAEHIRML        0.1581       9039.1                 50.00     Sequence
   DRB1_0405  398  AKELGPDGAAVLDAA  ELGPDGAAV        0.1575       9093.4                 50.00     Sequence
   DRB1_0405   44  IEDTDAQRDSEESYL  IEDTDAQRD        0.1564       9203.9                 50.00     Sequence
   DRB1_0405  118  ARHVAAGRNPKLGYD  HVAAGRNPK        0.1536       9492.9                 50.00     Sequence
   DRB1_0405  354  IALDEAAFAAAAELV  IALDEAAFA        0.1522       9634.1                 50.00     Sequence
   DRB1_0405  139  TDAQRAAYLAEGRQP  AQRAAYLAE        0.1477      10109.6                 50.00     Sequence
   DRB1_0405  317  RFDQKKADALNAEHI  FDQKKADAL        0.1464      10261.5                 50.00     Sequence
   DRB1_0405  397  AAKELGPDGAAVLDA  ELGPDGAAV        0.1451      10401.2                 50.00     Sequence
   DRB1_0405  318  FDQKKADALNAEHIR  FDQKKADAL        0.1421      10741.5                 50.00     Sequence
   DRB1_0405  138  LTDAQRAAYLAEGRQ  QRAAYLAEG        0.1407      10915.3                 50.00     Sequence
   DRB1_0405   69  LDWDEGPEVGGPYGP  LDWDEGPEV        0.1401      10986.8                 50.00     Sequence
   DRB1_0405  137  HLTDAQRAAYLAEGR  HLTDAQRAA        0.1387      11152.5                 50.00     Sequence
   DRB1_0405  120  HVAAGRNPKLGYDNF  GRNPKLGYD        0.1357      11518.8                 50.00     Sequence
   DRB1_0405  119  RHVAAGRNPKLGYDN  HVAAGRNPK        0.1341      11722.3                 50.00     Sequence
   DRB1_0405   75  PEVGGPYGPYRQSQR  GPYGPYRQS        0.1292      12355.6                 50.00     Sequence
   DRB1_0405  319  DQKKADALNAEHIRM  KKADALNAE        0.1190      13797.1                 50.00     Sequence
   DRB1_0405  109  AFSTPEEVEARHVAA  AFSTPEEVE        0.1171      14087.6                 50.00     Sequence
   DRB1_0405  111  STPEEVEARHVAAGR  EVEARHVAA        0.1044      16166.2                 50.00     Sequence
   DRB1_0405  110  FSTPEEVEARHVAAG  FSTPEEVEA        0.1005      16863.4                 50.00     Sequence
   DRB1_0405  396  AAAKELGPDGAAVLD  KELGPDGAA        0.0987      17185.0                 50.00     Sequence
   DRB1_0405   74  GPEVGGPYGPYRQSQ  GPYGPYRQS        0.0986      17200.2                 50.00     Sequence
   DRB1_0405   73  EGPEVGGPYGPYRQS  GPYGPYRQS        0.0877      19358.4                 50.00     Sequence
   DRB1_0405  395  KAAAKELGPDGAAVL  AAKELGPDG        0.0843      20087.3                 50.00     Sequence
   DRB1_0405  394  PKAAAKELGPDGAAV  AAKELGPDG        0.0828      20416.2                 50.00     Sequence
   DRB1_0405   70  DWDEGPEVGGPYGPY  DWDEGPEVG        0.0786      21364.2                 50.00     Sequence
   DRB1_0405  393  DPKAAAKELGPDGAA  AAAKELGPD        0.0771      21703.2                 50.00     Sequence
   DRB1_0405  392  IDPKAAAKELGPDGA  AAAKELGPD        0.0685      23834.1                 50.00     Sequence
   DRB1_0405  391  VIDPKAAAKELGPDG  VIDPKAAAK        0.0667      24285.2                 50.00     Sequence
   DRB1_0405   71  WDEGPEVGGPYGPYR  WDEGPEVGG        0.0601      26095.6                 50.00     Sequence
   DRB1_0405   72  DEGPEVGGPYGPYRQ  GPEVGGPYG        0.0562      27217.0                 50.00     Sequence
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Allele: DRB1_0405. Number of high binders 12. Number of weak binders 163. Number of peptides 476

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0701   87  SQRAEIYRDVLARLL  YRDVLARLL        0.8606          4.5           SB     2.00     Sequence
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DRB1_0701   88  QRAEIYRDVLARLLA  YRDVLARLL        0.8470          5.2          SB     2.00     Sequence
DRB1_0701   22  LVRTALFNWAYARHT  FNWAYARHT        0.8450          5.4          SB     2.00     Sequence
DRB1_0701   27  LFNWAYARHTGGTFV  FNWAYARHT        0.8392          5.7          SB     2.00     Sequence
DRB1_0701   24  RTALFNWAYARHTGG  FNWAYARHT        0.8275          6.5          SB     4.00     Sequence
DRB1_0701   89  RAEIYRDVLARLLAA  YRDVLARLL        0.8271          6.5          SB     4.00     Sequence
DRB1_0701  211  VLRGEDLLPSTPRQL  LLPSTPRQL        0.8231          6.8          SB     4.00     Sequence
DRB1_0701   23  VRTALFNWAYARHTG  FNWAYARHT        0.8224          6.8          SB     4.00     Sequence
DRB1_0701   28  FNWAYARHTGGTFVF  FNWAYARHT        0.8210          6.9          SB     4.00     Sequence
DRB1_0701  212  LRGEDLLPSTPRQLA  LLPSTPRQL        0.8144          7.5          SB     4.00     Sequence
DRB1_0701   26  ALFNWAYARHTGGTF  FNWAYARHT        0.8089          7.9          SB     4.00     Sequence
DRB1_0701  213  RGEDLLPSTPRQLAL  LLPSTPRQL        0.8041          8.3          SB     4.00     Sequence
DRB1_0701   25  TALFNWAYARHTGGT  FNWAYARHT        0.7975          8.9          SB     4.00     Sequence
DRB1_0701  473  DRSMQRLRAARQLVG  RLRAARQLV        0.7934          9.3          SB     4.00     Sequence
DRB1_0701  367  LVQTRIVVLGDAWEL  VVLGDAWEL        0.7919          9.5          SB     4.00     Sequence
DRB1_0701   90  AEIYRDVLARLLAAG  YRDVLARLL        0.7917          9.5          SB     4.00     Sequence
DRB1_0701  180  SVPDFALTRASGDPL  LTRASGDPL        0.7869         10.0          SB     4.00     Sequence
DRB1_0701   91  EIYRDVLARLLAAGE  YRDVLARLL        0.7776         11.1          SB     4.00     Sequence
DRB1_0701  214  GEDLLPSTPRQLALH  LLPSTPRQL        0.7760         11.3          SB     8.00     Sequence
DRB1_0701  472  RDRSMQRLRAARQLV  RLRAARQLV        0.7695         12.1          SB     8.00     Sequence
DRB1_0701  368  VQTRIVVLGDAWELL  VVLGDAWEL        0.7651         12.7          SB     8.00     Sequence
DRB1_0701  181  VPDFALTRASGDPLY  LTRASGDPL        0.7645         12.8          SB     8.00     Sequence
DRB1_0701   92  IYRDVLARLLAAGEA  YRDVLARLL        0.7607         13.3          SB     8.00     Sequence
DRB1_0701  474  RSMQRLRAARQLVGH  RLRAARQLV        0.7598         13.4          SB     8.00     Sequence
DRB1_0701  215  EDLLPSTPRQLALHQ  LLPSTPRQL        0.7569         13.9          SB     8.00     Sequence
DRB1_0701   93  YRDVLARLLAAGEAY  YRDVLARLL        0.7485         15.2          SB     8.00     Sequence
DRB1_0701  217  LLPSTPRQLALHQAL  LLPSTPRQL        0.7332         17.9          SB     8.00     Sequence
DRB1_0701  216  DLLPSTPRQLALHQA  LLPSTPRQL        0.7311         18.4          SB     8.00     Sequence
DRB1_0701  182  PDFALTRASGDPLYT  LTRASGDPL        0.7297         18.6          SB     8.00     Sequence
DRB1_0701  369  QTRIVVLGDAWELLK  VVLGDAWEL        0.7264         19.3          SB     8.00     Sequence
DRB1_0701  475  SMQRLRAARQLVGHA  RLRAARQLV        0.7212         20.4          SB     8.00     Sequence
DRB1_0701  445  KAFSPIRVAATGTTV  RVAATGTTV        0.7094         23.2          SB     8.00     Sequence
DRB1_0701  183  DFALTRASGDPLYTL  LTRASGDPL        0.7002         25.6          SB    16.00     Sequence
DRB1_0701  361  FAAAAELVQTRIVVL  LVQTRIVVL        0.6929         27.7          SB    16.00     Sequence
DRB1_0701  370  TRIVVLGDAWELLKF  VVLGDAWEL        0.6877         29.3          SB    16.00     Sequence
DRB1_0701   29  NWAYARHTGGTFVFR  ARHTGGTFV        0.6847         30.3          SB    16.00     Sequence
DRB1_0701  446  AFSPIRVAATGTTVS  RVAATGTTV        0.6800         31.9          SB    16.00     Sequence
DRB1_0701    0  VTATETVRVRFCPSP  VTATETVRV        0.6783         32.5          SB    16.00     Sequence
DRB1_0701  354  IALDEAAFAAAAELV  AFAAAAELV        0.6778         32.7          SB    16.00     Sequence
DRB1_0701  355  ALDEAAFAAAAELVQ  AFAAAAELV        0.6684         36.2          SB    16.00     Sequence
DRB1_0701  184  FALTRASGDPLYTLV  LTRASGDPL        0.6666         36.9          SB    16.00     Sequence
DRB1_0701  371  RIVVLGDAWELLKFF  VVLGDAWEL        0.6641         37.9          SB    16.00     Sequence
DRB1_0701   30  WAYARHTGGTFVFRI  ARHTGGTFV        0.6635         38.1          SB    16.00     Sequence
DRB1_0701  276  PEGLLNYLALLGWSI  YLALLGWSI        0.6569         41.0          SB    16.00     Sequence
DRB1_0701  353  HIALDEAAFAAAAEL  AAFAAAAEL        0.6515         43.4          SB    16.00     Sequence
DRB1_0701  410  DAALAALTSVTDWTA  LTSVTDWTA        0.6507         43.8          SB    16.00     Sequence
DRB1_0701  450  IRVAATGTTVSPPLF  GTTVSPPLF        0.6492         44.5          SB    16.00     Sequence
DRB1_0701  362  AAAAELVQTRIVVLG  LVQTRIVVL        0.6454         46.4          SB    16.00     Sequence
DRB1_0701  413  LAALTSVTDWTAPLI  LTSVTDWTA        0.6407         48.8          SB    16.00     Sequence
DRB1_0701   31  AYARHTGGTFVFRIE  ARHTGGTFV        0.6347         52.1          WB    16.00     Sequence
DRB1_0701  261  DPQSNLFAHRDRGFI  FAHRDRGFI        0.6329         53.1          WB    16.00     Sequence
DRB1_0701  320  QKKADALNAEHIRML  LNAEHIRML        0.6327         53.2          WB    16.00     Sequence
DRB1_0701  447  FSPIRVAATGTTVSP  RVAATGTTV        0.6317         53.8          WB    16.00     Sequence
DRB1_0701  444  RKAFSPIRVAATGTT  IRVAATGTT        0.6307         54.4          WB    16.00     Sequence
DRB1_0701  372  IVVLGDAWELLKFFN  VVLGDAWEL        0.6265         56.9          WB    16.00     Sequence
DRB1_0701  414  AALTSVTDWTAPLIE  LTSVTDWTA        0.6244         58.2          WB    16.00     Sequence
DRB1_0701  277  EGLLNYLALLGWSIA  YLALLGWSI        0.6233         58.9          WB    16.00     Sequence
DRB1_0701  282  YLALLGWSIADDHDL  WSIADDHDL        0.6210         60.4          WB    16.00     Sequence
DRB1_0701  356  LDEAAFAAAAELVQT  AFAAAAELV        0.6197         61.2          WB    16.00     Sequence
DRB1_0701  200  PCDDALMKITHVLRG  MKITHVLRG        0.6126         66.1          WB    16.00     Sequence
DRB1_0701  451  RVAATGTTVSPPLFE  GTTVSPPLF        0.6103         67.8          WB    16.00     Sequence
DRB1_0701   32  YARHTGGTFVFRIED  ARHTGGTFV        0.6097         68.2          WB    16.00     Sequence
DRB1_0701  411  AALAALTSVTDWTAP  LTSVTDWTA        0.6073         70.1          WB    16.00     Sequence
DRB1_0701  243  FAHLPTVLGEGTKKL  VLGEGTKKL        0.6021         74.0          WB    16.00     Sequence
DRB1_0701  363  AAAELVQTRIVVLGD  LVQTRIVVL        0.6012         74.8          WB    16.00     Sequence
DRB1_0701  415  ALTSVTDWTAPLIEA  LTSVTDWTA        0.5977         77.7          WB    32.00     Sequence
DRB1_0701  262  PQSNLFAHRDRGFIP  FAHRDRGFI        0.5973         78.0          WB    32.00     Sequence
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DRB1_0701  373  VVLGDAWELLKFFND  VVLGDAWEL        0.5963         78.9          WB    32.00     Sequence
DRB1_0701  185  ALTRASGDPLYTLVN  LTRASGDPL        0.5930         81.7          WB    32.00     Sequence
DRB1_0701  412  ALAALTSVTDWTAPL  LTSVTDWTA        0.5920         82.6          WB    32.00     Sequence
DRB1_0701  226  ALHQALIRIGVAERI  IRIGVAERI        0.5907         83.8          WB    32.00     Sequence
DRB1_0701  321  KKADALNAEHIRMLD  LNAEHIRML        0.5880         86.3          WB    32.00     Sequence
DRB1_0701  327  NAEHIRMLDVGDFTV  MLDVGDFTV        0.5875         86.8          WB    32.00     Sequence
DRB1_0701  448  SPIRVAATGTTVSPP  IRVAATGTT        0.5838         90.3          WB    32.00     Sequence
DRB1_0701  449  PIRVAATGTTVSPPL  RVAATGTTV        0.5837         90.4          WB    32.00     Sequence
DRB1_0701   16  GTPHVGLVRTALFNW  LVRTALFNW        0.5809         93.2          WB    32.00     Sequence
DRB1_0701  278  GLLNYLALLGWSIAD  YLALLGWSI        0.5749         99.4          WB    32.00     Sequence
DRB1_0701  244  AHLPTVLGEGTKKLS  VLGEGTKKL        0.5678        107.3          WB    32.00     Sequence
DRB1_0701  357  DEAAFAAAAELVQTR  AFAAAAELV        0.5657        109.9          WB    32.00     Sequence
DRB1_0701  416  LTSVTDWTAPLIEAA  LTSVTDWTA        0.5644        111.4          WB    32.00     Sequence
DRB1_0701  359  AAFAAAAELVQTRIV  AELVQTRIV        0.5642        111.7          WB    32.00     Sequence
DRB1_0701  322  KADALNAEHIRMLDV  LNAEHIRML        0.5629        113.3          WB    32.00     Sequence
DRB1_0701  263  QSNLFAHRDRGFIPE  FAHRDRGFI        0.5619        114.4          WB    32.00     Sequence
DRB1_0701  201  CDDALMKITHVLRGE  MKITHVLRG        0.5580        119.4          WB    32.00     Sequence
DRB1_0701  364  AAELVQTRIVVLGDA  LVQTRIVVL        0.5569        120.9          WB    32.00     Sequence
DRB1_0701  305  AFDVADVNSSPARFD  VNSSPARFD        0.5565        121.3          WB    32.00     Sequence
DRB1_0701  340  TVRLRDHLDTHGHHI  HLDTHGHHI        0.5523        127.0          WB    32.00     Sequence
DRB1_0701   14  PTGTPHVGLVRTALF  VGLVRTALF        0.5518        127.7          WB    32.00     Sequence
DRB1_0701  328  AEHIRMLDVGDFTVR  MLDVGDFTV        0.5484        132.5          WB    32.00     Sequence
DRB1_0701  186  LTRASGDPLYTLVNP  LTRASGDPL        0.5470        134.5          WB    32.00     Sequence
DRB1_0701  358  EAAFAAAAELVQTRI  AFAAAAELV        0.5417        142.4          WB    32.00     Sequence
DRB1_0701  227  LHQALIRIGVAERIP  IRIGVAERI        0.5417        142.5          WB    32.00     Sequence
DRB1_0701   15  TGTPHVGLVRTALFN  VGLVRTALF        0.5414        142.8          WB    32.00     Sequence
DRB1_0701   17  TPHVGLVRTALFNWA  LVRTALFNW        0.5397        145.5          WB    32.00     Sequence
DRB1_0701  333  MLDVGDFTVRLRDHL  FTVRLRDHL        0.5391        146.5          WB    32.00     Sequence
DRB1_0701  204  ALMKITHVLRGEDLL  HVLRGEDLL        0.5351        153.0          WB    32.00     Sequence
DRB1_0701  283  LALLGWSIADDHDLF  WSIADDHDL        0.5337        155.3          WB    32.00     Sequence
DRB1_0701  438  GLALKPRKAFSPIRV  RKAFSPIRV        0.5335        155.6          WB    32.00     Sequence
DRB1_0701   33  ARHTGGTFVFRIEDT  ARHTGGTFV        0.5315        159.0          WB    32.00     Sequence
DRB1_0701  341  VRLRDHLDTHGHHIA  HLDTHGHHI        0.5290        163.4          WB    32.00     Sequence
DRB1_0701  141  AQRAAYLAEGRQPVV  YLAEGRQPV        0.5266        167.7          WB    32.00     Sequence
DRB1_0701    4  ETVRVRFCPSPTGTP  FCPSPTGTP        0.5264        168.0          WB    32.00     Sequence
DRB1_0701  365  AELVQTRIVVLGDAW  LVQTRIVVL        0.5262        168.4          WB    32.00     Sequence
DRB1_0701  245  HLPTVLGEGTKKLSK  VLGEGTKKL        0.5253        170.0          WB    32.00     Sequence
DRB1_0701  306  FDVADVNSSPARFDQ  VNSSPARFD        0.5248        171.0          WB    32.00     Sequence
DRB1_0701    6  VRVRFCPSPTGTPHV  FCPSPTGTP        0.5231        174.2          WB    32.00     Sequence
DRB1_0701  199  NPCDDALMKITHVLR  LMKITHVLR        0.5224        175.4          WB    32.00     Sequence
DRB1_0701   18  PHVGLVRTALFNWAY  LVRTALFNW        0.5220        176.2          WB    32.00     Sequence
DRB1_0701  329  EHIRMLDVGDFTVRL  MLDVGDFTV        0.5201        180.0          WB    32.00     Sequence
DRB1_0701  140  DAQRAAYLAEGRQPV  YLAEGRQPV        0.5190        182.0          WB    32.00     Sequence
DRB1_0701  279  LLNYLALLGWSIADD  YLALLGWSI        0.5178        184.5          WB    32.00     Sequence
DRB1_0701  264  SNLFAHRDRGFIPEG  FAHRDRGFI        0.5173        185.4          WB    32.00     Sequence
DRB1_0701  360  AFAAAAELVQTRIVV  AFAAAAELV        0.5094        202.1          WB    32.00     Sequence
DRB1_0701  323  ADALNAEHIRMLDVG  LNAEHIRML        0.5094        202.1          WB    32.00     Sequence
DRB1_0701  342  RLRDHLDTHGHHIAL  HLDTHGHHI        0.5024        217.9          WB    32.00     Sequence
DRB1_0701  452  VAATGTTVSPPLFES  GTTVSPPLF        0.5011        220.9          WB    32.00     Sequence
DRB1_0701  202  DDALMKITHVLRGED  MKITHVLRG        0.5007        221.8          WB    32.00     Sequence
DRB1_0701  266  LFAHRDRGFIPEGLL  FAHRDRGFI        0.4982        228.0          WB    32.00     Sequence
DRB1_0701  219  PSTPRQLALHQALIR  RQLALHQAL        0.4940        238.5          WB    32.00     Sequence
DRB1_0701    8  VRFCPSPTGTPHVGL  FCPSPTGTP        0.4928        241.8          WB    32.00     Sequence
DRB1_0701    5  TVRVRFCPSPTGTPH  FCPSPTGTP        0.4921        243.5          WB    32.00     Sequence
DRB1_0701  265  NLFAHRDRGFIPEGL  FAHRDRGFI        0.4903        248.4          WB    32.00     Sequence
DRB1_0701  218  LPSTPRQLALHQALI  RQLALHQAL        0.4900        249.0          WB    32.00     Sequence
DRB1_0701   54  EESYLALLDALRWLG  LLDALRWLG        0.4889        252.0          WB    32.00     Sequence
DRB1_0701  280  LNYLALLGWSIADDH  YLALLGWSI        0.4881        254.4          WB    32.00     Sequence
DRB1_0701  307  DVADVNSSPARFDQK  VNSSPARFD        0.4874        256.3          WB    32.00     Sequence
DRB1_0701  228  HQALIRIGVAERIPK  IRIGVAERI        0.4852        262.4          WB    32.00     Sequence
DRB1_0701  366  ELVQTRIVVLGDAWE  LVQTRIVVL        0.4852        262.4          WB    32.00     Sequence
DRB1_0701   19  HVGLVRTALFNWAYA  LVRTALFNW        0.4842        265.3          WB    32.00     Sequence
DRB1_0701  237  AERIPKFAHLPTVLG  FAHLPTVLG        0.4827        269.6          WB    32.00     Sequence
DRB1_0701  403  PDGAAVLDAALAALT  LDAALAALT        0.4822        271.2          WB    32.00     Sequence
DRB1_0701  220  STPRQLALHQALIRI  RQLALHQAL        0.4817        272.7          WB    32.00     Sequence
DRB1_0701  205  LMKITHVLRGEDLLP  HVLRGEDLL        0.4813        273.7          WB    32.00     Sequence
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DRB1_0701  439  LALKPRKAFSPIRVA  RKAFSPIRV        0.4809        274.8         WB    32.00     Sequence
DRB1_0701   55  ESYLALLDALRWLGL  LLDALRWLG        0.4804        276.4         WB    32.00     Sequence
DRB1_0701  471  GRDRSMQRLRAARQL  QRLRAARQL        0.4797        278.7         WB    32.00     Sequence
DRB1_0701  324  DALNAEHIRMLDVGD  LNAEHIRML        0.4782        283.0         WB    32.00     Sequence
DRB1_0701  246  LPTVLGEGTKKLSKR  VLGEGTKKL        0.4743        295.2         WB    32.00     Sequence
DRB1_0701  443  PRKAFSPIRVAATGT  PIRVAATGT        0.4739        296.6         WB    32.00     Sequence
DRB1_0701  406  AAVLDAALAALTSVT  LDAALAALT        0.4717        303.7         WB    32.00     Sequence
DRB1_0701  284  ALLGWSIADDHDLFG  WSIADDHDL        0.4703        308.2         WB    32.00     Sequence
DRB1_0701  330  HIRMLDVGDFTVRLR  MLDVGDFTV        0.4702        308.8         WB    32.00     Sequence
DRB1_0701  325  ALNAEHIRMLDVGDF  LNAEHIRML        0.4694        311.3         WB    32.00     Sequence
DRB1_0701  319  DQKKADALNAEHIRM  ALNAEHIRM        0.4694        311.3         WB    32.00     Sequence
DRB1_0701  142  QRAAYLAEGRQPVVR  YLAEGRQPV        0.4663        321.9         WB    32.00     Sequence
DRB1_0701    7  RVRFCPSPTGTPHVG  FCPSPTGTP        0.4657        323.9         WB    32.00     Sequence
DRB1_0701  335  DVGDFTVRLRDHLDT  FTVRLRDHL        0.4590        348.5         WB    32.00     Sequence
DRB1_0701  178  AGSVPDFALTRASGD  FALTRASGD        0.4579        352.7         WB    32.00     Sequence
DRB1_0701  407  AVLDAALAALTSVTD  LDAALAALT        0.4562        359.2         WB    32.00     Sequence
DRB1_0701  281  NYLALLGWSIADDHD  YLALLGWSI        0.4554        362.2         WB    32.00     Sequence
DRB1_0701  453  AATGTTVSPPLFESL  GTTVSPPLF        0.4546        365.3         WB    32.00     Sequence
DRB1_0701  441  LKPRKAFSPIRVAAT  FSPIRVAAT        0.4541        367.2         WB    32.00     Sequence
DRB1_0701  404  DGAAVLDAALAALTS  LDAALAALT        0.4531        371.5         WB    50.00     Sequence
DRB1_0701  334  LDVGDFTVRLRDHLD  FTVRLRDHL        0.4531        371.6         WB    50.00     Sequence
DRB1_0701  203  DALMKITHVLRGEDL  LMKITHVLR        0.4522        375.1         WB    50.00     Sequence
DRB1_0701    2  ATETVRVRFCPSPTG  VRFCPSPTG        0.4517        377.2         WB    50.00     Sequence
DRB1_0701    9  RFCPSPTGTPHVGLV  FCPSPTGTP        0.4510        379.8         WB    50.00     Sequence
DRB1_0701  308  VADVNSSPARFDQKK  VNSSPARFD        0.4503        382.7         WB    50.00     Sequence
DRB1_0701   20  VGLVRTALFNWAYAR  LVRTALFNW        0.4497        385.4         WB    50.00     Sequence
DRB1_0701  221  TPRQLALHQALIRIG  RQLALHQAL        0.4492        387.3         WB    50.00     Sequence
DRB1_0701  343  LRDHLDTHGHHIALD  HLDTHGHHI        0.4481        392.0         WB    50.00     Sequence
DRB1_0701  405  GAAVLDAALAALTSV  LDAALAALT        0.4473        395.4         WB    50.00     Sequence
DRB1_0701  331  IRMLDVGDFTVRLRD  MLDVGDFTV        0.4442        408.9         WB    50.00     Sequence
DRB1_0701  247  PTVLGEGTKKLSKRD  VLGEGTKKL        0.4427        415.9         WB    50.00     Sequence
DRB1_0701  378  AWELLKFFNDDQYVI  FFNDDQYVI        0.4416        420.5         WB    50.00     Sequence
DRB1_0701  229  QALIRIGVAERIPKF  IRIGVAERI        0.4414        421.5         WB    50.00     Sequence
DRB1_0701   56  SYLALLDALRWLGLD  LLDALRWLG        0.4390        432.6         WB    50.00     Sequence
DRB1_0701  309  ADVNSSPARFDQKKA  VNSSPARFD        0.4378        438.1         WB    50.00     Sequence
DRB1_0701  285  LLGWSIADDHDLFGL  WSIADDHDL        0.4332        460.5         WB    50.00     Sequence
DRB1_0701  408  VLDAALAALTSVTDW  LDAALAALT        0.4308        472.5         WB    50.00     Sequence
DRB1_0701  238  ERIPKFAHLPTVLGE  FAHLPTVLG        0.4287        483.7         WB    50.00     Sequence
DRB1_0701  145  AYLAEGRQPVVRLRM  RQPVVRLRM        0.4246        505.5               50.00     Sequence
DRB1_0701  143  RAAYLAEGRQPVVRL  YLAEGRQPV        0.4243        507.4               50.00     Sequence
DRB1_0701  222  PRQLALHQALIRIGV  RQLALHQAL        0.4231        513.9               50.00     Sequence
DRB1_0701  260  RDPQSNLFAHRDRGF  LFAHRDRGF        0.4221        519.3               50.00     Sequence
DRB1_0701  310  DVNSSPARFDQKKAD  VNSSPARFD        0.4210        525.7               50.00     Sequence
DRB1_0701  248  TVLGEGTKKLSKRDP  VLGEGTKKL        0.4198        532.7               50.00     Sequence
DRB1_0701  225  LALHQALIRIGVAER  LIRIGVAER        0.4178        544.1               50.00     Sequence
DRB1_0701  332  RMLDVGDFTVRLRDH  MLDVGDFTV        0.4167        550.8               50.00     Sequence
DRB1_0701  172  GPVTFAAGSVPDFAL  AGSVPDFAL        0.4151        560.1               50.00     Sequence
DRB1_0701  170  VRGPVTFAAGSVPDF  VTFAAGSVP        0.4149        561.4               50.00     Sequence
DRB1_0701  440  ALKPRKAFSPIRVAA  RKAFSPIRV        0.4147        563.0               50.00     Sequence
DRB1_0701  454  ATGTTVSPPLFESLE  GTTVSPPLF        0.4142        565.6               50.00     Sequence
DRB1_0701   78  GGPYGPYRQSQRAEI  YRQSQRAEI        0.4136        569.6               50.00     Sequence
DRB1_0701  344  RDHLDTHGHHIALDE  HLDTHGHHI        0.4133        571.6               50.00     Sequence
DRB1_0701  267  FAHRDRGFIPEGLLN  FAHRDRGFI        0.4117        581.2               50.00     Sequence
DRB1_0701   10  FCPSPTGTPHVGLVR  FCPSPTGTP        0.4111        585.2               50.00     Sequence
DRB1_0701  437  EGLALKPRKAFSPIR  PRKAFSPIR        0.4067        613.7               50.00     Sequence
DRB1_0701  115  EVEARHVAAGRNPKL  VAAGRNPKL        0.4065        615.1               50.00     Sequence
DRB1_0701  168  DLVRGPVTFAAGSVP  VTFAAGSVP        0.4063        616.1               50.00     Sequence
DRB1_0701  230  ALIRIGVAERIPKFA  IRIGVAERI        0.4062        617.0               50.00     Sequence
DRB1_0701   57  YLALLDALRWLGLDW  LLDALRWLG        0.4041        631.2               50.00     Sequence
DRB1_0701   53  SEESYLALLDALRWL  LALLDALRW        0.4037        634.1               50.00     Sequence
DRB1_0701   52  DSEESYLALLDALRW  LALLDALRW        0.4037        634.2               50.00     Sequence
DRB1_0701  336  VGDFTVRLRDHLDTH  FTVRLRDHL        0.4007        654.5               50.00     Sequence
DRB1_0701  311  VNSSPARFDQKKADA  VNSSPARFD        0.4006        655.2               50.00     Sequence
DRB1_0701  102  AAGEAYHAFSTPEEV  HAFSTPEEV        0.4006        655.8               50.00     Sequence
DRB1_0701  379  WELLKFFNDDQYVID  FFNDDQYVI        0.3992        665.7               50.00     Sequence
DRB1_0701  442  KPRKAFSPIRVAATG  FSPIRVAAT        0.3972        680.2               50.00     Sequence
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DRB1_0701  286  LGWSIADDHDLFGLD  WSIADDHDL        0.3969        681.9                50.00     Sequence
DRB1_0701  179  GSVPDFALTRASGDP  FALTRASGD        0.3962        687.8                50.00     Sequence
DRB1_0701  268  AHRDRGFIPEGLLNY  FIPEGLLNY        0.3956        692.1                50.00     Sequence
DRB1_0701  456  GTTVSPPLFESLELL  GTTVSPPLF        0.3952        695.2                50.00     Sequence
DRB1_0701    3  TETVRVRFCPSPTGT  VRFCPSPTG        0.3937        706.4                50.00     Sequence
DRB1_0701  249  VLGEGTKKLSKRDPQ  VLGEGTKKL        0.3889        743.6                50.00     Sequence
DRB1_0701  223  RQLALHQALIRIGVA  RQLALHQAL        0.3879        752.0                50.00     Sequence
DRB1_0701   79  GPYGPYRQSQRAEIY  YRQSQRAEI        0.3871        758.6                50.00     Sequence
DRB1_0701  206  MKITHVLRGEDLLPS  HVLRGEDLL        0.3857        770.2                50.00     Sequence
DRB1_0701  455  TGTTVSPPLFESLEL  GTTVSPPLF        0.3797        822.2                50.00     Sequence
DRB1_0701  144  AAYLAEGRQPVVRLR  YLAEGRQPV        0.3775        842.1                50.00     Sequence
DRB1_0701  169  LVRGPVTFAAGSVPD  VTFAAGSVP        0.3767        848.8                50.00     Sequence
DRB1_0701  326  LNAEHIRMLDVGDFT  LNAEHIRML        0.3761        854.7                50.00     Sequence
DRB1_0701  231  LIRIGVAERIPKFAH  IRIGVAERI        0.3754        860.5                50.00     Sequence
DRB1_0701  345  DHLDTHGHHIALDEA  HLDTHGHHI        0.3747        867.1                50.00     Sequence
DRB1_0701  107  YHAFSTPEEVEARHV  PEEVEARHV        0.3747        867.8                50.00     Sequence
DRB1_0701  146  YLAEGRQPVVRLRMP  YLAEGRQPV        0.3746        868.2                50.00     Sequence
DRB1_0701  409  LDAALAALTSVTDWT  LDAALAALT        0.3719        894.0                50.00     Sequence
DRB1_0701  173  PVTFAAGSVPDFALT  AGSVPDFAL        0.3696        916.8                50.00     Sequence
DRB1_0701  198  VNPCDDALMKITHVL  ALMKITHVL        0.3681        931.5                50.00     Sequence
DRB1_0701  337  GDFTVRLRDHLDTHG  FTVRLRDHL        0.3650        963.0                50.00     Sequence
DRB1_0701  239  RIPKFAHLPTVLGEG  FAHLPTVLG        0.3638        976.5                50.00     Sequence
DRB1_0701  171  RGPVTFAAGSVPDFA  VTFAAGSVP        0.3630        984.8                50.00     Sequence
DRB1_0701   58  LALLDALRWLGLDWD  LLDALRWLG        0.3627        988.1                50.00     Sequence
DRB1_0701  269  HRDRGFIPEGLLNYL  FIPEGLLNY        0.3617        998.9                50.00     Sequence
DRB1_0701  287  GWSIADDHDLFGLDE  WSIADDHDL        0.3615       1000.5                50.00     Sequence
DRB1_0701  433  DALIEGLALKPRKAF  LALKPRKAF        0.3593       1025.0                50.00     Sequence
DRB1_0701  103  AGEAYHAFSTPEEVE  HAFSTPEEV        0.3547       1077.0                50.00     Sequence
DRB1_0701  346  HLDTHGHHIALDEAA  HLDTHGHHI        0.3456       1188.5                50.00     Sequence
DRB1_0701  116  VEARHVAAGRNPKLG  VAAGRNPKL        0.3453       1192.4                50.00     Sequence
DRB1_0701  380  ELLKFFNDDQYVIDP  FFNDDQYVI        0.3446       1201.7                50.00     Sequence
DRB1_0701  402  GPDGAAVLDAALAAL  VLDAALAAL        0.3402       1260.3                50.00     Sequence
DRB1_0701  312  NSSPARFDQKKADAL  FDQKKADAL        0.3372       1302.3                50.00     Sequence
DRB1_0701   80  PYGPYRQSQRAEIYR  YRQSQRAEI        0.3341       1345.4                50.00     Sequence
DRB1_0701   86  QSQRAEIYRDVLARL  IYRDVLARL        0.3339       1349.2                50.00     Sequence
DRB1_0701  112  TPEEVEARHVAAGRN  ARHVAAGRN        0.3333       1357.9                50.00     Sequence
DRB1_0701   21  GLVRTALFNWAYARH  LVRTALFNW        0.3331       1360.4                50.00     Sequence
DRB1_0701  288  WSIADDHDLFGLDEM  WSIADDHDL        0.3324       1371.6                50.00     Sequence
DRB1_0701  338  DFTVRLRDHLDTHGH  FTVRLRDHL        0.3324       1371.6                50.00     Sequence
DRB1_0701  104  GEAYHAFSTPEEVEA  HAFSTPEEV        0.3315       1384.2                50.00     Sequence
DRB1_0701  421  DWTAPLIEAALKDAL  LIEAALKDA        0.3315       1385.0                50.00     Sequence
DRB1_0701  434  ALIEGLALKPRKAFS  LALKPRKAF        0.3314       1385.3                50.00     Sequence
DRB1_0701  163  DLAWNDLVRGPVTFA  LVRGPVTFA        0.3309       1393.9                50.00     Sequence
DRB1_0701  174  VTFAAGSVPDFALTR  AGSVPDFAL        0.3297       1412.3                50.00     Sequence
DRB1_0701  192  DPLYTLVNPCDDALM  VNPCDDALM        0.3286       1429.3                50.00     Sequence
DRB1_0701  435  LIEGLALKPRKAFSP  LALKPRKAF        0.3273       1448.2                50.00     Sequence
DRB1_0701  422  WTAPLIEAALKDALI  LIEAALKDA        0.3273       1449.0                50.00     Sequence
DRB1_0701  270  RDRGFIPEGLLNYLA  FIPEGLLNY        0.3250       1484.9                50.00     Sequence
DRB1_0701  232  IRIGVAERIPKFAHL  IRIGVAERI        0.3216       1541.7                50.00     Sequence
DRB1_0701  236  VAERIPKFAHLPTVL  PKFAHLPTV        0.3206       1557.6                50.00     Sequence
DRB1_0701  240  IPKFAHLPTVLGEGT  FAHLPTVLG        0.3206       1558.5                50.00     Sequence
DRB1_0701  113  PEEVEARHVAAGRNP  ARHVAAGRN        0.3185       1593.7                50.00     Sequence
DRB1_0701  108  HAFSTPEEVEARHVA  PEEVEARHV        0.3155       1646.5                50.00     Sequence
DRB1_0701   59  ALLDALRWLGLDWDE  LLDALRWLG        0.3141       1671.7                50.00     Sequence
DRB1_0701  417  TSVTDWTAPLIEAAL  VTDWTAPLI        0.3131       1689.5                50.00     Sequence
DRB1_0701  339  FTVRLRDHLDTHGHH  FTVRLRDHL        0.3068       1809.1                50.00     Sequence
DRB1_0701  117  EARHVAAGRNPKLGY  VAAGRNPKL        0.3055       1834.6                50.00     Sequence
DRB1_0701  164  LAWNDLVRGPVTFAA  LVRGPVTFA        0.3031       1883.3                50.00     Sequence
DRB1_0701  241  PKFAHLPTVLGEGTK  FAHLPTVLG        0.3012       1920.8                50.00     Sequence
DRB1_0701  313  SSPARFDQKKADALN  FDQKKADAL        0.3004       1938.2                50.00     Sequence
DRB1_0701   95  DVLARLLAAGEAYHA  LLAAGEAYH        0.3000       1946.8                50.00     Sequence
DRB1_0701  207  KITHVLRGEDLLPST  HVLRGEDLL        0.2993       1961.5                50.00     Sequence
DRB1_0701  193  PLYTLVNPCDDALMK  VNPCDDALM        0.2980       1988.2                50.00     Sequence
DRB1_0701  167  NDLVRGPVTFAAGSV  PVTFAAGSV        0.2978       1994.4                50.00     Sequence
DRB1_0701  235  GVAERIPKFAHLPTV  PKFAHLPTV        0.2946       2063.2                50.00     Sequence
DRB1_0701  381  LLKFFNDDQYVIDPK  FFNDDQYVI        0.2928       2104.6                50.00     Sequence
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DRB1_0701  189  ASGDPLYTLVNPCDD  YTLVNPCDD        0.2915       2133.9              50.00     Sequence
DRB1_0701  418  SVTDWTAPLIEAALK  VTDWTAPLI        0.2881       2213.2              50.00     Sequence
DRB1_0701  101  LAAGEAYHAFSTPEE  AYHAFSTPE        0.2861       2262.4              50.00     Sequence
DRB1_0701  105  EAYHAFSTPEEVEAR  HAFSTPEEV        0.2861       2262.9              50.00     Sequence
DRB1_0701  271  DRGFIPEGLLNYLAL  FIPEGLLNY        0.2853       2283.1              50.00     Sequence
DRB1_0701  109  AFSTPEEVEARHVAA  PEEVEARHV        0.2849       2293.1              50.00     Sequence
DRB1_0701  224  QLALHQALIRIGVAE  ALHQALIRI        0.2823       2357.5              50.00     Sequence
DRB1_0701  272  RGFIPEGLLNYLALL  FIPEGLLNY        0.2823       2357.8              50.00     Sequence
DRB1_0701   94  RDVLARLLAAGEAYH  LLAAGEAYH        0.2821       2361.6              50.00     Sequence
DRB1_0701  436  IEGLALKPRKAFSPI  LALKPRKAF        0.2818       2371.0              50.00     Sequence
DRB1_0701   81  YGPYRQSQRAEIYRD  YRQSQRAEI        0.2817       2374.0              50.00     Sequence
DRB1_0701  194  LYTLVNPCDDALMKI  VNPCDDALM        0.2812       2385.4              50.00     Sequence
DRB1_0701  147  LAEGRQPVVRLRMPD  RQPVVRLRM        0.2809       2392.4              50.00     Sequence
DRB1_0701  457  TTVSPPLFESLELLG  LFESLELLG        0.2802       2411.9              50.00     Sequence
DRB1_0701  314  SPARFDQKKADALNA  FDQKKADAL        0.2795       2429.5              50.00     Sequence
DRB1_0701  273  GFIPEGLLNYLALLG  FIPEGLLNY        0.2789       2446.1              50.00     Sequence
DRB1_0701   11  CPSPTGTPHVGLVRT  PTGTPHVGL        0.2760       2522.8              50.00     Sequence
DRB1_0701  423  TAPLIEAALKDALIE  LIEAALKDA        0.2752       2545.6              50.00     Sequence
DRB1_0701  425  PLIEAALKDALIEGL  LKDALIEGL        0.2740       2579.8              50.00     Sequence
DRB1_0701   60  LLDALRWLGLDWDEG  LLDALRWLG        0.2685       2736.5              50.00     Sequence
DRB1_0701  100  LLAAGEAYHAFSTPE  AYHAFSTPE        0.2676       2763.0              50.00     Sequence
DRB1_0701  242  KFAHLPTVLGEGTKK  FAHLPTVLG        0.2674       2770.9              50.00     Sequence
DRB1_0701  317  RFDQKKADALNAEHI  FDQKKADAL        0.2667       2791.2              50.00     Sequence
DRB1_0701   96  VLARLLAAGEAYHAF  LLAAGEAYH        0.2666       2795.3              50.00     Sequence
DRB1_0701  274  FIPEGLLNYLALLGW  FIPEGLLNY        0.2660       2811.3              50.00     Sequence
DRB1_0701  382  LKFFNDDQYVIDPKA  FFNDDQYVI        0.2657       2821.9              50.00     Sequence
DRB1_0701  208  ITHVLRGEDLLPSTP  HVLRGEDLL        0.2618       2941.5              50.00     Sequence
DRB1_0701  191  GDPLYTLVNPCDDAL  YTLVNPCDD        0.2613       2958.3              50.00     Sequence
DRB1_0701  195  YTLVNPCDDALMKIT  VNPCDDALM        0.2573       3088.7              50.00     Sequence
DRB1_0701  118  ARHVAAGRNPKLGYD  VAAGRNPKL        0.2573       3089.8              50.00     Sequence
DRB1_0701   12  PSPTGTPHVGLVRTA  PSPTGTPHV        0.2570       3099.8              50.00     Sequence
DRB1_0701  106  AYHAFSTPEEVEARH  HAFSTPEEV        0.2568       3105.7              50.00     Sequence
DRB1_0701   82  GPYRQSQRAEIYRDV  YRQSQRAEI        0.2567       3109.3              50.00     Sequence
DRB1_0701  296  LFGLDEMVAAFDVAD  MVAAFDVAD        0.2562       3126.1              50.00     Sequence
DRB1_0701  420  TDWTAPLIEAALKDA  LIEAALKDA        0.2562       3128.1              50.00     Sequence
DRB1_0701  175  TFAAGSVPDFALTRA  AGSVPDFAL        0.2554       3153.1              50.00     Sequence
DRB1_0701   13  SPTGTPHVGLVRTAL  PTGTPHVGL        0.2546       3180.3              50.00     Sequence
DRB1_0701   83  PYRQSQRAEIYRDVL  YRQSQRAEI        0.2520       3272.2              50.00     Sequence
DRB1_0701  419  VTDWTAPLIEAALKD  VTDWTAPLI        0.2510       3307.2              50.00     Sequence
DRB1_0701  297  FGLDEMVAAFDVADV  MVAAFDVAD        0.2506       3321.2              50.00     Sequence
DRB1_0701  165  AWNDLVRGPVTFAAG  LVRGPVTFA        0.2501       3339.2              50.00     Sequence
DRB1_0701  190  SGDPLYTLVNPCDDA  YTLVNPCDD        0.2471       3449.3              50.00     Sequence
DRB1_0701  209  THVLRGEDLLPSTPR  HVLRGEDLL        0.2408       3692.1              50.00     Sequence
DRB1_0701  133  NFDRHLTDAQRAAYL  TDAQRAAYL        0.2406       3701.5              50.00     Sequence
DRB1_0701  395  KAAAKELGPDGAAVL  LGPDGAAVL        0.2387       3778.9              50.00     Sequence
DRB1_0701  318  FDQKKADALNAEHIR  FDQKKADAL        0.2379       3810.0              50.00     Sequence
DRB1_0701  110  FSTPEEVEARHVAAG  PEEVEARHV        0.2379       3811.0              50.00     Sequence
DRB1_0701  315  PARFDQKKADALNAE  FDQKKADAL        0.2378       3815.2              50.00     Sequence
DRB1_0701  426  LIEAALKDALIEGLA  LKDALIEGL        0.2368       3855.0              50.00     Sequence
DRB1_0701  114  EEVEARHVAAGRNPK  ARHVAAGRN        0.2358       3898.3              50.00     Sequence
DRB1_0701  294  HDLFGLDEMVAAFDV  DEMVAAFDV        0.2349       3939.2              50.00     Sequence
DRB1_0701  383  KFFNDDQYVIDPKAA  FFNDDQYVI        0.2330       4020.1              50.00     Sequence
DRB1_0701  458  TVSPPLFESLELLGR  LFESLELLG        0.2329       4021.8              50.00     Sequence
DRB1_0701  424  APLIEAALKDALIEG  IEAALKDAL        0.2326       4038.2              50.00     Sequence
DRB1_0701  304  AAFDVADVNSSPARF  VADVNSSPA        0.2318       4069.7              50.00     Sequence
DRB1_0701  130  GYDNFDRHLTDAQRA  RHLTDAQRA        0.2315       4086.0              50.00     Sequence
DRB1_0701  148  AEGRQPVVRLRMPDD  RQPVVRLRM        0.2313       4094.2              50.00     Sequence
DRB1_0701   84  YRQSQRAEIYRDVLA  YRQSQRAEI        0.2312       4099.1              50.00     Sequence
DRB1_0701  470  LGRDRSMQRLRAARQ  MQRLRAARQ        0.2304       4132.6              50.00     Sequence
DRB1_0701  302  MVAAFDVADVNSSPA  VADVNSSPA        0.2303       4136.0              50.00     Sequence
DRB1_0701   97  LARLLAAGEAYHAFS  LLAAGEAYH        0.2300       4153.6              50.00     Sequence
DRB1_0701   51  RDSEESYLALLDALR  YLALLDALR        0.2289       4203.1              50.00     Sequence
DRB1_0701    1  TATETVRVRFCPSPT  ATETVRVRF        0.2285       4219.3              50.00     Sequence
DRB1_0701  151  RQPVVRLRMPDDDLA  RQPVVRLRM        0.2259       4341.8              50.00     Sequence
DRB1_0701  462  PLFESLELLGRDRSM  ELLGRDRSM        0.2234       4460.1              50.00     Sequence
DRB1_0701  253  GTKKLSKRDPQSNLF  SKRDPQSNL        0.2231       4471.5              50.00     Sequence
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DRB1_0701  150  GRQPVVRLRMPDDDL  RQPVVRLRM         0.2216       4546.9                 50.00     Sequence
DRB1_0701  316  ARFDQKKADALNAEH  FDQKKADAL         0.2215       4549.3                 50.00     Sequence
DRB1_0701  176  FAAGSVPDFALTRAS  AGSVPDFAL         0.2196       4648.2                 50.00     Sequence
DRB1_0701  465  ESLELLGRDRSMQRL  LGRDRSMQR         0.2170       4776.6                 50.00     Sequence
DRB1_0701  464  FESLELLGRDRSMQR  LGRDRSMQR         0.2166       4798.8                 50.00     Sequence
DRB1_0701  162  DDLAWNDLVRGPVTF  DLVRGPVTF         0.2150       4881.9                 50.00     Sequence
DRB1_0701  166  WNDLVRGPVTFAAGS  LVRGPVTFA         0.2143       4920.9                 50.00     Sequence
DRB1_0701  119  RHVAAGRNPKLGYDN  VAAGRNPKL         0.2136       4958.2                 50.00     Sequence
DRB1_0701  134  FDRHLTDAQRAAYLA  TDAQRAAYL         0.2132       4976.7                 50.00     Sequence
DRB1_0701  298  GLDEMVAAFDVADVN  MVAAFDVAD         0.2127       5008.8                 50.00     Sequence
DRB1_0701  384  FFNDDQYVIDPKAAA  FFNDDQYVI         0.2113       5084.9                 50.00     Sequence
DRB1_0701  295  DLFGLDEMVAAFDVA  DEMVAAFDV         0.2110       5100.4                 50.00     Sequence
DRB1_0701  466  SLELLGRDRSMQRLR  LGRDRSMQR         0.2106       5121.6                 50.00     Sequence
DRB1_0701   34  RHTGGTFVFRIEDTD  FVFRIEDTD         0.2090       5208.4                 50.00     Sequence
DRB1_0701  396  AAAKELGPDGAAVLD  LGPDGAAVL         0.2089       5218.8                 50.00     Sequence
DRB1_0701  210  HVLRGEDLLPSTPRQ  HVLRGEDLL         0.2085       5239.7                 50.00     Sequence
DRB1_0701  300  DEMVAAFDVADVNSS  FDVADVNSS         0.2082       5258.2                 50.00     Sequence
DRB1_0701  124  GRNPKLGYDNFDRHL  GYDNFDRHL         0.2078       5280.0                 50.00     Sequence
DRB1_0701   98  ARLLAAGEAYHAFST  LLAAGEAYH         0.2072       5315.0                 50.00     Sequence
DRB1_0701  111  STPEEVEARHVAAGR  PEEVEARHV         0.2051       5437.5                 50.00     Sequence
DRB1_0701  149  EGRQPVVRLRMPDDD  RQPVVRLRM         0.2047       5460.3                 50.00     Sequence
DRB1_0701  399  KELGPDGAAVLDAAL  GAAVLDAAL         0.2024       5595.4                 50.00     Sequence
DRB1_0701  187  TRASGDPLYTLVNPC  PLYTLVNPC         0.2002       5731.6                 50.00     Sequence
DRB1_0701  427  IEAALKDALIEGLAL  LKDALIEGL         0.1986       5833.0                 50.00     Sequence
DRB1_0701  459  VSPPLFESLELLGRD  LFESLELLG         0.1945       6092.6                 50.00     Sequence
DRB1_0701  254  TKKLSKRDPQSNLFA  SKRDPQSNL         0.1944       6103.8                 50.00     Sequence
DRB1_0701  125  RNPKLGYDNFDRHLT  GYDNFDRHL         0.1940       6129.5                 50.00     Sequence
DRB1_0701  303  VAAFDVADVNSSPAR  VADVNSSPA         0.1924       6235.5                 50.00     Sequence
DRB1_0701  196  TLVNPCDDALMKITH  VNPCDDALM         0.1908       6342.9                 50.00     Sequence
DRB1_0701  429  AALKDALIEGLALKP  LIEGLALKP         0.1885       6502.5                 50.00     Sequence
DRB1_0701  463  LFESLELLGRDRSMQ  ELLGRDRSM         0.1885       6505.8                 50.00     Sequence
DRB1_0701  197  LVNPCDDALMKITHV  VNPCDDALM         0.1869       6616.0                 50.00     Sequence
DRB1_0701  397  AAKELGPDGAAVLDA  LGPDGAAVL         0.1849       6761.5                 50.00     Sequence
DRB1_0701   99  RLLAAGEAYHAFSTP  LLAAGEAYH         0.1822       6961.3                 50.00     Sequence
DRB1_0701  299  LDEMVAAFDVADVNS  MVAAFDVAD         0.1813       7033.5                 50.00     Sequence
DRB1_0701  233  RIGVAERIPKFAHLP  GVAERIPKF         0.1805       7092.7                 50.00     Sequence
DRB1_0701  135  DRHLTDAQRAAYLAE  TDAQRAAYL         0.1804       7101.4                 50.00     Sequence
DRB1_0701   44  IEDTDAQRDSEESYL  QRDSEESYL         0.1798       7148.4                 50.00     Sequence
DRB1_0701  160  PDDDLAWNDLVRGPV  WNDLVRGPV         0.1793       7186.9                 50.00     Sequence
DRB1_0701  120  HVAAGRNPKLGYDNF  VAAGRNPKL         0.1791       7204.6                 50.00     Sequence
DRB1_0701  400  ELGPDGAAVLDAALA  LGPDGAAVL         0.1786       7237.7                 50.00     Sequence
DRB1_0701  467  LELLGRDRSMQRLRA  LGRDRSMQR         0.1785       7247.0                 50.00     Sequence
DRB1_0701  401  LGPDGAAVLDAALAA  LGPDGAAVL         0.1754       7493.5                 50.00     Sequence
DRB1_0701  131  YDNFDRHLTDAQRAA  RHLTDAQRA         0.1739       7618.5                 50.00     Sequence
DRB1_0701  252  EGTKKLSKRDPQSNL  SKRDPQSNL         0.1700       7947.7                 50.00     Sequence
DRB1_0701  152  QPVVRLRMPDDDLAW  RLRMPDDDL         0.1677       8147.6                 50.00     Sequence
DRB1_0701  460  SPPLFESLELLGRDR  LFESLELLG         0.1672       8187.8                 50.00     Sequence
DRB1_0701  161  DDDLAWNDLVRGPVT  WNDLVRGPV         0.1664       8263.1                 50.00     Sequence
DRB1_0701  132  DNFDRHLTDAQRAAY  RHLTDAQRA         0.1649       8398.1                 50.00     Sequence
DRB1_0701  430  ALKDALIEGLALKPR  LIEGLALKP         0.1645       8429.0                 50.00     Sequence
DRB1_0701  121  VAAGRNPKLGYDNFD  VAAGRNPKL         0.1640       8483.0                 50.00     Sequence
DRB1_0701  255  KKLSKRDPQSNLFAH  SKRDPQSNL         0.1637       8509.2                 50.00     Sequence
DRB1_0701   35  HTGGTFVFRIEDTDA  TGGTFVFRI         0.1637       8510.8                 50.00     Sequence
DRB1_0701  126  NPKLGYDNFDRHLTD  GYDNFDRHL         0.1634       8535.5                 50.00     Sequence
DRB1_0701   45  EDTDAQRDSEESYLA  QRDSEESYL         0.1619       8670.0                 50.00     Sequence
DRB1_0701  275  IPEGLLNYLALLGWS  LLNYLALLG         0.1610       8758.0                 50.00     Sequence
DRB1_0701  234  IGVAERIPKFAHLPT  GVAERIPKF         0.1600       8858.1                 50.00     Sequence
DRB1_0701  177  AAGSVPDFALTRASG  AGSVPDFAL         0.1575       9092.3                 50.00     Sequence
DRB1_0701  398  AKELGPDGAAVLDAA  LGPDGAAVL         0.1572       9128.8                 50.00     Sequence
DRB1_0701  468  ELLGRDRSMQRLRAA  LGRDRSMQR         0.1560       9242.0                 50.00     Sequence
DRB1_0701  136  RHLTDAQRAAYLAEG  TDAQRAAYL         0.1536       9490.2                 50.00     Sequence
DRB1_0701   38  GTFVFRIEDTDAQRD  IEDTDAQRD         0.1520       9658.6                 50.00     Sequence
DRB1_0701  461  PPLFESLELLGRDRS  LFESLELLG         0.1500       9865.3                 50.00     Sequence
DRB1_0701  188  RASGDPLYTLVNPCD  PLYTLVNPC         0.1481      10074.5                 50.00     Sequence
DRB1_0701   47  TDAQRDSEESYLALL  QRDSEESYL         0.1458      10322.6                 50.00     Sequence
DRB1_0701  387  DDQYVIDPKAAAKEL  DPKAAAKEL         0.1456      10346.5                 50.00     Sequence
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DRB1_0701   46  DTDAQRDSEESYLAL  QRDSEESYL        0.1449      10429.2              50.00     Sequence
DRB1_0701  153  PVVRLRMPDDDLAWN  RLRMPDDDL        0.1430      10642.0              50.00     Sequence
DRB1_0701  432  KDALIEGLALKPRKA  GLALKPRKA        0.1423      10726.8              50.00     Sequence
DRB1_0701  428  EAALKDALIEGLALK  LKDALIEGL        0.1408      10900.6              50.00     Sequence
DRB1_0701  128  KLGYDNFDRHLTDAQ  GYDNFDRHL        0.1402      10967.0              50.00     Sequence
DRB1_0701   39  TFVFRIEDTDAQRDS  IEDTDAQRD        0.1400      10994.5              50.00     Sequence
DRB1_0701   36  TGGTFVFRIEDTDAQ  TGGTFVFRI        0.1399      11007.9              50.00     Sequence
DRB1_0701  256  KLSKRDPQSNLFAHR  SKRDPQSNL        0.1397      11029.3              50.00     Sequence
DRB1_0701  156  RLRMPDDDLAWNDLV  DDLAWNDLV        0.1373      11313.9              50.00     Sequence
DRB1_0701  127  PKLGYDNFDRHLTDA  GYDNFDRHL        0.1369      11367.4              50.00     Sequence
DRB1_0701  301  EMVAAFDVADVNSSP  FDVADVNSS        0.1347      11635.8              50.00     Sequence
DRB1_0701  257  LSKRDPQSNLFAHRD  SKRDPQSNL        0.1343      11696.7              50.00     Sequence
DRB1_0701  431  LKDALIEGLALKPRK  LKDALIEGL        0.1336      11783.1              50.00     Sequence
DRB1_0701  129  LGYDNFDRHLTDAQR  GYDNFDRHL        0.1331      11844.0              50.00     Sequence
DRB1_0701  377  DAWELLKFFNDDQYV  LKFFNDDQY        0.1330      11858.4              50.00     Sequence
DRB1_0701   48  DAQRDSEESYLALLD  QRDSEESYL        0.1316      12042.2              50.00     Sequence
DRB1_0701  385  FNDDQYVIDPKAAAK  VIDPKAAAK        0.1290      12384.8              50.00     Sequence
DRB1_0701  469  LLGRDRSMQRLRAAR  LGRDRSMQR        0.1290      12385.0              50.00     Sequence
DRB1_0701  154  VVRLRMPDDDLAWND  RLRMPDDDL        0.1288      12415.5              50.00     Sequence
DRB1_0701  376  GDAWELLKFFNDDQY  LKFFNDDQY        0.1282      12490.1              50.00     Sequence
DRB1_0701   40  FVFRIEDTDAQRDSE  IEDTDAQRD        0.1265      12715.8              50.00     Sequence
DRB1_0701  388  DQYVIDPKAAAKELG  DPKAAAKEL        0.1229      13228.2              50.00     Sequence
DRB1_0701  386  NDDQYVIDPKAAAKE  VIDPKAAAK        0.1180      13952.8              50.00     Sequence
DRB1_0701   85  RQSQRAEIYRDVLAR  RAEIYRDVL        0.1178      13982.2              50.00     Sequence
DRB1_0701  258  SKRDPQSNLFAHRDR  KRDPQSNLF        0.1177      13990.9              50.00     Sequence
DRB1_0701   49  AQRDSEESYLALLDA  QRDSEESYL        0.1176      14003.3              50.00     Sequence
DRB1_0701  155  VRLRMPDDDLAWNDL  RLRMPDDDL        0.1170      14097.7              50.00     Sequence
DRB1_0701   50  QRDSEESYLALLDAL  QRDSEESYL        0.1165      14179.7              50.00     Sequence
DRB1_0701  137  HLTDAQRAAYLAEGR  TDAQRAAYL        0.1150      14405.8              50.00     Sequence
DRB1_0701  251  GEGTKKLSKRDPQSN  LSKRDPQSN        0.1115      14966.1              50.00     Sequence
DRB1_0701  348  DTHGHHIALDEAAFA  IALDEAAFA        0.1105      15124.9              50.00     Sequence
DRB1_0701  139  TDAQRAAYLAEGRQP  TDAQRAAYL        0.1103      15153.5              50.00     Sequence
DRB1_0701  349  THGHHIALDEAAFAA  IALDEAAFA        0.1034      16325.7              50.00     Sequence
DRB1_0701  138  LTDAQRAAYLAEGRQ  TDAQRAAYL        0.1033      16352.9              50.00     Sequence
DRB1_0701   63  ALRWLGLDWDEGPEV  LDWDEGPEV        0.1012      16728.0              50.00     Sequence
DRB1_0701  389  QYVIDPKAAAKELGP  DPKAAAKEL        0.0998      16988.1              50.00     Sequence
DRB1_0701   43  RIEDTDAQRDSEESY  IEDTDAQRD        0.0997      16997.3              50.00     Sequence
DRB1_0701  157  LRMPDDDLAWNDLVR  DDLAWNDLV        0.0975      17404.8              50.00     Sequence
DRB1_0701   41  VFRIEDTDAQRDSEE  IEDTDAQRD        0.0975      17411.4              50.00     Sequence
DRB1_0701  290  IADDHDLFGLDEMVA  LFGLDEMVA        0.0971      17479.8              50.00     Sequence
DRB1_0701  347  LDTHGHHIALDEAAF  HIALDEAAF        0.0962      17663.8              50.00     Sequence
DRB1_0701   42  FRIEDTDAQRDSEES  IEDTDAQRD        0.0917      18536.9              50.00     Sequence
DRB1_0701   37  GGTFVFRIEDTDAQR  FVFRIEDTD        0.0908      18722.9              50.00     Sequence
DRB1_0701  374  VLGDAWELLKFFNDD  LGDAWELLK        0.0908      18726.4              50.00     Sequence
DRB1_0701  259  KRDPQSNLFAHRDRG  KRDPQSNLF        0.0881      19265.9              50.00     Sequence
DRB1_0701  350  HGHHIALDEAAFAAA  IALDEAAFA        0.0870      19509.0              50.00     Sequence
DRB1_0701  289  SIADDHDLFGLDEMV  SIADDHDLF        0.0834      20272.9              50.00     Sequence
DRB1_0701  158  RMPDDDLAWNDLVRG  DDLAWNDLV        0.0829      20384.7              50.00     Sequence
DRB1_0701   64  LRWLGLDWDEGPEVG  LDWDEGPEV        0.0820      20584.8              50.00     Sequence
DRB1_0701  390  YVIDPKAAAKELGPD  DPKAAAKEL        0.0816      20676.1              50.00     Sequence
DRB1_0701   61  LDALRWLGLDWDEGP  LDALRWLGL        0.0797      21119.2              50.00     Sequence
DRB1_0701  291  ADDHDLFGLDEMVAA  LFGLDEMVA        0.0768      21776.4              50.00     Sequence
DRB1_0701  293  DHDLFGLDEMVAAFD  LDEMVAAFD        0.0758      22010.2              50.00     Sequence
DRB1_0701  351  GHHIALDEAAFAAAA  IALDEAAFA        0.0723      22857.7              50.00     Sequence
DRB1_0701  250  LGEGTKKLSKRDPQS  GTKKLSKRD        0.0713      23113.6              50.00     Sequence
DRB1_0701   65  RWLGLDWDEGPEVGG  LDWDEGPEV        0.0709      23206.1              50.00     Sequence
DRB1_0701  292  DDHDLFGLDEMVAAF  LFGLDEMVA        0.0706      23301.4              50.00     Sequence
DRB1_0701  391  VIDPKAAAKELGPDG  DPKAAAKEL        0.0678      24006.5              50.00     Sequence
DRB1_0701  159  MPDDDLAWNDLVRGP  DDLAWNDLV        0.0663      24392.7              50.00     Sequence
DRB1_0701  375  LGDAWELLKFFNDDQ  LGDAWELLK        0.0661      24454.5              50.00     Sequence
DRB1_0701   76  EVGGPYGPYRQSQRA  YGPYRQSQR        0.0626      25391.5              50.00     Sequence
DRB1_0701   75  PEVGGPYGPYRQSQR  YGPYRQSQR        0.0613      25767.0              50.00     Sequence
DRB1_0701   66  WLGLDWDEGPEVGGP  LDWDEGPEV        0.0576      26806.7              50.00     Sequence
DRB1_0701  352  HHIALDEAAFAAAAE  IALDEAAFA        0.0575      26847.6              50.00     Sequence
DRB1_0701   77  VGGPYGPYRQSQRAE  YGPYRQSQR        0.0554      27442.4              50.00     Sequence
DRB1_0701  392  IDPKAAAKELGPDGA  DPKAAAKEL        0.0549      27597.5              50.00     Sequence
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   DRB1_0701   67  LGLDWDEGPEVGGPY  LDWDEGPEV        0.0542      27824.8                 50.00     Sequence
   DRB1_0701   68  GLDWDEGPEVGGPYG  LDWDEGPEV        0.0520      28500.0                 50.00     Sequence
   DRB1_0701  393  DPKAAAKELGPDGAA  DPKAAAKEL        0.0487      29520.9                 50.00     Sequence
   DRB1_0701   69  LDWDEGPEVGGPYGP  LDWDEGPEV        0.0482      29666.0                 50.00     Sequence
   DRB1_0701  122  AAGRNPKLGYDNFDR  PKLGYDNFD        0.0460      30386.5                 50.00     Sequence
   DRB1_0701   71  WDEGPEVGGPYGPYR  VGGPYGPYR        0.0417      31844.4                 50.00     Sequence
   DRB1_0701  394  PKAAAKELGPDGAAV  ELGPDGAAV        0.0414      31957.2                 50.00     Sequence
   DRB1_0701   62  DALRWLGLDWDEGPE  ALRWLGLDW        0.0381      33106.3                 50.00     Sequence
   DRB1_0701   72  DEGPEVGGPYGPYRQ  VGGPYGPYR        0.0376      33285.6                 50.00     Sequence
   DRB1_0701  123  AGRNPKLGYDNFDRH  GRNPKLGYD        0.0371      33476.3                 50.00     Sequence
   DRB1_0701   73  EGPEVGGPYGPYRQS  VGGPYGPYR        0.0342      34535.1                 50.00     Sequence
   DRB1_0701   70  DWDEGPEVGGPYGPY  EVGGPYGPY        0.0314      35607.8                 50.00     Sequence
   DRB1_0701   74  GPEVGGPYGPYRQSQ  VGGPYGPYR        0.0304      35990.4                 50.00     Sequence
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Allele: DRB1_0701. Number of high binders 49. Number of weak binders 122. Number of peptides 476

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0802  474  RSMQRLRAARQLVGH  RSMQRLRAA        0.6886         29.1          SB      0.80     Sequence
   DRB1_0802  472  RDRSMQRLRAARQLV  RSMQRLRAA        0.6836         30.7          SB      0.80     Sequence
   DRB1_0802  473  DRSMQRLRAARQLVG  RSMQRLRAA        0.6823         31.1          SB      0.80     Sequence
   DRB1_0802  475  SMQRLRAARQLVGHA  RLRAARQLV        0.6410         48.6          SB      2.00     Sequence
   DRB1_0802  471  GRDRSMQRLRAARQL  RSMQRLRAA        0.6364         51.1          WB      2.00     Sequence
   DRB1_0802  470  LGRDRSMQRLRAARQ  RSMQRLRAA        0.5986         77.0          WB      4.00     Sequence
   DRB1_0802  469  LLGRDRSMQRLRAAR  RSMQRLRAA        0.5506        129.3          WB      4.00     Sequence
   DRB1_0802  204  ALMKITHVLRGEDLL  LMKITHVLR        0.5383        147.7          WB      8.00     Sequence
   DRB1_0802   93  YRDVLARLLAAGEAY  YRDVLARLL        0.5341        154.6          WB      8.00     Sequence
   DRB1_0802  233  RIGVAERIPKFAHLP  RIGVAERIP        0.5268        167.3          WB      8.00     Sequence
   DRB1_0802   27  LFNWAYARHTGGTFV  FNWAYARHT        0.5266        167.7          WB      8.00     Sequence
   DRB1_0802   92  IYRDVLARLLAAGEA  YRDVLARLL        0.5204        179.4          WB      8.00     Sequence
   DRB1_0802  203  DALMKITHVLRGEDL  LMKITHVLR        0.5153        189.6          WB      8.00     Sequence
   DRB1_0802   26  ALFNWAYARHTGGTF  FNWAYARHT        0.5110        198.6          WB      8.00     Sequence
   DRB1_0802   18  PHVGLVRTALFNWAY  HVGLVRTAL        0.5108        198.9          WB      8.00     Sequence
   DRB1_0802   17  TPHVGLVRTALFNWA  HVGLVRTAL        0.5057        210.2          WB      8.00     Sequence
   DRB1_0802  239  RIPKFAHLPTVLGEG  RIPKFAHLP        0.5053        211.1          WB      8.00     Sequence
   DRB1_0802  468  ELLGRDRSMQRLRAA  RDRSMQRLR        0.5034        215.6          WB      8.00     Sequence
   DRB1_0802   91  EIYRDVLARLLAAGE  YRDVLARLL        0.5033        215.7          WB      8.00     Sequence
   DRB1_0802   28  FNWAYARHTGGTFVF  FNWAYARHT        0.5031        216.2          WB      8.00     Sequence
   DRB1_0802   16  GTPHVGLVRTALFNW  HVGLVRTAL        0.5004        222.7          WB      8.00     Sequence
   DRB1_0802  237  AERIPKFAHLPTVLG  RIPKFAHLP        0.4930        241.3          WB      8.00     Sequence
   DRB1_0802  205  LMKITHVLRGEDLLP  LMKITHVLR        0.4927        242.1          WB      8.00     Sequence
   DRB1_0802  202  DDALMKITHVLRGED  LMKITHVLR        0.4923        243.1          WB      8.00     Sequence
   DRB1_0802  238  ERIPKFAHLPTVLGE  RIPKFAHLP        0.4834        267.5          WB     16.00     Sequence
   DRB1_0802  201  CDDALMKITHVLRGE  LMKITHVLR        0.4778        284.2          WB     16.00     Sequence
   DRB1_0802  234  IGVAERIPKFAHLPT  RIPKFAHLP        0.4762        289.2          WB     16.00     Sequence
   DRB1_0802   90  AEIYRDVLARLLAAG  YRDVLARLL        0.4744        295.0          WB     16.00     Sequence
   DRB1_0802   25  TALFNWAYARHTGGT  FNWAYARHT        0.4694        311.2          WB     16.00     Sequence
   DRB1_0802   15  TGTPHVGLVRTALFN  HVGLVRTAL        0.4682        315.5          WB     16.00     Sequence
   DRB1_0802  232  IRIGVAERIPKFAHL  RIGVAERIP        0.4661        322.6          WB     16.00     Sequence
   DRB1_0802  236  VAERIPKFAHLPTVL  RIPKFAHLP        0.4649        326.7          WB     16.00     Sequence
   DRB1_0802  336  VGDFTVRLRDHLDTH  FTVRLRDHL        0.4635        332.1          WB     16.00     Sequence
   DRB1_0802  438  GLALKPRKAFSPIRV  GLALKPRKA        0.4614        339.4          WB     16.00     Sequence
   DRB1_0802  445  KAFSPIRVAATGTTV  AFSPIRVAA        0.4609        341.3          WB     16.00     Sequence
   DRB1_0802  235  GVAERIPKFAHLPTV  RIPKFAHLP        0.4495        386.3          WB     16.00     Sequence
   DRB1_0802   24  RTALFNWAYARHTGG  FNWAYARHT        0.4461        400.6          WB     16.00     Sequence
   DRB1_0802  338  DFTVRLRDHLDTHGH  FTVRLRDHL        0.4428        415.3          WB     16.00     Sequence
   DRB1_0802  337  GDFTVRLRDHLDTHG  FTVRLRDHL        0.4427        415.7          WB     16.00     Sequence
   DRB1_0802  335  DVGDFTVRLRDHLDT  FTVRLRDHL        0.4425        416.4          WB     16.00     Sequence
   DRB1_0802  231  LIRIGVAERIPKFAH  RIGVAERIP        0.4398        429.1          WB     16.00     Sequence
   DRB1_0802  467  LELLGRDRSMQRLRA  RDRSMQRLR        0.4396        429.7          WB     16.00     Sequence
   DRB1_0802  443  PRKAFSPIRVAATGT  AFSPIRVAA        0.4389        433.0          WB     16.00     Sequence
   DRB1_0802   14  PTGTPHVGLVRTALF  HVGLVRTAL        0.4387        434.2          WB     16.00     Sequence
   DRB1_0802   57  YLALLDALRWLGLDW  YLALLDALR        0.4376        439.2          WB     16.00     Sequence
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DRB1_0802  444  RKAFSPIRVAATGTT  AFSPIRVAA        0.4372        441.0          WB    16.00      Sequence
DRB1_0802   89  RAEIYRDVLARLLAA  YRDVLARLL        0.4359        447.5          WB    16.00      Sequence
DRB1_0802  146  YLAEGRQPVVRLRMP  YLAEGRQPV        0.4352        450.7          WB    16.00      Sequence
DRB1_0802  442  KPRKAFSPIRVAATG  AFSPIRVAA        0.4329        462.0          WB    16.00      Sequence
DRB1_0802  435  LIEGLALKPRKAFSP  GLALKPRKA        0.4307        473.3          WB    16.00      Sequence
DRB1_0802  339  FTVRLRDHLDTHGHH  FTVRLRDHL        0.4306        473.8          WB    16.00      Sequence
DRB1_0802  200  PCDDALMKITHVLRG  LMKITHVLR        0.4306        473.9          WB    16.00      Sequence
DRB1_0802  145  AYLAEGRQPVVRLRM  YLAEGRQPV        0.4283        485.6          WB    16.00      Sequence
DRB1_0802   79  GPYGPYRQSQRAEIY  GPYRQSQRA        0.4279        487.9          WB    16.00      Sequence
DRB1_0802   81  YGPYRQSQRAEIYRD  GPYRQSQRA        0.4270        492.4          WB    16.00      Sequence
DRB1_0802   19  HVGLVRTALFNWAYA  HVGLVRTAL        0.4250        503.6                16.00      Sequence
DRB1_0802  446  AFSPIRVAATGTTVS  AFSPIRVAA        0.4247        504.8                16.00      Sequence
DRB1_0802   78  GGPYGPYRQSQRAEI  PYRQSQRAE        0.4241        508.3                16.00      Sequence
DRB1_0802  437  EGLALKPRKAFSPIR  GLALKPRKA        0.4214        523.5                16.00      Sequence
DRB1_0802   80  PYGPYRQSQRAEIYR  GPYRQSQRA        0.4205        528.3                16.00      Sequence
DRB1_0802  230  ALIRIGVAERIPKFA  RIGVAERIP        0.4183        541.1                16.00      Sequence
DRB1_0802  436  IEGLALKPRKAFSPI  GLALKPRKA        0.4156        557.1                16.00      Sequence
DRB1_0802  144  AAYLAEGRQPVVRLR  YLAEGRQPV        0.4152        559.6                16.00      Sequence
DRB1_0802  439  LALKPRKAFSPIRVA  LALKPRKAF        0.4152        559.8                16.00      Sequence
DRB1_0802   56  SYLALLDALRWLGLD  YLALLDALR        0.4150        561.2                16.00      Sequence
DRB1_0802  441  LKPRKAFSPIRVAAT  PRKAFSPIR        0.4149        561.4                16.00      Sequence
DRB1_0802   13  SPTGTPHVGLVRTAL  HVGLVRTAL        0.4148        561.9                16.00      Sequence
DRB1_0802   55  ESYLALLDALRWLGL  YLALLDALR        0.4116        582.1                16.00      Sequence
DRB1_0802   88  QRAEIYRDVLARLLA  YRDVLARLL        0.4115        582.3                16.00      Sequence
DRB1_0802   94  RDVLARLLAAGEAYH  RDVLARLLA        0.4112        584.7                16.00      Sequence
DRB1_0802  440  ALKPRKAFSPIRVAA  PRKAFSPIR        0.4101        591.2                16.00      Sequence
DRB1_0802  206  MKITHVLRGEDLLPS  MKITHVLRG        0.4098        593.6                32.00      Sequence
DRB1_0802   82  GPYRQSQRAEIYRDV  GPYRQSQRA        0.4085        601.6                32.00      Sequence
DRB1_0802  136  RHLTDAQRAAYLAEG  HLTDAQRAA        0.4041        631.2                32.00      Sequence
DRB1_0802  150  GRQPVVRLRMPDDDL  QPVVRLRMP        0.4033        636.7                32.00      Sequence
DRB1_0802  434  ALIEGLALKPRKAFS  GLALKPRKA        0.4024        642.7                32.00      Sequence
DRB1_0802  143  RAAYLAEGRQPVVRL  YLAEGRQPV        0.3989        667.8                32.00      Sequence
DRB1_0802   58  LALLDALRWLGLDWD  LLDALRWLG        0.3890        743.4                32.00      Sequence
DRB1_0802   54  EESYLALLDALRWLG  YLALLDALR        0.3888        745.1                32.00      Sequence
DRB1_0802   23  VRTALFNWAYARHTG  FNWAYARHT        0.3887        745.7                32.00      Sequence
DRB1_0802  227  LHQALIRIGVAERIP  RIGVAERIP        0.3859        768.2                32.00      Sequence
DRB1_0802  151  RQPVVRLRMPDDDLA  QPVVRLRMP        0.3852        774.0                32.00      Sequence
DRB1_0802  240  IPKFAHLPTVLGEGT  KFAHLPTVL        0.3849        777.0                32.00      Sequence
DRB1_0802  466  SLELLGRDRSMQRLR  RDRSMQRLR        0.3847        778.5                32.00      Sequence
DRB1_0802   22  LVRTALFNWAYARHT  FNWAYARHT        0.3843        782.2                32.00      Sequence
DRB1_0802  433  DALIEGLALKPRKAF  GLALKPRKA        0.3834        789.9                32.00      Sequence
DRB1_0802  152  QPVVRLRMPDDDLAW  QPVVRLRMP        0.3825        796.9                32.00      Sequence
DRB1_0802  253  GTKKLSKRDPQSNLF  GTKKLSKRD        0.3788        829.7                32.00      Sequence
DRB1_0802  229  QALIRIGVAERIPKF  RIGVAERIP        0.3777        839.5                32.00      Sequence
DRB1_0802   77  VGGPYGPYRQSQRAE  YGPYRQSQR        0.3776        840.5                32.00      Sequence
DRB1_0802  149  EGRQPVVRLRMPDDD  QPVVRLRMP        0.3775        841.7                32.00      Sequence
DRB1_0802  142  QRAAYLAEGRQPVVR  YLAEGRQPV        0.3747        867.2                32.00      Sequence
DRB1_0802  249  VLGEGTKKLSKRDPQ  VLGEGTKKL        0.3738        875.5                32.00      Sequence
DRB1_0802  165  AWNDLVRGPVTFAAG  WNDLVRGPV        0.3705        907.7                32.00      Sequence
DRB1_0802  119  RHVAAGRNPKLGYDN  RHVAAGRNP        0.3704        908.5                32.00      Sequence
DRB1_0802  334  LDVGDFTVRLRDHLD  FTVRLRDHL        0.3676        937.1                32.00      Sequence
DRB1_0802  137  HLTDAQRAAYLAEGR  HLTDAQRAA        0.3675        937.6                32.00      Sequence
DRB1_0802  164  LAWNDLVRGPVTFAA  WNDLVRGPV        0.3669        943.8                32.00      Sequence
DRB1_0802  147  LAEGRQPVVRLRMPD  QPVVRLRMP        0.3663        949.8                32.00      Sequence
DRB1_0802  148  AEGRQPVVRLRMPDD  QPVVRLRMP        0.3636        977.8                32.00      Sequence
DRB1_0802    2  ATETVRVRFCPSPTG  ETVRVRFCP        0.3605       1011.8                32.00      Sequence
DRB1_0802  264  SNLFAHRDRGFIPEG  FAHRDRGFI        0.3601       1016.5                32.00      Sequence
DRB1_0802  131  YDNFDRHLTDAQRAA  HLTDAQRAA        0.3595       1022.9                32.00      Sequence
DRB1_0802    3  TETVRVRFCPSPTGT  ETVRVRFCP        0.3591       1027.4                32.00      Sequence
DRB1_0802  432  KDALIEGLALKPRKA  LIEGLALKP        0.3585       1033.9                32.00      Sequence
DRB1_0802  135  DRHLTDAQRAAYLAE  HLTDAQRAA        0.3568       1052.4                32.00      Sequence
DRB1_0802  252  EGTKKLSKRDPQSNL  GTKKLSKRD        0.3559       1062.7                32.00      Sequence
DRB1_0802  134  FDRHLTDAQRAAYLA  HLTDAQRAA        0.3547       1077.1                32.00      Sequence
DRB1_0802  199  NPCDDALMKITHVLR  LMKITHVLR        0.3537       1088.6                32.00      Sequence
DRB1_0802   59  ALLDALRWLGLDWDE  LLDALRWLG        0.3537       1089.2                32.00      Sequence
DRB1_0802  248  TVLGEGTKKLSKRDP  VLGEGTKKL        0.3535       1091.3                32.00      Sequence
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DRB1_0802  262  PQSNLFAHRDRGFIP  FAHRDRGFI        0.3522       1106.1                32.00     Sequence
DRB1_0802  251  GEGTKKLSKRDPQSN  GTKKLSKRD        0.3514       1115.9                32.00     Sequence
DRB1_0802  389  QYVIDPKAAAKELGP  YVIDPKAAA        0.3497       1136.9                32.00     Sequence
DRB1_0802  250  LGEGTKKLSKRDPQS  GTKKLSKRD        0.3493       1141.6                32.00     Sequence
DRB1_0802  366  ELVQTRIVVLGDAWE  VQTRIVVLG        0.3493       1141.9                32.00     Sequence
DRB1_0802    4  ETVRVRFCPSPTGTP  VRVRFCPSP        0.3493       1142.5                32.00     Sequence
DRB1_0802  241  PKFAHLPTVLGEGTK  FAHLPTVLG        0.3461       1182.1                32.00     Sequence
DRB1_0802  365  AELVQTRIVVLGDAW  VQTRIVVLG        0.3459       1184.5                32.00     Sequence
DRB1_0802  228  HQALIRIGVAERIPK  RIGVAERIP        0.3457       1187.0                32.00     Sequence
DRB1_0802  265  NLFAHRDRGFIPEGL  FAHRDRGFI        0.3448       1199.1                32.00     Sequence
DRB1_0802    1  TATETVRVRFCPSPT  VRVRFCPSP        0.3434       1217.5                32.00     Sequence
DRB1_0802  223  RQLALHQALIRIGVA  LHQALIRIG        0.3396       1268.5                32.00     Sequence
DRB1_0802   29  NWAYARHTGGTFVFR  WAYARHTGG        0.3384       1284.2                32.00     Sequence
DRB1_0802  247  PTVLGEGTKKLSKRD  VLGEGTKKL        0.3381       1289.0                32.00     Sequence
DRB1_0802  118  ARHVAAGRNPKLGYD  RHVAAGRNP        0.3368       1307.9                32.00     Sequence
DRB1_0802  263  QSNLFAHRDRGFIPE  FAHRDRGFI        0.3365       1311.1                32.00     Sequence
DRB1_0802  141  AQRAAYLAEGRQPVV  YLAEGRQPV        0.3352       1329.7                32.00     Sequence
DRB1_0802  222  PRQLALHQALIRIGV  LHQALIRIG        0.3336       1353.4                32.00     Sequence
DRB1_0802  242  KFAHLPTVLGEGTKK  FAHLPTVLG        0.3335       1355.0                32.00     Sequence
DRB1_0802  333  MLDVGDFTVRLRDHL  FTVRLRDHL        0.3332       1358.9                32.00     Sequence
DRB1_0802  225  LALHQALIRIGVAER  LHQALIRIG        0.3327       1367.2                32.00     Sequence
DRB1_0802  130  GYDNFDRHLTDAQRA  YDNFDRHLT        0.3325       1369.1                32.00     Sequence
DRB1_0802  163  DLAWNDLVRGPVTFA  WNDLVRGPV        0.3320       1377.0                32.00     Sequence
DRB1_0802  388  DQYVIDPKAAAKELG  YVIDPKAAA        0.3313       1387.8                32.00     Sequence
DRB1_0802  166  WNDLVRGPVTFAAGS  WNDLVRGPV        0.3307       1396.5                32.00     Sequence
DRB1_0802   21  GLVRTALFNWAYARH  GLVRTALFN        0.3303       1401.9                32.00     Sequence
DRB1_0802  447  FSPIRVAATGTTVSP  RVAATGTTV        0.3302       1403.7                32.00     Sequence
DRB1_0802  367  LVQTRIVVLGDAWEL  VQTRIVVLG        0.3301       1405.0                32.00     Sequence
DRB1_0802  226  ALHQALIRIGVAERI  LHQALIRIG        0.3285       1430.2                32.00     Sequence
DRB1_0802  207  KITHVLRGEDLLPST  KITHVLRGE        0.3284       1431.6                32.00     Sequence
DRB1_0802  254  TKKLSKRDPQSNLFA  KLSKRDPQS        0.3264       1463.3                32.00     Sequence
DRB1_0802  390  YVIDPKAAAKELGPD  YVIDPKAAA        0.3260       1468.7                32.00     Sequence
DRB1_0802  276  PEGLLNYLALLGWSI  LLNYLALLG        0.3239       1503.8                32.00     Sequence
DRB1_0802  261  DPQSNLFAHRDRGFI  FAHRDRGFI        0.3207       1556.2                32.00     Sequence
DRB1_0802  117  EARHVAAGRNPKLGY  RHVAAGRNP        0.3200       1567.9                32.00     Sequence
DRB1_0802   76  EVGGPYGPYRQSQRA  GPYRQSQRA        0.3199       1570.0                32.00     Sequence
DRB1_0802   12  PSPTGTPHVGLVRTA  PHVGLVRTA        0.3183       1596.9                50.00     Sequence
DRB1_0802  217  LLPSTPRQLALHQAL  LPSTPRQLA        0.3182       1599.0                50.00     Sequence
DRB1_0802  224  QLALHQALIRIGVAE  LHQALIRIG        0.3174       1612.5                50.00     Sequence
DRB1_0802  368  VQTRIVVLGDAWELL  VQTRIVVLG        0.3154       1648.2                50.00     Sequence
DRB1_0802  277  EGLLNYLALLGWSIA  LLNYLALLG        0.3144       1666.1                50.00     Sequence
DRB1_0802  448  SPIRVAATGTTVSPP  PIRVAATGT        0.3140       1673.5                50.00     Sequence
DRB1_0802    0  VTATETVRVRFCPSP  VRVRFCPSP        0.3139       1674.9                50.00     Sequence
DRB1_0802  278  GLLNYLALLGWSIAD  LLNYLALLG        0.3129       1693.4                50.00     Sequence
DRB1_0802   87  SQRAEIYRDVLARLL  YRDVLARLL        0.3124       1702.2                50.00     Sequence
DRB1_0802   83  PYRQSQRAEIYRDVL  PYRQSQRAE        0.3122       1705.0                50.00     Sequence
DRB1_0802   20  VGLVRTALFNWAYAR  GLVRTALFN        0.3117       1714.2                50.00     Sequence
DRB1_0802  221  TPRQLALHQALIRIG  LHQALIRIG        0.3110       1728.2                50.00     Sequence
DRB1_0802  133  NFDRHLTDAQRAAYL  HLTDAQRAA        0.3109       1729.5                50.00     Sequence
DRB1_0802  266  LFAHRDRGFIPEGLL  FAHRDRGFI        0.3096       1755.0                50.00     Sequence
DRB1_0802  129  LGYDNFDRHLTDAQR  YDNFDRHLT        0.3090       1765.7                50.00     Sequence
DRB1_0802   53  SEESYLALLDALRWL  YLALLDALR        0.3090       1766.4                50.00     Sequence
DRB1_0802    6  VRVRFCPSPTGTPHV  VRVRFCPSP        0.3073       1798.3                50.00     Sequence
DRB1_0802  140  DAQRAAYLAEGRQPV  YLAEGRQPV        0.3068       1808.3                50.00     Sequence
DRB1_0802  218  LPSTPRQLALHQALI  LPSTPRQLA        0.3065       1813.6                50.00     Sequence
DRB1_0802  128  KLGYDNFDRHLTDAQ  YDNFDRHLT        0.3061       1822.1                50.00     Sequence
DRB1_0802  116  VEARHVAAGRNPKLG  RHVAAGRNP        0.3060       1824.3                50.00     Sequence
DRB1_0802  243  FAHLPTVLGEGTKKL  FAHLPTVLG        0.3045       1854.9                50.00     Sequence
DRB1_0802  387  DDQYVIDPKAAAKEL  YVIDPKAAA        0.3039       1865.4                50.00     Sequence
DRB1_0802  115  EVEARHVAAGRNPKL  RHVAAGRNP        0.2996       1954.0                50.00     Sequence
DRB1_0802   30  WAYARHTGGTFVFRI  WAYARHTGG        0.2987       1974.4                50.00     Sequence
DRB1_0802  431  LKDALIEGLALKPRK  LIEGLALKP        0.2977       1995.4                50.00     Sequence
DRB1_0802  279  LLNYLALLGWSIADD  LLNYLALLG        0.2973       2005.0                50.00     Sequence
DRB1_0802  245  HLPTVLGEGTKKLSK  VLGEGTKKL        0.2942       2072.2                50.00     Sequence
DRB1_0802  255  KKLSKRDPQSNLFAH  KLSKRDPQS        0.2917       2130.2                50.00     Sequence
DRB1_0802  162  DDLAWNDLVRGPVTF  WNDLVRGPV        0.2915       2133.8                50.00     Sequence
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DRB1_0802  216  DLLPSTPRQLALHQA  LPSTPRQLA        0.2907       2153.6                 50.00     Sequence
DRB1_0802  267  FAHRDRGFIPEGLLN  FAHRDRGFI        0.2906       2154.8                 50.00     Sequence
DRB1_0802  465  ESLELLGRDRSMQRL  LLGRDRSMQ        0.2895       2181.0                 50.00     Sequence
DRB1_0802  132  DNFDRHLTDAQRAAY  HLTDAQRAA        0.2882       2212.7                 50.00     Sequence
DRB1_0802    5  TVRVRFCPSPTGTPH  VRVRFCPSP        0.2878       2220.9                 50.00     Sequence
DRB1_0802  246  LPTVLGEGTKKLSKR  VLGEGTKKL        0.2874       2230.8                 50.00     Sequence
DRB1_0802  364  AAELVQTRIVVLGDA  ELVQTRIVV        0.2848       2294.6                 50.00     Sequence
DRB1_0802  386  NDDQYVIDPKAAAKE  YVIDPKAAA        0.2847       2296.4                 50.00     Sequence
DRB1_0802   60  LLDALRWLGLDWDEG  LLDALRWLG        0.2834       2329.2                 50.00     Sequence
DRB1_0802  449  PIRVAATGTTVSPPL  PIRVAATGT        0.2816       2375.8                 50.00     Sequence
DRB1_0802  275  IPEGLLNYLALLGWS  LLNYLALLG        0.2796       2426.5                 50.00     Sequence
DRB1_0802  127  PKLGYDNFDRHLTDA  YDNFDRHLT        0.2763       2516.8                 50.00     Sequence
DRB1_0802  385  FNDDQYVIDPKAAAK  YVIDPKAAA        0.2756       2533.7                 50.00     Sequence
DRB1_0802  384  FFNDDQYVIDPKAAA  YVIDPKAAA        0.2756       2536.1                 50.00     Sequence
DRB1_0802  450  IRVAATGTTVSPPLF  RVAATGTTV        0.2725       2620.7                 50.00     Sequence
DRB1_0802  371  RIVVLGDAWELLKFF  RIVVLGDAW        0.2719       2639.2                 50.00     Sequence
DRB1_0802  220  STPRQLALHQALIRI  PRQLALHQA        0.2715       2651.2                 50.00     Sequence
DRB1_0802  430  ALKDALIEGLALKPR  LIEGLALKP        0.2696       2704.6                 50.00     Sequence
DRB1_0802  363  AAAELVQTRIVVLGD  ELVQTRIVV        0.2682       2745.7                 50.00     Sequence
DRB1_0802  161  DDDLAWNDLVRGPVT  WNDLVRGPV        0.2681       2750.4                 50.00     Sequence
DRB1_0802  114  EEVEARHVAAGRNPK  RHVAAGRNP        0.2673       2771.9                 50.00     Sequence
DRB1_0802  219  PSTPRQLALHQALIR  PRQLALHQA        0.2651       2839.4                 50.00     Sequence
DRB1_0802  120  HVAAGRNPKLGYDNF  HVAAGRNPK        0.2630       2904.8                 50.00     Sequence
DRB1_0802  370  TRIVVLGDAWELLKF  RIVVLGDAW        0.2627       2914.5                 50.00     Sequence
DRB1_0802  416  LTSVTDWTAPLIEAA  WTAPLIEAA        0.2621       2932.4                 50.00     Sequence
DRB1_0802  462  PLFESLELLGRDRSM  LFESLELLG        0.2620       2937.3                 50.00     Sequence
DRB1_0802  168  DLVRGPVTFAAGSVP  LVRGPVTFA        0.2599       3005.1                 50.00     Sequence
DRB1_0802  274  FIPEGLLNYLALLGW  LLNYLALLG        0.2597       3010.5                 50.00     Sequence
DRB1_0802  463  LFESLELLGRDRSMQ  LELLGRDRS        0.2588       3039.5                 50.00     Sequence
DRB1_0802  315  PARFDQKKADALNAE  PARFDQKKA        0.2585       3050.3                 50.00     Sequence
DRB1_0802  362  AAAAELVQTRIVVLG  LVQTRIVVL        0.2583       3056.6                 50.00     Sequence
DRB1_0802  273  GFIPEGLLNYLALLG  LLNYLALLG        0.2569       3103.8                 50.00     Sequence
DRB1_0802  126  NPKLGYDNFDRHLTD  YDNFDRHLT        0.2563       3123.6                 50.00     Sequence
DRB1_0802  169  LVRGPVTFAAGSVPD  LVRGPVTFA        0.2558       3141.9                 50.00     Sequence
DRB1_0802   95  DVLARLLAAGEAYHA  VLARLLAAG        0.2538       3208.1                 50.00     Sequence
DRB1_0802   75  PEVGGPYGPYRQSQR  GPYGPYRQS        0.2538       3208.8                 50.00     Sequence
DRB1_0802  125  RNPKLGYDNFDRHLT  YDNFDRHLT        0.2532       3228.6                 50.00     Sequence
DRB1_0802   96  VLARLLAAGEAYHAF  VLARLLAAG        0.2530       3236.5                 50.00     Sequence
DRB1_0802  256  KLSKRDPQSNLFAHR  KLSKRDPQS        0.2530       3237.3                 50.00     Sequence
DRB1_0802  208  ITHVLRGEDLLPSTP  HVLRGEDLL        0.2524       3257.0                 50.00     Sequence
DRB1_0802  210  HVLRGEDLLPSTPRQ  HVLRGEDLL        0.2523       3261.4                 50.00     Sequence
DRB1_0802  415  ALTSVTDWTAPLIEA  ALTSVTDWT        0.2523       3262.9                 50.00     Sequence
DRB1_0802  211  VLRGEDLLPSTPRQL  LRGEDLLPS        0.2522       3264.0                 50.00     Sequence
DRB1_0802  212  LRGEDLLPSTPRQLA  LPSTPRQLA        0.2522       3265.4                 50.00     Sequence
DRB1_0802  167  NDLVRGPVTFAAGSV  LVRGPVTFA        0.2520       3272.5                 50.00     Sequence
DRB1_0802  451  RVAATGTTVSPPLFE  RVAATGTTV        0.2516       3287.2                 50.00     Sequence
DRB1_0802  244  AHLPTVLGEGTKKLS  VLGEGTKKL        0.2508       3316.4                 50.00     Sequence
DRB1_0802  173  PVTFAAGSVPDFALT  VTFAAGSVP        0.2507       3317.3                 50.00     Sequence
DRB1_0802  113  PEEVEARHVAAGRNP  RHVAAGRNP        0.2507       3317.6                 50.00     Sequence
DRB1_0802   52  DSEESYLALLDALRW  YLALLDALR        0.2492       3372.1                 50.00     Sequence
DRB1_0802  369  QTRIVVLGDAWELLK  RIVVLGDAW        0.2482       3408.2                 50.00     Sequence
DRB1_0802   11  CPSPTGTPHVGLVRT  GTPHVGLVR        0.2476       3433.2                 50.00     Sequence
DRB1_0802  181  VPDFALTRASGDPLY  PDFALTRAS        0.2474       3439.4                 50.00     Sequence
DRB1_0802  426  LIEAALKDALIEGLA  LIEAALKDA        0.2466       3467.4                 50.00     Sequence
DRB1_0802  314  SPARFDQKKADALNA  PARFDQKKA        0.2455       3512.0                 50.00     Sequence
DRB1_0802  160  PDDDLAWNDLVRGPV  WNDLVRGPV        0.2450       3529.3                 50.00     Sequence
DRB1_0802  461  PPLFESLELLGRDRS  LFESLELLG        0.2448       3537.3                 50.00     Sequence
DRB1_0802  422  WTAPLIEAALKDALI  WTAPLIEAA        0.2444       3551.0                 50.00     Sequence
DRB1_0802  182  PDFALTRASGDPLYT  PDFALTRAS        0.2443       3556.7                 50.00     Sequence
DRB1_0802  215  EDLLPSTPRQLALHQ  LPSTPRQLA        0.2441       3563.8                 50.00     Sequence
DRB1_0802  209  THVLRGEDLLPSTPR  HVLRGEDLL        0.2435       3585.8                 50.00     Sequence
DRB1_0802  179  GSVPDFALTRASGDP  PDFALTRAS        0.2422       3639.5                 50.00     Sequence
DRB1_0802  412  ALAALTSVTDWTAPL  ALAALTSVT        0.2418       3654.4                 50.00     Sequence
DRB1_0802  464  FESLELLGRDRSMQR  LLGRDRSMQ        0.2413       3674.8                 50.00     Sequence
DRB1_0802  282  YLALLGWSIADDHDL  YLALLGWSI        0.2399       3728.5                 50.00     Sequence
DRB1_0802  414  AALTSVTDWTAPLIE  LTSVTDWTA        0.2387       3777.5                 50.00     Sequence
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DRB1_0802  214  GEDLLPSTPRQLALH  LPSTPRQLA        0.2367       3862.1              50.00     Sequence
DRB1_0802  280  LNYLALLGWSIADDH  YLALLGWSI        0.2358       3897.0              50.00     Sequence
DRB1_0802  180  SVPDFALTRASGDPL  PDFALTRAS        0.2352       3923.7              50.00     Sequence
DRB1_0802  281  NYLALLGWSIADDHD  YLALLGWSI        0.2346       3948.1              50.00     Sequence
DRB1_0802   84  YRQSQRAEIYRDVLA  YRQSQRAEI        0.2342       3967.9              50.00     Sequence
DRB1_0802  213  RGEDLLPSTPRQLAL  LPSTPRQLA        0.2336       3995.0              50.00     Sequence
DRB1_0802   10  FCPSPTGTPHVGLVR  GTPHVGLVR        0.2335       3998.8              50.00     Sequence
DRB1_0802   74  GPEVGGPYGPYRQSQ  GPEVGGPYG        0.2273       4276.3              50.00     Sequence
DRB1_0802  170  VRGPVTFAAGSVPDF  VRGPVTFAA        0.2268       4296.1              50.00     Sequence
DRB1_0802   37  GGTFVFRIEDTDAQR  GGTFVFRIE        0.2266       4306.0              50.00     Sequence
DRB1_0802  413  LAALTSVTDWTAPLI  ALTSVTDWT        0.2264       4316.4              50.00     Sequence
DRB1_0802  198  VNPCDDALMKITHVL  ALMKITHVL        0.2254       4363.7              50.00     Sequence
DRB1_0802  411  AALAALTSVTDWTAP  ALAALTSVT        0.2246       4403.2              50.00     Sequence
DRB1_0802   36  TGGTFVFRIEDTDAQ  GGTFVFRIE        0.2225       4501.9              50.00     Sequence
DRB1_0802  174  VTFAAGSVPDFALTR  VTFAAGSVP        0.2220       4528.2              50.00     Sequence
DRB1_0802  417  TSVTDWTAPLIEAAL  WTAPLIEAA        0.2211       4571.7              50.00     Sequence
DRB1_0802   51  RDSEESYLALLDALR  YLALLDALR        0.2173       4761.9              50.00     Sequence
DRB1_0802  425  PLIEAALKDALIEGL  LIEAALKDA        0.2167       4794.8              50.00     Sequence
DRB1_0802  429  AALKDALIEGLALKP  LIEGLALKP        0.2156       4850.9              50.00     Sequence
DRB1_0802  153  PVVRLRMPDDDLAWN  PVVRLRMPD        0.2153       4867.5              50.00     Sequence
DRB1_0802  373  VVLGDAWELLKFFND  VLGDAWELL        0.2146       4903.5              50.00     Sequence
DRB1_0802  178  AGSVPDFALTRASGD  PDFALTRAS        0.2143       4918.9              50.00     Sequence
DRB1_0802  332  RMLDVGDFTVRLRDH  VGDFTVRLR        0.2134       4966.4              50.00     Sequence
DRB1_0802  374  VLGDAWELLKFFNDD  VLGDAWELL        0.2131       4982.1              50.00     Sequence
DRB1_0802  410  DAALAALTSVTDWTA  ALAALTSVT        0.2125       5019.1              50.00     Sequence
DRB1_0802  260  RDPQSNLFAHRDRGF  RDPQSNLFA        0.2110       5098.8              50.00     Sequence
DRB1_0802  406  AAVLDAALAALTSVT  LDAALAALT        0.2096       5179.2              50.00     Sequence
DRB1_0802  421  DWTAPLIEAALKDAL  WTAPLIEAA        0.2095       5182.8              50.00     Sequence
DRB1_0802  341  VRLRDHLDTHGHHIA  HLDTHGHHI        0.2089       5213.7              50.00     Sequence
DRB1_0802  177  AAGSVPDFALTRASG  PDFALTRAS        0.2063       5362.2              50.00     Sequence
DRB1_0802  460  SPPLFESLELLGRDR  LFESLELLG        0.2056       5408.3              50.00     Sequence
DRB1_0802    7  RVRFCPSPTGTPHVG  RVRFCPSPT        0.2055       5412.2              50.00     Sequence
DRB1_0802  312  NSSPARFDQKKADAL  PARFDQKKA        0.2054       5417.1              50.00     Sequence
DRB1_0802   35  HTGGTFVFRIEDTDA  GGTFVFRIE        0.2051       5437.0              50.00     Sequence
DRB1_0802  139  TDAQRAAYLAEGRQP  AYLAEGRQP        0.2039       5508.7              50.00     Sequence
DRB1_0802  427  IEAALKDALIEGLAL  IEAALKDAL        0.2033       5541.4              50.00     Sequence
DRB1_0802  361  FAAAAELVQTRIVVL  LVQTRIVVL        0.2033       5542.1              50.00     Sequence
DRB1_0802  313  SSPARFDQKKADALN  PARFDQKKA        0.2030       5559.2              50.00     Sequence
DRB1_0802  372  IVVLGDAWELLKFFN  VLGDAWELL        0.2020       5618.1              50.00     Sequence
DRB1_0802  171  RGPVTFAAGSVPDFA  VTFAAGSVP        0.2014       5654.8              50.00     Sequence
DRB1_0802   32  YARHTGGTFVFRIED  GGTFVFRIE        0.2013       5660.8              50.00     Sequence
DRB1_0802  408  VLDAALAALTSVTDW  LDAALAALT        0.1983       5852.5              50.00     Sequence
DRB1_0802  407  AVLDAALAALTSVTD  LDAALAALT        0.1978       5879.4              50.00     Sequence
DRB1_0802  346  HLDTHGHHIALDEAA  LDTHGHHIA        0.1973       5911.4              50.00     Sequence
DRB1_0802  311  VNSSPARFDQKKADA  PARFDQKKA        0.1972       5918.5              50.00     Sequence
DRB1_0802  424  APLIEAALKDALIEG  LIEAALKDA        0.1969       5939.2              50.00     Sequence
DRB1_0802  409  LDAALAALTSVTDWT  LDAALAALT        0.1955       6027.8              50.00     Sequence
DRB1_0802  172  GPVTFAAGSVPDFAL  VTFAAGSVP        0.1952       6049.9              50.00     Sequence
DRB1_0802  138  LTDAQRAAYLAEGRQ  DAQRAAYLA        0.1946       6090.7              50.00     Sequence
DRB1_0802    8  VRFCPSPTGTPHVGL  VRFCPSPTG        0.1943       6108.0              50.00     Sequence
DRB1_0802   86  QSQRAEIYRDVLARL  IYRDVLARL        0.1943       6109.6              50.00     Sequence
DRB1_0802  272  RGFIPEGLLNYLALL  PEGLLNYLA        0.1942       6115.9              50.00     Sequence
DRB1_0802  342  RLRDHLDTHGHHIAL  LDTHGHHIA        0.1939       6133.1              50.00     Sequence
DRB1_0802   34  RHTGGTFVFRIEDTD  GGTFVFRIE        0.1934       6166.2              50.00     Sequence
DRB1_0802  270  RDRGFIPEGLLNYLA  RDRGFIPEG        0.1930       6192.9              50.00     Sequence
DRB1_0802   38  GTFVFRIEDTDAQRD  GTFVFRIED        0.1927       6217.3              50.00     Sequence
DRB1_0802  331  IRMLDVGDFTVRLRD  GDFTVRLRD        0.1913       6311.8              50.00     Sequence
DRB1_0802  340  TVRLRDHLDTHGHHI  TVRLRDHLD        0.1907       6349.2              50.00     Sequence
DRB1_0802  405  GAAVLDAALAALTSV  LDAALAALT        0.1900       6401.7              50.00     Sequence
DRB1_0802  459  VSPPLFESLELLGRD  LFESLELLG        0.1895       6433.0              50.00     Sequence
DRB1_0802  344  RDHLDTHGHHIALDE  HLDTHGHHI        0.1892       6456.7              50.00     Sequence
DRB1_0802  360  AFAAAAELVQTRIVV  AFAAAAELV        0.1884       6514.2              50.00     Sequence
DRB1_0802  192  DPLYTLVNPCDDALM  PLYTLVNPC        0.1877       6563.6              50.00     Sequence
DRB1_0802   33  ARHTGGTFVFRIEDT  GGTFVFRIE        0.1867       6630.9              50.00     Sequence
DRB1_0802  458  TVSPPLFESLELLGR  LFESLELLG        0.1867       6631.1              50.00     Sequence
DRB1_0802   73  EGPEVGGPYGPYRQS  GPYGPYRQS        0.1866       6636.7              50.00     Sequence
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DRB1_0802  345  DHLDTHGHHIALDEA  HLDTHGHHI        0.1855       6721.1              50.00     Sequence
DRB1_0802  317  RFDQKKADALNAEHI  RFDQKKADA        0.1852       6742.6              50.00     Sequence
DRB1_0802    9  RFCPSPTGTPHVGLV  PSPTGTPHV        0.1845       6790.5              50.00     Sequence
DRB1_0802  268  AHRDRGFIPEGLLNY  RDRGFIPEG        0.1843       6809.9              50.00     Sequence
DRB1_0802  343  LRDHLDTHGHHIALD  HLDTHGHHI        0.1842       6815.8              50.00     Sequence
DRB1_0802  316  ARFDQKKADALNAEH  RFDQKKADA        0.1836       6858.0              50.00     Sequence
DRB1_0802  418  SVTDWTAPLIEAALK  WTAPLIEAA        0.1830       6906.5              50.00     Sequence
DRB1_0802  191  GDPLYTLVNPCDDAL  PLYTLVNPC        0.1828       6920.7              50.00     Sequence
DRB1_0802  112  TPEEVEARHVAAGRN  EVEARHVAA        0.1820       6977.1              50.00     Sequence
DRB1_0802  423  TAPLIEAALKDALIE  LIEAALKDA        0.1816       7011.0              50.00     Sequence
DRB1_0802  271  DRGFIPEGLLNYLAL  PEGLLNYLA        0.1793       7181.6              50.00     Sequence
DRB1_0802  404  DGAAVLDAALAALTS  LDAALAALT        0.1793       7184.4              50.00     Sequence
DRB1_0802  259  KRDPQSNLFAHRDRG  RDPQSNLFA        0.1790       7205.1              50.00     Sequence
DRB1_0802  403  PDGAAVLDAALAALT  LDAALAALT        0.1786       7241.8              50.00     Sequence
DRB1_0802  176  FAAGSVPDFALTRAS  GSVPDFALT        0.1773       7342.2              50.00     Sequence
DRB1_0802  193  PLYTLVNPCDDALMK  PLYTLVNPC        0.1770       7365.1              50.00     Sequence
DRB1_0802  394  PKAAAKELGPDGAAV  PKAAAKELG        0.1754       7494.4              50.00     Sequence
DRB1_0802  420  TDWTAPLIEAALKDA  WTAPLIEAA        0.1749       7534.6              50.00     Sequence
DRB1_0802  383  KFFNDDQYVIDPKAA  FFNDDQYVI        0.1748       7545.0              50.00     Sequence
DRB1_0802  190  SGDPLYTLVNPCDDA  GDPLYTLVN        0.1735       7652.6              50.00     Sequence
DRB1_0802  375  LGDAWELLKFFNDDQ  LGDAWELLK        0.1733       7667.6              50.00     Sequence
DRB1_0802   85  RQSQRAEIYRDVLAR  RQSQRAEIY        0.1730       7689.3              50.00     Sequence
DRB1_0802  391  VIDPKAAAKELGPDG  PKAAAKELG        0.1728       7709.3              50.00     Sequence
DRB1_0802  393  DPKAAAKELGPDGAA  PKAAAKELG        0.1722       7761.7              50.00     Sequence
DRB1_0802  111  STPEEVEARHVAAGR  EVEARHVAA        0.1722       7761.9              50.00     Sequence
DRB1_0802  454  ATGTTVSPPLFESLE  TGTTVSPPL        0.1719       7785.2              50.00     Sequence
DRB1_0802  452  VAATGTTVSPPLFES  TGTTVSPPL        0.1714       7822.8              50.00     Sequence
DRB1_0802  269  HRDRGFIPEGLLNYL  RDRGFIPEG        0.1699       7951.1              50.00     Sequence
DRB1_0802  453  AATGTTVSPPLFESL  TGTTVSPPL        0.1695       7991.9              50.00     Sequence
DRB1_0802   31  AYARHTGGTFVFRIE  GGTFVFRIE        0.1694       7999.2              50.00     Sequence
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DRB1_0802  351  GHHIALDEAAFAAAA  HHIALDEAA        0.1683       8089.7              50.00     Sequence
DRB1_0802  175  TFAAGSVPDFALTRA  GSVPDFALT        0.1676       8155.2              50.00     Sequence
DRB1_0802  428  EAALKDALIEGLALK  KDALIEGLA        0.1667       8236.7              50.00     Sequence
DRB1_0802  359  AAFAAAAELVQTRIV  AFAAAAELV        0.1661       8286.6              50.00     Sequence
DRB1_0802  378  AWELLKFFNDDQYVI  AWELLKFFN        0.1660       8293.5              50.00     Sequence
DRB1_0802  183  DFALTRASGDPLYTL  ALTRASGDP        0.1657       8324.4              50.00     Sequence
DRB1_0802  110  FSTPEEVEARHVAAG  EVEARHVAA        0.1657       8327.6              50.00     Sequence
DRB1_0802   98  ARLLAAGEAYHAFST  RLLAAGEAY        0.1645       8430.4              50.00     Sequence
DRB1_0802  121  VAAGRNPKLGYDNFD  VAAGRNPKL        0.1635       8524.9              50.00     Sequence
DRB1_0802  455  TGTTVSPPLFESLEL  TGTTVSPPL        0.1633       8547.1              50.00     Sequence
DRB1_0802  392  IDPKAAAKELGPDGA  PKAAAKELG        0.1625       8616.4              50.00     Sequence
DRB1_0802  185  ALTRASGDPLYTLVN  ALTRASGDP        0.1625       8618.8              50.00     Sequence
DRB1_0802  189  ASGDPLYTLVNPCDD  GDPLYTLVN        0.1624       8631.5              50.00     Sequence
DRB1_0802  377  DAWELLKFFNDDQYV  AWELLKFFN        0.1621       8655.8              50.00     Sequence
DRB1_0802  419  VTDWTAPLIEAALKD  WTAPLIEAA        0.1610       8761.5              50.00     Sequence
DRB1_0802   99  RLLAAGEAYHAFSTP  RLLAAGEAY        0.1602       8833.9              50.00     Sequence
DRB1_0802  283  LALLGWSIADDHDLF  LALLGWSIA        0.1579       9061.7              50.00     Sequence
DRB1_0802  376  GDAWELLKFFNDDQY  DAWELLKFF        0.1578       9065.8              50.00     Sequence
DRB1_0802  309  ADVNSSPARFDQKKA  PARFDQKKA        0.1574       9106.8              50.00     Sequence
DRB1_0802  325  ALNAEHIRMLDVGDF  ALNAEHIRM        0.1568       9167.6              50.00     Sequence
DRB1_0802  330  HIRMLDVGDFTVRLR  VGDFTVRLR        0.1560       9250.0              50.00     Sequence
DRB1_0802  188  RASGDPLYTLVNPCD  GDPLYTLVN        0.1559       9257.3              50.00     Sequence
DRB1_0802  350  HGHHIALDEAAFAAA  HHIALDEAA        0.1552       9326.9              50.00     Sequence
DRB1_0802  194  LYTLVNPCDDALMKI  LYTLVNPCD        0.1531       9542.0              50.00     Sequence
DRB1_0802  358  EAAFAAAAELVQTRI  FAAAAELVQ        0.1525       9600.5              50.00     Sequence
DRB1_0802  457  TTVSPPLFESLELLG  LFESLELLG        0.1515       9702.1              50.00     Sequence
DRB1_0802  352  HHIALDEAAFAAAAE  HHIALDEAA        0.1506       9799.6              50.00     Sequence
DRB1_0802  347  LDTHGHHIALDEAAF  LDTHGHHIA        0.1502       9839.7              50.00     Sequence
DRB1_0802   72  DEGPEVGGPYGPYRQ  GPEVGGPYG        0.1480      10082.3              50.00     Sequence
DRB1_0802  124  GRNPKLGYDNFDRHL  GYDNFDRHL        0.1455      10353.9              50.00     Sequence
DRB1_0802  296  LFGLDEMVAAFDVAD  LFGLDEMVA        0.1443      10494.0              50.00     Sequence
DRB1_0802  324  DALNAEHIRMLDVGD  ALNAEHIRM        0.1441      10514.7              50.00     Sequence
DRB1_0802  357  DEAAFAAAAELVQTR  AFAAAAELV        0.1428      10670.1              50.00     Sequence
DRB1_0802  258  SKRDPQSNLFAHRDR  SNLFAHRDR        0.1421      10751.2              50.00     Sequence
DRB1_0802   97  LARLLAAGEAYHAFS  RLLAAGEAY        0.1406      10921.3              50.00     Sequence
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DRB1_0802  302  MVAAFDVADVNSSPA  VADVNSSPA        0.1401       10981.8                50.00     Sequence
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DRB1_0802  402  GPDGAAVLDAALAAL  AAVLDAALA        0.1375       11297.3                50.00     Sequence
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DRB1_0802  356  LDEAAFAAAAELVQT  AFAAAAELV        0.1354       11550.9                50.00     Sequence
DRB1_0802  349  THGHHIALDEAAFAA  HHIALDEAA        0.1350       11604.4                50.00     Sequence
DRB1_0802  456  GTTVSPPLFESLELL  GTTVSPPLF        0.1349       11611.7                50.00     Sequence
DRB1_0802  382  LKFFNDDQYVIDPKA  FFNDDQYVI        0.1342       11700.4                50.00     Sequence
DRB1_0802  306  FDVADVNSSPARFDQ  FDVADVNSS        0.1342       11702.5                50.00     Sequence
DRB1_0802  323  ADALNAEHIRMLDVG  ALNAEHIRM        0.1341       11715.7                50.00     Sequence
DRB1_0802  320  QKKADALNAEHIRML  ALNAEHIRM        0.1338       11750.1                50.00     Sequence
DRB1_0802  184  FALTRASGDPLYTLV  ALTRASGDP        0.1338       11761.3                50.00     Sequence
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DRB1_0802  379  WELLKFFNDDQYVID  FFNDDQYVI        0.1319       12005.6                50.00     Sequence
DRB1_0802  187  TRASGDPLYTLVNPC  GDPLYTLVN        0.1316       12036.3                50.00     Sequence
DRB1_0802  355  ALDEAAFAAAAELVQ  AFAAAAELV        0.1310       12112.9                50.00     Sequence
DRB1_0802  186  LTRASGDPLYTLVNP  LTRASGDPL        0.1310       12120.9                50.00     Sequence
DRB1_0802  197  LVNPCDDALMKITHV  LVNPCDDAL        0.1307       12158.8                50.00     Sequence
DRB1_0802  257  LSKRDPQSNLFAHRD  LSKRDPQSN        0.1303       12208.3                50.00     Sequence
DRB1_0802  107  YHAFSTPEEVEARHV  YHAFSTPEE        0.1300       12246.4                50.00     Sequence
DRB1_0802   50  QRDSEESYLALLDAL  RDSEESYLA        0.1295       12309.8                50.00     Sequence
DRB1_0802  106  AYHAFSTPEEVEARH  FSTPEEVEA        0.1295       12314.9                50.00     Sequence
DRB1_0802  122  AAGRNPKLGYDNFDR  AAGRNPKLG        0.1294       12323.8                50.00     Sequence
DRB1_0802  301  EMVAAFDVADVNSSP  FDVADVNSS        0.1287       12428.6                50.00     Sequence
DRB1_0802  159  MPDDDLAWNDLVRGP  LAWNDLVRG        0.1282       12496.6                50.00     Sequence
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DRB1_0802  305  AFDVADVNSSPARFD  FDVADVNSS        0.1237       13116.0                50.00     Sequence
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DRB1_0802  381  LLKFFNDDQYVIDPK  FFNDDQYVI        0.1232       13183.7                50.00     Sequence
DRB1_0802  104  GEAYHAFSTPEEVEA  YHAFSTPEE        0.1230       13214.9                50.00     Sequence
DRB1_0802  322  KADALNAEHIRMLDV  ALNAEHIRM        0.1224       13303.8                50.00     Sequence
DRB1_0802  329  EHIRMLDVGDFTVRL  RMLDVGDFT        0.1222       13320.7                50.00     Sequence
DRB1_0802   71  WDEGPEVGGPYGPYR  GPEVGGPYG        0.1204       13589.1                50.00     Sequence
DRB1_0802  297  FGLDEMVAAFDVADV  FGLDEMVAA        0.1201       13627.4                50.00     Sequence
DRB1_0802   63  ALRWLGLDWDEGPEV  ALRWLGLDW        0.1198       13674.5                50.00     Sequence
DRB1_0802  295  DLFGLDEMVAAFDVA  LFGLDEMVA        0.1189       13809.5                50.00     Sequence
DRB1_0802  298  GLDEMVAAFDVADVN  GLDEMVAAF        0.1177       13985.4                50.00     Sequence
DRB1_0802  308  VADVNSSPARFDQKK  VADVNSSPA        0.1173       14054.3                50.00     Sequence
DRB1_0802  294  HDLFGLDEMVAAFDV  LFGLDEMVA        0.1170       14092.4                50.00     Sequence
DRB1_0802  401  LGPDGAAVLDAALAA  AAVLDAALA        0.1170       14101.5                50.00     Sequence
DRB1_0802  348  DTHGHHIALDEAAFA  HHIALDEAA        0.1169       14109.6                50.00     Sequence
DRB1_0802  304  AAFDVADVNSSPARF  FDVADVNSS        0.1150       14406.1                50.00     Sequence
DRB1_0802  321  KKADALNAEHIRMLD  ALNAEHIRM        0.1132       14690.5                50.00     Sequence
DRB1_0802  400  ELGPDGAAVLDAALA  AAVLDAALA        0.1127       14764.6                50.00     Sequence
DRB1_0802  319  DQKKADALNAEHIRM  ALNAEHIRM        0.1125       14802.4                50.00     Sequence
DRB1_0802  380  ELLKFFNDDQYVIDP  FFNDDQYVI        0.1125       14810.4                50.00     Sequence
DRB1_0802  327  NAEHIRMLDVGDFTV  RMLDVGDFT        0.1109       15061.8                50.00     Sequence
DRB1_0802  353  HIALDEAAFAAAAEL  HIALDEAAF        0.1105       15120.5                50.00     Sequence
DRB1_0802  196  TLVNPCDDALMKITH  CDDALMKIT        0.1103       15163.9                50.00     Sequence
DRB1_0802   49  AQRDSEESYLALLDA  RDSEESYLA        0.1095       15292.7                50.00     Sequence
DRB1_0802   61  LDALRWLGLDWDEGP  WLGLDWDEG        0.1088       15407.1                50.00     Sequence
DRB1_0802   62  DALRWLGLDWDEGPE  WLGLDWDEG        0.1085       15454.1                50.00     Sequence
DRB1_0802   40  FVFRIEDTDAQRDSE  FVFRIEDTD        0.1064       15804.4                50.00     Sequence
DRB1_0802  328  AEHIRMLDVGDFTVR  RMLDVGDFT        0.1064       15818.5                50.00     Sequence
DRB1_0802  303  VAAFDVADVNSSPAR  FDVADVNSS        0.1045       16149.5                50.00     Sequence
DRB1_0802  293  DHDLFGLDEMVAAFD  LFGLDEMVA        0.1044       16151.5                50.00     Sequence
DRB1_0802  307  DVADVNSSPARFDQK  VADVNSSPA        0.1044       16159.4                50.00     Sequence
DRB1_0802  102  AAGEAYHAFSTPEEV  AGEAYHAFS        0.1040       16233.4                50.00     Sequence
DRB1_0802   66  WLGLDWDEGPEVGGP  WLGLDWDEG        0.1034       16341.0                50.00     Sequence
DRB1_0802   65  RWLGLDWDEGPEVGG  WLGLDWDEG        0.1032       16369.4                50.00     Sequence
DRB1_0802  100  LLAAGEAYHAFSTPE  LLAAGEAYH        0.1031       16385.5                50.00     Sequence
DRB1_0802  123  AGRNPKLGYDNFDRH  GRNPKLGYD        0.1012       16727.4                50.00     Sequence
DRB1_0802  103  AGEAYHAFSTPEEVE  AGEAYHAFS        0.1011       16750.1                50.00     Sequence
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   DRB1_0802  101  LAAGEAYHAFSTPEE  AGEAYHAFS        0.1007      16824.6                 50.00     Sequence
   DRB1_0802  195  YTLVNPCDDALMKIT  CDDALMKIT        0.0981      17296.1                 50.00     Sequence
   DRB1_0802  292  DDHDLFGLDEMVAAF  LFGLDEMVA        0.0975      17405.0                 50.00     Sequence
   DRB1_0802  284  ALLGWSIADDHDLFG  WSIADDHDL        0.0975      17410.1                 50.00     Sequence
   DRB1_0802   64  LRWLGLDWDEGPEVG  WLGLDWDEG        0.0956      17763.1                 50.00     Sequence
   DRB1_0802   48  DAQRDSEESYLALLD  RDSEESYLA        0.0907      18732.1                 50.00     Sequence
   DRB1_0802  286  LGWSIADDHDLFGLD  WSIADDHDL        0.0886      19175.8                 50.00     Sequence
   DRB1_0802  158  RMPDDDLAWNDLVRG  LAWNDLVRG        0.0872      19463.7                 50.00     Sequence
   DRB1_0802   47  TDAQRDSEESYLALL  RDSEESYLA        0.0864      19640.5                 50.00     Sequence
   DRB1_0802  285  LLGWSIADDHDLFGL  WSIADDHDL        0.0858      19752.2                 50.00     Sequence
   DRB1_0802  299  LDEMVAAFDVADVNS  MVAAFDVAD        0.0841      20134.1                 50.00     Sequence
   DRB1_0802   42  FRIEDTDAQRDSEES  FRIEDTDAQ        0.0805      20917.1                 50.00     Sequence
   DRB1_0802  291  ADDHDLFGLDEMVAA  LFGLDEMVA        0.0799      21053.8                 50.00     Sequence
   DRB1_0802   46  DTDAQRDSEESYLAL  RDSEESYLA        0.0782      21454.3                 50.00     Sequence
   DRB1_0802  399  KELGPDGAAVLDAAL  GAAVLDAAL        0.0781      21475.7                 50.00     Sequence
   DRB1_0802   41  VFRIEDTDAQRDSEE  FRIEDTDAQ        0.0772      21677.2                 50.00     Sequence
   DRB1_0802  287  GWSIADDHDLFGLDE  WSIADDHDL        0.0771      21699.7                 50.00     Sequence
   DRB1_0802   70  DWDEGPEVGGPYGPY  GPEVGGPYG        0.0767      21794.1                 50.00     Sequence
   DRB1_0802  154  VVRLRMPDDDLAWND  VVRLRMPDD        0.0740      22461.0                 50.00     Sequence
   DRB1_0802   69  LDWDEGPEVGGPYGP  GPEVGGPYG        0.0735      22561.9                 50.00     Sequence
   DRB1_0802   68  GLDWDEGPEVGGPYG  GPEVGGPYG        0.0732      22642.1                 50.00     Sequence
   DRB1_0802  395  KAAAKELGPDGAAVL  KAAAKELGP        0.0701      23426.6                 50.00     Sequence
   DRB1_0802   45  EDTDAQRDSEESYLA  RDSEESYLA        0.0696      23558.0                 50.00     Sequence
   DRB1_0802  288  WSIADDHDLFGLDEM  WSIADDHDL        0.0681      23921.2                 50.00     Sequence
   DRB1_0802  157  LRMPDDDLAWNDLVR  LRMPDDDLA        0.0668      24270.8                 50.00     Sequence
   DRB1_0802  290  IADDHDLFGLDEMVA  LFGLDEMVA        0.0635      25143.5                 50.00     Sequence
   DRB1_0802  397  AAKELGPDGAAVLDA  AAKELGPDG        0.0627      25362.6                 50.00     Sequence
   DRB1_0802  396  AAAKELGPDGAAVLD  AAKELGPDG        0.0578      26743.8                 50.00     Sequence
   DRB1_0802  155  VRLRMPDDDLAWNDL  LRMPDDDLA        0.0543      27794.4                 50.00     Sequence
   DRB1_0802  156  RLRMPDDDLAWNDLV  LRMPDDDLA        0.0532      28125.3                 50.00     Sequence
   DRB1_0802   43  RIEDTDAQRDSEESY  RIEDTDAQR        0.0517      28577.8                 50.00     Sequence
   DRB1_0802  398  AKELGPDGAAVLDAA  LGPDGAAVL        0.0504      28980.7                 50.00     Sequence
   DRB1_0802   67  LGLDWDEGPEVGGPY  WDEGPEVGG        0.0436      31200.8                 50.00     Sequence
   DRB1_0802   44  IEDTDAQRDSEESYL  DAQRDSEES        0.0436      31203.1                 50.00     Sequence
   DRB1_0802  289  SIADDHDLFGLDEMV  SIADDHDLF        0.0375      33321.6                 50.00     Sequence
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Allele: DRB1_0802. Number of high binders 4. Number of weak binders 51. Number of peptides 476

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0901   92  IYRDVLARLLAAGEA  IYRDVLARL        0.6068         70.4          WB     4.00     Sequence
   DRB1_0901  433  DALIEGLALKPRKAF  ALIEGLALK        0.5905         84.0          WB     8.00     Sequence
   DRB1_0901  444  RKAFSPIRVAATGTT  KAFSPIRVA        0.5898         84.6          WB     8.00     Sequence
   DRB1_0901  432  KDALIEGLALKPRKA  ALIEGLALK        0.5849         89.2          WB     8.00     Sequence
   DRB1_0901  358  EAAFAAAAELVQTRI  AFAAAAELV        0.5843         89.8          WB     8.00     Sequence
   DRB1_0901  104  GEAYHAFSTPEEVEA  YHAFSTPEE        0.5785         95.6          WB     8.00     Sequence
   DRB1_0901  105  EAYHAFSTPEEVEAR  YHAFSTPEE        0.5778         96.4          WB     8.00     Sequence
   DRB1_0901  359  AAFAAAAELVQTRIV  AFAAAAELV        0.5745         99.8          WB     8.00     Sequence
   DRB1_0901   27  LFNWAYARHTGGTFV  FNWAYARHT        0.5723        102.3          WB     8.00     Sequence
   DRB1_0901   91  EIYRDVLARLLAAGE  IYRDVLARL        0.5692        105.8          WB     8.00     Sequence
   DRB1_0901  445  KAFSPIRVAATGTTV  IRVAATGTT        0.5684        106.7          WB     8.00     Sequence
   DRB1_0901  431  LKDALIEGLALKPRK  ALIEGLALK        0.5683        106.8          WB     8.00     Sequence
   DRB1_0901   90  AEIYRDVLARLLAAG  IYRDVLARL        0.5659        109.6          WB     8.00     Sequence
   DRB1_0901  441  LKPRKAFSPIRVAAT  RKAFSPIRV        0.5638        112.1          WB     8.00     Sequence
   DRB1_0901  238  ERIPKFAHLPTVLGE  FAHLPTVLG        0.5624        113.8          WB     8.00     Sequence
   DRB1_0901  356  LDEAAFAAAAELVQT  AFAAAAELV        0.5598        117.0          WB     8.00     Sequence
   DRB1_0901  439  LALKPRKAFSPIRVA  RKAFSPIRV        0.5589        118.2          WB     8.00     Sequence
   DRB1_0901  357  DEAAFAAAAELVQTR  AFAAAAELV        0.5584        118.9          WB     8.00     Sequence
   DRB1_0901  440  ALKPRKAFSPIRVAA  RKAFSPIRV        0.5581        119.3          WB     8.00     Sequence
   DRB1_0901  239  RIPKFAHLPTVLGEG  FAHLPTVLG        0.5561        121.9          WB     8.00     Sequence
   DRB1_0901   26  ALFNWAYARHTGGTF  FNWAYARHT        0.5554        122.9          WB     8.00     Sequence
   DRB1_0901  103  AGEAYHAFSTPEEVE  YHAFSTPEE        0.5520        127.3          WB     8.00     Sequence
   DRB1_0901  166  WNDLVRGPVTFAAGS  WNDLVRGPV        0.5515        128.1          WB     8.00     Sequence
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DRB1_0901  106  AYHAFSTPEEVEARH  YHAFSTPEE         0.5507         129.2         WB     8.00     Sequence
DRB1_0901  297  FGLDEMVAAFDVADV  FGLDEMVAA         0.5507         129.3         WB     8.00     Sequence
DRB1_0901  296  LFGLDEMVAAFDVAD  EMVAAFDVA         0.5466         135.1         WB    16.00     Sequence
DRB1_0901  355  ALDEAAFAAAAELVQ  AFAAAAELV         0.5444         138.3         WB    16.00     Sequence
DRB1_0901  446  AFSPIRVAATGTTVS  IRVAATGTT         0.5425         141.2         WB    16.00     Sequence
DRB1_0901  442  KPRKAFSPIRVAATG  KAFSPIRVA         0.5422         141.6         WB    16.00     Sequence
DRB1_0901   89  RAEIYRDVLARLLAA  IYRDVLARL         0.5413         143.1         WB    16.00     Sequence
DRB1_0901  434  ALIEGLALKPRKAFS  ALIEGLALK         0.5406         144.1         WB    16.00     Sequence
DRB1_0901   93  YRDVLARLLAAGEAY  YRDVLARLL         0.5402         144.7         WB    16.00     Sequence
DRB1_0901  237  AERIPKFAHLPTVLG  FAHLPTVLG         0.5387         147.1         WB    16.00     Sequence
DRB1_0901  419  VTDWTAPLIEAALKD  DWTAPLIEA         0.5334         155.7         WB    16.00     Sequence
DRB1_0901   28  FNWAYARHTGGTFVF  FNWAYARHT         0.5323         157.6         WB    16.00     Sequence
DRB1_0901  165  AWNDLVRGPVTFAAG  LVRGPVTFA         0.5319         158.4         WB    16.00     Sequence
DRB1_0901  443  PRKAFSPIRVAATGT  KAFSPIRVA         0.5319         158.4         WB    16.00     Sequence
DRB1_0901  430  ALKDALIEGLALKPR  ALIEGLALK         0.5307         160.4         WB    16.00     Sequence
DRB1_0901  299  LDEMVAAFDVADVNS  EMVAAFDVA         0.5264         168.1         WB    16.00     Sequence
DRB1_0901   88  QRAEIYRDVLARLLA  IYRDVLARL         0.5249         170.8         WB    16.00     Sequence
DRB1_0901  173  PVTFAAGSVPDFALT  VTFAAGSVP         0.5229         174.5         WB    16.00     Sequence
DRB1_0901  174  VTFAAGSVPDFALTR  VTFAAGSVP         0.5224         175.5         WB    16.00     Sequence
DRB1_0901  240  IPKFAHLPTVLGEGT  FAHLPTVLG         0.5223         175.7         WB    16.00     Sequence
DRB1_0901  298  GLDEMVAAFDVADVN  EMVAAFDVA         0.5213         177.6         WB    16.00     Sequence
DRB1_0901  447  FSPIRVAATGTTVSP  IRVAATGTT         0.5207         178.8         WB    16.00     Sequence
DRB1_0901  270  RDRGFIPEGLLNYLA  RGFIPEGLL         0.5194         181.2         WB    16.00     Sequence
DRB1_0901  164  LAWNDLVRGPVTFAA  WNDLVRGPV         0.5176         184.9         WB    16.00     Sequence
DRB1_0901  474  RSMQRLRAARQLVGH  QRLRAARQL         0.5175         185.0         WB    16.00     Sequence
DRB1_0901   25  TALFNWAYARHTGGT  FNWAYARHT         0.5167         186.7         WB    16.00     Sequence
DRB1_0901  360  AFAAAAELVQTRIVV  AFAAAAELV         0.5164         187.2         WB    16.00     Sequence
DRB1_0901  167  NDLVRGPVTFAAGSV  LVRGPVTFA         0.5158         188.5         WB    16.00     Sequence
DRB1_0901  295  DLFGLDEMVAAFDVA  EMVAAFDVA         0.5154         189.2         WB    16.00     Sequence
DRB1_0901  475  SMQRLRAARQLVGHA  QRLRAARQL         0.5146         190.8         WB    16.00     Sequence
DRB1_0901  269  HRDRGFIPEGLLNYL  RGFIPEGLL         0.5137         192.9         WB    16.00     Sequence
DRB1_0901  107  YHAFSTPEEVEARHV  YHAFSTPEE         0.5111         198.3         WB    16.00     Sequence
DRB1_0901  271  DRGFIPEGLLNYLAL  RGFIPEGLL         0.5109         198.7         WB    16.00     Sequence
DRB1_0901   79  GPYGPYRQSQRAEIY  YRQSQRAEI         0.5105         199.6         WB    16.00     Sequence
DRB1_0901  229  QALIRIGVAERIPKF  IRIGVAERI         0.5095         201.8         WB    16.00     Sequence
DRB1_0901  272  RGFIPEGLLNYLALL  RGFIPEGLL         0.5089         203.0         WB    16.00     Sequence
DRB1_0901  226  ALHQALIRIGVAERI  IRIGVAERI         0.5081         204.9         WB    16.00     Sequence
DRB1_0901   78  GGPYGPYRQSQRAEI  YRQSQRAEI         0.5043         213.5         WB    16.00     Sequence
DRB1_0901  449  PIRVAATGTTVSPPL  IRVAATGTT         0.5034         215.6         WB    16.00     Sequence
DRB1_0901   23  VRTALFNWAYARHTG  FNWAYARHT         0.5018         219.2         WB    16.00     Sequence
DRB1_0901  450  IRVAATGTTVSPPLF  IRVAATGTT         0.5006         222.1         WB    16.00     Sequence
DRB1_0901  448  SPIRVAATGTTVSPP  IRVAATGTT         0.4997         224.3         WB    16.00     Sequence
DRB1_0901  354  IALDEAAFAAAAELV  AFAAAAELV         0.4997         224.4         WB    16.00     Sequence
DRB1_0901  473  DRSMQRLRAARQLVG  QRLRAARQL         0.4993         225.2         WB    16.00     Sequence
DRB1_0901   22  LVRTALFNWAYARHT  FNWAYARHT         0.4987         226.8         WB    16.00     Sequence
DRB1_0901  241  PKFAHLPTVLGEGTK  FAHLPTVLG         0.4981         228.3         WB    16.00     Sequence
DRB1_0901  168  DLVRGPVTFAAGSVP  LVRGPVTFA         0.4975         229.8         WB    16.00     Sequence
DRB1_0901  102  AAGEAYHAFSTPEEV  YHAFSTPEE         0.4970         231.1         WB    16.00     Sequence
DRB1_0901  230  ALIRIGVAERIPKFA  IRIGVAERI         0.4966         232.0         WB    16.00     Sequence
DRB1_0901   87  SQRAEIYRDVLARLL  IYRDVLARL         0.4966         232.1         WB    16.00     Sequence
DRB1_0901   95  DVLARLLAAGEAYHA  ARLLAAGEA         0.4950         236.1         WB    16.00     Sequence
DRB1_0901  300  DEMVAAFDVADVNSS  EMVAAFDVA         0.4941         238.3         WB    16.00     Sequence
DRB1_0901   83  PYRQSQRAEIYRDVL  YRQSQRAEI         0.4937         239.3         WB    32.00     Sequence
DRB1_0901   94  RDVLARLLAAGEAYH  ARLLAAGEA         0.4933         240.5         WB    32.00     Sequence
DRB1_0901  242  KFAHLPTVLGEGTKK  FAHLPTVLG         0.4910         246.6         WB    32.00     Sequence
DRB1_0901  418  SVTDWTAPLIEAALK  VTDWTAPLI         0.4884         253.6         WB    32.00     Sequence
DRB1_0901  163  DLAWNDLVRGPVTFA  WNDLVRGPV         0.4883         253.7         WB    32.00     Sequence
DRB1_0901  228  HQALIRIGVAERIPK  IRIGVAERI         0.4883         253.9         WB    32.00     Sequence
DRB1_0901   24  RTALFNWAYARHTGG  FNWAYARHT         0.4880         254.7         WB    32.00     Sequence
DRB1_0901    5  TVRVRFCPSPTGTPH  VRFCPSPTG         0.4873         256.5         WB    32.00     Sequence
DRB1_0901  169  LVRGPVTFAAGSVPD  LVRGPVTFA         0.4863         259.2         WB    32.00     Sequence
DRB1_0901  227  LHQALIRIGVAERIP  IRIGVAERI         0.4858         260.8         WB    32.00     Sequence
DRB1_0901  172  GPVTFAAGSVPDFAL  VTFAAGSVP         0.4851         262.7         WB    32.00     Sequence
DRB1_0901  461  PPLFESLELLGRDRS  PLFESLELL         0.4840         265.8         WB    32.00     Sequence
DRB1_0901   82  GPYRQSQRAEIYRDV  YRQSQRAEI         0.4840         265.9         WB    32.00     Sequence
DRB1_0901   81  YGPYRQSQRAEIYRD  YRQSQRAEI         0.4828         269.3         WB    32.00     Sequence
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DRB1_0901  231  LIRIGVAERIPKFAH  IRIGVAERI        0.4812        274.1         WB    32.00     Sequence
DRB1_0901  458  TVSPPLFESLELLGR  PLFESLELL        0.4803        276.6         WB    32.00     Sequence
DRB1_0901  150  GRQPVVRLRMPDDDL  RLRMPDDDL        0.4801        277.4         WB    32.00     Sequence
DRB1_0901  420  TDWTAPLIEAALKDA  DWTAPLIEA        0.4794        279.6         WB    32.00     Sequence
DRB1_0901   80  PYGPYRQSQRAEIYR  YRQSQRAEI        0.4788        281.3         WB    32.00     Sequence
DRB1_0901  459  VSPPLFESLELLGRD  PLFESLELL        0.4781        283.5         WB    32.00     Sequence
DRB1_0901  101  LAAGEAYHAFSTPEE  YHAFSTPEE        0.4774        285.7         WB    32.00     Sequence
DRB1_0901  175  TFAAGSVPDFALTRA  TFAAGSVPD        0.4773        285.8         WB    32.00     Sequence
DRB1_0901  149  EGRQPVVRLRMPDDD  EGRQPVVRL        0.4760        289.9         WB    32.00     Sequence
DRB1_0901  192  DPLYTLVNPCDDALM  LYTLVNPCD        0.4758        290.4         WB    32.00     Sequence
DRB1_0901  171  RGPVTFAAGSVPDFA  VTFAAGSVP        0.4758        290.5         WB    32.00     Sequence
DRB1_0901  146  YLAEGRQPVVRLRMP  EGRQPVVRL        0.4751        292.8         WB    32.00     Sequence
DRB1_0901  390  YVIDPKAAAKELGPD  YVIDPKAAA        0.4749        293.3         WB    32.00     Sequence
DRB1_0901  472  RDRSMQRLRAARQLV  QRLRAARQL        0.4744        294.9         WB    32.00     Sequence
DRB1_0901  268  AHRDRGFIPEGLLNY  RGFIPEGLL        0.4742        295.5         WB    32.00     Sequence
DRB1_0901  389  QYVIDPKAAAKELGP  YVIDPKAAA        0.4734        298.0         WB    32.00     Sequence
DRB1_0901  421  DWTAPLIEAALKDAL  DWTAPLIEA        0.4733        298.6         WB    32.00     Sequence
DRB1_0901    4  ETVRVRFCPSPTGTP  VRFCPSPTG        0.4731        299.2         WB    32.00     Sequence
DRB1_0901  267  FAHRDRGFIPEGLLN  RGFIPEGLL        0.4720        302.8         WB    32.00     Sequence
DRB1_0901    6  VRVRFCPSPTGTPHV  VRFCPSPTG        0.4704        308.1         WB    32.00     Sequence
DRB1_0901  429  AALKDALIEGLALKP  LKDALIEGL        0.4704        308.1         WB    32.00     Sequence
DRB1_0901   84  YRQSQRAEIYRDVLA  YRQSQRAEI        0.4701        309.0         WB    32.00     Sequence
DRB1_0901  460  SPPLFESLELLGRDR  PLFESLELL        0.4697        310.3         WB    32.00     Sequence
DRB1_0901  193  PLYTLVNPCDDALMK  LYTLVNPCD        0.4666        320.8         WB    32.00     Sequence
DRB1_0901  147  LAEGRQPVVRLRMPD  LAEGRQPVV        0.4653        325.4         WB    32.00     Sequence
DRB1_0901  170  VRGPVTFAAGSVPDF  PVTFAAGSV        0.4652        325.7         WB    32.00     Sequence
DRB1_0901  417  TSVTDWTAPLIEAAL  VTDWTAPLI        0.4647        327.4         WB    32.00     Sequence
DRB1_0901  232  IRIGVAERIPKFAHL  IRIGVAERI        0.4638        330.8         WB    32.00     Sequence
DRB1_0901  438  GLALKPRKAFSPIRV  RKAFSPIRV        0.4632        332.8         WB    32.00     Sequence
DRB1_0901  457  TTVSPPLFESLELLG  PLFESLELL        0.4631        333.2         WB    32.00     Sequence
DRB1_0901  181  VPDFALTRASGDPLY  LTRASGDPL        0.4631        333.3         WB    32.00     Sequence
DRB1_0901    7  RVRFCPSPTGTPHVG  VRFCPSPTG        0.4630        333.7         WB    32.00     Sequence
DRB1_0901   96  VLARLLAAGEAYHAF  ARLLAAGEA        0.4627        334.8         WB    32.00     Sequence
DRB1_0901  388  DQYVIDPKAAAKELG  YVIDPKAAA        0.4620        337.2         WB    32.00     Sequence
DRB1_0901  243  FAHLPTVLGEGTKKL  FAHLPTVLG        0.4614        339.5         WB    32.00     Sequence
DRB1_0901  406  AAVLDAALAALTSVT  VLDAALAAL        0.4597        345.7         WB    32.00     Sequence
DRB1_0901  306  FDVADVNSSPARFDQ  VNSSPARFD        0.4588        349.2         WB    32.00     Sequence
DRB1_0901  223  RQLALHQALIRIGVA  QLALHQALI        0.4587        349.4         WB    32.00     Sequence
DRB1_0901  400  ELGPDGAAVLDAALA  LGPDGAAVL        0.4573        355.0         WB    32.00     Sequence
DRB1_0901  308  VADVNSSPARFDQKK  VNSSPARFD        0.4556        361.6         WB    32.00     Sequence
DRB1_0901  422  WTAPLIEAALKDALI  PLIEAALKD        0.4548        364.6         WB    32.00     Sequence
DRB1_0901  423  TAPLIEAALKDALIE  PLIEAALKD        0.4538        368.8         WB    32.00     Sequence
DRB1_0901  349  THGHHIALDEAAFAA  THGHHIALD        0.4535        369.8         WB    32.00     Sequence
DRB1_0901  236  VAERIPKFAHLPTVL  KFAHLPTVL        0.4534        370.1         WB    32.00     Sequence
DRB1_0901  401  LGPDGAAVLDAALAA  LGPDGAAVL        0.4526        373.3         WB    32.00     Sequence
DRB1_0901   97  LARLLAAGEAYHAFS  ARLLAAGEA        0.4520        375.9         WB    32.00     Sequence
DRB1_0901  399  KELGPDGAAVLDAAL  LGPDGAAVL        0.4515        377.9         WB    32.00     Sequence
DRB1_0901  348  DTHGHHIALDEAAFA  THGHHIALD        0.4509        380.5         WB    32.00     Sequence
DRB1_0901  424  APLIEAALKDALIEG  PLIEAALKD        0.4492        387.6         WB    32.00     Sequence
DRB1_0901  182  PDFALTRASGDPLYT  LTRASGDPL        0.4482        391.6         WB    32.00     Sequence
DRB1_0901  151  RQPVVRLRMPDDDLA  RLRMPDDDL        0.4476        394.2         WB    32.00     Sequence
DRB1_0901  148  AEGRQPVVRLRMPDD  EGRQPVVRL        0.4462        400.1         WB    32.00     Sequence
DRB1_0901  108  HAFSTPEEVEARHVA  HAFSTPEEV        0.4453        404.3         WB    32.00     Sequence
DRB1_0901  305  AFDVADVNSSPARFD  VNSSPARFD        0.4453        404.3         WB    32.00     Sequence
DRB1_0901  310  DVNSSPARFDQKKAD  VNSSPARFD        0.4446        407.1         WB    32.00     Sequence
DRB1_0901  416  LTSVTDWTAPLIEAA  VTDWTAPLI        0.4443        408.5         WB    32.00     Sequence
DRB1_0901  347  LDTHGHHIALDEAAF  THGHHIALD        0.4427        415.5         WB    32.00     Sequence
DRB1_0901  184  FALTRASGDPLYTLV  LTRASGDPL        0.4422        418.1         WB    32.00     Sequence
DRB1_0901  215  EDLLPSTPRQLALHQ  LLPSTPRQL        0.4407        424.9         WB    32.00     Sequence
DRB1_0901  309  ADVNSSPARFDQKKA  VNSSPARFD        0.4405        425.8         WB    32.00     Sequence
DRB1_0901  225  LALHQALIRIGVAER  LALHQALIR        0.4398        428.9         WB    32.00     Sequence
DRB1_0901   98  ARLLAAGEAYHAFST  ARLLAAGEA        0.4397        429.5         WB    32.00     Sequence
DRB1_0901  346  HLDTHGHHIALDEAA  THGHHIALD        0.4394        430.9         WB    32.00     Sequence
DRB1_0901  407  AVLDAALAALTSVTD  VLDAALAAL        0.4375        439.6         WB    32.00     Sequence
DRB1_0901  307  DVADVNSSPARFDQK  VNSSPARFD        0.4375        439.9         WB    32.00     Sequence
DRB1_0901    3  TETVRVRFCPSPTGT  VRFCPSPTG        0.4373        440.7         WB    32.00     Sequence
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DRB1_0901   19  HVGLVRTALFNWAYA  VGLVRTALF        0.4368        443.3         WB    32.00     Sequence
DRB1_0901  183  DFALTRASGDPLYTL  LTRASGDPL        0.4357        448.3         WB    32.00     Sequence
DRB1_0901  222  PRQLALHQALIRIGV  QLALHQALI        0.4354        449.9         WB    32.00     Sequence
DRB1_0901  180  SVPDFALTRASGDPL  LTRASGDPL        0.4338        457.8         WB    32.00     Sequence
DRB1_0901  387  DDQYVIDPKAAAKEL  YVIDPKAAA        0.4317        468.2         WB    32.00     Sequence
DRB1_0901  145  AYLAEGRQPVVRLRM  YLAEGRQPV        0.4317        468.3         WB    32.00     Sequence
DRB1_0901   17  TPHVGLVRTALFNWA  HVGLVRTAL        0.4300        477.1         WB    32.00     Sequence
DRB1_0901  214  GEDLLPSTPRQLALH  LLPSTPRQL        0.4295        479.6         WB    32.00     Sequence
DRB1_0901  266  LFAHRDRGFIPEGLL  RGFIPEGLL        0.4290        482.0         WB    32.00     Sequence
DRB1_0901  216  DLLPSTPRQLALHQA  LLPSTPRQL        0.4290        482.2         WB    32.00     Sequence
DRB1_0901  294  HDLFGLDEMVAAFDV  DLFGLDEMV        0.4280        487.3         WB    32.00     Sequence
DRB1_0901  408  VLDAALAALTSVTDW  VLDAALAAL        0.4268        493.6         WB    32.00     Sequence
DRB1_0901  398  AKELGPDGAAVLDAA  LGPDGAAVL        0.4267        494.5         WB    32.00     Sequence
DRB1_0901  455  TGTTVSPPLFESLEL  GTTVSPPLF        0.4266        494.8         WB    32.00     Sequence
DRB1_0901  194  LYTLVNPCDDALMKI  LVNPCDDAL        0.4265        495.1         WB    32.00     Sequence
DRB1_0901  425  PLIEAALKDALIEGL  EAALKDALI        0.4254        501.2               50.00     Sequence
DRB1_0901  462  PLFESLELLGRDRSM  PLFESLELL        0.4235        511.6               50.00     Sequence
DRB1_0901    8  VRFCPSPTGTPHVGL  VRFCPSPTG        0.4228        515.3               50.00     Sequence
DRB1_0901  224  QLALHQALIRIGVAE  LALHQALIR        0.4221        519.5               50.00     Sequence
DRB1_0901  428  EAALKDALIEGLALK  LKDALIEGL        0.4217        521.6               50.00     Sequence
DRB1_0901  364  AAELVQTRIVVLGDA  ELVQTRIVV        0.4216        522.5               50.00     Sequence
DRB1_0901  221  TPRQLALHQALIRIG  QLALHQALI        0.4213        523.8               50.00     Sequence
DRB1_0901  456  GTTVSPPLFESLELL  GTTVSPPLF        0.4210        525.8               50.00     Sequence
DRB1_0901  162  DDLAWNDLVRGPVTF  WNDLVRGPV        0.4195        534.5               50.00     Sequence
DRB1_0901   21  GLVRTALFNWAYARH  VRTALFNWA        0.4186        539.2               50.00     Sequence
DRB1_0901   86  QSQRAEIYRDVLARL  IYRDVLARL        0.4173        547.2               50.00     Sequence
DRB1_0901  402  GPDGAAVLDAALAAL  GPDGAAVLD        0.4166        551.4               50.00     Sequence
DRB1_0901  452  VAATGTTVSPPLFES  TGTTVSPPL        0.4157        556.5               50.00     Sequence
DRB1_0901  405  GAAVLDAALAALTSV  VLDAALAAL        0.4140        567.2               50.00     Sequence
DRB1_0901  451  RVAATGTTVSPPLFE  TGTTVSPPL        0.4132        572.1               50.00     Sequence
DRB1_0901  379  WELLKFFNDDQYVID  LKFFNDDQY        0.4126        575.5               50.00     Sequence
DRB1_0901  152  QPVVRLRMPDDDLAW  RLRMPDDDL        0.4120        579.4               50.00     Sequence
DRB1_0901  144  AAYLAEGRQPVVRLR  LAEGRQPVV        0.4117        581.4               50.00     Sequence
DRB1_0901   15  TGTPHVGLVRTALFN  HVGLVRTAL        0.4104        589.5               50.00     Sequence
DRB1_0901   29  NWAYARHTGGTFVFR  YARHTGGTF        0.4096        594.4               50.00     Sequence
DRB1_0901  176  FAAGSVPDFALTRAS  FAAGSVPDF        0.4084        602.4               50.00     Sequence
DRB1_0901    2  ATETVRVRFCPSPTG  VRFCPSPTG        0.4080        605.1               50.00     Sequence
DRB1_0901  415  ALTSVTDWTAPLIEA  VTDWTAPLI        0.4071        610.8               50.00     Sequence
DRB1_0901   20  VGLVRTALFNWAYAR  VGLVRTALF        0.4062        616.9               50.00     Sequence
DRB1_0901  365  AELVQTRIVVLGDAW  ELVQTRIVV        0.4060        618.1               50.00     Sequence
DRB1_0901  191  GDPLYTLVNPCDDAL  LYTLVNPCD        0.4053        623.1               50.00     Sequence
DRB1_0901  213  RGEDLLPSTPRQLAL  LLPSTPRQL        0.4048        626.2               50.00     Sequence
DRB1_0901   30  WAYARHTGGTFVFRI  YARHTGGTF        0.4042        630.6               50.00     Sequence
DRB1_0901  471  GRDRSMQRLRAARQL  QRLRAARQL        0.4031        637.9               50.00     Sequence
DRB1_0901  283  LALLGWSIADDHDLF  LALLGWSIA        0.4015        649.3               50.00     Sequence
DRB1_0901  301  EMVAAFDVADVNSSP  EMVAAFDVA        0.4011        652.3               50.00     Sequence
DRB1_0901  435  LIEGLALKPRKAFSP  LIEGLALKP        0.4010        652.5               50.00     Sequence
DRB1_0901  391  VIDPKAAAKELGPDG  DPKAAAKEL        0.3991        666.1               50.00     Sequence
DRB1_0901   32  YARHTGGTFVFRIED  YARHTGGTF        0.3973        679.1               50.00     Sequence
DRB1_0901  361  FAAAAELVQTRIVVL  FAAAAELVQ        0.3968        683.1               50.00     Sequence
DRB1_0901  217  LLPSTPRQLALHQAL  LLPSTPRQL        0.3959        689.4               50.00     Sequence
DRB1_0901  453  AATGTTVSPPLFESL  TGTTVSPPL        0.3952        694.8               50.00     Sequence
DRB1_0901  363  AAAELVQTRIVVLGD  AELVQTRIV        0.3952        695.3               50.00     Sequence
DRB1_0901   16  GTPHVGLVRTALFNW  VGLVRTALF        0.3934        708.6               50.00     Sequence
DRB1_0901  220  STPRQLALHQALIRI  QLALHQALI        0.3932        710.2               50.00     Sequence
DRB1_0901  116  VEARHVAAGRNPKLG  EARHVAAGR        0.3928        713.1               50.00     Sequence
DRB1_0901  282  YLALLGWSIADDHDL  LALLGWSIA        0.3915        723.7               50.00     Sequence
DRB1_0901  397  AAKELGPDGAAVLDA  LGPDGAAVL        0.3911        726.7               50.00     Sequence
DRB1_0901  362  AAAAELVQTRIVVLG  AELVQTRIV        0.3898        736.8               50.00     Sequence
DRB1_0901  185  ALTRASGDPLYTLVN  LTRASGDPL        0.3885        747.2               50.00     Sequence
DRB1_0901  179  GSVPDFALTRASGDP  VPDFALTRA        0.3884        748.0               50.00     Sequence
DRB1_0901  212  LRGEDLLPSTPRQLA  LLPSTPRQL        0.3882        749.4               50.00     Sequence
DRB1_0901  204  ALMKITHVLRGEDLL  MKITHVLRG        0.3875        755.0               50.00     Sequence
DRB1_0901   36  TGGTFVFRIEDTDAQ  FVFRIEDTD        0.3869        760.2               50.00     Sequence
DRB1_0901   18  PHVGLVRTALFNWAY  VGLVRTALF        0.3859        768.4               50.00     Sequence
DRB1_0901   37  GGTFVFRIEDTDAQR  FVFRIEDTD        0.3858        769.2               50.00     Sequence
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DRB1_0901  205  LMKITHVLRGEDLLP  MKITHVLRG        0.3848        778.1                 50.00     Sequence
DRB1_0901  385  FNDDQYVIDPKAAAK  YVIDPKAAA        0.3836        787.7                 50.00     Sequence
DRB1_0901  118  ARHVAAGRNPKLGYD  ARHVAAGRN        0.3832        790.9                 50.00     Sequence
DRB1_0901  353  HIALDEAAFAAAAEL  AAFAAAAEL        0.3828        794.9                 50.00     Sequence
DRB1_0901  404  DGAAVLDAALAALTS  VLDAALAAL        0.3826        796.4                 50.00     Sequence
DRB1_0901  366  ELVQTRIVVLGDAWE  LVQTRIVVL        0.3824        797.8                 50.00     Sequence
DRB1_0901  195  YTLVNPCDDALMKIT  VNPCDDALM        0.3823        798.9                 50.00     Sequence
DRB1_0901  386  NDDQYVIDPKAAAKE  YVIDPKAAA        0.3820        801.3                 50.00     Sequence
DRB1_0901  115  EVEARHVAAGRNPKL  EARHVAAGR        0.3817        804.5                 50.00     Sequence
DRB1_0901   31  AYARHTGGTFVFRIE  YARHTGGTF        0.3815        805.7                 50.00     Sequence
DRB1_0901  454  ATGTTVSPPLFESLE  TGTTVSPPL        0.3814        806.9                 50.00     Sequence
DRB1_0901  234  IGVAERIPKFAHLPT  IPKFAHLPT        0.3806        813.6                 50.00     Sequence
DRB1_0901  161  DDDLAWNDLVRGPVT  WNDLVRGPV        0.3802        817.0                 50.00     Sequence
DRB1_0901  345  DHLDTHGHHIALDEA  THGHHIALD        0.3785        832.7                 50.00     Sequence
DRB1_0901   14  PTGTPHVGLVRTALF  TGTPHVGLV        0.3783        834.7                 50.00     Sequence
DRB1_0901  235  GVAERIPKFAHLPTV  IPKFAHLPT        0.3771        845.4                 50.00     Sequence
DRB1_0901  277  EGLLNYLALLGWSIA  EGLLNYLAL        0.3749        865.6                 50.00     Sequence
DRB1_0901  249  VLGEGTKKLSKRDPQ  LGEGTKKLS        0.3746        868.2                 50.00     Sequence
DRB1_0901  396  AAAKELGPDGAAVLD  LGPDGAAVL        0.3738        876.1                 50.00     Sequence
DRB1_0901  100  LLAAGEAYHAFSTPE  AYHAFSTPE        0.3737        876.7                 50.00     Sequence
DRB1_0901  248  TVLGEGTKKLSKRDP  LGEGTKKLS        0.3736        877.9                 50.00     Sequence
DRB1_0901  378  AWELLKFFNDDQYVI  LKFFNDDQY        0.3730        883.2                 50.00     Sequence
DRB1_0901   35  HTGGTFVFRIEDTDA  FVFRIEDTD        0.3673        939.7                 50.00     Sequence
DRB1_0901  153  PVVRLRMPDDDLAWN  RLRMPDDDL        0.3669        944.4                 50.00     Sequence
DRB1_0901   34  RHTGGTFVFRIEDTD  FVFRIEDTD        0.3667        946.2                 50.00     Sequence
DRB1_0901  136  RHLTDAQRAAYLAEG  RHLTDAQRA        0.3663        949.9                 50.00     Sequence
DRB1_0901   77  VGGPYGPYRQSQRAE  GPYGPYRQS        0.3660        952.8                 50.00     Sequence
DRB1_0901  219  PSTPRQLALHQALIR  QLALHQALI        0.3654        959.1                 50.00     Sequence
DRB1_0901  380  ELLKFFNDDQYVIDP  LKFFNDDQY        0.3654        959.4                 50.00     Sequence
DRB1_0901  403  PDGAAVLDAALAALT  VLDAALAAL        0.3635        979.5                 50.00     Sequence
DRB1_0901  186  LTRASGDPLYTLVNP  LTRASGDPL        0.3633        981.8                 50.00     Sequence
DRB1_0901  275  IPEGLLNYLALLGWS  EGLLNYLAL        0.3627        987.7                 50.00     Sequence
DRB1_0901   76  EVGGPYGPYRQSQRA  GPYGPYRQS        0.3624        991.0                 50.00     Sequence
DRB1_0901  244  AHLPTVLGEGTKKLS  LGEGTKKLS        0.3620        995.4                 50.00     Sequence
DRB1_0901  284  ALLGWSIADDHDLFG  WSIADDHDL        0.3617        998.4                 50.00     Sequence
DRB1_0901   99  RLLAAGEAYHAFSTP  RLLAAGEAY        0.3613       1002.6                 50.00     Sequence
DRB1_0901  233  RIGVAERIPKFAHLP  VAERIPKFA        0.3611       1004.7                 50.00     Sequence
DRB1_0901  384  FFNDDQYVIDPKAAA  YVIDPKAAA        0.3598       1019.1                 50.00     Sequence
DRB1_0901  178  AGSVPDFALTRASGD  VPDFALTRA        0.3595       1022.4                 50.00     Sequence
DRB1_0901  350  HGHHIALDEAAFAAA  HGHHIALDE        0.3588       1030.2                 50.00     Sequence
DRB1_0901  247  PTVLGEGTKKLSKRD  LGEGTKKLS        0.3584       1034.9                 50.00     Sequence
DRB1_0901  190  SGDPLYTLVNPCDDA  LYTLVNPCD        0.3583       1036.0                 50.00     Sequence
DRB1_0901  119  RHVAAGRNPKLGYDN  RHVAAGRNP        0.3576       1043.7                 50.00     Sequence
DRB1_0901  160  PDDDLAWNDLVRGPV  WNDLVRGPV        0.3575       1044.4                 50.00     Sequence
DRB1_0901  143  RAAYLAEGRQPVVRL  LAEGRQPVV        0.3572       1048.6                 50.00     Sequence
DRB1_0901  293  DHDLFGLDEMVAAFD  DLFGLDEMV        0.3571       1049.1                 50.00     Sequence
DRB1_0901  285  LLGWSIADDHDLFGL  WSIADDHDL        0.3566       1055.3                 50.00     Sequence
DRB1_0901  211  VLRGEDLLPSTPRQL  LLPSTPRQL        0.3559       1063.4                 50.00     Sequence
DRB1_0901  109  AFSTPEEVEARHVAA  AFSTPEEVE        0.3549       1075.2                 50.00     Sequence
DRB1_0901  206  MKITHVLRGEDLLPS  MKITHVLRG        0.3548       1076.0                 50.00     Sequence
DRB1_0901  203  DALMKITHVLRGEDL  MKITHVLRG        0.3547       1077.2                 50.00     Sequence
DRB1_0901    0  VTATETVRVRFCPSP  VTATETVRV        0.3532       1094.4                 50.00     Sequence
DRB1_0901  311  VNSSPARFDQKKADA  VNSSPARFD        0.3531       1096.0                 50.00     Sequence
DRB1_0901  274  FIPEGLLNYLALLGW  EGLLNYLAL        0.3528       1099.8                 50.00     Sequence
DRB1_0901  273  GFIPEGLLNYLALLG  EGLLNYLAL        0.3517       1112.3                 50.00     Sequence
DRB1_0901  117  EARHVAAGRNPKLGY  EARHVAAGR        0.3514       1116.1                 50.00     Sequence
DRB1_0901  141  AQRAAYLAEGRQPVV  AQRAAYLAE        0.3506       1126.5                 50.00     Sequence
DRB1_0901  218  LPSTPRQLALHQALI  QLALHQALI        0.3503       1130.0                 50.00     Sequence
DRB1_0901  135  DRHLTDAQRAAYLAE  RHLTDAQRA        0.3499       1135.0                 50.00     Sequence
DRB1_0901  326  LNAEHIRMLDVGDFT  LNAEHIRML        0.3498       1135.9                 50.00     Sequence
DRB1_0901  344  RDHLDTHGHHIALDE  THGHHIALD        0.3494       1140.9                 50.00     Sequence
DRB1_0901  177  AAGSVPDFALTRASG  AGSVPDFAL        0.3478       1160.0                 50.00     Sequence
DRB1_0901  137  HLTDAQRAAYLAEGR  HLTDAQRAA        0.3456       1188.4                 50.00     Sequence
DRB1_0901   38  GTFVFRIEDTDAQRD  FVFRIEDTD        0.3446       1201.1                 50.00     Sequence
DRB1_0901  325  ALNAEHIRMLDVGDF  LNAEHIRML        0.3445       1203.2                 50.00     Sequence
DRB1_0901  437  EGLALKPRKAFSPIR  PRKAFSPIR        0.3432       1220.0                 50.00     Sequence
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DRB1_0901   75  PEVGGPYGPYRQSQR  GPYGPYRQS        0.3426       1227.1                 50.00     Sequence
DRB1_0901  377  DAWELLKFFNDDQYV  LKFFNDDQY        0.3424       1229.8                 50.00     Sequence
DRB1_0901  250  LGEGTKKLSKRDPQS  LGEGTKKLS        0.3420       1236.0                 50.00     Sequence
DRB1_0901    9  RFCPSPTGTPHVGLV  FCPSPTGTP        0.3417       1239.3                 50.00     Sequence
DRB1_0901  414  AALTSVTDWTAPLIE  VTDWTAPLI        0.3404       1257.6                 50.00     Sequence
DRB1_0901  154  VVRLRMPDDDLAWND  RLRMPDDDL        0.3392       1274.0                 50.00     Sequence
DRB1_0901  426  LIEAALKDALIEGLA  EAALKDALI        0.3382       1287.8                 50.00     Sequence
DRB1_0901  276  PEGLLNYLALLGWSI  EGLLNYLAL        0.3375       1297.5                 50.00     Sequence
DRB1_0901  427  IEAALKDALIEGLAL  EAALKDALI        0.3367       1308.5                 50.00     Sequence
DRB1_0901  352  HHIALDEAAFAAAAE  HHIALDEAA        0.3366       1310.7                 50.00     Sequence
DRB1_0901  324  DALNAEHIRMLDVGD  LNAEHIRML        0.3363       1315.0                 50.00     Sequence
DRB1_0901  392  IDPKAAAKELGPDGA  DPKAAAKEL        0.3360       1319.0                 50.00     Sequence
DRB1_0901  280  LNYLALLGWSIADDH  LALLGWSIA        0.3356       1323.6                 50.00     Sequence
DRB1_0901  114  EEVEARHVAAGRNPK  EARHVAAGR        0.3351       1332.1                 50.00     Sequence
DRB1_0901  367  LVQTRIVVLGDAWEL  VQTRIVVLG        0.3349       1334.5                 50.00     Sequence
DRB1_0901   33  ARHTGGTFVFRIEDT  ARHTGGTFV        0.3348       1335.2                 50.00     Sequence
DRB1_0901  304  AAFDVADVNSSPARF  FDVADVNSS        0.3343       1342.8                 50.00     Sequence
DRB1_0901  372  IVVLGDAWELLKFFN  IVVLGDAWE        0.3331       1361.1                 50.00     Sequence
DRB1_0901  262  PQSNLFAHRDRGFIP  LFAHRDRGF        0.3328       1365.1                 50.00     Sequence
DRB1_0901   55  ESYLALLDALRWLGL  YLALLDALR        0.3316       1383.6                 50.00     Sequence
DRB1_0901  245  HLPTVLGEGTKKLSK  VLGEGTKKL        0.3302       1403.6                 50.00     Sequence
DRB1_0901  189  ASGDPLYTLVNPCDD  LYTLVNPCD        0.3298       1410.3                 50.00     Sequence
DRB1_0901  196  TLVNPCDDALMKITH  LVNPCDDAL        0.3287       1426.7                 50.00     Sequence
DRB1_0901  134  FDRHLTDAQRAAYLA  RHLTDAQRA        0.3285       1430.7                 50.00     Sequence
DRB1_0901  281  NYLALLGWSIADDHD  LALLGWSIA        0.3281       1436.4                 50.00     Sequence
DRB1_0901  263  QSNLFAHRDRGFIPE  QSNLFAHRD        0.3270       1453.7                 50.00     Sequence
DRB1_0901   53  SEESYLALLDALRWL  SEESYLALL        0.3262       1465.7                 50.00     Sequence
DRB1_0901  409  LDAALAALTSVTDWT  AALAALTSV        0.3261       1468.2                 50.00     Sequence
DRB1_0901  302  MVAAFDVADVNSSPA  MVAAFDVAD        0.3251       1483.5                 50.00     Sequence
DRB1_0901  371  RIVVLGDAWELLKFF  IVVLGDAWE        0.3237       1505.9                 50.00     Sequence
DRB1_0901   13  SPTGTPHVGLVRTAL  TGTPHVGLV        0.3235       1509.1                 50.00     Sequence
DRB1_0901  138  LTDAQRAAYLAEGRQ  LTDAQRAAY        0.3234       1511.7                 50.00     Sequence
DRB1_0901  436  IEGLALKPRKAFSPI  ALKPRKAFS        0.3227       1521.9                 50.00     Sequence
DRB1_0901  393  DPKAAAKELGPDGAA  DPKAAAKEL        0.3226       1524.0                 50.00     Sequence
DRB1_0901  197  LVNPCDDALMKITHV  LVNPCDDAL        0.3221       1532.7                 50.00     Sequence
DRB1_0901  261  DPQSNLFAHRDRGFI  LFAHRDRGF        0.3218       1537.9                 50.00     Sequence
DRB1_0901  381  LLKFFNDDQYVIDPK  LKFFNDDQY        0.3215       1543.3                 50.00     Sequence
DRB1_0901  202  DDALMKITHVLRGED  MKITHVLRG        0.3210       1550.2                 50.00     Sequence
DRB1_0901   39  TFVFRIEDTDAQRDS  FVFRIEDTD        0.3206       1557.1                 50.00     Sequence
DRB1_0901  376  GDAWELLKFFNDDQY  LKFFNDDQY        0.3206       1557.9                 50.00     Sequence
DRB1_0901  335  DVGDFTVRLRDHLDT  VGDFTVRLR        0.3206       1558.5                 50.00     Sequence
DRB1_0901  113  PEEVEARHVAAGRNP  EARHVAAGR        0.3191       1583.9                 50.00     Sequence
DRB1_0901  368  VQTRIVVLGDAWELL  VQTRIVVLG        0.3180       1602.1                 50.00     Sequence
DRB1_0901   56  SYLALLDALRWLGLD  YLALLDALR        0.3172       1616.6                 50.00     Sequence
DRB1_0901  413  LAALTSVTDWTAPLI  VTDWTAPLI        0.3169       1621.1                 50.00     Sequence
DRB1_0901  246  LPTVLGEGTKKLSKR  VLGEGTKKL        0.3145       1664.7                 50.00     Sequence
DRB1_0901  208  ITHVLRGEDLLPSTP  HVLRGEDLL        0.3140       1673.0                 50.00     Sequence
DRB1_0901  382  LKFFNDDQYVIDPKA  LKFFNDDQY        0.3137       1678.8                 50.00     Sequence
DRB1_0901  279  LLNYLALLGWSIADD  LALLGWSIA        0.3136       1679.6                 50.00     Sequence
DRB1_0901    1  TATETVRVRFCPSPT  RVRFCPSPT        0.3132       1686.7                 50.00     Sequence
DRB1_0901  207  KITHVLRGEDLLPST  HVLRGEDLL        0.3125       1700.0                 50.00     Sequence
DRB1_0901  278  GLLNYLALLGWSIAD  GLLNYLALL        0.3125       1700.6                 50.00     Sequence
DRB1_0901  334  LDVGDFTVRLRDHLD  VGDFTVRLR        0.3118       1712.5                 50.00     Sequence
DRB1_0901  336  VGDFTVRLRDHLDTH  VGDFTVRLR        0.3113       1721.8                 50.00     Sequence
DRB1_0901  121  VAAGRNPKLGYDNFD  VAAGRNPKL        0.3108       1731.3                 50.00     Sequence
DRB1_0901  370  TRIVVLGDAWELLKF  VLGDAWELL        0.3105       1738.4                 50.00     Sequence
DRB1_0901   85  RQSQRAEIYRDVLAR  QRAEIYRDV        0.3099       1748.8                 50.00     Sequence
DRB1_0901  374  VLGDAWELLKFFNDD  VLGDAWELL        0.3092       1762.3                 50.00     Sequence
DRB1_0901   52  DSEESYLALLDALRW  SEESYLALL        0.3087       1771.5                 50.00     Sequence
DRB1_0901  133  NFDRHLTDAQRAAYL  RHLTDAQRA        0.3081       1783.4                 50.00     Sequence
DRB1_0901  463  LFESLELLGRDRSMQ  LFESLELLG        0.3078       1789.8                 50.00     Sequence
DRB1_0901  373  VVLGDAWELLKFFND  VLGDAWELL        0.3076       1793.2                 50.00     Sequence
DRB1_0901  351  GHHIALDEAAFAAAA  HHIALDEAA        0.3049       1845.1                 50.00     Sequence
DRB1_0901   54  EESYLALLDALRWLG  YLALLDALR        0.3049       1846.0                 50.00     Sequence
DRB1_0901  155  VRLRMPDDDLAWNDL  RLRMPDDDL        0.3041       1862.9                 50.00     Sequence
DRB1_0901  343  LRDHLDTHGHHIALD  THGHHIALD        0.3030       1883.4                 50.00     Sequence
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DRB1_0901  327  NAEHIRMLDVGDFTV  NAEHIRMLD        0.3023       1899.4                50.00     Sequence
DRB1_0901  292  DDHDLFGLDEMVAAF  HDLFGLDEM        0.3016       1913.9                50.00     Sequence
DRB1_0901  333  MLDVGDFTVRLRDHL  VGDFTVRLR        0.3008       1928.8                50.00     Sequence
DRB1_0901  120  HVAAGRNPKLGYDNF  VAAGRNPKL        0.3006       1933.9                50.00     Sequence
DRB1_0901  131  YDNFDRHLTDAQRAA  HLTDAQRAA        0.2999       1948.4                50.00     Sequence
DRB1_0901  323  ADALNAEHIRMLDVG  LNAEHIRML        0.2971       2008.5                50.00     Sequence
DRB1_0901  140  DAQRAAYLAEGRQPV  AQRAAYLAE        0.2969       2012.1                50.00     Sequence
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DRB1_0901  395  KAAAKELGPDGAAVL  LGPDGAAVL        0.2959       2035.9                50.00     Sequence
DRB1_0901  142  QRAAYLAEGRQPVVR  QRAAYLAEG        0.2955       2042.9                50.00     Sequence
DRB1_0901  132  DNFDRHLTDAQRAAY  RHLTDAQRA        0.2954       2047.0                50.00     Sequence
DRB1_0901  468  ELLGRDRSMQRLRAA  LGRDRSMQR        0.2952       2050.2                50.00     Sequence
DRB1_0901  470  LGRDRSMQRLRAARQ  LGRDRSMQR        0.2948       2059.1                50.00     Sequence
DRB1_0901  210  HVLRGEDLLPSTPRQ  HVLRGEDLL        0.2924       2112.5                50.00     Sequence
DRB1_0901  467  LELLGRDRSMQRLRA  LGRDRSMQR        0.2916       2132.1                50.00     Sequence
DRB1_0901  410  DAALAALTSVTDWTA  AALAALTSV        0.2913       2139.1                50.00     Sequence
DRB1_0901   74  GPEVGGPYGPYRQSQ  GPYGPYRQS        0.2912       2141.5                50.00     Sequence
DRB1_0901  265  NLFAHRDRGFIPEGL  FAHRDRGFI        0.2899       2171.9                50.00     Sequence
DRB1_0901   57  YLALLDALRWLGLDW  YLALLDALR        0.2889       2194.3                50.00     Sequence
DRB1_0901   10  FCPSPTGTPHVGLVR  FCPSPTGTP        0.2888       2197.0                50.00     Sequence
DRB1_0901  369  QTRIVVLGDAWELLK  VLGDAWELL        0.2875       2227.3                50.00     Sequence
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DRB1_0901  320  QKKADALNAEHIRML  LNAEHIRML        0.2863       2258.7                50.00     Sequence
DRB1_0901   12  PSPTGTPHVGLVRTA  TGTPHVGLV        0.2853       2282.9                50.00     Sequence
DRB1_0901  201  CDDALMKITHVLRGE  MKITHVLRG        0.2840       2313.6                50.00     Sequence
DRB1_0901  198  VNPCDDALMKITHVL  VNPCDDALM        0.2837       2322.3                50.00     Sequence
DRB1_0901  110  FSTPEEVEARHVAAG  FSTPEEVEA        0.2818       2369.8                50.00     Sequence
DRB1_0901  383  KFFNDDQYVIDPKAA  QYVIDPKAA        0.2813       2383.1                50.00     Sequence
DRB1_0901  466  SLELLGRDRSMQRLR  LELLGRDRS        0.2809       2393.6                50.00     Sequence
DRB1_0901  112  TPEEVEARHVAAGRN  ARHVAAGRN        0.2804       2405.4                50.00     Sequence
DRB1_0901  286  LGWSIADDHDLFGLD  WSIADDHDL        0.2801       2413.8                50.00     Sequence
DRB1_0901  156  RLRMPDDDLAWNDLV  RLRMPDDDL        0.2799       2420.1                50.00     Sequence
DRB1_0901  264  SNLFAHRDRGFIPEG  FAHRDRGFI        0.2795       2430.7                50.00     Sequence
DRB1_0901  322  KADALNAEHIRMLDV  LNAEHIRML        0.2749       2554.1                50.00     Sequence
DRB1_0901   51  RDSEESYLALLDALR  SEESYLALL        0.2742       2572.5                50.00     Sequence
DRB1_0901  187  TRASGDPLYTLVNPC  TRASGDPLY        0.2741       2576.5                50.00     Sequence
DRB1_0901  291  ADDHDLFGLDEMVAA  LFGLDEMVA        0.2739       2582.8                50.00     Sequence
DRB1_0901  465  ESLELLGRDRSMQRL  LELLGRDRS        0.2738       2585.6                50.00     Sequence
DRB1_0901  328  AEHIRMLDVGDFTVR  HIRMLDVGD        0.2735       2591.8                50.00     Sequence
DRB1_0901   40  FVFRIEDTDAQRDSE  FVFRIEDTD        0.2708       2671.1                50.00     Sequence
DRB1_0901  258  SKRDPQSNLFAHRDR  KRDPQSNLF        0.2707       2672.3                50.00     Sequence
DRB1_0901  255  KKLSKRDPQSNLFAH  SKRDPQSNL        0.2702       2688.2                50.00     Sequence
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DRB1_0901   73  EGPEVGGPYGPYRQS  GPYGPYRQS        0.2679       2756.3                50.00     Sequence
DRB1_0901  188  RASGDPLYTLVNPCD  LYTLVNPCD        0.2677       2761.7                50.00     Sequence
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DRB1_0901  411  AALAALTSVTDWTAP  AALAALTSV        0.2633       2894.4                50.00     Sequence
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DRB1_0901  130  GYDNFDRHLTDAQRA  RHLTDAQRA        0.2614       2954.5                50.00     Sequence
DRB1_0901  253  GTKKLSKRDPQSNLF  KRDPQSNLF        0.2596       3012.9                50.00     Sequence
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DRB1_0901   50  QRDSEESYLALLDAL  QRDSEESYL        0.2582       3058.4                50.00     Sequence
DRB1_0901  316  ARFDQKKADALNAEH  FDQKKADAL        0.2553       3158.5                50.00     Sequence
DRB1_0901  315  PARFDQKKADALNAE  FDQKKADAL        0.2552       3162.0                50.00     Sequence
DRB1_0901  259  KRDPQSNLFAHRDRG  KRDPQSNLF        0.2540       3202.0                50.00     Sequence
DRB1_0901   11  CPSPTGTPHVGLVRT  TGTPHVGLV        0.2518       3279.4                50.00     Sequence
DRB1_0901   64  LRWLGLDWDEGPEVG  LRWLGLDWD        0.2498       3349.2                50.00     Sequence
DRB1_0901  257  LSKRDPQSNLFAHRD  SKRDPQSNL        0.2497       3355.7                50.00     Sequence
DRB1_0901  337  GDFTVRLRDHLDTHG  GDFTVRLRD        0.2491       3377.1                50.00     Sequence
DRB1_0901  314  SPARFDQKKADALNA  FDQKKADAL        0.2489       3383.6                50.00     Sequence
DRB1_0901  332  RMLDVGDFTVRLRDH  VGDFTVRLR        0.2484       3403.0                50.00     Sequence
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   DRB1_0901  256  KLSKRDPQSNLFAHR  SKRDPQSNL        0.2459       3495.8                50.00     Sequence
   DRB1_0901  329  EHIRMLDVGDFTVRL  IRMLDVGDF        0.2458       3497.9                50.00     Sequence
   DRB1_0901  122  AAGRNPKLGYDNFDR  AGRNPKLGY        0.2449       3532.2                50.00     Sequence
   DRB1_0901  464  FESLELLGRDRSMQR  LELLGRDRS        0.2440       3569.8                50.00     Sequence
   DRB1_0901   66  WLGLDWDEGPEVGGP  LDWDEGPEV        0.2428       3613.7                50.00     Sequence
   DRB1_0901   65  RWLGLDWDEGPEVGG  LDWDEGPEV        0.2428       3615.6                50.00     Sequence
   DRB1_0901  200  PCDDALMKITHVLRG  MKITHVLRG        0.2424       3629.6                50.00     Sequence
   DRB1_0901   49  AQRDSEESYLALLDA  QRDSEESYL        0.2414       3668.7                50.00     Sequence
   DRB1_0901  252  EGTKKLSKRDPQSNL  GTKKLSKRD        0.2407       3696.3                50.00     Sequence
   DRB1_0901   68  GLDWDEGPEVGGPYG  LDWDEGPEV        0.2386       3781.1                50.00     Sequence
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   DRB1_0901   67  LGLDWDEGPEVGGPY  LDWDEGPEV        0.2363       3877.2                50.00     Sequence
   DRB1_0901   69  LDWDEGPEVGGPYGP  LDWDEGPEV        0.2337       3988.4                50.00     Sequence
   DRB1_0901  318  FDQKKADALNAEHIR  FDQKKADAL        0.2322       4053.9                50.00     Sequence
   DRB1_0901  123  AGRNPKLGYDNFDRH  AGRNPKLGY        0.2322       4054.0                50.00     Sequence
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   DRB1_0901  290  IADDHDLFGLDEMVA  DLFGLDEMV        0.2294       4178.4                50.00     Sequence
   DRB1_0901   58  LALLDALRWLGLDWD  LALLDALRW        0.2285       4221.2                50.00     Sequence
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   DRB1_0901  341  VRLRDHLDTHGHHIA  VRLRDHLDT        0.2203       4612.7                50.00     Sequence
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   DRB1_0901  319  DQKKADALNAEHIRM  QKKADALNA        0.2150       4883.7                50.00     Sequence
   DRB1_0901   70  DWDEGPEVGGPYGPY  WDEGPEVGG        0.2149       4886.6                50.00     Sequence
   DRB1_0901   45  EDTDAQRDSEESYLA  QRDSEESYL        0.2141       4931.0                50.00     Sequence
   DRB1_0901  312  NSSPARFDQKKADAL  RFDQKKADA        0.2140       4934.8                50.00     Sequence
   DRB1_0901   71  WDEGPEVGGPYGPYR  WDEGPEVGG        0.2120       5044.8                50.00     Sequence
   DRB1_0901  288  WSIADDHDLFGLDEM  WSIADDHDL        0.2115       5072.1                50.00     Sequence
   DRB1_0901  339  FTVRLRDHLDTHGHH  VRLRDHLDT        0.2111       5092.8                50.00     Sequence
   DRB1_0901  129  LGYDNFDRHLTDAQR  DRHLTDAQR        0.2097       5173.4                50.00     Sequence
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   DRB1_0901   48  DAQRDSEESYLALLD  QRDSEESYL        0.2055       5412.8                50.00     Sequence
   DRB1_0901  340  TVRLRDHLDTHGHHI  VRLRDHLDT        0.2043       5480.5                50.00     Sequence
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   DRB1_0901  157  LRMPDDDLAWNDLVR  LRMPDDDLA        0.2021       5615.1                50.00     Sequence
   DRB1_0901   63  ALRWLGLDWDEGPEV  LRWLGLDWD        0.2012       5667.2                50.00     Sequence
   DRB1_0901   59  ALLDALRWLGLDWDE  DALRWLGLD        0.2000       5744.2                50.00     Sequence
   DRB1_0901  124  GRNPKLGYDNFDRHL  GRNPKLGYD        0.2000       5746.3                50.00     Sequence
   DRB1_0901   72  DEGPEVGGPYGPYRQ  GPEVGGPYG        0.1996       5771.0                50.00     Sequence
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   DRB1_0901   46  DTDAQRDSEESYLAL  QRDSEESYL        0.1983       5848.5                50.00     Sequence
   DRB1_0901  159  MPDDDLAWNDLVRGP  DLAWNDLVR        0.1935       6160.2                50.00     Sequence
   DRB1_0901  126  NPKLGYDNFDRHLTD  GYDNFDRHL        0.1863       6663.9                50.00     Sequence
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   DRB1_0901   61  LDALRWLGLDWDEGP  LRWLGLDWD        0.1776       7318.3                50.00     Sequence
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   DRB1_0901  128  KLGYDNFDRHLTDAQ  GYDNFDRHL        0.1706       7890.9                50.00     Sequence
   DRB1_0901  127  PKLGYDNFDRHLTDA  YDNFDRHLT        0.1702       7927.7                50.00     Sequence
   DRB1_0901   43  RIEDTDAQRDSEESY  IEDTDAQRD        0.1659       8306.3                50.00     Sequence
   DRB1_0901  158  RMPDDDLAWNDLVRG  DLAWNDLVR        0.1646       8419.7                50.00     Sequence
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Allele: DRB1_0901. Number of high binders 0. Number of weak binders 170. Number of peptides 476

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1101  475  SMQRLRAARQLVGHA  RLRAARQLV        0.6722         34.7           SB     4.00     Sequence
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DRB1_1101  473  DRSMQRLRAARQLVG  RLRAARQLV         0.6606          39.3          SB     4.00     Sequence
DRB1_1101  443  PRKAFSPIRVAATGT  FSPIRVAAT         0.6472          45.5          SB     4.00     Sequence
DRB1_1101  240  IPKFAHLPTVLGEGT  FAHLPTVLG         0.6400          49.2          SB     8.00     Sequence
DRB1_1101  472  RDRSMQRLRAARQLV  RLRAARQLV         0.6311          54.1          WB     8.00     Sequence
DRB1_1101  239  RIPKFAHLPTVLGEG  FAHLPTVLG         0.6306          54.4          WB     8.00     Sequence
DRB1_1101  445  KAFSPIRVAATGTTV  FSPIRVAAT         0.6273          56.4          WB     8.00     Sequence
DRB1_1101   55  ESYLALLDALRWLGL  LALLDALRW         0.6238          58.6          WB     8.00     Sequence
DRB1_1101  466  SLELLGRDRSMQRLR  LELLGRDRS         0.6234          58.9          WB     8.00     Sequence
DRB1_1101  467  LELLGRDRSMQRLRA  LELLGRDRS         0.6176          62.6          WB     8.00     Sequence
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DRB1_1101  465  ESLELLGRDRSMQRL  LELLGRDRS         0.6067          70.5          WB     8.00     Sequence
DRB1_1101  442  KPRKAFSPIRVAATG  FSPIRVAAT         0.6003          75.5          WB     8.00     Sequence
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DRB1_1101   54  EESYLALLDALRWLG  LALLDALRW         0.5957          79.4          WB     8.00     Sequence
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DRB1_1101  225  LALHQALIRIGVAER  LHQALIRIG         0.5931          81.6          WB     8.00     Sequence
DRB1_1101  204  ALMKITHVLRGEDLL  LMKITHVLR         0.5905          84.0          WB     8.00     Sequence
DRB1_1101  446  AFSPIRVAATGTTVS  FSPIRVAAT         0.5879          86.4          WB     8.00     Sequence
DRB1_1101  226  ALHQALIRIGVAERI  LHQALIRIG         0.5879          86.4          WB     8.00     Sequence
DRB1_1101  464  FESLELLGRDRSMQR  LELLGRDRS         0.5838          90.3          WB     8.00     Sequence
DRB1_1101   57  YLALLDALRWLGLDW  LALLDALRW         0.5823          91.8          WB     8.00     Sequence
DRB1_1101  202  DDALMKITHVLRGED  LMKITHVLR         0.5823          91.8          WB     8.00     Sequence
DRB1_1101  463  LFESLELLGRDRSMQ  LELLGRDRS         0.5819          92.1          WB     8.00     Sequence
DRB1_1101  227  LHQALIRIGVAERIP  LHQALIRIG         0.5746          99.8          WB     8.00     Sequence
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DRB1_1101  242  KFAHLPTVLGEGTKK  FAHLPTVLG         0.5652         110.5          WB    16.00     Sequence
DRB1_1101   58  LALLDALRWLGLDWD  LALLDALRW         0.5645         111.2          WB    16.00     Sequence
DRB1_1101   26  ALFNWAYARHTGGTF  LFNWAYARH         0.5645         111.3          WB    16.00     Sequence
DRB1_1101  237  AERIPKFAHLPTVLG  FAHLPTVLG         0.5639         112.0          WB    16.00     Sequence
DRB1_1101   91  EIYRDVLARLLAAGE  RDVLARLLA         0.5639         112.0          WB    16.00     Sequence
DRB1_1101  205  LMKITHVLRGEDLLP  LMKITHVLR         0.5634         112.5          WB    16.00     Sequence
DRB1_1101   27  LFNWAYARHTGGTFV  FNWAYARHT         0.5631         113.0          WB    16.00     Sequence
DRB1_1101  435  LIEGLALKPRKAFSP  LALKPRKAF         0.5610         115.6          WB    16.00     Sequence
DRB1_1101  441  LKPRKAFSPIRVAAT  FSPIRVAAT         0.5557         122.5          WB    16.00     Sequence
DRB1_1101  223  RQLALHQALIRIGVA  LALHQALIR         0.5537         125.0          WB    16.00     Sequence
DRB1_1101  201  CDDALMKITHVLRGE  LMKITHVLR         0.5498         130.4          WB    16.00     Sequence
DRB1_1101  471  GRDRSMQRLRAARQL  RDRSMQRLR         0.5494         131.1          WB    16.00     Sequence
DRB1_1101  434  ALIEGLALKPRKAFS  LIEGLALKP         0.5487         132.0          WB    16.00     Sequence
DRB1_1101   93  YRDVLARLLAAGEAY  RDVLARLLA         0.5483         132.6          WB    16.00     Sequence
DRB1_1101   24  RTALFNWAYARHTGG  LFNWAYARH         0.5477         133.4          WB    16.00     Sequence
DRB1_1101  462  PLFESLELLGRDRSM  LFESLELLG         0.5429         140.6          WB    16.00     Sequence
DRB1_1101  470  LGRDRSMQRLRAARQ  RDRSMQRLR         0.5418         142.2          WB    16.00     Sequence
DRB1_1101   90  AEIYRDVLARLLAAG  YRDVLARLL         0.5406         144.1          WB    16.00     Sequence
DRB1_1101  436  IEGLALKPRKAFSPI  LALKPRKAF         0.5330         156.5          WB    16.00     Sequence
DRB1_1101  469  LLGRDRSMQRLRAAR  RDRSMQRLR         0.5284         164.4          WB    16.00     Sequence
DRB1_1101  222  PRQLALHQALIRIGV  LALHQALIR         0.5211         177.9          WB    16.00     Sequence
DRB1_1101  437  EGLALKPRKAFSPIR  LALKPRKAF         0.5188         182.5          WB    16.00     Sequence
DRB1_1101  279  LLNYLALLGWSIADD  YLALLGWSI         0.5185         183.0          WB    16.00     Sequence
DRB1_1101  278  GLLNYLALLGWSIAD  LLNYLALLG         0.5161         187.8          WB    16.00     Sequence
DRB1_1101  447  FSPIRVAATGTTVSP  FSPIRVAAT         0.5147         190.8          WB    16.00     Sequence
DRB1_1101   94  RDVLARLLAAGEAYH  DVLARLLAA         0.5140         192.1          WB    16.00     Sequence
DRB1_1101    5  TVRVRFCPSPTGTPH  VRFCPSPTG         0.5112         198.1          WB    16.00     Sequence
DRB1_1101  433  DALIEGLALKPRKAF  LIEGLALKP         0.5090         202.8          WB    16.00     Sequence
DRB1_1101  438  GLALKPRKAFSPIRV  LALKPRKAF         0.5047         212.6          WB    16.00     Sequence
DRB1_1101   53  SEESYLALLDALRWL  LALLDALRW         0.5038         214.7          WB    16.00     Sequence
DRB1_1101  293  DHDLFGLDEMVAAFD  LFGLDEMVA         0.5027         217.3          WB    16.00     Sequence
DRB1_1101   89  RAEIYRDVLARLLAA  YRDVLARLL         0.5022         218.3          WB    16.00     Sequence
DRB1_1101   23  VRTALFNWAYARHTG  LFNWAYARH         0.5004         222.6          WB    16.00     Sequence
DRB1_1101   95  DVLARLLAAGEAYHA  DVLARLLAA         0.4961         233.3          WB    16.00     Sequence
DRB1_1101  200  PCDDALMKITHVLRG  LMKITHVLR         0.4934         240.0          WB    16.00     Sequence
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DRB1_1101    4  ETVRVRFCPSPTGTP  VRFCPSPTG        0.4924        242.7          WB    16.00     Sequence
DRB1_1101  294  HDLFGLDEMVAAFDV  LFGLDEMVA        0.4914        245.5          WB    16.00     Sequence
DRB1_1101  292  DDHDLFGLDEMVAAF  LFGLDEMVA        0.4881        254.3          WB    16.00     Sequence
DRB1_1101  461  PPLFESLELLGRDRS  LFESLELLG        0.4856        261.2          WB    16.00     Sequence
DRB1_1101  277  EGLLNYLALLGWSIA  LLNYLALLG        0.4849        263.3          WB    16.00     Sequence
DRB1_1101   17  TPHVGLVRTALFNWA  VGLVRTALF        0.4800        277.5          WB    16.00     Sequence
DRB1_1101   22  LVRTALFNWAYARHT  RTALFNWAY        0.4781        283.3          WB    16.00     Sequence
DRB1_1101    6  VRVRFCPSPTGTPHV  VRFCPSPTG        0.4725        301.1          WB    32.00     Sequence
DRB1_1101  228  HQALIRIGVAERIPK  HQALIRIGV        0.4696        310.9          WB    32.00     Sequence
DRB1_1101    3  TETVRVRFCPSPTGT  TVRVRFCPS        0.4635        331.8          WB    32.00     Sequence
DRB1_1101  280  LNYLALLGWSIADDH  YLALLGWSI        0.4629        333.9          WB    32.00     Sequence
DRB1_1101   16  GTPHVGLVRTALFNW  VGLVRTALF        0.4552        363.1          WB    32.00     Sequence
DRB1_1101  295  DLFGLDEMVAAFDVA  LFGLDEMVA        0.4537        368.9          WB    32.00     Sequence
DRB1_1101    2  ATETVRVRFCPSPTG  TVRVRFCPS        0.4493        387.1          WB    32.00     Sequence
DRB1_1101  206  MKITHVLRGEDLLPS  ITHVLRGED        0.4490        388.4          WB    32.00     Sequence
DRB1_1101   18  PHVGLVRTALFNWAY  VGLVRTALF        0.4465        398.8          WB    32.00     Sequence
DRB1_1101  231  LIRIGVAERIPKFAH  IGVAERIPK        0.4448        406.2          WB    32.00     Sequence
DRB1_1101   96  VLARLLAAGEAYHAF  RLLAAGEAY        0.4380        437.1          WB    32.00     Sequence
DRB1_1101  291  ADDHDLFGLDEMVAA  LFGLDEMVA        0.4375        439.8          WB    32.00     Sequence
DRB1_1101  276  PEGLLNYLALLGWSI  LLNYLALLG        0.4367        443.7          WB    32.00     Sequence
DRB1_1101  199  NPCDDALMKITHVLR  LMKITHVLR        0.4343        455.1          WB    32.00     Sequence
DRB1_1101  164  LAWNDLVRGPVTFAA  WNDLVRGPV        0.4339        457.3          WB    32.00     Sequence
DRB1_1101  229  QALIRIGVAERIPKF  LIRIGVAER        0.4338        457.9          WB    32.00     Sequence
DRB1_1101    7  RVRFCPSPTGTPHVG  VRFCPSPTG        0.4334        459.7          WB    32.00     Sequence
DRB1_1101   52  DSEESYLALLDALRW  LALLDALRW        0.4300        477.1          WB    32.00     Sequence
DRB1_1101  230  ALIRIGVAERIPKFA  IRIGVAERI        0.4299        477.2          WB    32.00     Sequence
DRB1_1101  163  DLAWNDLVRGPVTFA  WNDLVRGPV        0.4288        483.4          WB    32.00     Sequence
DRB1_1101   59  ALLDALRWLGLDWDE  LLDALRWLG        0.4254        501.2                32.00     Sequence
DRB1_1101  221  TPRQLALHQALIRIG  LALHQALIR        0.4239        509.2                32.00     Sequence
DRB1_1101  432  KDALIEGLALKPRKA  LIEGLALKP        0.4222        519.1                32.00     Sequence
DRB1_1101   15  TGTPHVGLVRTALFN  VGLVRTALF        0.4221        519.4                32.00     Sequence
DRB1_1101  439  LALKPRKAFSPIRVA  LALKPRKAF        0.4196        533.6                32.00     Sequence
DRB1_1101  460  SPPLFESLELLGRDR  LFESLELLG        0.4192        536.2                32.00     Sequence
DRB1_1101  448  SPIRVAATGTTVSPP  IRVAATGTT        0.4191        536.5                32.00     Sequence
DRB1_1101   19  HVGLVRTALFNWAYA  VGLVRTALF        0.4143        565.3                32.00     Sequence
DRB1_1101   28  FNWAYARHTGGTFVF  FNWAYARHT        0.4141        566.6                32.00     Sequence
DRB1_1101   21  GLVRTALFNWAYARH  RTALFNWAY        0.4103        589.9                32.00     Sequence
DRB1_1101  325  ALNAEHIRMLDVGDF  AEHIRMLDV        0.4074        609.2                32.00     Sequence
DRB1_1101  243  FAHLPTVLGEGTKKL  FAHLPTVLG        0.4000        659.6                32.00     Sequence
DRB1_1101  440  ALKPRKAFSPIRVAA  RKAFSPIRV        0.3996        662.9                32.00     Sequence
DRB1_1101  232  IRIGVAERIPKFAHL  IGVAERIPK        0.3971        680.9                32.00     Sequence
DRB1_1101   20  VGLVRTALFNWAYAR  VGLVRTALF        0.3959        689.9                32.00     Sequence
DRB1_1101  281  NYLALLGWSIADDHD  YLALLGWSI        0.3953        694.2                32.00     Sequence
DRB1_1101   88  QRAEIYRDVLARLLA  YRDVLARLL        0.3948        697.9                32.00     Sequence
DRB1_1101  449  PIRVAATGTTVSPPL  IRVAATGTT        0.3916        722.2                32.00     Sequence
DRB1_1101   97  LARLLAAGEAYHAFS  RLLAAGEAY        0.3900        735.3                32.00     Sequence
DRB1_1101  162  DDLAWNDLVRGPVTF  WNDLVRGPV        0.3886        746.3                32.00     Sequence
DRB1_1101  275  IPEGLLNYLALLGWS  LLNYLALLG        0.3880        751.0                32.00     Sequence
DRB1_1101  327  NAEHIRMLDVGDFTV  AEHIRMLDV        0.3784        833.5                32.00     Sequence
DRB1_1101   60  LLDALRWLGLDWDEG  LLDALRWLG        0.3778        838.8                32.00     Sequence
DRB1_1101  387  DDQYVIDPKAAAKEL  YVIDPKAAA        0.3744        870.3                32.00     Sequence
DRB1_1101  388  DQYVIDPKAAAKELG  YVIDPKAAA        0.3699        913.6                32.00     Sequence
DRB1_1101  326  LNAEHIRMLDVGDFT  AEHIRMLDV        0.3689        923.9                32.00     Sequence
DRB1_1101  251  GEGTKKLSKRDPQSN  TKKLSKRDP        0.3659        954.3                32.00     Sequence
DRB1_1101  150  GRQPVVRLRMPDDDL  PVVRLRMPD        0.3651        962.0                32.00     Sequence
DRB1_1101  165  AWNDLVRGPVTFAAG  WNDLVRGPV        0.3650        963.7                32.00     Sequence
DRB1_1101  324  DALNAEHIRMLDVGD  AEHIRMLDV        0.3648        965.1                32.00     Sequence
DRB1_1101  151  RQPVVRLRMPDDDLA  PVVRLRMPD        0.3644        969.4                32.00     Sequence
DRB1_1101   14  PTGTPHVGLVRTALF  PHVGLVRTA        0.3619        996.8                32.00     Sequence
DRB1_1101  236  VAERIPKFAHLPTVL  AERIPKFAH        0.3577       1042.4                32.00     Sequence
DRB1_1101  409  LDAALAALTSVTDWT  LAALTSVTD        0.3577       1042.7                32.00     Sequence
DRB1_1101  410  DAALAALTSVTDWTA  LAALTSVTD        0.3571       1049.1                32.00     Sequence
DRB1_1101  274  FIPEGLLNYLALLGW  LLNYLALLG        0.3552       1070.8                32.00     Sequence
DRB1_1101  431  LKDALIEGLALKPRK  LIEGLALKP        0.3550       1073.8                32.00     Sequence
DRB1_1101  207  KITHVLRGEDLLPST  ITHVLRGED        0.3533       1093.4                50.00     Sequence
DRB1_1101  459  VSPPLFESLELLGRD  LFESLELLG        0.3528       1099.5                50.00     Sequence
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DRB1_1101    1  TATETVRVRFCPSPT  TVRVRFCPS         0.3509       1121.8                    50.00     Sequence
DRB1_1101  358  EAAFAAAAELVQTRI  FAAAAELVQ         0.3506       1126.2                    50.00     Sequence
DRB1_1101  328  AEHIRMLDVGDFTVR  HIRMLDVGD         0.3496       1137.7                    50.00     Sequence
DRB1_1101  252  EGTKKLSKRDPQSNL  TKKLSKRDP         0.3495       1139.2                    50.00     Sequence
DRB1_1101  375  LGDAWELLKFFNDDQ  AWELLKFFN         0.3461       1182.5                    50.00     Sequence
DRB1_1101  389  QYVIDPKAAAKELGP  YVIDPKAAA         0.3459       1184.9                    50.00     Sequence
DRB1_1101  296  LFGLDEMVAAFDVAD  LFGLDEMVA         0.3447       1200.2                    50.00     Sequence
DRB1_1101  264  SNLFAHRDRGFIPEG  LFAHRDRGF         0.3447       1200.2                    50.00     Sequence
DRB1_1101  250  LGEGTKKLSKRDPQS  GTKKLSKRD         0.3434       1216.7                    50.00     Sequence
DRB1_1101  220  STPRQLALHQALIRI  LALHQALIR         0.3426       1228.0                    50.00     Sequence
DRB1_1101  374  VLGDAWELLKFFNDD  AWELLKFFN         0.3419       1237.3                    50.00     Sequence
DRB1_1101  359  AAFAAAAELVQTRIV  AFAAAAELV         0.3415       1242.7                    50.00     Sequence
DRB1_1101  233  RIGVAERIPKFAHLP  AERIPKFAH         0.3404       1257.7                    50.00     Sequence
DRB1_1101  408  VLDAALAALTSVTDW  DAALAALTS         0.3398       1265.5                    50.00     Sequence
DRB1_1101  149  EGRQPVVRLRMPDDD  RQPVVRLRM         0.3370       1303.9                    50.00     Sequence
DRB1_1101  161  DDDLAWNDLVRGPVT  WNDLVRGPV         0.3368       1307.7                    50.00     Sequence
DRB1_1101  263  QSNLFAHRDRGFIPE  LFAHRDRGF         0.3363       1314.9                    50.00     Sequence
DRB1_1101    8  VRFCPSPTGTPHVGL  VRFCPSPTG         0.3346       1338.2                    50.00     Sequence
DRB1_1101  338  DFTVRLRDHLDTHGH  VRLRDHLDT         0.3344       1341.3                    50.00     Sequence
DRB1_1101  407  AVLDAALAALTSVTD  DAALAALTS         0.3338       1350.2                    50.00     Sequence
DRB1_1101  373  VVLGDAWELLKFFND  AWELLKFFN         0.3335       1354.4                    50.00     Sequence
DRB1_1101  376  GDAWELLKFFNDDQY  AWELLKFFN         0.3315       1384.8                    50.00     Sequence
DRB1_1101  253  GTKKLSKRDPQSNLF  TKKLSKRDP         0.3306       1397.4                    50.00     Sequence
DRB1_1101  357  DEAAFAAAAELVQTR  FAAAAELVQ         0.3299       1409.1                    50.00     Sequence
DRB1_1101  377  DAWELLKFFNDDQYV  AWELLKFFN         0.3285       1430.4                    50.00     Sequence
DRB1_1101  386  NDDQYVIDPKAAAKE  YVIDPKAAA         0.3284       1432.2                    50.00     Sequence
DRB1_1101  181  VPDFALTRASGDPLY  DFALTRASG         0.3256       1476.2                    50.00     Sequence
DRB1_1101  135  DRHLTDAQRAAYLAE  LTDAQRAAY         0.3253       1481.1                    50.00     Sequence
DRB1_1101  323  ADALNAEHIRMLDVG  AEHIRMLDV         0.3241       1500.6                    50.00     Sequence
DRB1_1101  180  SVPDFALTRASGDPL  DFALTRASG         0.3235       1510.0                    50.00     Sequence
DRB1_1101  166  WNDLVRGPVTFAAGS  LVRGPVTFA         0.3227       1522.1                    50.00     Sequence
DRB1_1101  411  AALAALTSVTDWTAP  LAALTSVTD         0.3218       1536.9                    50.00     Sequence
DRB1_1101  265  NLFAHRDRGFIPEGL  LFAHRDRGF         0.3213       1546.6                    50.00     Sequence
DRB1_1101  337  GDFTVRLRDHLDTHG  VRLRDHLDT         0.3182       1597.8                    50.00     Sequence
DRB1_1101  148  AEGRQPVVRLRMPDD  RQPVVRLRM         0.3181       1599.7                    50.00     Sequence
DRB1_1101  339  FTVRLRDHLDTHGHH  VRLRDHLDT         0.3173       1614.9                    50.00     Sequence
DRB1_1101  134  FDRHLTDAQRAAYLA  LTDAQRAAY         0.3149       1657.0                    50.00     Sequence
DRB1_1101  290  IADDHDLFGLDEMVA  LFGLDEMVA         0.3149       1657.0                    50.00     Sequence
DRB1_1101  406  AAVLDAALAALTSVT  LDAALAALT         0.3136       1680.6                    50.00     Sequence
DRB1_1101  234  IGVAERIPKFAHLPT  AERIPKFAH         0.3136       1681.1                    50.00     Sequence
DRB1_1101   98  ARLLAAGEAYHAFST  RLLAAGEAY         0.3118       1714.2                    50.00     Sequence
DRB1_1101  282  YLALLGWSIADDHDL  YLALLGWSI         0.3087       1771.2                    50.00     Sequence
DRB1_1101  360  AFAAAAELVQTRIVV  FAAAAELVQ         0.3079       1787.6                    50.00     Sequence
DRB1_1101  136  RHLTDAQRAAYLAEG  LTDAQRAAY         0.3073       1798.1                    50.00     Sequence
DRB1_1101   29  NWAYARHTGGTFVFR  WAYARHTGG         0.3069       1805.8                    50.00     Sequence
DRB1_1101  117  EARHVAAGRNPKLGY  ARHVAAGRN         0.3069       1806.0                    50.00     Sequence
DRB1_1101  450  IRVAATGTTVSPPLF  IRVAATGTT         0.3069       1807.3                    50.00     Sequence
DRB1_1101  118  ARHVAAGRNPKLGYD  ARHVAAGRN         0.3041       1862.8                    50.00     Sequence
DRB1_1101  152  QPVVRLRMPDDDLAW  PVVRLRMPD         0.3038       1868.5                    50.00     Sequence
DRB1_1101  262  PQSNLFAHRDRGFIP  NLFAHRDRG         0.3038       1868.6                    50.00     Sequence
DRB1_1101  458  TVSPPLFESLELLGR  LFESLELLG         0.3019       1907.1                    50.00     Sequence
DRB1_1101  430  ALKDALIEGLALKPR  LIEGLALKP         0.3018       1910.0                    50.00     Sequence
DRB1_1101  372  IVVLGDAWELLKFFN  AWELLKFFN         0.3016       1913.4                    50.00     Sequence
DRB1_1101  273  GFIPEGLLNYLALLG  FIPEGLLNY         0.3016       1914.1                    50.00     Sequence
DRB1_1101  182  PDFALTRASGDPLYT  DFALTRASG         0.3010       1925.0                    50.00     Sequence
DRB1_1101  336  VGDFTVRLRDHLDTH  FTVRLRDHL         0.3010       1925.9                    50.00     Sequence
DRB1_1101  192  DPLYTLVNPCDDALM  YTLVNPCDD         0.2994       1960.2                    50.00     Sequence
DRB1_1101  193  PLYTLVNPCDDALMK  YTLVNPCDD         0.2969       2012.2                    50.00     Sequence
DRB1_1101  364  AAELVQTRIVVLGDA  LVQTRIVVL         0.2969       2012.5                    50.00     Sequence
DRB1_1101  147  LAEGRQPVVRLRMPD  RQPVVRLRM         0.2967       2018.0                    50.00     Sequence
DRB1_1101    0  VTATETVRVRFCPSP  TVRVRFCPS         0.2924       2113.7                    50.00     Sequence
DRB1_1101  145  AYLAEGRQPVVRLRM  RQPVVRLRM         0.2918       2127.2                    50.00     Sequence
DRB1_1101   87  SQRAEIYRDVLARLL  EIYRDVLAR         0.2917       2130.5                    50.00     Sequence
DRB1_1101  249  VLGEGTKKLSKRDPQ  TKKLSKRDP         0.2900       2169.9                    50.00     Sequence
DRB1_1101  365  AELVQTRIVVLGDAW  VQTRIVVLG         0.2890       2192.0                    50.00     Sequence
DRB1_1101  191  GDPLYTLVNPCDDAL  LYTLVNPCD         0.2868       2245.4                    50.00     Sequence
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DRB1_1101	378	AWELLKFFNDDQYVI	AWELLKFFN	0.2867	2246.7	50.00	Sequence
DRB1_1101	356	LDEAAFAAAAELVQT	FAAAAELVQ	0.2848	2295.2	50.00	Sequence
DRB1_1101	405	GAAVLDAALAALTSV	LDAALAALT	0.2837	2321.7	50.00	Sequence
DRB1_1101	366	ELVQTRIVVLGDAWE	VQTRIVVLG	0.2831	2338.2	50.00	Sequence
DRB1_1101	133	NFDRHLTDAQRAAYL	RHLTDAQRA	0.2809	2393.8	50.00	Sequence
DRB1_1101	146	YLAEGRQPVVRLRMP	RQPVVRLRM	0.2802	2411.7	50.00	Sequence
DRB1_1101	329	EHIRMLDVGDFTVRL	HIRMLDVGD	0.2798	2422.7	50.00	Sequence
DRB1_1101	330	HIRMLDVGDFTVRLR	HIRMLDVGD	0.2798	2423.0	50.00	Sequence
DRB1_1101	322	KADALNAEHIRMLDV	ALNAEHIRM	0.2784	2459.3	50.00	Sequence
DRB1_1101	235	GVAERIPKFAHLPTV	AERIPKFAH	0.2776	2480.6	50.00	Sequence
DRB1_1101	385	FNDDQYVIDPKAAAK	YVIDPKAAA	0.2775	2483.5	50.00	Sequence
DRB1_1101	412	ALAALTSVTDWTAPL	LAALTSVTD	0.2754	2539.8	50.00	Sequence
DRB1_1101	367	LVQTRIVVLGDAWEL	VQTRIVVLG	0.2751	2549.6	50.00	Sequence
DRB1_1101	266	LFAHRDRGFIPEGLL	FAHRDRGFI	0.2739	2582.0	50.00	Sequence
DRB1_1101	144	AAYLAEGRQPVVRLR	YLAEGRQPV	0.2722	2630.6	50.00	Sequence
DRB1_1101	272	RGFIPEGLLNYLALL	FIPEGLLNY	0.2708	2670.2	50.00	Sequence
DRB1_1101	198	VNPCDDALMKITHVL	DDALMKITH	0.2686	2733.0	50.00	Sequence
DRB1_1101	128	KLGYDNFDRHLTDAQ	YDNFDRHLT	0.2680	2753.3	50.00	Sequence
DRB1_1101	143	RAAYLAEGRQPVVRL	YLAEGRQPV	0.2677	2760.6	50.00	Sequence
DRB1_1101	30	WAYARHTGGTFVFRI	WAYARHTGG	0.2668	2788.7	50.00	Sequence
DRB1_1101	61	LDALRWLGLDWDEGP	ALRWLGLDW	0.2664	2800.7	50.00	Sequence
DRB1_1101	248	TVLGEGTKKLSKRDP	LGEGTKKLS	0.2664	2801.2	50.00	Sequence
DRB1_1101	179	GSVPDFALTRASGDP	DFALTRASG	0.2662	2806.7	50.00	Sequence
DRB1_1101	219	PSTPRQLALHQALIR	LALHQALIR	0.2656	2823.3	50.00	Sequence
DRB1_1101	363	AAAELVQTRIVVLGD	LVQTRIVVL	0.2653	2832.1	50.00	Sequence
DRB1_1101	99	RLLAAGEAYHAFSTP	RLLAAGEAY	0.2640	2874.0	50.00	Sequence
DRB1_1101	160	PDDDLAWNDLVRGPV	WNDLVRGPV	0.2626	2916.9	50.00	Sequence
DRB1_1101	208	ITHVLRGEDLLPSTP	ITHVLRGED	0.2623	2928.6	50.00	Sequence
DRB1_1101	335	DVGDFTVRLRDHLDT	FTVRLRDHL	0.2617	2947.0	50.00	Sequence
DRB1_1101	153	PVVRLRMPDDDLAWN	VVRLRMPDD	0.2602	2995.8	50.00	Sequence
DRB1_1101	104	GEAYHAFSTPEEVEA	YHAFSTPEE	0.2601	2998.3	50.00	Sequence
DRB1_1101	271	DRGFIPEGLLNYLAL	FIPEGLLNY	0.2578	3074.1	50.00	Sequence
DRB1_1101	247	PTVLGEGTKKLSKRD	LGEGTKKLS	0.2568	3106.9	50.00	Sequence
DRB1_1101	51	RDSEESYLALLDALR	ESYLALLDA	0.2559	3136.2	50.00	Sequence
DRB1_1101	115	EVEARHVAAGRNPKL	ARHVAAGRN	0.2558	3139.2	50.00	Sequence
DRB1_1101	390	YVIDPKAAAKELGPD	YVIDPKAAA	0.2550	3168.0	50.00	Sequence
DRB1_1101	261	DPQSNLFAHRDRGFI	NLFAHRDRG	0.2532	3230.4	50.00	Sequence
DRB1_1101	129	LGYDNFDRHLTDAQR	YDNFDRHLT	0.2531	3233.0	50.00	Sequence
DRB1_1101	130	GYDNFDRHLTDAQRA	YDNFDRHLT	0.2516	3285.1	50.00	Sequence
DRB1_1101	105	EAYHAFSTPEEVEAR	YHAFSTPEE	0.2494	3364.4	50.00	Sequence
DRB1_1101	119	RHVAAGRNPKLGYDN	HVAAGRNPK	0.2486	3396.1	50.00	Sequence
DRB1_1101	190	SGDPLYTLVNPCDDA	LYTLVNPCD	0.2450	3530.1	50.00	Sequence
DRB1_1101	13	SPTGTPHVGLVRTAL	HVGLVRTAL	0.2441	3563.0	50.00	Sequence
DRB1_1101	404	DGAAVLDAALAALTS	AAVLDAALA	0.2432	3598.4	50.00	Sequence
DRB1_1101	183	DFALTRASGDPLYTL	DFALTRASG	0.2431	3603.6	50.00	Sequence
DRB1_1101	116	VEARHVAAGRNPKLG	ARHVAAGRN	0.2423	3632.6	50.00	Sequence
DRB1_1101	362	AAAAELVQTRIVVLG	LVQTRIVVL	0.2418	3654.4	50.00	Sequence
DRB1_1101	270	RDRGFIPEGLLNYLA	FIPEGLLNY	0.2416	3661.6	50.00	Sequence
DRB1_1101	429	AALKDALIEGLALKP	LIEGLALKP	0.2394	3749.0	50.00	Sequence
DRB1_1101	368	VQTRIVVLGDAWELL	RIVVLGDAW	0.2388	3775.9	50.00	Sequence
DRB1_1101	106	AYHAFSTPEEVEARH	YHAFSTPEE	0.2386	3784.4	50.00	Sequence
DRB1_1101	355	ALDEAAFAAAAELVQ	FAAAAELVQ	0.2378	3814.2	50.00	Sequence
DRB1_1101	361	FAAAAELVQTRIVVL	AAELVQTRI	0.2375	3829.4	50.00	Sequence
DRB1_1101	103	AGEAYHAFSTPEEVE	YHAFSTPEE	0.2330	4019.1	50.00	Sequence
DRB1_1101	246	LPTVLGEGTKKLSKR	LGEGTKKLS	0.2327	4032.7	50.00	Sequence
DRB1_1101	127	PKLGYDNFDRHLTDA	YDNFDRHLT	0.2313	4092.7	50.00	Sequence
DRB1_1101	62	DALRWLGLDWDEGPE	ALRWLGLDW	0.2308	4116.5	50.00	Sequence
DRB1_1101	63	ALRWLGLDWDEGPEV	ALRWLGLDW	0.2306	4126.6	50.00	Sequence
DRB1_1101	142	QRAAYLAEGRQPVVR	YLAEGRQPV	0.2302	4141.4	50.00	Sequence
DRB1_1101	371	RIVVLGDAWELLKFF	RIVVLGDAW	0.2266	4309.2	50.00	Sequence
DRB1_1101	167	NDLVRGPVTFAAGSV	LVRGPVTFA	0.2254	4361.7	50.00	Sequence
DRB1_1101	370	TRIVVLGDAWELLKF	RIVVLGDAW	0.2250	4383.6	50.00	Sequence
DRB1_1101	194	LYTLVNPCDDALMKI	LYTLVNPCD	0.2245	4407.4	50.00	Sequence
DRB1_1101	215	EDLLPSTPRQLALHQ	LPSTPRQLA	0.2243	4414.3	50.00	Sequence
DRB1_1101	254	TKKLSKRDPQSNLFA	TKKLSKRDP	0.2227	4490.7	50.00	Sequence
DRB1_1101	384	FFNDDQYVIDPKAAA	YVIDPKAAA	0.2224	4508.2	50.00	Sequence

DRB1_1101	137	HLTDAQRAAYLAEGR	LTDAQRAAY	0.2221	4521.3	50.00	Sequence
DRB1_1101	132	DNFDRHLTDAQRAAY	LTDAQRAAY	0.2211	4572.7	50.00	Sequence
DRB1_1101	114	EEVEARHVAAGRNPK	ARHVAAGRN	0.2205	4598.8	50.00	Sequence
DRB1_1101	340	TVRLRDHLDTHGHHI	VRLRDHLDT	0.2201	4621.9	50.00	Sequence
DRB1_1101	334	LDVGDFTVRLRDHLD	FTVRLRDHL	0.2186	4696.8	50.00	Sequence
DRB1_1101	131	YDNFDRHLTDAQRAA	YDNFDRHLT	0.2185	4699.7	50.00	Sequence
DRB1_1101	81	YGPYRQSQRAEIYRD	YRQSQRAEI	0.2172	4767.8	50.00	Sequence
DRB1_1101	369	QTRIVVLGDAWELLK	RIVVLGDAW	0.2160	4829.4	50.00	Sequence
DRB1_1101	80	PYGPYRQSQRAEIYR	YRQSQRAEI	0.2152	4872.4	50.00	Sequence
DRB1_1101	79	GPYGPYRQSQRAEIY	YGPYRQSQR	0.2131	4983.2	50.00	Sequence
DRB1_1101	214	GEDLLPSTPRQLALH	LPSTPRQLA	0.2082	5255.5	50.00	Sequence
DRB1_1101	178	AGSVPDFALTRASGD	DFALTRASG	0.2072	5313.5	50.00	Sequence
DRB1_1101	120	HVAAGRNPKLGYDNF	AGRNPKLGY	0.2070	5322.6	50.00	Sequence
DRB1_1101	78	GGPYGPYRQSQRAEI	YRQSQRAEI	0.2040	5498.9	50.00	Sequence
DRB1_1101	245	HLPTVLGEGTKKLSK	LGEGTKKLS	0.2023	5600.8	50.00	Sequence
DRB1_1101	217	LLPSTPRQLALHQAL	LPSTPRQLA	0.1980	5871.9	50.00	Sequence
DRB1_1101	216	DLLPSTPRQLALHQA	LPSTPRQLA	0.1972	5922.2	50.00	Sequence
DRB1_1101	297	FGLDEMVAAFDVADV	FGLDEMVAA	0.1963	5979.8	50.00	Sequence
DRB1_1101	403	PDGAAVLDAALAALT	AAVLDAALA	0.1936	6156.6	50.00	Sequence
DRB1_1101	333	MLDVGDFTVRLRDHL	FTVRLRDHL	0.1930	6192.1	50.00	Sequence
DRB1_1101	269	HRDRGFIPEGLLNYL	RGFIPEGLL	0.1929	6203.4	50.00	Sequence
DRB1_1101	189	ASGDPLYTLVNPCDD	LYTLVNPCD	0.1917	6283.2	50.00	Sequence
DRB1_1101	197	LVNPCDDALMKITHV	DDALMKITH	0.1909	6336.7	50.00	Sequence
DRB1_1101	267	FAHRDRGFIPEGLLN	FAHRDRGFI	0.1898	6415.5	50.00	Sequence
DRB1_1101	126	NPKLGYDNFDRHLTD	YDNFDRHLT	0.1879	6548.4	50.00	Sequence
DRB1_1101	82	GPYRQSQRAEIYRDV	YRQSQRAEI	0.1875	6575.5	50.00	Sequence
DRB1_1101	413	LAALTSVTDWTAPLI	LAALTSVTD	0.1873	6590.9	50.00	Sequence
DRB1_1101	283	LALLGWSIADDHDLF	LALLGWSIA	0.1862	6671.2	50.00	Sequence
DRB1_1101	141	AQRAAYLAEGRQPVV	YLAEGRQPV	0.1859	6692.8	50.00	Sequence
DRB1_1101	350	HGHHIALDEAAFAAA	HIALDEAAF	0.1847	6778.1	50.00	Sequence
DRB1_1101	244	AHLPTVLGEGTKKLS	PTVLGEGTK	0.1846	6785.7	50.00	Sequence
DRB1_1101	457	TTVSPPLFESLELLG	LFESLELLG	0.1845	6795.1	50.00	Sequence
DRB1_1101	113	PEEVEARHVAAGRNP	EVEARHVAA	0.1841	6824.8	50.00	Sequence
DRB1_1101	331	IRMLDVGDFTVRLRD	IRMLDVGDF	0.1822	6964.9	50.00	Sequence
DRB1_1101	138	LTDAQRAAYLAEGRQ	LTDAQRAAY	0.1817	6999.5	50.00	Sequence
DRB1_1101	102	AAGEAYHAFSTPEEV	YHAFSTPEE	0.1801	7124.4	50.00	Sequence
DRB1_1101	86	QSQRAEIYRDVLARL	EIYRDVLAR	0.1779	7295.0	50.00	Sequence
DRB1_1101	168	DLVRGPVTFAAGSVP	LVRGPVTFA	0.1761	7438.1	50.00	Sequence
DRB1_1101	341	VRLRDHLDTHGHHIA	VRLRDHLDT	0.1755	7483.6	50.00	Sequence
DRB1_1101	213	RGEDLLPSTPRQLAL	LPSTPRQLA	0.1754	7493.9	50.00	Sequence
DRB1_1101	218	LPSTPRQLALHQALI	LPSTPRQLA	0.1751	7518.0	50.00	Sequence
DRB1_1101	379	WELLKFFNDDQYVID	WELLKFFND	0.1745	7567.8	50.00	Sequence
DRB1_1101	351	GHHIALDEAAFAAAA	HIALDEAAF	0.1745	7570.1	50.00	Sequence
DRB1_1101	38	GTFVFRIEDTDAQRD	TFVFRIEDT	0.1731	7682.3	50.00	Sequence
DRB1_1101	305	AFDVADVNSSPARFD	FDVADVNSS	0.1716	7808.6	50.00	Sequence
DRB1_1101	169	LVRGPVTFAAGSVPD	LVRGPVTFA	0.1711	7856.1	50.00	Sequence
DRB1_1101	349	THGHHIALDEAAFAA	HIALDEAAF	0.1704	7912.5	50.00	Sequence
DRB1_1101	37	GGTFVFRIEDTDAQR	TFVFRIEDT	0.1688	8046.6	50.00	Sequence
DRB1_1101	451	RVAATGTTVSPPLFE	RVAATGTTV	0.1683	8092.1	50.00	Sequence
DRB1_1101	381	LLKFFNDDQYVIDPK	FFNDDQYVI	0.1681	8112.1	50.00	Sequence
DRB1_1101	107	YHAFSTPEEVEARHV	YHAFSTPEE	0.1681	8115.0	50.00	Sequence
DRB1_1101	421	DWTAPLIEAALKDAL	DWTAPLIEA	0.1677	8147.1	50.00	Sequence
DRB1_1101	321	KKADALNAEHIRMLD	ALNAEHIRM	0.1657	8325.0	50.00	Sequence
DRB1_1101	419	VTDWTAPLIEAALKD	DWTAPLIEA	0.1634	8538.4	50.00	Sequence
DRB1_1101	380	ELLKFFNDDQYVIDP	KFFNDDQYV	0.1625	8614.1	50.00	Sequence
DRB1_1101	172	GPVTFAAGSVPDFAL	VTFAAGSVP	0.1623	8640.0	50.00	Sequence
DRB1_1101	260	RDPQSNLFAHRDRGF	NLFAHRDRG	0.1618	8687.8	50.00	Sequence
DRB1_1101	382	LKFFNDDQYVIDPKA	FFNDDQYVI	0.1608	8778.5	50.00	Sequence
DRB1_1101	418	SVTDWTAPLIEAALK	DWTAPLIEA	0.1606	8792.2	50.00	Sequence
DRB1_1101	39	TFVFRIEDTDAQRDS	VFRIEDTDA	0.1602	8838.3	50.00	Sequence
DRB1_1101	212	LRGEDLLPSTPRQLA	LLPSTPRQL	0.1601	8846.5	50.00	Sequence
DRB1_1101	31	AYARHTGGTFVFRIE	YARHTGGTF	0.1599	8866.0	50.00	Sequence
DRB1_1101	100	LLAAGEAYHAFSTPE	LLAAGEAYH	0.1598	8872.2	50.00	Sequence
DRB1_1101	209	THVLRGEDLLPSTPR	LRGEDLLPS	0.1581	9036.3	50.00	Sequence
DRB1_1101	121	VAAGRNPKLGYDNFD	AGRNPKLGY	0.1577	9072.5	50.00	Sequence
DRB1_1101	304	AAFDVADVNSSPARF	FDVADVNSS	0.1577	9080.0	50.00	Sequence

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DRB1_1101  420  TDWTAPLIEAALKDA  DWTAPLIEA        0.1567       9172.7               50.00     Sequence
DRB1_1101   36  TGGTFVFRIEDTDAQ  TFVFRIEDT        0.1566       9182.5               50.00     Sequence
DRB1_1101  268  AHRDRGFIPEGLLNY  RGFIPEGLL        0.1560       9244.8               50.00     Sequence
DRB1_1101  354  IALDEAAFAAAAELV  AFAAAAELV        0.1552       9320.8               50.00     Sequence
DRB1_1101  352  HHIALDEAAFAAAAE  HIALDEAAF        0.1551       9337.2               50.00     Sequence
DRB1_1101  173  PVTFAAGSVPDFALT  VTFAAGSVP        0.1543       9412.7               50.00     Sequence
DRB1_1101  383  KFFNDDQYVIDPKAA  KFFNDDQYV        0.1540       9452.2               50.00     Sequence
DRB1_1101  211  VLRGEDLLPSTPRQL  LRGEDLLPS        0.1530       9550.1               50.00     Sequence
DRB1_1101  171  RGPVTFAAGSVPDFA  VTFAAGSVP        0.1523       9626.9               50.00     Sequence
DRB1_1101  415  ALTSVTDWTAPLIEA  LTSVTDWTA        0.1521       9642.3               50.00     Sequence
DRB1_1101  112  TPEEVEARHVAAGRN  EVEARHVAA        0.1515       9710.5               50.00     Sequence
DRB1_1101  210  HVLRGEDLLPSTPRQ  LRGEDLLPS        0.1513       9724.8               50.00     Sequence
DRB1_1101  416  LTSVTDWTAPLIEAA  LTSVTDWTA        0.1511       9748.7               50.00     Sequence
DRB1_1101  195  YTLVNPCDDALMKIT  YTLVNPCDD        0.1507       9795.4               50.00     Sequence
DRB1_1101   12  PSPTGTPHVGLVRTA  PHVGLVRTA        0.1504       9822.9               50.00     Sequence
DRB1_1101  125  RNPKLGYDNFDRHLT  YDNFDRHLT        0.1503       9831.6               50.00     Sequence
DRB1_1101   83  PYRQSQRAEIYRDVL  YRQSQRAEI        0.1489       9988.4               50.00     Sequence
DRB1_1101   50  QRDSEESYLALLDAL  ESYLALLDA        0.1486      10012.0               50.00     Sequence
DRB1_1101  306  FDVADVNSSPARFDQ  FDVADVNSS        0.1485      10024.4               50.00     Sequence
DRB1_1101  314  SPARFDQKKADALNA  RFDQKKADA        0.1483      10044.5               50.00     Sequence
DRB1_1101  422  WTAPLIEAALKDALI  LIEAALKDA        0.1477      10119.0               50.00     Sequence
DRB1_1101  424  APLIEAALKDALIEG  LIEAALKDA        0.1452      10397.2               50.00     Sequence
DRB1_1101  154  VVRLRMPDDDLAWND  VVRLRMPDD        0.1451      10399.2               50.00     Sequence
DRB1_1101   35  HTGGTFVFRIEDTDA  GTFVFRIED        0.1449      10426.8               50.00     Sequence
DRB1_1101  177  AAGSVPDFALTRASG  DFALTRASG        0.1436      10570.2               50.00     Sequence
DRB1_1101  315  PARFDQKKADALNAE  RFDQKKADA        0.1431      10632.8               50.00     Sequence
DRB1_1101  423  TAPLIEAALKDALIE  LIEAALKDA        0.1430      10636.8               50.00     Sequence
DRB1_1101  303  VAAFDVADVNSSPAR  FDVADVNSS        0.1423      10728.3               50.00     Sequence
DRB1_1101   77  VGGPYGPYRQSQRAE  YGPYRQSQR        0.1421      10741.3               50.00     Sequence
DRB1_1101   32  YARHTGGTFVFRIED  YARHTGGTF        0.1413      10844.9               50.00     Sequence
DRB1_1101  140  DAQRAAYLAEGRQPV  YLAEGRQPV        0.1395      11056.2               50.00     Sequence
DRB1_1101  332  RMLDVGDFTVRLRDH  VGDFTVRLR        0.1391      11102.3               50.00     Sequence
DRB1_1101  417  TSVTDWTAPLIEAAL  VTDWTAPLI        0.1383      11202.5               50.00     Sequence
DRB1_1101  348  DTHGHHIALDEAAFA  HHIALDEAA        0.1371      11348.1               50.00     Sequence
DRB1_1101  188  RASGDPLYTLVNPCD  LYTLVNPCD        0.1366      11401.8               50.00     Sequence
DRB1_1101  184  FALTRASGDPLYTLV  FALTRASGD        0.1346      11656.1               50.00     Sequence
DRB1_1101  101  LAAGEAYHAFSTPEE  YHAFSTPEE        0.1341      11722.9               50.00     Sequence
DRB1_1101  170  VRGPVTFAAGSVPDF  PVTFAAGSV        0.1338      11758.5               50.00     Sequence
DRB1_1101  308  VADVNSSPARFDQKK  VADVNSSPA        0.1320      11992.8               50.00     Sequence
DRB1_1101  313  SSPARFDQKKADALN  RFDQKKADA        0.1315      12047.2               50.00     Sequence
DRB1_1101  428  EAALKDALIEGLALK  DALIEGLAL        0.1314      12067.0               50.00     Sequence
DRB1_1101  320  QKKADALNAEHIRML  ALNAEHIRM        0.1312      12095.4               50.00     Sequence
DRB1_1101  425  PLIEAALKDALIEGL  LIEAALKDA        0.1303      12206.4               50.00     Sequence
DRB1_1101  353  HIALDEAAFAAAAEL  HIALDEAAF        0.1297      12283.7               50.00     Sequence
DRB1_1101  402  GPDGAAVLDAALAAL  AAVLDAALA        0.1285      12444.3               50.00     Sequence
DRB1_1101  174  VTFAAGSVPDFALTR  VTFAAGSVP        0.1280      12522.5               50.00     Sequence
DRB1_1101   64  LRWLGLDWDEGPEVG  LRWLGLDWD        0.1278      12548.8               50.00     Sequence
DRB1_1101  307  DVADVNSSPARFDQK  DVNSSPARF        0.1273      12612.3               50.00     Sequence
DRB1_1101  414  AALTSVTDWTAPLIE  LTSVTDWTA        0.1248      12954.4               50.00     Sequence
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DRB1_1101   40  FVFRIEDTDAQRDSE  VFRIEDTDA        0.1231      13193.3               50.00     Sequence
DRB1_1101   34  RHTGGTFVFRIEDTD  GTFVFRIED        0.1214      13436.6               50.00     Sequence
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DRB1_1101  312  NSSPARFDQKKADAL  RFDQKKADA        0.1188      13824.1               50.00     Sequence
DRB1_1101  289  SIADDHDLFGLDEMV  DLFGLDEMV        0.1180      13952.9               50.00     Sequence
DRB1_1101  159  MPDDDLAWNDLVRGP  LAWNDLVRG        0.1166      14163.4               50.00     Sequence
DRB1_1101  196  TLVNPCDDALMKITH  DDALMKITH        0.1164      14192.9               50.00     Sequence
DRB1_1101  316  ARFDQKKADALNAEH  RFDQKKADA        0.1138      14592.1               50.00     Sequence
DRB1_1101   76  EVGGPYGPYRQSQRA  YGPYRQSQR        0.1130      14728.7               50.00     Sequence
DRB1_1101  347  LDTHGHHIALDEAAF  HHIALDEAA        0.1123      14831.2               50.00     Sequence
DRB1_1101  302  MVAAFDVADVNSSPA  FDVADVNSS        0.1121      14862.9               50.00     Sequence
DRB1_1101   33  ARHTGGTFVFRIEDT  HTGGTFVFR        0.1121      14864.8               50.00     Sequence
DRB1_1101   84  YRQSQRAEIYRDVLA  YRQSQRAEI        0.1102      15179.5               50.00     Sequence
DRB1_1101  427  IEAALKDALIEGLAL  DALIEGLAL        0.1093      15331.1               50.00     Sequence
DRB1_1101   65  RWLGLDWDEGPEVGG  RWLGLDWDE        0.1088      15413.6               50.00     Sequence
DRB1_1101  123  AGRNPKLGYDNFDRH  AGRNPKLGY        0.1082      15499.1               50.00     Sequence
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DRB1_1101  452  VAATGTTVSPPLFES  VAATGTTVS        0.1075      15617.1                 50.00     Sequence
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DRB1_1101  255  KKLSKRDPQSNLFAH  KKLSKRDPQ        0.1057      15928.7                 50.00     Sequence
DRB1_1101  111  STPEEVEARHVAAGR  EVEARHVAA        0.1040      16233.2                 50.00     Sequence
DRB1_1101  311  VNSSPARFDQKKADA  RFDQKKADA        0.1025      16499.0                 50.00     Sequence
DRB1_1101  175  TFAAGSVPDFALTRA  TFAAGSVPD        0.1019      16605.5                 50.00     Sequence
DRB1_1101    9  RFCPSPTGTPHVGLV  FCPSPTGTP        0.1013      16704.8                 50.00     Sequence
DRB1_1101  187  TRASGDPLYTLVNPC  RASGDPLYT        0.1006      16828.4                 50.00     Sequence
DRB1_1101  176  FAAGSVPDFALTRAS  PDFALTRAS        0.0987      17182.6                 50.00     Sequence
DRB1_1101  319  DQKKADALNAEHIRM  ALNAEHIRM        0.0986      17196.5                 50.00     Sequence
DRB1_1101  108  HAFSTPEEVEARHVA  AFSTPEEVE        0.0976      17393.4                 50.00     Sequence
DRB1_1101   41  VFRIEDTDAQRDSEE  VFRIEDTDA        0.0969      17515.5                 50.00     Sequence
DRB1_1101  109  AFSTPEEVEARHVAA  AFSTPEEVE        0.0964      17617.0                 50.00     Sequence
DRB1_1101  284  ALLGWSIADDHDLFG  ALLGWSIAD        0.0954      17803.3                 50.00     Sequence
DRB1_1101  453  AATGTTVSPPLFESL  GTTVSPPLF        0.0952      17847.5                 50.00     Sequence
DRB1_1101   85  RQSQRAEIYRDVLAR  EIYRDVLAR        0.0910      18688.9                 50.00     Sequence
DRB1_1101   49  AQRDSEESYLALLDA  ESYLALLDA        0.0905      18786.7                 50.00     Sequence
DRB1_1101  259  KRDPQSNLFAHRDRG  NLFAHRDRG        0.0899      18911.3                 50.00     Sequence
DRB1_1101  309  ADVNSSPARFDQKKA  ADVNSSPAR        0.0872      19463.9                 50.00     Sequence
DRB1_1101  256  KLSKRDPQSNLFAHR  KLSKRDPQS        0.0870      19498.6                 50.00     Sequence
DRB1_1101  342  RLRDHLDTHGHHIAL  RDHLDTHGH        0.0861      19699.0                 50.00     Sequence
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DRB1_1101  301  EMVAAFDVADVNSSP  FDVADVNSS        0.0835      20256.5                 50.00     Sequence
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DRB1_1101  110  FSTPEEVEARHVAAG  EVEARHVAA        0.0811      20784.6                 50.00     Sequence
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DRB1_1101  298  GLDEMVAAFDVADVN  LDEMVAAFD        0.0791      21253.6                 50.00     Sequence
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DRB1_1101  401  LGPDGAAVLDAALAA  AAVLDAALA        0.0785      21385.3                 50.00     Sequence
DRB1_1101   11  CPSPTGTPHVGLVRT  TPHVGLVRT        0.0754      22121.0                 50.00     Sequence
DRB1_1101   10  FCPSPTGTPHVGLVR  FCPSPTGTP        0.0748      22264.1                 50.00     Sequence
DRB1_1101  285  LLGWSIADDHDLFGL  LGWSIADDH        0.0737      22514.8                 50.00     Sequence
DRB1_1101  257  LSKRDPQSNLFAHRD  RDPQSNLFA        0.0716      23034.0                 50.00     Sequence
DRB1_1101  185  ALTRASGDPLYTLVN  LTRASGDPL        0.0715      23065.1                 50.00     Sequence
DRB1_1101  300  DEMVAAFDVADVNSS  FDVADVNSS        0.0709      23215.6                 50.00     Sequence
DRB1_1101  286  LGWSIADDHDLFGLD  LGWSIADDH        0.0679      23981.5                 50.00     Sequence
DRB1_1101  344  RDHLDTHGHHIALDE  RDHLDTHGH        0.0678      24006.2                 50.00     Sequence
DRB1_1101  343  LRDHLDTHGHHIALD  RDHLDTHGH        0.0669      24231.7                 50.00     Sequence
DRB1_1101  124  GRNPKLGYDNFDRHL  LGYDNFDRH        0.0666      24312.8                 50.00     Sequence
DRB1_1101  345  DHLDTHGHHIALDEA  DTHGHHIAL        0.0644      24917.9                 50.00     Sequence
DRB1_1101  299  LDEMVAAFDVADVNS  LDEMVAAFD        0.0622      25502.4                 50.00     Sequence
DRB1_1101  391  VIDPKAAAKELGPDG  PKAAAKELG        0.0618      25630.8                 50.00     Sequence
DRB1_1101  288  WSIADDHDLFGLDEM  SIADDHDLF        0.0584      26571.4                 50.00     Sequence
DRB1_1101  258  SKRDPQSNLFAHRDR  RDPQSNLFA        0.0569      27021.6                 50.00     Sequence
DRB1_1101  318  FDQKKADALNAEHIR  QKKADALNA        0.0564      27172.3                 50.00     Sequence
DRB1_1101  186  LTRASGDPLYTLVNP  LTRASGDPL        0.0561      27246.8                 50.00     Sequence
DRB1_1101   66  WLGLDWDEGPEVGGP  WLGLDWDEG        0.0530      28185.3                 50.00     Sequence
DRB1_1101   74  GPEVGGPYGPYRQSQ  EVGGPYGPY        0.0523      28400.5                 50.00     Sequence
DRB1_1101   73  EGPEVGGPYGPYRQS  EVGGPYGPY        0.0485      29594.8                 50.00     Sequence
DRB1_1101  400  ELGPDGAAVLDAALA  AAVLDAALA        0.0458      30449.4                 50.00     Sequence
DRB1_1101  392  IDPKAAAKELGPDGA  PKAAAKELG        0.0445      30878.4                 50.00     Sequence
DRB1_1101  287  GWSIADDHDLFGLDE  WSIADDHDL        0.0444      30934.6                 50.00     Sequence
DRB1_1101  394  PKAAAKELGPDGAAV  PKAAAKELG        0.0427      31490.1                 50.00     Sequence
DRB1_1101  393  DPKAAAKELGPDGAA  PKAAAKELG        0.0422      31681.1                 50.00     Sequence
DRB1_1101   71  WDEGPEVGGPYGPYR  WDEGPEVGG        0.0416      31865.4                 50.00     Sequence
DRB1_1101   67  LGLDWDEGPEVGGPY  WDEGPEVGG        0.0416      31887.4                 50.00     Sequence
DRB1_1101   68  GLDWDEGPEVGGPYG  WDEGPEVGG        0.0414      31931.3                 50.00     Sequence
DRB1_1101   69  LDWDEGPEVGGPYGP  WDEGPEVGG        0.0383      33022.3                 50.00     Sequence
DRB1_1101   72  DEGPEVGGPYGPYRQ  EVGGPYGPY        0.0377      33253.2                 50.00     Sequence
DRB1_1101  155  VRLRMPDDDLAWNDL  VRLRMPDDD        0.0375      33332.1                 50.00     Sequence
DRB1_1101  395  KAAAKELGPDGAAVL  KAAAKELGP        0.0372      33441.9                 50.00     Sequence
DRB1_1101   42  FRIEDTDAQRDSEES  FRIEDTDAQ        0.0370      33517.6                 50.00     Sequence
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   DRB1_1101   70  DWDEGPEVGGPYGPY  WDEGPEVGG         0.0353      34130.2                50.00     Sequence
   DRB1_1101  397  AAKELGPDGAAVLDA  KELGPDGAA         0.0328      35069.0                50.00     Sequence
   DRB1_1101  396  AAAKELGPDGAAVLD  AAKELGPDG         0.0316      35538.1                50.00     Sequence
   DRB1_1101   48  DAQRDSEESYLALLD  AQRDSEESY         0.0312      35665.2                50.00     Sequence
   DRB1_1101   43  RIEDTDAQRDSEESY  IEDTDAQRD         0.0296      36290.4                50.00     Sequence
   DRB1_1101   47  TDAQRDSEESYLALL  AQRDSEESY         0.0286      36680.4                50.00     Sequence
   DRB1_1101  399  KELGPDGAAVLDAAL  KELGPDGAA         0.0285      36737.2                50.00     Sequence
   DRB1_1101   46  DTDAQRDSEESYLAL  AQRDSEESY         0.0272      37270.9                50.00     Sequence
   DRB1_1101  398  AKELGPDGAAVLDAA  KELGPDGAA         0.0263      37607.1                50.00     Sequence
   DRB1_1101  156  RLRMPDDDLAWNDLV  RLRMPDDDL         0.0260      37735.5                50.00     Sequence
   DRB1_1101  157  LRMPDDDLAWNDLVR  DLAWNDLVR         0.0251      38110.1                50.00     Sequence
   DRB1_1101   45  EDTDAQRDSEESYLA  AQRDSEESY         0.0248      38216.2                50.00     Sequence
   DRB1_1101   44  IEDTDAQRDSEESYL  IEDTDAQRD         0.0247      38272.5                50.00     Sequence
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Allele: DRB1_1101. Number of high binders 6. Number of weak binders 88. Number of peptides 476

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1302   18  PHVGLVRTALFNWAY  VGLVRTALF         0.5906         83.9          WB     8.00     Sequence
   DRB1_1302  226  ALHQALIRIGVAERI  IRIGVAERI         0.5889         85.5          WB     8.00     Sequence
   DRB1_1302   16  GTPHVGLVRTALFNW  VGLVRTALF         0.5845         89.6          WB     8.00     Sequence
   DRB1_1302   19  HVGLVRTALFNWAYA  VGLVRTALF         0.5817         92.4          WB     8.00     Sequence
   DRB1_1302  367  LVQTRIVVLGDAWEL  LVQTRIVVL         0.5792         95.0          WB     8.00     Sequence
   DRB1_1302   17  TPHVGLVRTALFNWA  VGLVRTALF         0.5759         98.3          WB     8.00     Sequence
   DRB1_1302  361  FAAAAELVQTRIVVL  LVQTRIVVL         0.5710        103.7          WB     8.00     Sequence
   DRB1_1302  445  KAFSPIRVAATGTTV  IRVAATGTT         0.5701        104.8          WB     8.00     Sequence
   DRB1_1302  362  AAAAELVQTRIVVLG  LVQTRIVVL         0.5683        106.8          WB     8.00     Sequence
   DRB1_1302   20  VGLVRTALFNWAYAR  VGLVRTALF         0.5607        116.0          WB     8.00     Sequence
   DRB1_1302   15  TGTPHVGLVRTALFN  VGLVRTALF         0.5606        116.0          WB     8.00     Sequence
   DRB1_1302  446  AFSPIRVAATGTTVS  IRVAATGTT         0.5582        119.1          WB     8.00     Sequence
   DRB1_1302   14  PTGTPHVGLVRTALF  VGLVRTALF         0.5541        124.5          WB     8.00     Sequence
   DRB1_1302  363  AAAELVQTRIVVLGD  LVQTRIVVL         0.5496        130.7          WB     8.00     Sequence
   DRB1_1302  365  AELVQTRIVVLGDAW  LVQTRIVVL         0.5438        139.2          WB     8.00     Sequence
   DRB1_1302  220  STPRQLALHQALIRI  ALHQALIRI         0.5394        145.9          WB     8.00     Sequence
   DRB1_1302  447  FSPIRVAATGTTVSP  RVAATGTTV         0.5390        146.6          WB     8.00     Sequence
   DRB1_1302  227  LHQALIRIGVAERIP  IRIGVAERI         0.5365        150.6          WB     8.00     Sequence
   DRB1_1302  364  AAELVQTRIVVLGDA  LVQTRIVVL         0.5311        159.8          WB    16.00     Sequence
   DRB1_1302  221  TPRQLALHQALIRIG  ALHQALIRI         0.5295        162.5          WB    16.00     Sequence
   DRB1_1302  368  VQTRIVVLGDAWELL  VVLGDAWEL         0.5283        164.6          WB    16.00     Sequence
   DRB1_1302  473  DRSMQRLRAARQLVG  MQRLRAARQ         0.5234        173.5          WB    16.00     Sequence
   DRB1_1302  366  ELVQTRIVVLGDAWE  LVQTRIVVL         0.5234        173.6          WB    16.00     Sequence
   DRB1_1302  228  HQALIRIGVAERIPK  IRIGVAERI         0.5202        179.6          WB    16.00     Sequence
   DRB1_1302  370  TRIVVLGDAWELLKF  VVLGDAWEL         0.5180        183.9          WB    16.00     Sequence
   DRB1_1302  223  RQLALHQALIRIGVA  QLALHQALI         0.5176        184.9          WB    16.00     Sequence
   DRB1_1302  229  QALIRIGVAERIPKF  IRIGVAERI         0.5143        191.4          WB    16.00     Sequence
   DRB1_1302  222  PRQLALHQALIRIGV  ALHQALIRI         0.5135        193.2          WB    16.00     Sequence
   DRB1_1302  472  RDRSMQRLRAARQLV  MQRLRAARQ         0.5110        198.4          WB    16.00     Sequence
   DRB1_1302  369  QTRIVVLGDAWELLK  VVLGDAWEL         0.5109        198.7          WB    16.00     Sequence
   DRB1_1302  474  RSMQRLRAARQLVGH  MQRLRAARQ         0.5095        201.8          WB    16.00     Sequence
   DRB1_1302  371  RIVVLGDAWELLKFF  VVLGDAWEL         0.4976        229.4          WB    16.00     Sequence
   DRB1_1302  448  SPIRVAATGTTVSPP  RVAATGTTV         0.4955        234.7          WB    16.00     Sequence
   DRB1_1302  450  IRVAATGTTVSPPLF  RVAATGTTV         0.4908        247.1          WB    16.00     Sequence
   DRB1_1302  475  SMQRLRAARQLVGHA  MQRLRAARQ         0.4882        254.1          WB    16.00     Sequence
   DRB1_1302  224  QLALHQALIRIGVAE  QLALHQALI         0.4854        261.9          WB    16.00     Sequence
   DRB1_1302  449  PIRVAATGTTVSPPL  RVAATGTTV         0.4802        276.9          WB    16.00     Sequence
   DRB1_1302  444  RKAFSPIRVAATGTT  IRVAATGTT         0.4793        279.7          WB    16.00     Sequence
   DRB1_1302  471  GRDRSMQRLRAARQL  MQRLRAARQ         0.4793        279.7          WB    16.00     Sequence
   DRB1_1302   87  SQRAEIYRDVLARLL  IYRDVLARL         0.4630        333.7          WB    16.00     Sequence
   DRB1_1302  470  LGRDRSMQRLRAARQ  MQRLRAARQ         0.4613        339.8          WB    16.00     Sequence
   DRB1_1302  230  ALIRIGVAERIPKFA  IRIGVAERI         0.4516        377.4          WB    16.00     Sequence
   DRB1_1302  219  PSTPRQLALHQALIR  QLALHQALI         0.4441        409.4          WB    32.00     Sequence
   DRB1_1302   88  QRAEIYRDVLARLLA  IYRDVLARL         0.4417        420.2          WB    32.00     Sequence
   DRB1_1302   86  QSQRAEIYRDVLARL  IYRDVLARL         0.4389        433.1          WB    32.00     Sequence
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DRB1_1302   89  RAEIYRDVLARLLAA  IYRDVLARL        0.4377       439.0          WB    32.00     Sequence
DRB1_1302  225  LALHQALIRIGVAER  ALHQALIRI        0.4275       490.0          WB    32.00     Sequence
DRB1_1302  231  LIRIGVAERIPKFAH  IRIGVAERI        0.4261       497.6          WB    32.00     Sequence
DRB1_1302  116  VEARHVAAGRNPKLG  VAAGRNPKL        0.4254       501.1                32.00     Sequence
DRB1_1302  115  EVEARHVAAGRNPKL  VAAGRNPKL        0.4251       502.8                32.00     Sequence
DRB1_1302   53  SEESYLALLDALRWL  LALLDALRW        0.4183       541.5                32.00     Sequence
DRB1_1302  117  EARHVAAGRNPKLGY  VAAGRNPKL        0.4178       544.1                32.00     Sequence
DRB1_1302  218  LPSTPRQLALHQALI  QLALHQALI        0.4147       562.9                32.00     Sequence
DRB1_1302  451  RVAATGTTVSPPLFE  RVAATGTTV        0.4136       569.4                32.00     Sequence
DRB1_1302   54  EESYLALLDALRWLG  LALLDALRW        0.4107       587.7                32.00     Sequence
DRB1_1302  403  PDGAAVLDAALAALT  VLDAALAAL        0.4091       597.7                32.00     Sequence
DRB1_1302  200  PCDDALMKITHVLRG  ALMKITHVL        0.4086       601.1                32.00     Sequence
DRB1_1302   55  ESYLALLDALRWLGL  LALLDALRW        0.4072       610.1                32.00     Sequence
DRB1_1302  118  ARHVAAGRNPKLGYD  VAAGRNPKL        0.4067       613.6                32.00     Sequence
DRB1_1302  232  IRIGVAERIPKFAHL  IRIGVAERI        0.4021       644.8                32.00     Sequence
DRB1_1302  405  GAAVLDAALAALTSV  VLDAALAAL        0.3999       660.5                32.00     Sequence
DRB1_1302   91  EIYRDVLARLLAAGE  IYRDVLARL        0.3991       666.0                32.00     Sequence
DRB1_1302    0  VTATETVRVRFCPSP  VTATETVRV        0.3984       670.9                32.00     Sequence
DRB1_1302  272  RGFIPEGLLNYLALL  GLLNYLALL        0.3982       672.5                32.00     Sequence
DRB1_1302  404  DGAAVLDAALAALTS  VLDAALAAL        0.3945       700.2                32.00     Sequence
DRB1_1302   90  AEIYRDVLARLLAAG  IYRDVLARL        0.3940       704.1                32.00     Sequence
DRB1_1302  395  KAAAKELGPDGAAVL  LGPDGAAVL        0.3868       761.2                32.00     Sequence
DRB1_1302   92  IYRDVLARLLAAGEA  IYRDVLARL        0.3866       763.0                32.00     Sequence
DRB1_1302   56  SYLALLDALRWLGLD  LALLDALRW        0.3856       771.2                32.00     Sequence
DRB1_1302  396  AAAKELGPDGAAVLD  LGPDGAAVL        0.3852       774.5                32.00     Sequence
DRB1_1302  146  YLAEGRQPVVRLRMP  LAEGRQPVV        0.3844       780.6                32.00     Sequence
DRB1_1302  274  FIPEGLLNYLALLGW  GLLNYLALL        0.3842       782.3                32.00     Sequence
DRB1_1302  201  CDDALMKITHVLRGE  DALMKITHV        0.3829       794.0                32.00     Sequence
DRB1_1302  119  RHVAAGRNPKLGYDN  VAAGRNPKL        0.3822       800.0                32.00     Sequence
DRB1_1302   30  WAYARHTGGTFVFRI  ARHTGGTFV        0.3768       848.2                32.00     Sequence
DRB1_1302  273  GFIPEGLLNYLALLG  GLLNYLALL        0.3766       850.0                32.00     Sequence
DRB1_1302  402  GPDGAAVLDAALAAL  VLDAALAAL        0.3765       851.1                32.00     Sequence
DRB1_1302   28  FNWAYARHTGGTFVF  ARHTGGTFV        0.3752       862.9                32.00     Sequence
DRB1_1302   52  DSEESYLALLDALRW  LALLDALRW        0.3748       866.3                32.00     Sequence
DRB1_1302  397  AAKELGPDGAAVLDA  LGPDGAAVL        0.3748       866.5                32.00     Sequence
DRB1_1302   29  NWAYARHTGGTFVFR  ARHTGGTFV        0.3739       874.7                32.00     Sequence
DRB1_1302  120  HVAAGRNPKLGYDNF  VAAGRNPKL        0.3711       902.1                32.00     Sequence
DRB1_1302  199  NPCDDALMKITHVLR  DALMKITHV        0.3700       912.6                32.00     Sequence
DRB1_1302  372  IVVLGDAWELLKFFN  VVLGDAWEL        0.3682       930.8                32.00     Sequence
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DRB1_1302   57  YLALLDALRWLGLDW  LALLDALRW        0.3647       966.3                32.00     Sequence
DRB1_1302  202  DDALMKITHVLRGED  DALMKITHV        0.3645       968.4                32.00     Sequence
DRB1_1302  406  AAVLDAALAALTSVT  VLDAALAAL        0.3638       976.0                32.00     Sequence
DRB1_1302  275  IPEGLLNYLALLGWS  GLLNYLALL        0.3611      1005.6                32.00     Sequence
DRB1_1302  203  DALMKITHVLRGEDL  ALMKITHVL        0.3608      1008.7                32.00     Sequence
DRB1_1302  360  AFAAAAELVQTRIVV  AAELVQTRI        0.3604      1012.2                32.00     Sequence
DRB1_1302  400  ELGPDGAAVLDAALA  LGPDGAAVL        0.3597      1019.9                32.00     Sequence
DRB1_1302  304  AAFDVADVNSSPARF  VADVNSSPA        0.3590      1028.4                32.00     Sequence
DRB1_1302  398  AKELGPDGAAVLDAA  LGPDGAAVL        0.3584      1035.3                32.00     Sequence
DRB1_1302  399  KELGPDGAAVLDAAL  LGPDGAAVL        0.3583      1035.6                32.00     Sequence
DRB1_1302  276  PEGLLNYLALLGWSI  GLLNYLALL        0.3577      1042.4                32.00     Sequence
DRB1_1302  182  PDFALTRASGDPLYT  LTRASGDPL        0.3533      1093.6                32.00     Sequence
DRB1_1302  325  ALNAEHIRMLDVGDF  IRMLDVGDF        0.3529      1098.1                32.00     Sequence
DRB1_1302  183  DFALTRASGDPLYTL  LTRASGDPL        0.3522      1106.1                32.00     Sequence
DRB1_1302  407  AVLDAALAALTSVTD  VLDAALAAL        0.3507      1124.8                32.00     Sequence
DRB1_1302  145  AYLAEGRQPVVRLRM  LAEGRQPVV        0.3504      1129.0                32.00     Sequence
DRB1_1302  181  VPDFALTRASGDPLY  LTRASGDPL        0.3496      1138.7                32.00     Sequence
DRB1_1302  121  VAAGRNPKLGYDNFD  VAAGRNPKL        0.3474      1165.4                32.00     Sequence
DRB1_1302  198  VNPCDDALMKITHVL  DALMKITHV        0.3474      1165.8                32.00     Sequence
DRB1_1302  305  AFDVADVNSSPARFD  VADVNSSPA        0.3474      1165.8                32.00     Sequence
DRB1_1302   32  YARHTGGTFVFRIED  ARHTGGTFV        0.3471      1169.7                32.00     Sequence
DRB1_1302  147  LAEGRQPVVRLRMPD  RQPVVRLRM        0.3446      1200.9                32.00     Sequence
DRB1_1302   95  DVLARLLAAGEAYHA  RLLAAGEAY        0.3446      1202.0                32.00     Sequence
DRB1_1302  184  FALTRASGDPLYTLV  LTRASGDPL        0.3438      1211.8                32.00     Sequence
DRB1_1302  326  LNAEHIRMLDVGDFT  IRMLDVGDF        0.3421      1234.9                32.00     Sequence
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DRB1_1302  430  ALKDALIEGLALKPR  LIEGLALKP        0.3414       1243.9              32.00     Sequence
DRB1_1302   58  LALLDALRWLGLDWD  LALLDALRW        0.3407       1253.5              32.00     Sequence
DRB1_1302  322  KADALNAEHIRMLDV  AEHIRMLDV        0.3405       1255.8              32.00     Sequence
DRB1_1302  401  LGPDGAAVLDAALAA  LGPDGAAVL        0.3372       1301.7              32.00     Sequence
DRB1_1302  429  AALKDALIEGLALKP  DALIEGLAL        0.3370       1304.3              32.00     Sequence
DRB1_1302  329  EHIRMLDVGDFTVRL  IRMLDVGDF        0.3354       1327.0              32.00     Sequence
DRB1_1302  306  FDVADVNSSPARFDQ  VADVNSSPA        0.3349       1334.3              32.00     Sequence
DRB1_1302  185  ALTRASGDPLYTLVN  LTRASGDPL        0.3345       1340.1              32.00     Sequence
DRB1_1302   96  VLARLLAAGEAYHAF  RLLAAGEAY        0.3325       1368.8              32.00     Sequence
DRB1_1302  278  GLLNYLALLGWSIAD  GLLNYLALL        0.3291       1420.5              50.00     Sequence
DRB1_1302  180  SVPDFALTRASGDPL  LTRASGDPL        0.3279       1439.0              50.00     Sequence
DRB1_1302  433  DALIEGLALKPRKAF  LIEGLALKP        0.3247       1489.9              50.00     Sequence
DRB1_1302  330  HIRMLDVGDFTVRLR  DVGDFTVRL        0.3232       1514.7              50.00     Sequence
DRB1_1302  359  AAFAAAAELVQTRIV  AAELVQTRI        0.3230       1517.7              50.00     Sequence
DRB1_1302  320  QKKADALNAEHIRML  LNAEHIRML        0.3230       1518.3              50.00     Sequence
DRB1_1302  431  LKDALIEGLALKPRK  LIEGLALKP        0.3226       1524.2              50.00     Sequence
DRB1_1302  323  ADALNAEHIRMLDVG  AEHIRMLDV        0.3225       1526.3              50.00     Sequence
DRB1_1302   93  YRDVLARLLAAGEAY  RLLAAGEAY        0.3215       1542.2              50.00     Sequence
DRB1_1302  307  DVADVNSSPARFDQK  VADVNSSPA        0.3210       1550.4              50.00     Sequence
DRB1_1302   97  LARLLAAGEAYHAFS  RLLAAGEAY        0.3201       1565.9              50.00     Sequence
DRB1_1302   27  LFNWAYARHTGGTFV  ARHTGGTFV        0.3201       1566.9              50.00     Sequence
DRB1_1302  432  KDALIEGLALKPRKA  LIEGLALKP        0.3181       1599.8              50.00     Sequence
DRB1_1302  327  NAEHIRMLDVGDFTV  IRMLDVGDF        0.3149       1656.2              50.00     Sequence
DRB1_1302  408  VLDAALAALTSVTDW  VLDAALAAL        0.3149       1657.1              50.00     Sequence
DRB1_1302  373  VVLGDAWELLKFFND  VVLGDAWEL        0.3117       1715.6              50.00     Sequence
DRB1_1302  308  VADVNSSPARFDQKK  VADVNSSPA        0.3105       1737.0              50.00     Sequence
DRB1_1302   33  ARHTGGTFVFRIEDT  ARHTGGTFV        0.3102       1742.8              50.00     Sequence
DRB1_1302   94  RDVLARLLAAGEAYH  RLLAAGEAY        0.3073       1798.9              50.00     Sequence
DRB1_1302  204  ALMKITHVLRGEDLL  ALMKITHVL        0.3062       1820.4              50.00     Sequence
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DRB1_1302  328  AEHIRMLDVGDFTVR  IRMLDVGDF        0.3041       1862.6              50.00     Sequence
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DRB1_1302  331  IRMLDVGDFTVRLRD  DVGDFTVRL        0.2979       1991.5              50.00     Sequence
DRB1_1302  321  KKADALNAEHIRMLD  LNAEHIRML        0.2958       2037.8              50.00     Sequence
DRB1_1302  144  AAYLAEGRQPVVRLR  LAEGRQPVV        0.2954       2046.5              50.00     Sequence
DRB1_1302  324  DALNAEHIRMLDVGD  AEHIRMLDV        0.2947       2060.6              50.00     Sequence
DRB1_1302  303  VAAFDVADVNSSPAR  VADVNSSPA        0.2890       2193.3              50.00     Sequence
DRB1_1302   22  LVRTALFNWAYARHT  RTALFNWAY        0.2888       2197.1              50.00     Sequence
DRB1_1302  385  FNDDQYVIDPKAAAK  VIDPKAAAK        0.2863       2258.0              50.00     Sequence
DRB1_1302  443  PRKAFSPIRVAATGT  RKAFSPIRV        0.2854       2278.9              50.00     Sequence
DRB1_1302  211  VLRGEDLLPSTPRQL  LLPSTPRQL        0.2843       2306.7              50.00     Sequence
DRB1_1302  386  NDDQYVIDPKAAAKE  YVIDPKAAA        0.2817       2372.2              50.00     Sequence
DRB1_1302  255  KKLSKRDPQSNLFAH  KRDPQSNLF        0.2799       2419.5              50.00     Sequence
DRB1_1302   99  RLLAAGEAYHAFSTP  RLLAAGEAY        0.2790       2444.3              50.00     Sequence
DRB1_1302  257  LSKRDPQSNLFAHRD  KRDPQSNLF        0.2782       2464.2              50.00     Sequence
DRB1_1302  197  LVNPCDDALMKITHV  DALMKITHV        0.2777       2477.9              50.00     Sequence
DRB1_1302  302  MVAAFDVADVNSSPA  VADVNSSPA        0.2772       2492.6              50.00     Sequence
DRB1_1302  256  KLSKRDPQSNLFAHR  KRDPQSNLF        0.2743       2571.8              50.00     Sequence
DRB1_1302  358  EAAFAAAAELVQTRI  AAELVQTRI        0.2722       2631.0              50.00     Sequence
DRB1_1302  212  LRGEDLLPSTPRQLA  LLPSTPRQL        0.2711       2660.7              50.00     Sequence
DRB1_1302  213  RGEDLLPSTPRQLAL  LLPSTPRQL        0.2709       2666.9              50.00     Sequence
DRB1_1302  148  AEGRQPVVRLRMPDD  RQPVVRLRM        0.2701       2689.6              50.00     Sequence
DRB1_1302  217  LLPSTPRQLALHQAL  LLPSTPRQL        0.2696       2705.4              50.00     Sequence
DRB1_1302  237  AERIPKFAHLPTVLG  FAHLPTVLG        0.2695       2706.9              50.00     Sequence
DRB1_1302  141  AQRAAYLAEGRQPVV  LAEGRQPVV        0.2689       2723.9              50.00     Sequence
DRB1_1302  238  ERIPKFAHLPTVLGE  FAHLPTVLG        0.2678       2759.1              50.00     Sequence
DRB1_1302   84  YRQSQRAEIYRDVLA  RAEIYRDVL        0.2676       2763.2              50.00     Sequence
DRB1_1302  441  LKPRKAFSPIRVAAT  RKAFSPIRV        0.2672       2775.8              50.00     Sequence
DRB1_1302  258  SKRDPQSNLFAHRDR  KRDPQSNLF        0.2671       2779.0              50.00     Sequence
DRB1_1302  387  DDQYVIDPKAAAKEL  YVIDPKAAA        0.2662       2806.4              50.00     Sequence
DRB1_1302  167  NDLVRGPVTFAAGSV  LVRGPVTFA        0.2650       2842.6              50.00     Sequence
DRB1_1302  142  QRAAYLAEGRQPVVR  LAEGRQPVV        0.2617       2944.8              50.00     Sequence
DRB1_1302   79  GPYGPYRQSQRAEIY  RQSQRAEIY        0.2617       2946.6              50.00     Sequence
DRB1_1302  468  ELLGRDRSMQRLRAA  LGRDRSMQR        0.2610       2969.9              50.00     Sequence
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DRB1_1302  434  ALIEGLALKPRKAFS  LIEGLALKP        0.2608       2974.1                 50.00     Sequence
DRB1_1302  168  DLVRGPVTFAAGSVP  LVRGPVTFA        0.2607       2979.3                 50.00     Sequence
DRB1_1302   23  VRTALFNWAYARHTG  RTALFNWAY        0.2585       3051.5                 50.00     Sequence
DRB1_1302  214  GEDLLPSTPRQLALH  LLPSTPRQL        0.2576       3078.3                 50.00     Sequence
DRB1_1302  134  FDRHLTDAQRAAYLA  LTDAQRAAY        0.2571       3097.6                 50.00     Sequence
DRB1_1302  442  KPRKAFSPIRVAATG  RKAFSPIRV        0.2555       3149.2                 50.00     Sequence
DRB1_1302  465  ESLELLGRDRSMQRL  LGRDRSMQR        0.2541       3198.5                 50.00     Sequence
DRB1_1302  354  IALDEAAFAAAAELV  AAFAAAAEL        0.2527       3247.6                 50.00     Sequence
DRB1_1302   83  PYRQSQRAEIYRDVL  RAEIYRDVL        0.2523       3260.2                 50.00     Sequence
DRB1_1302  254  TKKLSKRDPQSNLFA  KRDPQSNLF        0.2522       3263.7                 50.00     Sequence
DRB1_1302   80  PYGPYRQSQRAEIYR  RQSQRAEIY        0.2520       3271.3                 50.00     Sequence
DRB1_1302  133  NFDRHLTDAQRAAYL  LTDAQRAAY        0.2518       3278.9                 50.00     Sequence
DRB1_1302  388  DQYVIDPKAAAKELG  YVIDPKAAA        0.2505       3324.3                 50.00     Sequence
DRB1_1302  253  GTKKLSKRDPQSNLF  KRDPQSNLF        0.2502       3336.6                 50.00     Sequence
DRB1_1302  435  LIEGLALKPRKAFSP  LIEGLALKP        0.2497       3353.3                 50.00     Sequence
DRB1_1302  469  LLGRDRSMQRLRAAR  LGRDRSMQR        0.2484       3402.9                 50.00     Sequence
DRB1_1302  412  ALAALTSVTDWTAPL  SVTDWTAPL        0.2481       3412.7                 50.00     Sequence
DRB1_1302  215  EDLLPSTPRQLALHQ  LLPSTPRQL        0.2478       3425.8                 50.00     Sequence
DRB1_1302  149  EGRQPVVRLRMPDDD  RQPVVRLRM        0.2474       3439.3                 50.00     Sequence
DRB1_1302  163  DLAWNDLVRGPVTFA  LVRGPVTFA        0.2473       3442.5                 50.00     Sequence
DRB1_1302  112  TPEEVEARHVAAGRN  ARHVAAGRN        0.2461       3488.8                 50.00     Sequence
DRB1_1302  135  DRHLTDAQRAAYLAE  LTDAQRAAY        0.2436       3582.0                 50.00     Sequence
DRB1_1302  466  SLELLGRDRSMQRLR  LGRDRSMQR        0.2434       3593.0                 50.00     Sequence
DRB1_1302  239  RIPKFAHLPTVLGEG  KFAHLPTVL        0.2425       3627.5                 50.00     Sequence
DRB1_1302  271  DRGFIPEGLLNYLAL  EGLLNYLAL        0.2418       3655.9                 50.00     Sequence
DRB1_1302   81  YGPYRQSQRAEIYRD  RQSQRAEIY        0.2415       3664.6                 50.00     Sequence
DRB1_1302  205  LMKITHVLRGEDLLP  MKITHVLRG        0.2401       3721.8                 50.00     Sequence
DRB1_1302  164  LAWNDLVRGPVTFAA  LVRGPVTFA        0.2386       3782.0                 50.00     Sequence
DRB1_1302  438  GLALKPRKAFSPIRV  RKAFSPIRV        0.2382       3800.7                 50.00     Sequence
DRB1_1302  353  HIALDEAAFAAAAEL  AAFAAAAEL        0.2380       3808.2                 50.00     Sequence
DRB1_1302  259  KRDPQSNLFAHRDRG  KRDPQSNLF        0.2378       3815.3                 50.00     Sequence
DRB1_1302  136  RHLTDAQRAAYLAEG  TDAQRAAYL        0.2377       3820.2                 50.00     Sequence
DRB1_1302  282  YLALLGWSIADDHDL  WSIADDHDL        0.2374       3830.2                 50.00     Sequence
DRB1_1302  428  EAALKDALIEGLALK  DALIEGLAL        0.2355       3912.7                 50.00     Sequence
DRB1_1302  216  DLLPSTPRQLALHQA  LLPSTPRQL        0.2351       3929.1                 50.00     Sequence
DRB1_1302  389  QYVIDPKAAAKELGP  YVIDPKAAA        0.2348       3942.0                 50.00     Sequence
DRB1_1302  342  RLRDHLDTHGHHIAL  DTHGHHIAL        0.2347       3947.6                 50.00     Sequence
DRB1_1302  332  RMLDVGDFTVRLRDH  DVGDFTVRL        0.2329       4021.3                 50.00     Sequence
DRB1_1302  113  PEEVEARHVAAGRNP  ARHVAAGRN        0.2328       4027.0                 50.00     Sequence
DRB1_1302  244  AHLPTVLGEGTKKLS  VLGEGTKKL        0.2326       4035.7                 50.00     Sequence
DRB1_1302  467  LELLGRDRSMQRLRA  LGRDRSMQR        0.2323       4051.5                 50.00     Sequence
DRB1_1302   24  RTALFNWAYARHTGG  RTALFNWAY        0.2312       4099.4                 50.00     Sequence
DRB1_1302  413  LAALTSVTDWTAPLI  SVTDWTAPL        0.2310       4105.1                 50.00     Sequence
DRB1_1302  165  AWNDLVRGPVTFAAG  LVRGPVTFA        0.2309       4109.2                 50.00     Sequence
DRB1_1302   85  RQSQRAEIYRDVLAR  RAEIYRDVL        0.2282       4235.2                 50.00     Sequence
DRB1_1302  243  FAHLPTVLGEGTKKL  VLGEGTKKL        0.2279       4245.5                 50.00     Sequence
DRB1_1302  169  LVRGPVTFAAGSVPD  LVRGPVTFA        0.2278       4251.3                 50.00     Sequence
DRB1_1302  240  IPKFAHLPTVLGEGT  KFAHLPTVL        0.2256       4354.1                 50.00     Sequence
DRB1_1302  384  FFNDDQYVIDPKAAA  QYVIDPKAA        0.2256       4355.4                 50.00     Sequence
DRB1_1302   82  GPYRQSQRAEIYRDV  RQSQRAEIY        0.2256       4356.0                 50.00     Sequence
DRB1_1302  100  LLAAGEAYHAFSTPE  LAAGEAYHA        0.2248       4389.5                 50.00     Sequence
DRB1_1302  132  DNFDRHLTDAQRAAY  LTDAQRAAY        0.2238       4437.4                 50.00     Sequence
DRB1_1302  343  LRDHLDTHGHHIALD  DTHGHHIAL        0.2236       4449.4                 50.00     Sequence
DRB1_1302  319  DQKKADALNAEHIRM  ALNAEHIRM        0.2227       4494.4                 50.00     Sequence
DRB1_1302  279  LLNYLALLGWSIADD  YLALLGWSI        0.2224       4506.0                 50.00     Sequence
DRB1_1302  355  ALDEAAFAAAAELVQ  AAFAAAAEL        0.2213       4561.7                 50.00     Sequence
DRB1_1302  439  LALKPRKAFSPIRVA  RKAFSPIRV        0.2206       4594.0                 50.00     Sequence
DRB1_1302  464  FESLELLGRDRSMQR  LGRDRSMQR        0.2203       4611.6                 50.00     Sequence
DRB1_1302  348  DTHGHHIALDEAAFA  IALDEAAFA        0.2198       4636.3                 50.00     Sequence
DRB1_1302  427  IEAALKDALIEGLAL  DALIEGLAL        0.2197       4643.3                 50.00     Sequence
DRB1_1302  166  WNDLVRGPVTFAAGS  LVRGPVTFA        0.2187       4693.4                 50.00     Sequence
DRB1_1302  422  WTAPLIEAALKDALI  EAALKDALI        0.2182       4718.6                 50.00     Sequence
DRB1_1302  150  GRQPVVRLRMPDDDL  RQPVVRLRM        0.2179       4730.2                 50.00     Sequence
DRB1_1302  344  RDHLDTHGHHIALDE  DTHGHHIAL        0.2175       4755.0                 50.00     Sequence
DRB1_1302  417  TSVTDWTAPLIEAAL  SVTDWTAPL        0.2160       4829.8                 50.00     Sequence
DRB1_1302  245  HLPTVLGEGTKKLSK  VLGEGTKKL        0.2159       4833.9                 50.00     Sequence
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DRB1_1302  101  LAAGEAYHAFSTPEE  LAAGEAYHA      0.2144     4913.6          50.00   Sequence
DRB1_1302  261  DPQSNLFAHRDRGFI  FAHRDRGFI      0.2143     4918.9          50.00   Sequence
DRB1_1302  345  DHLDTHGHHIALDEA  DTHGHHIAL      0.2131     4983.6          50.00   Sequence
DRB1_1302  280  LNYLALLGWSIADDH  YLALLGWSI      0.2129     4995.0          50.00   Sequence
DRB1_1302  151  RQPVVRLRMPDDDLA  RQPVVRLRM      0.2122     5032.2          50.00   Sequence
DRB1_1302  333  MLDVGDFTVRLRDHL  DVGDFTVRL      0.2112     5089.7          50.00   Sequence
DRB1_1302  418  SVTDWTAPLIEAALK  SVTDWTAPL      0.2104     5129.5          50.00   Sequence
DRB1_1302  236  VAERIPKFAHLPTVL  KFAHLPTVL      0.2102     5142.9          50.00   Sequence
DRB1_1302  114  EEVEARHVAAGRNPK  ARHVAAGRN      0.2098     5166.9          50.00   Sequence
DRB1_1302  453  AATGTTVSPPLFESL  GTTVSPPLF      0.2094     5186.9          50.00   Sequence
DRB1_1302  414  AALTSVTDWTAPLIE  SVTDWTAPL      0.2090     5210.2          50.00   Sequence
DRB1_1302  350  HGHHIALDEAAFAAA  IALDEAAFA      0.2086     5231.8          50.00   Sequence
DRB1_1302  246  LPTVLGEGTKKLSKR  VLGEGTKKL      0.2071     5320.6          50.00   Sequence
DRB1_1302   78  GGPYGPYRQSQRAEI  YRQSQRAEI      0.2063     5364.5          50.00   Sequence
DRB1_1302  317  RFDQKKADALNAEHI  ADALNAEHI      0.2055     5409.7          50.00   Sequence
DRB1_1302  341  VRLRDHLDTHGHHIA  HLDTHGHHI      0.2046     5461.8          50.00   Sequence
DRB1_1302  241  PKFAHLPTVLGEGTK  KFAHLPTVL      0.2044     5476.3          50.00   Sequence
DRB1_1302  349  THGHHIALDEAAFAA  IALDEAAFA      0.2044     5477.9          50.00   Sequence
DRB1_1302  356  LDEAAFAAAAELVQT  AAFAAAAEL      0.2024     5594.0          50.00   Sequence
DRB1_1302  346  HLDTHGHHIALDEAA  DTHGHHIAL      0.2022     5609.4          50.00   Sequence
DRB1_1302  269  HRDRGFIPEGLLNYL  IPEGLLNYL      0.2021     5615.8          50.00   Sequence
DRB1_1302  452  VAATGTTVSPPLFES  GTTVSPPLF      0.2017     5638.2          50.00   Sequence
DRB1_1302  137  HLTDAQRAAYLAEGR  TDAQRAAYL      0.2005     5711.6          50.00   Sequence
DRB1_1302  423  TAPLIEAALKDALIE  EAALKDALI      0.1998     5756.9          50.00   Sequence
DRB1_1302  206  MKITHVLRGEDLLPS  MKITHVLRG      0.1981     5865.6          50.00   Sequence
DRB1_1302  315  PARFDQKKADALNAE  QKKADALNA      0.1975     5903.8          50.00   Sequence
DRB1_1302  415  ALTSVTDWTAPLIEA  SVTDWTAPL      0.1965     5965.6          50.00   Sequence
DRB1_1302  440  ALKPRKAFSPIRVAA  RKAFSPIRV      0.1964     5972.9          50.00   Sequence
DRB1_1302  309  ADVNSSPARFDQKKA  DVNSSPARF      0.1959     6003.9          50.00   Sequence
DRB1_1302  270  RDRGFIPEGLLNYLA  IPEGLLNYL      0.1958     6008.2          50.00   Sequence
DRB1_1302  233  RIGVAERIPKFAHLP  ERIPKFAHL      0.1956     6022.5          50.00   Sequence
DRB1_1302  351  GHHIALDEAAFAAAA  IALDEAAFA      0.1940     6126.9          50.00   Sequence
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DRB1_1302  357  DEAAFAAAAELVQTR  AAFAAAAEL      0.1929     6200.7          50.00   Sequence
DRB1_1302  316  ARFDQKKADALNAEH  QKKADALNA      0.1923     6245.7          50.00   Sequence
DRB1_1302  409  LDAALAALTSVTDWT  AALAALTSV      0.1911     6322.2          50.00   Sequence
DRB1_1302  283  LALLGWSIADDHDLF  WSIADDHDL      0.1907     6354.8          50.00   Sequence
DRB1_1302   26  ALFNWAYARHTGGTF  YARHTGGTF      0.1880     6537.7          50.00   Sequence
DRB1_1302  383  KFFNDDQYVIDPKAA  QYVIDPKAA      0.1875     6572.3          50.00   Sequence
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DRB1_1302  454  ATGTTVSPPLFESLE  GTTVSPPLF      0.1873     6588.7          50.00   Sequence
DRB1_1302  352  HHIALDEAAFAAAAE  IALDEAAFA      0.1866     6639.6          50.00   Sequence
DRB1_1302  247  PTVLGEGTKKLSKRD  VLGEGTKKL      0.1865     6649.1          50.00   Sequence
DRB1_1302  455  TGTTVSPPLFESLEL  GTTVSPPLF      0.1853     6731.3          50.00   Sequence
DRB1_1302  234  IGVAERIPKFAHLPT  ERIPKFAHL      0.1853     6731.9          50.00   Sequence
DRB1_1302  138  LTDAQRAAYLAEGRQ  LTDAQRAAY      0.1849     6760.2          50.00   Sequence
DRB1_1302  170  VRGPVTFAAGSVPDF  PVTFAAGSV      0.1839     6837.4          50.00   Sequence
DRB1_1302  262  PQSNLFAHRDRGFIP  FAHRDRGFI      0.1837     6852.6          50.00   Sequence
DRB1_1302  318  FDQKKADALNAEHIR  QKKADALNA      0.1825     6939.2          50.00   Sequence
DRB1_1302  416  LTSVTDWTAPLIEAA  SVTDWTAPL      0.1811     7046.9          50.00   Sequence
DRB1_1302  421  DWTAPLIEAALKDAL  IEAALKDAL      0.1806     7084.9          50.00   Sequence
DRB1_1302  425  PLIEAALKDALIEGL  EAALKDALI      0.1798     7150.2          50.00   Sequence
DRB1_1302  111  STPEEVEARHVAAGR  EVEARHVAA      0.1786     7238.3          50.00   Sequence
DRB1_1302  110  FSTPEEVEARHVAAG  EVEARHVAA      0.1778     7304.0          50.00   Sequence
DRB1_1302  249  VLGEGTKKLSKRDPQ  VLGEGTKKL      0.1766     7401.3          50.00   Sequence
DRB1_1302  310  DVNSSPARFDQKKAD  DVNSSPARF      0.1762     7431.8          50.00   Sequence
DRB1_1302  248  TVLGEGTKKLSKRDP  VLGEGTKKL      0.1761     7440.9          50.00   Sequence
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DRB1_1302  424  APLIEAALKDALIEG  IEAALKDAL      0.1737     7630.7          50.00   Sequence
DRB1_1302  410  DAALAALTSVTDWTA  AALAALTSV      0.1714     7825.9          50.00   Sequence
DRB1_1302  335  DVGDFTVRLRDHLDT  DVGDFTVRL      0.1710     7860.3          50.00   Sequence
DRB1_1302  437  EGLALKPRKAFSPIR  LALKPRKAF      0.1708     7877.8          50.00   Sequence
DRB1_1302  436  IEGLALKPRKAFSPI  LALKPRKAF      0.1700     7944.0          50.00   Sequence
DRB1_1302  294  HDLFGLDEMVAAFDV  GLDEMVAAF      0.1698     7959.8          50.00   Sequence
DRB1_1302  456  GTTVSPPLFESLELL  GTTVSPPLF      0.1691     8024.4          50.00   Sequence
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DRB1_1302  293  DHDLFGLDEMVAAFD  GLDEMVAAF        0.1681       8111.0              50.00     Sequence
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DRB1_1302  314  SPARFDQKKADALNA  QKKADALNA        0.1672       8190.8              50.00     Sequence
DRB1_1302  284  ALLGWSIADDHDLFG  WSIADDHDL        0.1669       8218.7              50.00     Sequence
DRB1_1302  426  LIEAALKDALIEGLA  EAALKDALI        0.1664       8259.6              50.00     Sequence
DRB1_1302  102  AAGEAYHAFSTPEEV  AYHAFSTPE        0.1656       8332.3              50.00     Sequence
DRB1_1302   34  RHTGGTFVFRIEDTD  RHTGGTFVF        0.1645       8435.3              50.00     Sequence
DRB1_1302  235  GVAERIPKFAHLPTV  ERIPKFAHL        0.1644       8442.2              50.00     Sequence
DRB1_1302  266  LFAHRDRGFIPEGLL  RGFIPEGLL        0.1634       8533.4              50.00     Sequence
DRB1_1302  260  RDPQSNLFAHRDRGF  LFAHRDRGF        0.1630       8566.6              50.00     Sequence
DRB1_1302  171  RGPVTFAAGSVPDFA  PVTFAAGSV        0.1626       8607.3              50.00     Sequence
DRB1_1302    9  RFCPSPTGTPHVGLV  TGTPHVGLV        0.1611       8745.6              50.00     Sequence
DRB1_1302  378  AWELLKFFNDDQYVI  FFNDDQYVI        0.1609       8763.7              50.00     Sequence
DRB1_1302  292  DDHDLFGLDEMVAAF  GLDEMVAAF        0.1609       8765.7              50.00     Sequence
DRB1_1302  411  AALAALTSVTDWTAP  AALAALTSV        0.1605       8803.8              50.00     Sequence
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DRB1_1302  340  TVRLRDHLDTHGHHI  HLDTHGHHI        0.1592       8931.9              50.00     Sequence
DRB1_1302   11  CPSPTGTPHVGLVRT  TGTPHVGLV        0.1580       9052.0              50.00     Sequence
DRB1_1302  295  DLFGLDEMVAAFDVA  GLDEMVAAF        0.1549       9354.9              50.00     Sequence
DRB1_1302  172  GPVTFAAGSVPDFAL  PVTFAAGSV        0.1547       9381.3              50.00     Sequence
DRB1_1302  296  LFGLDEMVAAFDVAD  GLDEMVAAF        0.1545       9398.3              50.00     Sequence
DRB1_1302  297  FGLDEMVAAFDVADV  GLDEMVAAF        0.1534       9512.1              50.00     Sequence
DRB1_1302  379  WELLKFFNDDQYVID  FFNDDQYVI        0.1513       9724.9              50.00     Sequence
DRB1_1302  285  LLGWSIADDHDLFGL  WSIADDHDL        0.1504       9824.2              50.00     Sequence
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DRB1_1302   10  FCPSPTGTPHVGLVR  TGTPHVGLV        0.1431      10630.7              50.00     Sequence
DRB1_1302  267  FAHRDRGFIPEGLLN  RGFIPEGLL        0.1431      10634.7              50.00     Sequence
DRB1_1302  158  RMPDDDLAWNDLVRG  RMPDDDLAW        0.1422      10733.2              50.00     Sequence
DRB1_1302  173  PVTFAAGSVPDFALT  PVTFAAGSV        0.1417      10792.7              50.00     Sequence
DRB1_1302  192  DPLYTLVNPCDDALM  LVNPCDDAL        0.1404      10949.3              50.00     Sequence
DRB1_1302  420  TDWTAPLIEAALKDA  TAPLIEAAL        0.1403      10952.6              50.00     Sequence
DRB1_1302  381  LLKFFNDDQYVIDPK  FFNDDQYVI        0.1397      11029.2              50.00     Sequence
DRB1_1302  382  LKFFNDDQYVIDPKA  FFNDDQYVI        0.1393      11074.7              50.00     Sequence
DRB1_1302  265  NLFAHRDRGFIPEGL  FAHRDRGFI        0.1381      11224.6              50.00     Sequence
DRB1_1302  193  PLYTLVNPCDDALMK  LVNPCDDAL        0.1380      11237.4              50.00     Sequence
DRB1_1302  194  LYTLVNPCDDALMKI  LVNPCDDAL        0.1377      11266.5              50.00     Sequence
DRB1_1302  103  AGEAYHAFSTPEEVE  AYHAFSTPE        0.1376      11282.1              50.00     Sequence
DRB1_1302  391  VIDPKAAAKELGPDG  VIDPKAAAK        0.1350      11607.9              50.00     Sequence
DRB1_1302  286  LGWSIADDHDLFGLD  WSIADDHDL        0.1349      11620.0              50.00     Sequence
DRB1_1302  195  YTLVNPCDDALMKIT  LVNPCDDAL        0.1292      12353.8              50.00     Sequence
DRB1_1302  287  GWSIADDHDLFGLDE  WSIADDHDL        0.1282      12491.6              50.00     Sequence
DRB1_1302  109  AFSTPEEVEARHVAA  EVEARHVAA        0.1278      12545.9              50.00     Sequence
DRB1_1302  419  VTDWTAPLIEAALKD  TAPLIEAAL        0.1275      12581.3              50.00     Sequence
DRB1_1302   59  ALLDALRWLGLDWDE  LDALRWLGL        0.1224      13299.2              50.00     Sequence
DRB1_1302  288  WSIADDHDLFGLDEM  WSIADDHDL        0.1193      13753.3              50.00     Sequence
DRB1_1302  159  MPDDDLAWNDLVRGP  DDLAWNDLV        0.1177      13996.5              50.00     Sequence
DRB1_1302  156  RLRMPDDDLAWNDLV  RLRMPDDDL        0.1175      14030.3              50.00     Sequence
DRB1_1302  153  PVVRLRMPDDDLAWN  RLRMPDDDL        0.1165      14174.8              50.00     Sequence
DRB1_1302  207  KITHVLRGEDLLPST  VLRGEDLLP        0.1153      14359.9              50.00     Sequence
DRB1_1302  196  TLVNPCDDALMKITH  LVNPCDDAL        0.1146      14465.1              50.00     Sequence
DRB1_1302  377  DAWELLKFFNDDQYV  LKFFNDDQY        0.1136      14632.5              50.00     Sequence
DRB1_1302  313  SSPARFDQKKADALN  RFDQKKADA        0.1126      14788.3              50.00     Sequence
DRB1_1302  104  GEAYHAFSTPEEVEA  AYHAFSTPE        0.1125      14802.2              50.00     Sequence
DRB1_1302  312  NSSPARFDQKKADAL  FDQKKADAL        0.1115      14966.6              50.00     Sequence
DRB1_1302  157  LRMPDDDLAWNDLVR  RMPDDDLAW        0.1107      15096.7              50.00     Sequence
DRB1_1302    1  TATETVRVRFCPSPT  RVRFCPSPT        0.1099      15221.9              50.00     Sequence
DRB1_1302  154  VVRLRMPDDDLAWND  RLRMPDDDL        0.1095      15290.9              50.00     Sequence
DRB1_1302  299  LDEMVAAFDVADVNS  VAAFDVADV        0.1084      15477.7              50.00     Sequence
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DRB1_1302	160	PDDDLAWNDLVRGPV	LAWNDLVRG	0.1072	15679.4	50.00	Sequence
DRB1_1302	131	YDNFDRHLTDAQRAA	RHLTDAQRA	0.1063	15829.6	50.00	Sequence
DRB1_1302	155	VRLRMPDDDLAWNDL	LRMPDDDLA	0.1039	16242.3	50.00	Sequence
DRB1_1302	191	GDPLYTLVNPCDDAL	LVNPCDDAL	0.1039	16254.1	50.00	Sequence
DRB1_1302	208	ITHVLRGEDLLPSTP	THVLRGEDL	0.1034	16337.2	50.00	Sequence
DRB1_1302	139	TDAQRAAYLAEGRQP	TDAQRAAYL	0.1031	16391.3	50.00	Sequence
DRB1_1302	291	ADDHDLFGLDEMVAA	FGLDEMVAA	0.1016	16651.4	50.00	Sequence
DRB1_1302	123	AGRNPKLGYDNFDRH	AGRNPKLGY	0.1016	16663.7	50.00	Sequence
DRB1_1302	161	DDDLAWNDLVRGPVT	LAWNDLVRG	0.1015	16665.1	50.00	Sequence
DRB1_1302	300	DEMVAAFDVADVNSS	DEMVAAFDV	0.1009	16786.0	50.00	Sequence
DRB1_1302	252	EGTKKLSKRDPQSNL	SKRDPQSNL	0.1004	16874.7	50.00	Sequence
DRB1_1302	2	ATETVRVRFCPSPTG	RVRFCPSPT	0.0992	17102.8	50.00	Sequence
DRB1_1302	6	VRVRFCPSPTGTPHV	PSPTGTPHV	0.0989	17154.7	50.00	Sequence
DRB1_1302	7	RVRFCPSPTGTPHVG	PSPTGTPHV	0.0987	17190.9	50.00	Sequence
DRB1_1302	130	GYDNFDRHLTDAQRA	RHLTDAQRA	0.0981	17294.6	50.00	Sequence
DRB1_1302	394	PKAAAKELGPDGAAV	ELGPDGAAV	0.0949	17908.4	50.00	Sequence
DRB1_1302	250	LGEGTKKLSKRDPQS	LGEGTKKLS	0.0948	17928.9	50.00	Sequence
DRB1_1302	374	VLGDAWELLKFFNDD	VLGDAWELL	0.0938	18116.9	50.00	Sequence
DRB1_1302	209	THVLRGEDLLPSTPR	VLRGEDLLP	0.0921	18458.8	50.00	Sequence
DRB1_1302	122	AAGRNPKLGYDNFDR	AGRNPKLGY	0.0920	18472.8	50.00	Sequence
DRB1_1302	47	TDAQRDSEESYLALL	SEESYLALL	0.0918	18510.2	50.00	Sequence
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DRB1_1302	463	LFESLELLGRDRSMQ	ELLGRDRSM	0.0909	18705.3	50.00	Sequence
DRB1_1302	3	TETVRVRFCPSPTGT	RVRFCPSPT	0.0895	18990.4	50.00	Sequence
DRB1_1302	124	GRNPKLGYDNFDRHL	LGYDNFDRH	0.0894	19008.7	50.00	Sequence
DRB1_1302	108	HAFSTPEEVEARHVA	PEEVEARHV	0.0885	19201.8	50.00	Sequence
DRB1_1302	336	VGDFTVRLRDHLDTH	RLRDHLDTH	0.0875	19400.4	50.00	Sequence
DRB1_1302	36	TGGTFVFRIEDTDAQ	VFRIEDTDA	0.0859	19730.0	50.00	Sequence
DRB1_1302	376	GDAWELLKFFNDDQY	LKFFNDDQY	0.0855	19818.1	50.00	Sequence
DRB1_1302	187	TRASGDPLYTLVNPC	RASGDPLYT	0.0854	19837.2	50.00	Sequence
DRB1_1302	60	LLDALRWLGLDWDEG	LDALRWLGL	0.0844	20062.1	50.00	Sequence
DRB1_1302	37	GGTFVFRIEDTDAQR	VFRIEDTDA	0.0844	20069.7	50.00	Sequence
DRB1_1302	301	EMVAAFDVADVNSSP	VAAFDVADV	0.0835	20247.5	50.00	Sequence
DRB1_1302	8	VRFCPSPTGTPHVGL	PSPTGTPHV	0.0835	20260.6	50.00	Sequence
DRB1_1302	125	RNPKLGYDNFDRHLT	LGYDNFDRH	0.0831	20342.8	50.00	Sequence
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DRB1_1302	174	VTFAAGSVPDFALTR	VTFAAGSVP	0.0822	20548.1	50.00	Sequence
DRB1_1302	140	DAQRAAYLAEGRQPV	YLAEGRQPV	0.0820	20592.8	50.00	Sequence
DRB1_1302	38	GTFVFRIEDTDAQRD	VFRIEDTDA	0.0819	20612.7	50.00	Sequence
DRB1_1302	51	RDSEESYLALLDALR	SEESYLALL	0.0809	20830.6	50.00	Sequence
DRB1_1302	338	DFTVRLRDHLDTHGH	RDHLDTHGH	0.0801	21026.9	50.00	Sequence
DRB1_1302	105	EAYHAFSTPEEVEAR	AYHAFSTPE	0.0791	21234.9	50.00	Sequence
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DRB1_1302	462	PLFESLELLGRDRSM	ELLGRDRSM	0.0784	21404.3	50.00	Sequence
DRB1_1302	76	EVGGPYGPYRQSQRA	GPYRQSQRA	0.0763	21889.5	50.00	Sequence
DRB1_1302	49	AQRDSEESYLALLDA	SEESYLALL	0.0751	22174.2	50.00	Sequence
DRB1_1302	39	TFVFRIEDTDAQRDS	VFRIEDTDA	0.0750	22214.0	50.00	Sequence
DRB1_1302	72	DEGPEVGGPYGPYRQ	GGPYGPYRQ	0.0745	22319.5	50.00	Sequence
DRB1_1302	73	EGPEVGGPYGPYRQS	GGPYGPYRQ	0.0745	22341.1	50.00	Sequence
DRB1_1302	61	LDALRWLGLDWDEGP	LDALRWLGL	0.0737	22527.2	50.00	Sequence
DRB1_1302	178	AGSVPDFALTRASGD	FALTRASGD	0.0735	22562.4	50.00	Sequence
DRB1_1302	4	ETVRVRFCPSPTGTP	RVRFCPSPT	0.0734	22587.7	50.00	Sequence
DRB1_1302	126	NPKLGYDNFDRHLTD	LGYDNFDRH	0.0732	22642.8	50.00	Sequence
DRB1_1302	337	GDFTVRLRDHLDTHG	TVRLRDHLD	0.0730	22684.0	50.00	Sequence
DRB1_1302	458	TVSPPLFESLELLGR	PLFESLELL	0.0727	22778.0	50.00	Sequence
DRB1_1302	251	GEGTKKLSKRDPQSN	LSKRDPQSN	0.0724	22847.3	50.00	Sequence
DRB1_1302	5	TVRVRFCPSPTGTPH	RFCPSPTGT	0.0723	22877.0	50.00	Sequence
DRB1_1302	457	TTVSPPLFESLELLG	PLFESLELL	0.0717	23005.3	50.00	Sequence
DRB1_1302	75	PEVGGPYGPYRQSQR	GGPYGPYRQ	0.0708	23237.0	50.00	Sequence
DRB1_1302	175	TFAAGSVPDFALTRA	VPDFALTRA	0.0705	23325.6	50.00	Sequence
DRB1_1302	35	HTGGTFVFRIEDTDA	VFRIEDTDA	0.0702	23401.2	50.00	Sequence
DRB1_1302	77	VGGPYGPYRQSQRAE	GPYRQSQRA	0.0701	23412.4	50.00	Sequence
DRB1_1302	290	IADDHDLFGLDEMVA	LFGLDEMVA	0.0675	24095.7	50.00	Sequence
DRB1_1302	459	VSPPLFESLELLGRD	PPLFESLEL	0.0675	24098.3	50.00	Sequence
DRB1_1302	127	PKLGYDNFDRHLTDA	LGYDNFDRH	0.0668	24262.4	50.00	Sequence
DRB1_1302	128	KLGYDNFDRHLTDAQ	LGYDNFDRH	0.0656	24594.6	50.00	Sequence

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   DRB1_1302  107  YHAFSTPEEVEARHV  PEEVEARHV        0.0655      24616.4                 50.00     Sequence
   DRB1_1302  210  HVLRGEDLLPSTPRQ  VLRGEDLLP        0.0654      24630.3                 50.00     Sequence
   DRB1_1302   74  GPEVGGPYGPYRQSQ  GGPYGPYRQ        0.0653      24660.7                 50.00     Sequence
   DRB1_1302  106  AYHAFSTPEEVEARH  AYHAFSTPE        0.0647      24818.1                 50.00     Sequence
   DRB1_1302   40  FVFRIEDTDAQRDSE  VFRIEDTDA        0.0647      24831.5                 50.00     Sequence
   DRB1_1302  339  FTVRLRDHLDTHGHH  RDHLDTHGH        0.0640      25004.6                 50.00     Sequence
   DRB1_1302  176  FAAGSVPDFALTRAS  VPDFALTRA        0.0635      25154.4                 50.00     Sequence
   DRB1_1302  392  IDPKAAAKELGPDGA  DPKAAAKEL        0.0622      25522.6                 50.00     Sequence
   DRB1_1302  311  VNSSPARFDQKKADA  RFDQKKADA        0.0619      25598.6                 50.00     Sequence
   DRB1_1302  188  RASGDPLYTLVNPCD  RASGDPLYT        0.0611      25805.0                 50.00     Sequence
   DRB1_1302  393  DPKAAAKELGPDGAA  DPKAAAKEL        0.0608      25886.9                 50.00     Sequence
   DRB1_1302   41  VFRIEDTDAQRDSEE  VFRIEDTDA        0.0590      26412.9                 50.00     Sequence
   DRB1_1302  129  LGYDNFDRHLTDAQR  DRHLTDAQR        0.0585      26537.2                 50.00     Sequence
   DRB1_1302  177  AAGSVPDFALTRASG  VPDFALTRA        0.0583      26604.2                 50.00     Sequence
   DRB1_1302  461  PPLFESLELLGRDRS  PPLFESLEL        0.0576      26825.0                 50.00     Sequence
   DRB1_1302  375  LGDAWELLKFFNDDQ  LLKFFNDDQ        0.0565      27134.1                 50.00     Sequence
   DRB1_1302   46  DTDAQRDSEESYLAL  DSEESYLAL        0.0548      27631.3                 50.00     Sequence
   DRB1_1302  460  SPPLFESLELLGRDR  PPLFESLEL        0.0534      28060.0                 50.00     Sequence
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   DRB1_1302   42  FRIEDTDAQRDSEES  FRIEDTDAQ        0.0465      30231.4                 50.00     Sequence
   DRB1_1302   63  ALRWLGLDWDEGPEV  LDWDEGPEV        0.0462      30344.1                 50.00     Sequence
   DRB1_1302   70  DWDEGPEVGGPYGPY  EVGGPYGPY        0.0458      30461.6                 50.00     Sequence
   DRB1_1302   44  IEDTDAQRDSEESYL  QRDSEESYL        0.0441      31012.3                 50.00     Sequence
   DRB1_1302   45  EDTDAQRDSEESYLA  QRDSEESYL        0.0417      31855.7                 50.00     Sequence
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   DRB1_1302   67  LGLDWDEGPEVGGPY  EGPEVGGPY        0.0367      33600.7                 50.00     Sequence
   DRB1_1302   43  RIEDTDAQRDSEESY  IEDTDAQRD        0.0366      33659.3                 50.00     Sequence
   DRB1_1302   68  GLDWDEGPEVGGPYG  EGPEVGGPY        0.0355      34046.1                 50.00     Sequence
   DRB1_1302  190  SGDPLYTLVNPCDDA  PLYTLVNPC        0.0342      34537.3                 50.00     Sequence
   DRB1_1302   64  LRWLGLDWDEGPEVG  LDWDEGPEV        0.0322      35295.5                 50.00     Sequence
   DRB1_1302   62  DALRWLGLDWDEGPE  ALRWLGLDW        0.0301      36099.6                 50.00     Sequence
   DRB1_1302   65  RWLGLDWDEGPEVGG  LDWDEGPEV        0.0275      37119.9                 50.00     Sequence
   DRB1_1302   66  WLGLDWDEGPEVGGP  LDWDEGPEV        0.0238      38631.5                 50.00     Sequence
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Allele: DRB1_1302. Number of high binders 0. Number of weak binders 48. Number of peptides 476

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1501  432  KDALIEGLALKPRKA  LIEGLALKP        0.7042         24.5           SB     2.00     Sequence
   DRB1_1501  472  RDRSMQRLRAARQLV  SMQRLRAAR        0.7014         25.3           SB     2.00     Sequence
   DRB1_1501  473  DRSMQRLRAARQLVG  SMQRLRAAR        0.6856         30.0           SB     2.00     Sequence
   DRB1_1501  433  DALIEGLALKPRKAF  LIEGLALKP        0.6822         31.1           SB     2.00     Sequence
   DRB1_1501  434  ALIEGLALKPRKAFS  LIEGLALKP        0.6821         31.2           SB     2.00     Sequence
   DRB1_1501  471  GRDRSMQRLRAARQL  SMQRLRAAR        0.6808         31.6           SB     2.00     Sequence
   DRB1_1501  474  RSMQRLRAARQLVGH  SMQRLRAAR        0.6767         33.1           SB     4.00     Sequence
   DRB1_1501  431  LKDALIEGLALKPRK  ALIEGLALK        0.6747         33.8           SB     4.00     Sequence
   DRB1_1501   21  GLVRTALFNWAYARH  LFNWAYARH        0.6670         36.7           SB     4.00     Sequence
   DRB1_1501   22  LVRTALFNWAYARHT  LFNWAYARH        0.6660         37.1           SB     4.00     Sequence
   DRB1_1501   19  HVGLVRTALFNWAYA  HVGLVRTAL        0.6619         38.8           SB     4.00     Sequence
   DRB1_1501  430  ALKDALIEGLALKPR  ALIEGLALK        0.6607         39.3           SB     4.00     Sequence
   DRB1_1501   23  VRTALFNWAYARHTG  LFNWAYARH        0.6539         42.3           SB     4.00     Sequence
   DRB1_1501   94  RDVLARLLAAGEAYH  VLARLLAAG        0.6527         42.8           SB     4.00     Sequence
   DRB1_1501   18  PHVGLVRTALFNWAY  HVGLVRTAL        0.6520         43.2           SB     4.00     Sequence
   DRB1_1501   95  DVLARLLAAGEAYHA  VLARLLAAG        0.6504         43.9           SB     4.00     Sequence
   DRB1_1501   91  EIYRDVLARLLAAGE  EIYRDVLAR        0.6472         45.5           SB     4.00     Sequence
   DRB1_1501  470  LGRDRSMQRLRAARQ  SMQRLRAAR        0.6463         45.9           SB     4.00     Sequence
   DRB1_1501   17  TPHVGLVRTALFNWA  HVGLVRTAL        0.6356         51.5           WB     4.00     Sequence
   DRB1_1501  475  SMQRLRAARQLVGHA  SMQRLRAAR        0.6322         53.5           WB     4.00     Sequence
   DRB1_1501  429  AALKDALIEGLALKP  LIEGLALKP        0.6282         55.8           WB     4.00     Sequence
   DRB1_1501   90  AEIYRDVLARLLAAG  EIYRDVLAR        0.6258         57.3           WB     8.00     Sequence
   DRB1_1501   24  RTALFNWAYARHTGG  LFNWAYARH        0.6230         59.1           WB     8.00     Sequence
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DRB1_1501   92  IYRDVLARLLAAGEA  VLARLLAAG        0.6221          59.7          WB     8.00     Sequence
DRB1_1501   93  YRDVLARLLAAGEAY  VLARLLAAG        0.6211          60.3          WB     8.00     Sequence
DRB1_1501   20  VGLVRTALFNWAYAR  LVRTALFNW        0.6170          63.1          WB     8.00     Sequence
DRB1_1501   16  GTPHVGLVRTALFNW  HVGLVRTAL        0.6134          65.5          WB     8.00     Sequence
DRB1_1501   96  VLARLLAAGEAYHAF  VLARLLAAG        0.6122          66.4          WB     8.00     Sequence
DRB1_1501  277  EGLLNYLALLGWSIA  YLALLGWSI        0.6114          67.0          WB     8.00     Sequence
DRB1_1501   89  RAEIYRDVLARLLAA  EIYRDVLAR        0.6110          67.3          WB     8.00     Sequence
DRB1_1501  466  SLELLGRDRSMQRLR  LLGRDRSMQ        0.5959          79.2          WB     8.00     Sequence
DRB1_1501  276  PEGLLNYLALLGWSI  LLNYLALLG        0.5959          79.3          WB     8.00     Sequence
DRB1_1501  469  LLGRDRSMQRLRAAR  SMQRLRAAR        0.5948          80.2          WB     8.00     Sequence
DRB1_1501  278  GLLNYLALLGWSIAD  YLALLGWSI        0.5920          82.6          WB     8.00     Sequence
DRB1_1501  435  LIEGLALKPRKAFSP  LIEGLALKP        0.5903          84.2          WB     8.00     Sequence
DRB1_1501   88  QRAEIYRDVLARLLA  EIYRDVLAR        0.5842          90.0          WB     8.00     Sequence
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DRB1_1501  465  ESLELLGRDRSMQRL  LLGRDRSMQ        0.5675         107.7          WB    16.00     Sequence
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DRB1_1501  442  KPRKAFSPIRVAATG  AFSPIRVAA        0.5580         119.4          WB    16.00     Sequence
DRB1_1501   25  TALFNWAYARHTGGT  LFNWAYARH        0.5557         122.4          WB    16.00     Sequence
DRB1_1501  279  LLNYLALLGWSIADD  YLALLGWSI        0.5538         124.9          WB    16.00     Sequence
DRB1_1501  148  AEGRQPVVRLRMPDD  PVVRLRMPD        0.5534         125.5          WB    16.00     Sequence
DRB1_1501  222  PRQLALHQALIRIGV  LALHQALIR        0.5518         127.6          WB    16.00     Sequence
DRB1_1501   86  QSQRAEIYRDVLARL  EIYRDVLAR        0.5511         128.7          WB    16.00     Sequence
DRB1_1501  149  EGRQPVVRLRMPDDD  PVVRLRMPD        0.5481         132.9          WB    16.00     Sequence
DRB1_1501  221  TPRQLALHQALIRIG  LALHQALIR        0.5469         134.6          WB    16.00     Sequence
DRB1_1501  226  ALHQALIRIGVAERI  LIRIGVAER        0.5429         140.6          WB    16.00     Sequence
DRB1_1501  225  LALHQALIRIGVAER  ALIRIGVAE        0.5414         142.9          WB    16.00     Sequence
DRB1_1501  443  PRKAFSPIRVAATGT  AFSPIRVAA        0.5408         143.8          WB    16.00     Sequence
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DRB1_1501   15  TGTPHVGLVRTALFN  HVGLVRTAL        0.5393         146.2          WB    16.00     Sequence
DRB1_1501  223  RQLALHQALIRIGVA  LALHQALIR        0.5382         147.9          WB    16.00     Sequence
DRB1_1501  220  STPRQLALHQALIRI  LALHQALIR        0.5357         151.9          WB    16.00     Sequence
DRB1_1501  468  ELLGRDRSMQRLRAA  LLGRDRSMQ        0.5344         154.0          WB    16.00     Sequence
DRB1_1501  439  LALKPRKAFSPIRVA  ALKPRKAFS        0.5336         155.5          WB    16.00     Sequence
DRB1_1501  227  LHQALIRIGVAERIP  LIRIGVAER        0.5331         156.4          WB    16.00     Sequence
DRB1_1501  150  GRQPVVRLRMPDDDL  PVVRLRMPD        0.5328         156.8          WB    16.00     Sequence
DRB1_1501  410  DAALAALTSVTDWTA  ALAALTSVT        0.5324         157.5          WB    16.00     Sequence
DRB1_1501  409  LDAALAALTSVTDWT  ALAALTSVT        0.5283         164.6          WB    16.00     Sequence
DRB1_1501  274  FIPEGLLNYLALLGW  GLLNYLALL        0.5280         165.1          WB    16.00     Sequence
DRB1_1501  464  FESLELLGRDRSMQR  LLGRDRSMQ        0.5252         170.2          WB    16.00     Sequence
DRB1_1501  228  HQALIRIGVAERIPK  LIRIGVAER        0.5219         176.5          WB    16.00     Sequence
DRB1_1501  329  EHIRMLDVGDFTVRL  DVGDFTVRL        0.5185         183.1          WB    16.00     Sequence
DRB1_1501  273  GFIPEGLLNYLALLG  GLLNYLALL        0.5158         188.5          WB    16.00     Sequence
DRB1_1501   14  PTGTPHVGLVRTALF  HVGLVRTAL        0.5157         188.7          WB    16.00     Sequence
DRB1_1501  147  LAEGRQPVVRLRMPD  PVVRLRMPD        0.5127         194.9          WB    16.00     Sequence
DRB1_1501  229  QALIRIGVAERIPKF  LIRIGVAER        0.5119         196.7          WB    16.00     Sequence
DRB1_1501   26  ALFNWAYARHTGGTF  LFNWAYARH        0.5079         205.3          WB    16.00     Sequence
DRB1_1501  411  AALAALTSVTDWTAP  ALAALTSVT        0.5062         209.1          WB    16.00     Sequence
DRB1_1501  444  RKAFSPIRVAATGTT  AFSPIRVAA        0.5061         209.4          WB    16.00     Sequence
DRB1_1501  463  LFESLELLGRDRSMQ  ELLGRDRSM        0.5039         214.4          WB    16.00     Sequence
DRB1_1501  408  VLDAALAALTSVTDW  ALAALTSVT        0.5024         217.8          WB    16.00     Sequence
DRB1_1501  151  RQPVVRLRMPDDDLA  PVVRLRMPD        0.4969         231.2          WB    16.00     Sequence
DRB1_1501  280  LNYLALLGWSIADDH  YLALLGWSI        0.4929         241.5          WB    16.00     Sequence
DRB1_1501  230  ALIRIGVAERIPKFA  LIRIGVAER        0.4880         254.5          WB    32.00     Sequence
DRB1_1501  330  HIRMLDVGDFTVRLR  DVGDFTVRL        0.4877         255.3          WB    32.00     Sequence
DRB1_1501   99  RLLAAGEAYHAFSTP  LLAAGEAYH        0.4875         255.9          WB    32.00     Sequence
DRB1_1501  438  GLALKPRKAFSPIRV  ALKPRKAFS        0.4873         256.5          WB    32.00     Sequence
DRB1_1501  362  AAAAELVQTRIVVLG  AAELVQTRI        0.4863         259.4          WB    32.00     Sequence
DRB1_1501   97  LARLLAAGEAYHAFS  RLLAAGEAY        0.4850         263.0          WB    32.00     Sequence
DRB1_1501  445  KAFSPIRVAATGTTV  AFSPIRVAA        0.4826         270.0          WB    32.00     Sequence
DRB1_1501  407  AVLDAALAALTSVTD  ALAALTSVT        0.4807         275.4          WB    32.00     Sequence
DRB1_1501  376  GDAWELLKFFNDDQY  ELLKFFNDD        0.4796         278.7          WB    32.00     Sequence
DRB1_1501  371  RIVVLGDAWELLKFF  RIVVLGDAW        0.4773         285.7          WB    32.00     Sequence
DRB1_1501  368  VQTRIVVLGDAWELL  RIVVLGDAW        0.4773         285.9          WB    32.00     Sequence
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DRB1_1501   57  YLALLDALRWLGLDW  ALRWLGLDW        0.4770         286.7          WB    32.00     Sequence
DRB1_1501  363  AAAELVQTRIVVLGD  AAELVQTRI        0.4765         288.2          WB    32.00     Sequence
DRB1_1501  369  QTRIVVLGDAWELLK  RIVVLGDAW        0.4758         290.7          WB    32.00     Sequence
DRB1_1501  335  DVGDFTVRLRDHLDT  DVGDFTVRL        0.4748         293.7          WB    32.00     Sequence
DRB1_1501  370  TRIVVLGDAWELLKF  RIVVLGDAW        0.4706         307.4          WB    32.00     Sequence
DRB1_1501   85  RQSQRAEIYRDVLAR  EIYRDVLAR        0.4696         310.8          WB    32.00     Sequence
DRB1_1501  378  AWELLKFFNDDQYVI  ELLKFFNDD        0.4690         312.7          WB    32.00     Sequence
DRB1_1501  377  DAWELLKFFNDDQYV  ELLKFFNDD        0.4678         316.8          WB    32.00     Sequence
DRB1_1501  237  AERIPKFAHLPTVLG  KFAHLPTVL        0.4652         325.8          WB    32.00     Sequence
DRB1_1501  437  EGLALKPRKAFSPIR  ALKPRKAFS        0.4636         331.6          WB    32.00     Sequence
DRB1_1501  361  FAAAAELVQTRIVVL  AAELVQTRI        0.4633         332.7          WB    32.00     Sequence
DRB1_1501  334  LDVGDFTVRLRDHLD  DVGDFTVRL        0.4608         341.9          WB    32.00     Sequence
DRB1_1501   98  ARLLAAGEAYHAFST  RLLAAGEAY        0.4590         348.4          WB    32.00     Sequence
DRB1_1501  219  PSTPRQLALHQALIR  LALHQALIR        0.4574         354.6          WB    32.00     Sequence
DRB1_1501  375  LGDAWELLKFFNDDQ  ELLKFFNDD        0.4568         356.8          WB    32.00     Sequence
DRB1_1501  332  RMLDVGDFTVRLRDH  DVGDFTVRL        0.4567         357.4          WB    32.00     Sequence
DRB1_1501  462  PLFESLELLGRDRSM  LFESLELLG        0.4559         360.4          WB    32.00     Sequence
DRB1_1501  412  ALAALTSVTDWTAPL  ALAALTSVT        0.4557         361.3          WB    32.00     Sequence
DRB1_1501  152  QPVVRLRMPDDDLAW  PVVRLRMPD        0.4555         362.1          WB    32.00     Sequence
DRB1_1501  281  NYLALLGWSIADDHD  YLALLGWSI        0.4554         362.3          WB    32.00     Sequence
DRB1_1501  367  LVQTRIVVLGDAWEL  RIVVLGDAW        0.4540         367.8          WB    32.00     Sequence
DRB1_1501  406  AAVLDAALAALTSVT  ALAALTSVT        0.4539         368.2          WB    32.00     Sequence
DRB1_1501  272  RGFIPEGLLNYLALL  GLLNYLALL        0.4531         371.4          WB    32.00     Sequence
DRB1_1501  436  IEGLALKPRKAFSPI  ALKPRKAFS        0.4517         376.9          WB    32.00     Sequence
DRB1_1501  238  ERIPKFAHLPTVLGE  KFAHLPTVL        0.4510         379.8          WB    32.00     Sequence
DRB1_1501  100  LLAAGEAYHAFSTPE  EAYHAFSTP        0.4499         384.6          WB    32.00     Sequence
DRB1_1501  231  LIRIGVAERIPKFAH  LIRIGVAER        0.4495         386.1          WB    32.00     Sequence
DRB1_1501  333  MLDVGDFTVRLRDHL  DVGDFTVRL        0.4468         397.8          WB    32.00     Sequence
DRB1_1501  374  VLGDAWELLKFFNDD  ELLKFFNDD        0.4465         398.7          WB    32.00     Sequence
DRB1_1501  379  WELLKFFNDDQYVID  ELLKFFNDD        0.4455         403.4          WB    32.00     Sequence
DRB1_1501    3  TETVRVRFCPSPTGT  VRVRFCPSP        0.4448         406.4          WB    32.00     Sequence
DRB1_1501    5  TVRVRFCPSPTGTPH  VRVRFCPSP        0.4447         406.7          WB    32.00     Sequence
DRB1_1501   58  LALLDALRWLGLDWD  ALRWLGLDW        0.4442         409.2          WB    32.00     Sequence
DRB1_1501  239  RIPKFAHLPTVLGEG  KFAHLPTVL        0.4435         411.9          WB    32.00     Sequence
DRB1_1501    4  ETVRVRFCPSPTGTP  VRVRFCPSP        0.4421         418.3          WB    32.00     Sequence
DRB1_1501  336  VGDFTVRLRDHLDTH  FTVRLRDHL        0.4421         418.5          WB    32.00     Sequence
DRB1_1501  236  VAERIPKFAHLPTVL  KFAHLPTVL        0.4407         424.9          WB    32.00     Sequence
DRB1_1501  364  AAELVQTRIVVLGDA  AAELVQTRI        0.4400         428.2          WB    32.00     Sequence
DRB1_1501  458  TVSPPLFESLELLGR  LFESLELLG        0.4398         428.9          WB    32.00     Sequence
DRB1_1501   59  ALLDALRWLGLDWDE  ALRWLGLDW        0.4388         433.4          WB    32.00     Sequence
DRB1_1501  365  AELVQTRIVVLGDAW  RIVVLGDAW        0.4386         434.6          WB    32.00     Sequence
DRB1_1501  104  GEAYHAFSTPEEVEA  AYHAFSTPE        0.4384         435.5          WB    32.00     Sequence
DRB1_1501  102  AAGEAYHAFSTPEEV  AYHAFSTPE        0.4381         436.7          WB    32.00     Sequence
DRB1_1501  103  AGEAYHAFSTPEEVE  AYHAFSTPE        0.4370         442.1          WB    32.00     Sequence
DRB1_1501  207  KITHVLRGEDLLPST  HVLRGEDLL        0.4369         442.6          WB    32.00     Sequence
DRB1_1501   27  LFNWAYARHTGGTFV  LFNWAYARH        0.4333         460.2          WB    32.00     Sequence
DRB1_1501   13  SPTGTPHVGLVRTAL  HVGLVRTAL        0.4316         468.5          WB    32.00     Sequence
DRB1_1501   55  ESYLALLDALRWLGL  YLALLDALR        0.4312         471.0          WB    32.00     Sequence
DRB1_1501   56  SYLALLDALRWLGLD  YLALLDALR        0.4305         474.3          WB    32.00     Sequence
DRB1_1501  372  IVVLGDAWELLKFFN  VVLGDAWEL        0.4304         474.7          WB    32.00     Sequence
DRB1_1501  326  LNAEHIRMLDVGDFT  EHIRMLDVG        0.4298         477.7          WB    32.00     Sequence
DRB1_1501  205  LMKITHVLRGEDLLP  HVLRGEDLL        0.4296         479.0          WB    32.00     Sequence
DRB1_1501  428  EAALKDALIEGLALK  ALIEGLALK        0.4296         479.0          WB    32.00     Sequence
DRB1_1501  331  IRMLDVGDFTVRLRD  DVGDFTVRL        0.4291         481.3          WB    32.00     Sequence
DRB1_1501  328  AEHIRMLDVGDFTVR  HIRMLDVGD        0.4290         482.2          WB    32.00     Sequence
DRB1_1501  206  MKITHVLRGEDLLPS  HVLRGEDLL        0.4282         486.4          WB    32.00     Sequence
DRB1_1501  325  ALNAEHIRMLDVGDF  EHIRMLDVG        0.4278         488.2          WB    32.00     Sequence
DRB1_1501    2  ATETVRVRFCPSPTG  VRVRFCPSP        0.4275         490.0          WB    32.00     Sequence
DRB1_1501  461  PPLFESLELLGRDRS  LFESLELLG        0.4254         501.3                32.00     Sequence
DRB1_1501  373  VVLGDAWELLKFFND  VVLGDAWEL        0.4215         522.6                32.00     Sequence
DRB1_1501  459  VSPPLFESLELLGRD  LFESLELLG        0.4213         523.8                32.00     Sequence
DRB1_1501    6  VRVRFCPSPTGTPHV  VRVRFCPSP        0.4211         525.0                32.00     Sequence
DRB1_1501  208  ITHVLRGEDLLPSTP  HVLRGEDLL        0.4200         531.4                32.00     Sequence
DRB1_1501  101  LAAGEAYHAFSTPEE  AYHAFSTPE        0.4182         541.8                32.00     Sequence
DRB1_1501  446  AFSPIRVAATGTTVS  AFSPIRVAA        0.4170         548.8                32.00     Sequence
DRB1_1501  327  NAEHIRMLDVGDFTV  EHIRMLDVG        0.4159         555.4                32.00     Sequence
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DRB1_1501  457  TTVSPPLFESLELLG  LFESLELLG       0.4152       559.7              32.00    Sequence
DRB1_1501  324  DALNAEHIRMLDVGD  EHIRMLDVG       0.4132       572.2              32.00    Sequence
DRB1_1501  337  GDFTVRLRDHLDTHG  FTVRLRDHL       0.4131       572.3              32.00    Sequence
DRB1_1501  282  YLALLGWSIADDHDL  LALLGWSIA       0.4125       576.2              32.00    Sequence
DRB1_1501   60  LLDALRWLGLDWDEG  ALRWLGLDW       0.4104       589.8              32.00    Sequence
DRB1_1501  460  SPPLFESLELLGRDR  LFESLELLG       0.4063       616.1              32.00    Sequence
DRB1_1501  105  EAYHAFSTPEEVEAR  AYHAFSTPE       0.4036       634.4              32.00    Sequence
DRB1_1501  380  ELLKFFNDDQYVIDP  ELLKFFNDD       0.4016       648.2              32.00    Sequence
DRB1_1501  413  LAALTSVTDWTAPLI  AALTSVTDW       0.4015       649.3              32.00    Sequence
DRB1_1501  366  ELVQTRIVVLGDAWE  RIVVLGDAW       0.4003       657.9              32.00    Sequence
DRB1_1501  168  DLVRGPVTFAAGSVP  LVRGPVTFA       0.3996       662.9              32.00    Sequence
DRB1_1501  190  SGDPLYTLVNPCDDA  PLYTLVNPC       0.3993       664.5              32.00    Sequence
DRB1_1501  240  IPKFAHLPTVLGEGT  KFAHLPTVL       0.3953       694.4              32.00    Sequence
DRB1_1501  360  AFAAAAELVQTRIVV  AAELVQTRI       0.3949       696.9              32.00    Sequence
DRB1_1501  117  EARHVAAGRNPKLGY  HVAAGRNPK       0.3946       699.8              32.00    Sequence
DRB1_1501  164  LAWNDLVRGPVTFAA  DLVRGPVTF       0.3945       700.1              32.00    Sequence
DRB1_1501  146  YLAEGRQPVVRLRMP  LAEGRQPVV       0.3930       711.7              32.00    Sequence
DRB1_1501  188  RASGDPLYTLVNPCD  PLYTLVNPC       0.3925       715.3              32.00    Sequence
DRB1_1501    1  TATETVRVRFCPSPT  VRVRFCPSP       0.3919       720.0              32.00    Sequence
DRB1_1501  414  AALTSVTDWTAPLIE  SVTDWTAPL       0.3914       724.4              32.00    Sequence
DRB1_1501  189  ASGDPLYTLVNPCDD  PLYTLVNPC       0.3912       725.7              32.00    Sequence
DRB1_1501   54  EESYLALLDALRWLG  YLALLDALR       0.3897       737.3              32.00    Sequence
DRB1_1501  209  THVLRGEDLLPSTPR  HVLRGEDLL       0.3887       745.4              32.00    Sequence
DRB1_1501   53  SEESYLALLDALRWL  YLALLDALR       0.3884       748.2              32.00    Sequence
DRB1_1501  204  ALMKITHVLRGEDLL  HVLRGEDLL       0.3879       751.9              32.00    Sequence
DRB1_1501  165  AWNDLVRGPVTFAAG  DLVRGPVTF       0.3876       754.2              32.00    Sequence
DRB1_1501  116  VEARHVAAGRNPKLG  HVAAGRNPK       0.3821       801.0              50.00    Sequence
DRB1_1501  166  WNDLVRGPVTFAAGS  LVRGPVTFA       0.3818       803.6              50.00    Sequence
DRB1_1501  338  DFTVRLRDHLDTHGH  FTVRLRDHL       0.3814       806.5              50.00    Sequence
DRB1_1501  167  NDLVRGPVTFAAGSV  LVRGPVTFA       0.3805       814.7              50.00    Sequence
DRB1_1501  191  GDPLYTLVNPCDDAL  PLYTLVNPC       0.3801       818.3              50.00    Sequence
DRB1_1501  163  DLAWNDLVRGPVTFA  DLVRGPVTF       0.3797       822.0              50.00    Sequence
DRB1_1501  118  ARHVAAGRNPKLGYD  HVAAGRNPK       0.3783       834.6              50.00    Sequence
DRB1_1501  241  PKFAHLPTVLGEGTK  KFAHLPTVL       0.3778       838.6              50.00    Sequence
DRB1_1501  115  EVEARHVAAGRNPKL  VEARHVAAG       0.3760       855.5              50.00    Sequence
DRB1_1501  169  LVRGPVTFAAGSVPD  LVRGPVTFA       0.3733       880.7              50.00    Sequence
DRB1_1501  339  FTVRLRDHLDTHGHH  RLRDHLDTH       0.3730       883.7              50.00    Sequence
DRB1_1501  187  TRASGDPLYTLVNPC  PLYTLVNPC       0.3707       905.9              50.00    Sequence
DRB1_1501  153  PVVRLRMPDDDLAWN  PVVRLRMPD       0.3683       930.1              50.00    Sequence
DRB1_1501   61  LDALRWLGLDWDEGP  ALRWLGLDW       0.3668       944.6              50.00    Sequence
DRB1_1501  405  GAAVLDAALAALTSV  AAVLDAALA       0.3668       944.6              50.00    Sequence
DRB1_1501  245  HLPTVLGEGTKKLSK  TVLGEGTKK       0.3657       956.3              50.00    Sequence
DRB1_1501  246  LPTVLGEGTKKLSKR  VLGEGTKKL       0.3653       960.2              50.00    Sequence
DRB1_1501  210  HVLRGEDLLPSTPRQ  HVLRGEDLL       0.3646       967.2              50.00    Sequence
DRB1_1501  283  LALLGWSIADDHDLF  LALLGWSIA       0.3592      1026.3              50.00    Sequence
DRB1_1501  145  AYLAEGRQPVVRLRM  LAEGRQPVV       0.3591      1026.5              50.00    Sequence
DRB1_1501  119  RHVAAGRNPKLGYDN  HVAAGRNPK       0.3572      1048.4              50.00    Sequence
DRB1_1501   31  AYARHTGGTFVFRIE  YARHTGGTF       0.3572      1048.8              50.00    Sequence
DRB1_1501   52  DSEESYLALLDALRW  YLALLDALR       0.3567      1054.3              50.00    Sequence
DRB1_1501  244  AHLPTVLGEGTKKLS  TVLGEGTKK       0.3550      1074.0              50.00    Sequence
DRB1_1501  271  DRGFIPEGLLNYLAL  EGLLNYLAL       0.3545      1079.1              50.00    Sequence
DRB1_1501  247  PTVLGEGTKKLSKRD  VLGEGTKKL       0.3495      1138.9              50.00    Sequence
DRB1_1501  295  DLFGLDEMVAAFDVA  LFGLDEMVA       0.3479      1159.8              50.00    Sequence
DRB1_1501  192  DPLYTLVNPCDDALM  PLYTLVNPC       0.3476      1163.6              50.00    Sequence
DRB1_1501   30  WAYARHTGGTFVFRI  YARHTGGTF       0.3440      1209.6              50.00    Sequence
DRB1_1501    0  VTATETVRVRFCPSP  VRVRFCPSP       0.3361      1316.6              50.00    Sequence
DRB1_1501  243  FAHLPTVLGEGTKKL  TVLGEGTKK       0.3329      1364.2              50.00    Sequence
DRB1_1501  449  PIRVAATGTTVSPPL  RVAATGTTV       0.3312      1388.7              50.00    Sequence
DRB1_1501  235  GVAERIPKFAHLPTV  RIPKFAHLP       0.3300      1406.8              50.00    Sequence
DRB1_1501  415  ALTSVTDWTAPLIEA  SVTDWTAPL       0.3299      1408.1              50.00    Sequence
DRB1_1501  448  SPIRVAATGTTVSPP  RVAATGTTV       0.3290      1422.3              50.00    Sequence
DRB1_1501  293  DHDLFGLDEMVAAFD  LFGLDEMVA       0.3280      1437.2              50.00    Sequence
DRB1_1501   32  YARHTGGTFVFRIED  YARHTGGTF       0.3266      1459.2              50.00    Sequence
DRB1_1501  292  DDHDLFGLDEMVAAF  LFGLDEMVA       0.3252      1481.6              50.00    Sequence
DRB1_1501  262  PQSNLFAHRDRGFIP  NLFAHRDRG       0.3243      1496.1              50.00    Sequence
DRB1_1501   62  DALRWLGLDWDEGPE  ALRWLGLDW       0.3239      1502.7              50.00    Sequence
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DRB1_1501  294  HDLFGLDEMVAAFDV  LFGLDEMVA        0.3231       1516.6                 50.00     Sequence
DRB1_1501  114  EEVEARHVAAGRNPK  VEARHVAAG        0.3216       1540.5                 50.00     Sequence
DRB1_1501  120  HVAAGRNPKLGYDNF  HVAAGRNPK        0.3205       1559.3                 50.00     Sequence
DRB1_1501  263  QSNLFAHRDRGFIPE  NLFAHRDRG        0.3204       1561.6                 50.00     Sequence
DRB1_1501  340  TVRLRDHLDTHGHHI  RLRDHLDTH        0.3187       1590.0                 50.00     Sequence
DRB1_1501  264  SNLFAHRDRGFIPEG  NLFAHRDRG        0.3187       1590.3                 50.00     Sequence
DRB1_1501  248  TVLGEGTKKLSKRDP  VLGEGTKKL        0.3181       1599.9                 50.00     Sequence
DRB1_1501  261  DPQSNLFAHRDRGFI  NLFAHRDRG        0.3179       1604.5                 50.00     Sequence
DRB1_1501  296  LFGLDEMVAAFDVAD  LFGLDEMVA        0.3177       1606.9                 50.00     Sequence
DRB1_1501  203  DALMKITHVLRGEDL  DALMKITHV        0.3151       1652.8                 50.00     Sequence
DRB1_1501  144  AAYLAEGRQPVVRLR  LAEGRQPVV        0.3144       1665.2                 50.00     Sequence
DRB1_1501  323  ADALNAEHIRMLDVG  EHIRMLDVG        0.3118       1712.8                 50.00     Sequence
DRB1_1501  342  RLRDHLDTHGHHIAL  RLRDHLDTH        0.3100       1746.5                 50.00     Sequence
DRB1_1501  180  SVPDFALTRASGDPL  SVPDFALTR        0.3092       1761.4                 50.00     Sequence
DRB1_1501   29  NWAYARHTGGTFVFR  YARHTGGTF        0.3084       1777.1                 50.00     Sequence
DRB1_1501  450  IRVAATGTTVSPPLF  RVAATGTTV        0.3071       1802.6                 50.00     Sequence
DRB1_1501   63  ALRWLGLDWDEGPEV  ALRWLGLDW        0.3070       1804.6                 50.00     Sequence
DRB1_1501  202  DDALMKITHVLRGED  DALMKITHV        0.3039       1865.6                 50.00     Sequence
DRB1_1501  242  KFAHLPTVLGEGTKK  KFAHLPTVL        0.3029       1887.3                 50.00     Sequence
DRB1_1501  218  LPSTPRQLALHQALI  QLALHQALI        0.3021       1903.2                 50.00     Sequence
DRB1_1501  201  CDDALMKITHVLRGE  DALMKITHV        0.3021       1903.5                 50.00     Sequence
DRB1_1501  341  VRLRDHLDTHGHHIA  RLRDHLDTH        0.3020       1905.7                 50.00     Sequence
DRB1_1501  416  LTSVTDWTAPLIEAA  SVTDWTAPL        0.3003       1939.9                 50.00     Sequence
DRB1_1501  447  FSPIRVAATGTTVSP  RVAATGTTV        0.2986       1975.6                 50.00     Sequence
DRB1_1501  417  TSVTDWTAPLIEAAL  SVTDWTAPL        0.2975       2000.0                 50.00     Sequence
DRB1_1501  193  PLYTLVNPCDDALMK  PLYTLVNPC        0.2959       2034.3                 50.00     Sequence
DRB1_1501  179  GSVPDFALTRASGDP  SVPDFALTR        0.2956       2040.8                 50.00     Sequence
DRB1_1501  403  PDGAAVLDAALAALT  AVLDAALAA        0.2955       2042.7                 50.00     Sequence
DRB1_1501  113  PEEVEARHVAAGRNP  VEARHVAAG        0.2945       2065.4                 50.00     Sequence
DRB1_1501  200  PCDDALMKITHVLRG  ALMKITHVL        0.2939       2079.3                 50.00     Sequence
DRB1_1501  162  DDLAWNDLVRGPVTF  DLVRGPVTF        0.2926       2108.3                 50.00     Sequence
DRB1_1501  265  NLFAHRDRGFIPEGL  NLFAHRDRG        0.2887       2199.7                 50.00     Sequence
DRB1_1501   51  RDSEESYLALLDALR  YLALLDALR        0.2873       2233.2                 50.00     Sequence
DRB1_1501  451  RVAATGTTVSPPLFE  RVAATGTTV        0.2869       2242.2                 50.00     Sequence
DRB1_1501  260  RDPQSNLFAHRDRGF  NLFAHRDRG        0.2867       2247.4                 50.00     Sequence
DRB1_1501  404  DGAAVLDAALAALTS  AVLDAALAA        0.2840       2315.6                 50.00     Sequence
DRB1_1501  199  NPCDDALMKITHVLR  DALMKITHV        0.2838       2320.4                 50.00     Sequence
DRB1_1501  270  RDRGFIPEGLLNYLA  FIPEGLLNY        0.2829       2343.1                 50.00     Sequence
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DRB1_1501  143  RAAYLAEGRQPVVRL  LAEGRQPVV        0.2780       2470.5                 50.00     Sequence
DRB1_1501  418  SVTDWTAPLIEAALK  SVTDWTAPL        0.2756       2535.0                 50.00     Sequence
DRB1_1501  170  VRGPVTFAAGSVPDF  VRGPVTFAA        0.2734       2597.2                 50.00     Sequence
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DRB1_1501  359  AAFAAAAELVQTRIV  AAELVQTRI        0.2684       2738.9                 50.00     Sequence
DRB1_1501   34  RHTGGTFVFRIEDTD  HTGGTFVFR        0.2666       2794.7                 50.00     Sequence
DRB1_1501  456  GTTVSPPLFESLELL  PLFESLELL        0.2660       2812.4                 50.00     Sequence
DRB1_1501  181  VPDFALTRASGDPLY  DFALTRASG        0.2649       2846.5                 50.00     Sequence
DRB1_1501  284  ALLGWSIADDHDLFG  ALLGWSIAD        0.2623       2928.6                 50.00     Sequence
DRB1_1501   35  HTGGTFVFRIEDTDA  FVFRIEDTD        0.2620       2935.5                 50.00     Sequence
DRB1_1501   33  ARHTGGTFVFRIEDT  HTGGTFVFR        0.2615       2953.9                 50.00     Sequence
DRB1_1501   36  TGGTFVFRIEDTDAQ  FVFRIEDTD        0.2610       2966.9                 50.00     Sequence
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DRB1_1501  132  DNFDRHLTDAQRAAY  NFDRHLTDA        0.2447       3540.1               50.00     Sequence
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DRB1_1501  171  RGPVTFAAGSVPDFA  TFAAGSVPD        0.2303       4136.4               50.00     Sequence
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DRB1_1501  267  FAHRDRGFIPEGLLN  GFIPEGLLN        0.1914       6301.6                 50.00     Sequence
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   DRB1_1501  257  LSKRDPQSNLFAHRD  PQSNLFAHR        0.1145      14490.5                  50.00     Sequence
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   DRB1_1501   48  DAQRDSEESYLALLD  SEESYLALL        0.1051      16043.7                  50.00     Sequence
   DRB1_1501  454  ATGTTVSPPLFESLE  ATGTTVSPP        0.1041      16208.3                  50.00     Sequence
   DRB1_1501  309  ADVNSSPARFDQKKA  ADVNSSPAR        0.1041      16208.6                  50.00     Sequence
   DRB1_1501  156  RLRMPDDDLAWNDLV  LRMPDDDLA        0.0983      17257.8                  50.00     Sequence
   DRB1_1501   47  TDAQRDSEESYLALL  SEESYLALL        0.0962      17657.1                  50.00     Sequence
   DRB1_1501  286  LGWSIADDHDLFGLD  LGWSIADDH        0.0954      17816.0                  50.00     Sequence
   DRB1_1501   43  RIEDTDAQRDSEESY  RIEDTDAQR        0.0930      18277.2                  50.00     Sequence
   DRB1_1501   10  FCPSPTGTPHVGLVR  GTPHVGLVR        0.0923      18413.2                  50.00     Sequence
   DRB1_1501  393  DPKAAAKELGPDGAA  AAKELGPDG        0.0905      18782.4                  50.00     Sequence
   DRB1_1501   42  FRIEDTDAQRDSEES  RIEDTDAQR        0.0890      19082.9                  50.00     Sequence
   DRB1_1501   67  LGLDWDEGPEVGGPY  GLDWDEGPE        0.0881      19283.0                  50.00     Sequence
   DRB1_1501  155  VRLRMPDDDLAWNDL  LRMPDDDLA        0.0873      19445.6                  50.00     Sequence
   DRB1_1501    9  RFCPSPTGTPHVGLV  RFCPSPTGT        0.0864      19639.9                  50.00     Sequence
   DRB1_1501  109  AFSTPEEVEARHVAA  EVEARHVAA        0.0840      20144.6                  50.00     Sequence
   DRB1_1501   68  GLDWDEGPEVGGPYG  GLDWDEGPE        0.0811      20798.1                  50.00     Sequence
   DRB1_1501  392  IDPKAAAKELGPDGA  AAKELGPDG        0.0793      21198.0                  50.00     Sequence
   DRB1_1501   46  DTDAQRDSEESYLAL  DAQRDSEES        0.0762      21934.6                  50.00     Sequence
   DRB1_1501  288  WSIADDHDLFGLDEM  SIADDHDLF        0.0761      21947.9                  50.00     Sequence
   DRB1_1501  311  VNSSPARFDQKKADA  RFDQKKADA        0.0753      22146.6                  50.00     Sequence
   DRB1_1501  310  DVNSSPARFDQKKAD  DVNSSPARF        0.0723      22879.5                  50.00     Sequence
   DRB1_1501  287  GWSIADDHDLFGLDE  SIADDHDLF        0.0657      24550.2                  50.00     Sequence
   DRB1_1501   44  IEDTDAQRDSEESYL  DAQRDSEES        0.0654      24637.2                  50.00     Sequence
   DRB1_1501   45  EDTDAQRDSEESYLA  DAQRDSEES        0.0652      24696.5                  50.00     Sequence
   DRB1_1501   69  LDWDEGPEVGGPYGP  LDWDEGPEV        0.0616      25668.2                  50.00     Sequence
   DRB1_1501  107  YHAFSTPEEVEARHV  YHAFSTPEE        0.0535      28031.2                  50.00     Sequence
   DRB1_1501  108  HAFSTPEEVEARHVA  HAFSTPEEV        0.0454      30607.3                  50.00     Sequence
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Allele: DRB1_1501. Number of high binders 18. Number of weak binders 129. Number of peptides 476

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB3_0101  378  AWELLKFFNDDQYVI  FFNDDQYVI        0.7898          9.7           SB     0.05     Sequence
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DRB3_0101  379  WELLKFFNDDQYVID  FFNDDQYVI         0.7864          10.1          SB     0.05     Sequence
DRB3_0101  380  ELLKFFNDDQYVIDP  FFNDDQYVI         0.7683          12.3          SB     0.10     Sequence
DRB3_0101  381  LLKFFNDDQYVIDPK  FFNDDQYVI         0.7461          15.6          SB     0.10     Sequence
DRB3_0101  382  LKFFNDDQYVIDPKA  FFNDDQYVI         0.7157          21.7          SB     0.20     Sequence
DRB3_0101  383  KFFNDDQYVIDPKAA  FFNDDQYVI         0.6767          33.1          SB     0.40     Sequence
DRB3_0101  291  ADDHDLFGLDEMVAA  FGLDEMVAA         0.6715          34.9          SB     0.40     Sequence
DRB3_0101  384  FFNDDQYVIDPKAAA  FFNDDQYVI         0.6574          40.7          SB     0.80     Sequence
DRB3_0101  292  DDHDLFGLDEMVAAF  FGLDEMVAA         0.6558          41.4          SB     0.80     Sequence
DRB3_0101  293  DHDLFGLDEMVAAFD  FGLDEMVAA         0.6256          57.5          WB     0.80     Sequence
DRB3_0101  294  HDLFGLDEMVAAFDV  FGLDEMVAA         0.5915          83.1          WB     2.00     Sequence
DRB3_0101  295  DLFGLDEMVAAFDVA  FGLDEMVAA         0.5574         120.2          WB     2.00     Sequence
DRB3_0101   63  ALRWLGLDWDEGPEV  LDWDEGPEV         0.5303         161.1          WB     2.00     Sequence
DRB3_0101  296  LFGLDEMVAAFDVAD  FGLDEMVAA         0.5269         167.2          WB     4.00     Sequence
DRB3_0101   64  LRWLGLDWDEGPEVG  LDWDEGPEV         0.5186         182.9          WB     4.00     Sequence
DRB3_0101   65  RWLGLDWDEGPEVGG  LDWDEGPEV         0.5116         197.2          WB     4.00     Sequence
DRB3_0101  297  FGLDEMVAAFDVADV  FGLDEMVAA         0.5072         206.9          WB     4.00     Sequence
DRB3_0101   66  WLGLDWDEGPEVGGP  LDWDEGPEV         0.5014         220.2          WB     4.00     Sequence
DRB3_0101  385  FNDDQYVIDPKAAAK  YVIDPKAAA         0.4985         227.4          WB     4.00     Sequence
DRB3_0101   67  LGLDWDEGPEVGGPY  LDWDEGPEV         0.4915         245.3          WB     4.00     Sequence
DRB3_0101   68  GLDWDEGPEVGGPYG  LDWDEGPEV         0.4778         284.4          WB     4.00     Sequence
DRB3_0101  386  NDDQYVIDPKAAAKE  YVIDPKAAA         0.4522         375.0          WB     8.00     Sequence
DRB3_0101   69  LDWDEGPEVGGPYGP  LDWDEGPEV         0.4491         387.8          WB     8.00     Sequence
DRB3_0101  286  LGWSIADDHDLFGLD  SIADDHDLF         0.4471         396.5          WB     8.00     Sequence
DRB3_0101  284  ALLGWSIADDHDLFG  SIADDHDLF         0.4409         424.0          WB     8.00     Sequence
DRB3_0101  285  LLGWSIADDHDLFGL  SIADDHDLF         0.4400         427.9          WB     8.00     Sequence
DRB3_0101  283  LALLGWSIADDHDLF  SIADDHDLF         0.4354         449.8          WB     8.00     Sequence
DRB3_0101   87  SQRAEIYRDVLARLL  IYRDVLARL         0.4296         478.9          WB     8.00     Sequence
DRB3_0101  287  GWSIADDHDLFGLDE  SIADDHDLF         0.4210         525.8                 8.00     Sequence
DRB3_0101  387  DDQYVIDPKAAAKEL  YVIDPKAAA         0.4193         535.2                 8.00     Sequence
DRB3_0101  300  DEMVAAFDVADVNSS  FDVADVNSS         0.4107         587.5                 8.00     Sequence
DRB3_0101   88  QRAEIYRDVLARLLA  IYRDVLARL         0.4054         622.3                 8.00     Sequence
DRB3_0101  288  WSIADDHDLFGLDEM  SIADDHDLF         0.4010         652.4                 8.00     Sequence
DRB3_0101   53  SEESYLALLDALRWL  ALLDALRWL         0.3943         702.1                 8.00     Sequence
DRB3_0101  301  EMVAAFDVADVNSSP  FDVADVNSS         0.3938         705.7                 8.00     Sequence
DRB3_0101  388  DQYVIDPKAAAKELG  YVIDPKAAA         0.3869         760.3                 8.00     Sequence
DRB3_0101   54  EESYLALLDALRWLG  ALLDALRWL         0.3785         832.3                16.00     Sequence
DRB3_0101   89  RAEIYRDVLARLLAA  IYRDVLARL         0.3770         846.0                16.00     Sequence
DRB3_0101  302  MVAAFDVADVNSSPA  FDVADVNSS         0.3750         864.4                16.00     Sequence
DRB3_0101   36  TGGTFVFRIEDTDAQ  FRIEDTDAQ         0.3703         909.4                16.00     Sequence
DRB3_0101  282  YLALLGWSIADDHDL  WSIADDHDL         0.3670         942.9                16.00     Sequence
DRB3_0101   55  ESYLALLDALRWLGL  ALLDALRWL         0.3657         956.6                16.00     Sequence
DRB3_0101   37  GGTFVFRIEDTDAQR  FRIEDTDAQ         0.3642         972.1                16.00     Sequence
DRB3_0101  389  QYVIDPKAAAKELGP  YVIDPKAAA         0.3610        1005.9                16.00     Sequence
DRB3_0101   38  GTFVFRIEDTDAQRD  FRIEDTDAQ         0.3560        1061.6                16.00     Sequence
DRB3_0101  170  VRGPVTFAAGSVPDF  FAAGSVPDF         0.3546        1077.8                16.00     Sequence
DRB3_0101  183  DFALTRASGDPLYTL  ASGDPLYTL         0.3536        1089.6                16.00     Sequence
DRB3_0101  303  VAAFDVADVNSSPAR  FDVADVNSS         0.3518        1111.8                16.00     Sequence
DRB3_0101   86  QSQRAEIYRDVLARL  IYRDVLARL         0.3483        1154.8                16.00     Sequence
DRB3_0101  172  GPVTFAAGSVPDFAL  FAAGSVPDF         0.3479        1159.6                16.00     Sequence
DRB3_0101  184  FALTRASGDPLYTLV  ASGDPLYTL         0.3476        1162.7                16.00     Sequence
DRB3_0101  171  RGPVTFAAGSVPDFA  FAAGSVPDF         0.3471        1169.0                16.00     Sequence
DRB3_0101  261  DPQSNLFAHRDRGFI  FAHRDRGFI         0.3441        1208.4                16.00     Sequence
DRB3_0101  185  ALTRASGDPLYTLVN  ASGDPLYTL         0.3440        1208.9                16.00     Sequence
DRB3_0101   56  SYLALLDALRWLGLD  ALLDALRWL         0.3438        1212.5                16.00     Sequence
DRB3_0101  289  SIADDHDLFGLDEMV  SIADDHDLF         0.3405        1256.2                16.00     Sequence
DRB3_0101  326  LNAEHIRMLDVGDFT  LNAEHIRML         0.3345        1339.9                16.00     Sequence
DRB3_0101  262  PQSNLFAHRDRGFIP  FAHRDRGFI         0.3336        1353.6                16.00     Sequence
DRB3_0101  390  YVIDPKAAAKELGPD  YVIDPKAAA         0.3320        1376.8                16.00     Sequence
DRB3_0101  173  PVTFAAGSVPDFALT  FAAGSVPDF         0.3311        1391.0                16.00     Sequence
DRB3_0101   39  TFVFRIEDTDAQRDS  FRIEDTDAQ         0.3291        1421.4                16.00     Sequence
DRB3_0101  325  ALNAEHIRMLDVGDF  LNAEHIRML         0.3271        1451.8                16.00     Sequence
DRB3_0101  304  AAFDVADVNSSPARF  FDVADVNSS         0.3269        1454.7                16.00     Sequence
DRB3_0101   90  AEIYRDVLARLLAAG  IYRDVLARL         0.3264        1462.9                16.00     Sequence
DRB3_0101  174  VTFAAGSVPDFALTR  FAAGSVPDF         0.3230        1518.0                16.00     Sequence
DRB3_0101  186  LTRASGDPLYTLVNP  ASGDPLYTL         0.3227        1522.7                16.00     Sequence
DRB3_0101   57  YLALLDALRWLGLDW  ALLDALRWL         0.3201        1565.6                16.00     Sequence
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DRB3_0101	348	DTHGHHIALDEAAFA	IALDEAAFA	0.3137	1679.2	16.00	Sequence
DRB3_0101	263	QSNLFAHRDRGFIPE	FAHRDRGFI	0.3135	1681.9	16.00	Sequence
DRB3_0101	40	FVFRIEDTDAQRDSE	FRIEDTDAQ	0.3117	1715.8	16.00	Sequence
DRB3_0101	187	TRASGDPLYTLVNPC	ASGDPLYTL	0.3106	1735.2	16.00	Sequence
DRB3_0101	91	EIYRDVLARLLAAGE	IYRDVLARL	0.3094	1757.7	16.00	Sequence
DRB3_0101	22	LVRTALFNWAYARHT	FNWAYARHT	0.3028	1889.5	16.00	Sequence
DRB3_0101	175	TFAAGSVPDFALTRA	FAAGSVPDF	0.3016	1912.3	16.00	Sequence
DRB3_0101	305	AFDVADVNSSPARFD	FDVADVNSS	0.3008	1929.5	16.00	Sequence
DRB3_0101	368	VQTRIVVLGDAWELL	VLGDAWELL	0.3001	1944.7	16.00	Sequence
DRB3_0101	189	ASGDPLYTLVNPCDD	ASGDPLYTL	0.2995	1957.6	16.00	Sequence
DRB3_0101	188	RASGDPLYTLVNPCD	ASGDPLYTL	0.2983	1981.8	16.00	Sequence
DRB3_0101	58	LALLDALRWLGLDWD	ALLDALRWL	0.2983	1983.7	16.00	Sequence
DRB3_0101	327	NAEHIRMLDVGDFTV	IRMLDVGDF	0.2961	2030.0	16.00	Sequence
DRB3_0101	176	FAAGSVPDFALTRAS	FAAGSVPDF	0.2958	2036.6	16.00	Sequence
DRB3_0101	320	QKKADALNAEHIRML	LNAEHIRML	0.2943	2069.5	16.00	Sequence
DRB3_0101	264	SNLFAHRDRGFIPEG	FAHRDRGFI	0.2926	2110.0	32.00	Sequence
DRB3_0101	349	THGHHIALDEAAFAA	IALDEAAFA	0.2916	2131.1	32.00	Sequence
DRB3_0101	41	VFRIEDTDAQRDSEE	FRIEDTDAQ	0.2913	2137.6	32.00	Sequence
DRB3_0101	329	EHIRMLDVGDFTVRL	IRMLDVGDF	0.2910	2145.6	32.00	Sequence
DRB3_0101	466	SLELLGRDRSMQRLR	LGRDRSMQR	0.2901	2167.2	32.00	Sequence
DRB3_0101	47	TDAQRDSEESYLALL	AQRDSEESY	0.2898	2172.7	32.00	Sequence
DRB3_0101	321	KKADALNAEHIRMLD	LNAEHIRML	0.2893	2184.7	32.00	Sequence
DRB3_0101	465	ESLELLGRDRSMQRL	LGRDRSMQR	0.2891	2190.9	32.00	Sequence
DRB3_0101	48	DAQRDSEESYLALLD	AQRDSEESY	0.2867	2248.4	32.00	Sequence
DRB3_0101	369	QTRIVVLGDAWELLK	VLGDAWELL	0.2858	2269.2	32.00	Sequence
DRB3_0101	467	LELLGRDRSMQRLRA	LGRDRSMQR	0.2823	2356.9	32.00	Sequence
DRB3_0101	92	IYRDVLARLLAAGEA	IYRDVLARL	0.2822	2359.6	32.00	Sequence
DRB3_0101	322	KADALNAEHIRMLDV	LNAEHIRML	0.2822	2361.3	32.00	Sequence
DRB3_0101	464	FESLELLGRDRSMQR	LGRDRSMQR	0.2805	2404.9	32.00	Sequence
DRB3_0101	23	VRTALFNWAYARHTG	FNWAYARHT	0.2803	2408.3	32.00	Sequence
DRB3_0101	265	NLFAHRDRGFIPEGL	FAHRDRGFI	0.2795	2430.7	32.00	Sequence
DRB3_0101	46	DTDAQRDSEESYLAL	AQRDSEESY	0.2794	2433.2	32.00	Sequence
DRB3_0101	269	HRDRGFIPEGLLNYL	FIPEGLLNY	0.2780	2469.3	32.00	Sequence
DRB3_0101	306	FDVADVNSSPARFDQ	FDVADVNSS	0.2773	2487.5	32.00	Sequence
DRB3_0101	328	AEHIRMLDVGDFTVR	IRMLDVGDF	0.2768	2502.0	32.00	Sequence
DRB3_0101	45	EDTDAQRDSEESYLA	AQRDSEESY	0.2756	2534.9	32.00	Sequence
DRB3_0101	312	NSSPARFDQKKADAL	FDQKKADAL	0.2753	2543.5	32.00	Sequence
DRB3_0101	370	TRIVVLGDAWELLKF	VLGDAWELL	0.2749	2552.8	32.00	Sequence
DRB3_0101	330	HIRMLDVGDFTVRLR	IRMLDVGDF	0.2747	2560.6	32.00	Sequence
DRB3_0101	371	RIVVLGDAWELLKFF	VLGDAWELL	0.2743	2571.6	32.00	Sequence
DRB3_0101	350	HGHHIALDEAAFAAA	IALDEAAFA	0.2730	2607.6	32.00	Sequence
DRB3_0101	401	LGPDGAAVLDAALAA	LGPDGAAVL	0.2724	2625.2	32.00	Sequence
DRB3_0101	26	ALFNWAYARHTGGTF	FNWAYARHT	0.2724	2625.4	32.00	Sequence
DRB3_0101	49	AQRDSEESYLALLDA	AQRDSEESY	0.2722	2629.0	32.00	Sequence
DRB3_0101	268	AHRDRGFIPEGLLNY	FIPEGLLNY	0.2712	2658.1	32.00	Sequence
DRB3_0101	468	ELLGRDRSMQRLRAA	LGRDRSMQR	0.2698	2699.9	32.00	Sequence
DRB3_0101	313	SSPARFDQKKADALN	FDQKKADAL	0.2688	2727.9	32.00	Sequence
DRB3_0101	272	RGFIPEGLLNYLALL	FIPEGLLNY	0.2675	2766.3	32.00	Sequence
DRB3_0101	469	LLGRDRSMQRLRAAR	LGRDRSMQR	0.2673	2772.6	32.00	Sequence
DRB3_0101	270	RDRGFIPEGLLNYLA	FIPEGLLNY	0.2659	2815.3	32.00	Sequence
DRB3_0101	59	ALLDALRWLGLDWDE	ALLDALRWL	0.2659	2816.3	32.00	Sequence
DRB3_0101	377	DAWELLKFFNDDQYV	LKFFNDDQY	0.2641	2872.1	32.00	Sequence
DRB3_0101	323	ADALNAEHIRMLDVG	LNAEHIRML	0.2634	2891.1	32.00	Sequence
DRB3_0101	281	NYLALLGWSIADDHD	LGWSIADDH	0.2600	3000.3	32.00	Sequence
DRB3_0101	331	IRMLDVGDFTVRLRD	IRMLDVGDF	0.2595	3016.9	32.00	Sequence
DRB3_0101	271	DRGFIPEGLLNYLAL	FIPEGLLNY	0.2587	3042.4	32.00	Sequence
DRB3_0101	314	SPARFDQKKADALNA	FDQKKADAL	0.2577	3077.7	32.00	Sequence
DRB3_0101	27	LFNWAYARHTGGTFV	FNWAYARHT	0.2575	3082.5	32.00	Sequence
DRB3_0101	412	ALAALTSVTDWTAPL	SVTDWTAPL	0.2559	3136.5	32.00	Sequence
DRB3_0101	140	DAQRAAYLAEGRQPV	YLAEGRQPV	0.2540	3203.0	32.00	Sequence
DRB3_0101	372	IVVLGDAWELLKFFN	VLGDAWELL	0.2538	3209.8	32.00	Sequence
DRB3_0101	141	AQRAAYLAEGRQPVV	YLAEGRQPV	0.2528	3242.2	32.00	Sequence
DRB3_0101	397	AAKELGPDGAAVLDA	LGPDGAAVL	0.2527	3246.7	32.00	Sequence
DRB3_0101	273	GFIPEGLLNYLALLG	FIPEGLLNY	0.2526	3251.2	32.00	Sequence
DRB3_0101	396	AAAKELGPDGAAVLD	LGPDGAAVL	0.2524	3259.2	32.00	Sequence
DRB3_0101	373	VVLGDAWELLKFFND	VLGDAWELL	0.2516	3286.8	32.00	Sequence

DRB3_0101	266	LFAHRDRGFIPEGLL	FAHRDRGFI	0.2515	3288.1	32.00	Sequence
DRB3_0101	351	GHHIALDEAAFAAAA	IALDEAAFA	0.2504	3328.5	32.00	Sequence
DRB3_0101	315	PARFDQKKADALNAE	FDQKKADAL	0.2487	3390.0	32.00	Sequence
DRB3_0101	324	DALNAEHIRMLDVGD	LNAEHIRML	0.2471	3451.4	32.00	Sequence
DRB3_0101	413	LAALTSVTDWTAPLI	SVTDWTAPL	0.2470	3453.2	32.00	Sequence
DRB3_0101	395	KAAAKELGPDGAAVL	LGPDGAAVL	0.2468	3460.0	32.00	Sequence
DRB3_0101	24	RTALFNWAYARHTGG	FNWAYARHT	0.2468	3461.5	32.00	Sequence
DRB3_0101	400	ELGPDGAAVLDAALA	LGPDGAAVL	0.2463	3479.5	32.00	Sequence
DRB3_0101	280	LNYLALLGWSIADDH	LGWSIADDH	0.2429	3612.1	32.00	Sequence
DRB3_0101	156	RLRMPDDDLAWNDLV	RMPDDDLAW	0.2415	3665.4	32.00	Sequence
DRB3_0101	142	QRAAYLAEGRQPVVR	YLAEGRQPV	0.2408	3693.1	32.00	Sequence
DRB3_0101	28	FNWAYARHTGGTFVF	FNWAYARHT	0.2407	3696.5	32.00	Sequence
DRB3_0101	470	LGRDRSMQRLRAARQ	LGRDRSMQR	0.2404	3710.5	32.00	Sequence
DRB3_0101	154	VVRLRMPDDDLAWND	RMPDDDLAW	0.2399	3728.2	32.00	Sequence
DRB3_0101	398	AKELGPDGAAVLDAA	LGPDGAAVL	0.2377	3820.9	32.00	Sequence
DRB3_0101	316	ARFDQKKADALNAEH	FDQKKADAL	0.2373	3834.6	32.00	Sequence
DRB3_0101	14	PTGTPHVGLVRTALF	VGLVRTALF	0.2370	3850.3	32.00	Sequence
DRB3_0101	42	FRIEDTDAQRDSEES	FRIEDTDAQ	0.2364	3874.2	32.00	Sequence
DRB3_0101	336	VGDFTVRLRDHLDTH	RLRDHLDTH	0.2364	3874.3	32.00	Sequence
DRB3_0101	274	FIPEGLLNYLALLGW	FIPEGLLNY	0.2362	3882.2	32.00	Sequence
DRB3_0101	155	VRLRMPDDDLAWNDL	RMPDDDLAW	0.2355	3912.9	32.00	Sequence
DRB3_0101	125	RNPKLGYDNFDRHLT	YDNFDRHLT	0.2353	3920.0	32.00	Sequence
DRB3_0101	414	AALTSVTDWTAPLIE	SVTDWTAPL	0.2350	3931.3	32.00	Sequence
DRB3_0101	131	YDNFDRHLTDAQRAA	YDNFDRHLT	0.2343	3961.8	32.00	Sequence
DRB3_0101	128	KLGYDNFDRHLTDAQ	YDNFDRHLT	0.2335	3998.4	32.00	Sequence
DRB3_0101	352	HHIALDEAAFAAAAE	IALDEAAFA	0.2323	4049.0	32.00	Sequence
DRB3_0101	126	NPKLGYDNFDRHLTD	YDNFDRHLT	0.2317	4076.9	32.00	Sequence
DRB3_0101	399	KELGPDGAAVLDAAL	LGPDGAAVL	0.2308	4116.8	32.00	Sequence
DRB3_0101	337	GDFTVRLRDHLDTHG	RLRDHLDTH	0.2276	4262.0	32.00	Sequence
DRB3_0101	374	VLGDAWELLKFFNDD	VLGDAWELL	0.2275	4263.6	32.00	Sequence
DRB3_0101	15	TGTPHVGLVRTALFN	VGLVRTALF	0.2275	4267.0	32.00	Sequence
DRB3_0101	157	LRMPDDDLAWNDLVR	RMPDDDLAW	0.2273	4272.5	32.00	Sequence
DRB3_0101	129	LGYDNFDRHLTDAQR	YDNFDRHLT	0.2269	4291.7	32.00	Sequence
DRB3_0101	143	RAAYLAEGRQPVVRL	YLAEGRQPV	0.2259	4339.2	32.00	Sequence
DRB3_0101	127	PKLGYDNFDRHLTDA	YDNFDRHLT	0.2250	4383.5	32.00	Sequence
DRB3_0101	16	GTPHVGLVRTALFNW	VGLVRTALF	0.2240	4430.6	32.00	Sequence
DRB3_0101	367	LVQTRIVVLGDAWEL	VVLGDAWEL	0.2239	4435.8	32.00	Sequence
DRB3_0101	317	RFDQKKADALNAEHI	FDQKKADAL	0.2231	4475.7	32.00	Sequence
DRB3_0101	211	VLRGEDLLPSTPRQL	LLPSTPRQL	0.2230	4476.9	32.00	Sequence
DRB3_0101	25	TALFNWAYARHTGGT	FNWAYARHT	0.2215	4551.5	32.00	Sequence
DRB3_0101	353	HIALDEAAFAAAAEL	IALDEAAFA	0.2211	4570.7	32.00	Sequence
DRB3_0101	191	GDPLYTLVNPCDDAL	TLVNPCDDA	0.2201	4620.0	32.00	Sequence
DRB3_0101	158	RMPDDDLAWNDLVRG	RMPDDDLAW	0.2194	4655.0	32.00	Sequence
DRB3_0101	213	RGEDLLPSTPRQLAL	LLPSTPRQL	0.2178	4735.6	32.00	Sequence
DRB3_0101	78	GGPYGPYRQSQRAEI	YRQSQRAEI	0.2178	4738.6	32.00	Sequence
DRB3_0101	267	FAHRDRGFIPEGLLN	FAHRDRGFI	0.2170	4778.3	32.00	Sequence
DRB3_0101	212	LRGEDLLPSTPRQLA	LLPSTPRQL	0.2169	4785.4	32.00	Sequence
DRB3_0101	194	LYTLVNPCDDALMKI	LVNPCDDAL	0.2162	4818.9	32.00	Sequence
DRB3_0101	44	IEDTDAQRDSEESYL	AQRDSEESY	0.2157	4843.8	32.00	Sequence
DRB3_0101	338	DFTVRLRDHLDTHGH	RLRDHLDTH	0.2156	4849.0	32.00	Sequence
DRB3_0101	195	YTLVNPCDDALMKIT	LVNPCDDAL	0.2143	4919.1	32.00	Sequence
DRB3_0101	79	GPYGPYRQSQRAEIY	YRQSQRAEI	0.2140	4935.9	32.00	Sequence
DRB3_0101	376	GDAWELLKFFNDDQY	LKFFNDDQY	0.2138	4946.3	32.00	Sequence
DRB3_0101	17	TPHVGLVRTALFNWA	VGLVRTALF	0.2135	4964.7	32.00	Sequence
DRB3_0101	130	GYDNFDRHLTDAQRA	YDNFDRHLT	0.2124	5020.3	32.00	Sequence
DRB3_0101	192	DPLYTLVNPCDDALM	TLVNPCDDA	0.2094	5190.6	32.00	Sequence
DRB3_0101	43	RIEDTDAQRDSEESY	AQRDSEESY	0.2091	5205.3	32.00	Sequence
DRB3_0101	318	FDQKKADALNAEHIR	FDQKKADAL	0.2084	5245.9	32.00	Sequence
DRB3_0101	144	AAYLAEGRQPVVRLR	YLAEGRQPV	0.2068	5337.8	50.00	Sequence
DRB3_0101	20	VGLVRTALFNWAYAR	VGLVRTALF	0.2058	5392.2	50.00	Sequence
DRB3_0101	339	FTVRLRDHLDTHGHH	RLRDHLDTH	0.2058	5395.3	50.00	Sequence
DRB3_0101	403	PDGAAVLDAALAALT	AVLDAALAA	0.2051	5437.1	50.00	Sequence
DRB3_0101	276	PEGLLNYLALLGWSI	YLALLGWSI	0.2041	5493.6	50.00	Sequence
DRB3_0101	193	PLYTLVNPCDDALMK	LVNPCDDAL	0.2040	5497.4	50.00	Sequence
DRB3_0101	153	PVVRLRMPDDDLAWN	RMPDDDLAW	0.2033	5544.4	50.00	Sequence
DRB3_0101	415	ALTSVTDWTAPLIEA	SVTDWTAPL	0.2016	5641.9	50.00	Sequence

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DRB3_0101   18  PHVGLVRTALFNWAY  VGLVRTALF        0.2010       5679.6                  50.00     Sequence
DRB3_0101  214  GEDLLPSTPRQLALH  LLPSTPRQL        0.2006       5706.7                  50.00     Sequence
DRB3_0101  333  MLDVGDFTVRLRDHL  FTVRLRDHL        0.1999       5750.1                  50.00     Sequence
DRB3_0101   80  PYGPYRQSQRAEIYR  YRQSQRAEI        0.1972       5919.6                  50.00     Sequence
DRB3_0101  145  AYLAEGRQPVVRLRM  YLAEGRQPV        0.1968       5948.3                  50.00     Sequence
DRB3_0101   19  HVGLVRTALFNWAYA  VGLVRTALF        0.1964       5974.7                  50.00     Sequence
DRB3_0101  237  AERIPKFAHLPTVLG  FAHLPTVLG        0.1942       6114.7                  50.00     Sequence
DRB3_0101  354  IALDEAAFAAAAELV  IALDEAAFA        0.1936       6153.0                  50.00     Sequence
DRB3_0101  159  MPDDDLAWNDLVRGP  DDLAWNDLV        0.1929       6200.2                  50.00     Sequence
DRB3_0101   83  PYRQSQRAEIYRDVL  YRQSQRAEI        0.1926       6221.6                  50.00     Sequence
DRB3_0101  402  GPDGAAVLDAALAAL  AVLDAALAA        0.1925       6230.2                  50.00     Sequence
DRB3_0101  196  TLVNPCDDALMKITH  LVNPCDDAL        0.1911       6320.9                  50.00     Sequence
DRB3_0101   51  RDSEESYLALLDALR  RDSEESYLA        0.1911       6326.9                  50.00     Sequence
DRB3_0101   81  YGPYRQSQRAEIYRD  YRQSQRAEI        0.1894       6443.6                  50.00     Sequence
DRB3_0101  332  RMLDVGDFTVRLRDH  RMLDVGDFT        0.1894       6444.6                  50.00     Sequence
DRB3_0101  290  IADDHDLFGLDEMVA  IADDHDLFG        0.1889       6477.6                  50.00     Sequence
DRB3_0101  160  PDDDLAWNDLVRGPV  DDLAWNDLV        0.1886       6500.1                  50.00     Sequence
DRB3_0101  334  LDVGDFTVRLRDHLD  FTVRLRDHL        0.1885       6506.6                  50.00     Sequence
DRB3_0101  340  TVRLRDHLDTHGHHI  RLRDHLDTH        0.1873       6588.0                  50.00     Sequence
DRB3_0101  215  EDLLPSTPRQLALHQ  LLPSTPRQL        0.1868       6625.9                  50.00     Sequence
DRB3_0101  132  DNFDRHLTDAQRAAY  HLTDAQRAA        0.1862       6669.1                  50.00     Sequence
DRB3_0101   30  WAYARHTGGTFVFRI  YARHTGGTF        0.1857       6703.4                  50.00     Sequence
DRB3_0101  341  VRLRDHLDTHGHHIA  RLRDHLDTH        0.1857       6706.7                  50.00     Sequence
DRB3_0101  335  DVGDFTVRLRDHLDT  FTVRLRDHL        0.1856       6710.1                  50.00     Sequence
DRB3_0101   84  YRQSQRAEIYRDVLA  YRQSQRAEI        0.1847       6778.0                  50.00     Sequence
DRB3_0101  197  LVNPCDDALMKITHV  LVNPCDDAL        0.1840       6828.8                  50.00     Sequence
DRB3_0101  416  LTSVTDWTAPLIEAA  SVTDWTAPL        0.1836       6860.5                  50.00     Sequence
DRB3_0101  277  EGLLNYLALLGWSIA  YLALLGWSI        0.1835       6864.2                  50.00     Sequence
DRB3_0101   29  NWAYARHTGGTFVFR  YARHTGGTF        0.1828       6915.7                  50.00     Sequence
DRB3_0101  404  DGAAVLDAALAALTS  AVLDAALAA        0.1827       6927.0                  50.00     Sequence
DRB3_0101  298  GLDEMVAAFDVADVN  AAFDVADVN        0.1813       7028.8                  50.00     Sequence
DRB3_0101  190  SGDPLYTLVNPCDDA  TLVNPCDDA        0.1811       7046.1                  50.00     Sequence
DRB3_0101   82  GPYRQSQRAEIYRDV  YRQSQRAEI        0.1811       7050.3                  50.00     Sequence
DRB3_0101  133  NFDRHLTDAQRAAYL  HLTDAQRAA        0.1807       7080.6                  50.00     Sequence
DRB3_0101  178  AGSVPDFALTRASGD  FALTRASGD        0.1800       7131.2                  50.00     Sequence
DRB3_0101  152  QPVVRLRMPDDDLAW  RMPDDDLAW        0.1792       7193.4                  50.00     Sequence
DRB3_0101  342  RLRDHLDTHGHHIAL  RLRDHLDTH        0.1787       7233.0                  50.00     Sequence
DRB3_0101  238  ERIPKFAHLPTVLGE  FAHLPTVLG        0.1783       7260.6                  50.00     Sequence
DRB3_0101  216  DLLPSTPRQLALHQA  LLPSTPRQL        0.1782       7267.6                  50.00     Sequence
DRB3_0101   50  QRDSEESYLALLDAL  RDSEESYLA        0.1778       7304.9                  50.00     Sequence
DRB3_0101   31  AYARHTGGTFVFRIE  YARHTGGTF        0.1768       7381.2                  50.00     Sequence
DRB3_0101   34  RHTGGTFVFRIEDTD  FVFRIEDTD        0.1767       7392.5                  50.00     Sequence
DRB3_0101   93  YRDVLARLLAAGEAY  YRDVLARLL        0.1763       7418.9                  50.00     Sequence
DRB3_0101  361  FAAAAELVQTRIVVL  LVQTRIVVL        0.1757       7470.2                  50.00     Sequence
DRB3_0101   61  LDALRWLGLDWDEGP  LGLDWDEGP        0.1752       7512.3                  50.00     Sequence
DRB3_0101  181  VPDFALTRASGDPLY  FALTRASGD        0.1741       7598.3                  50.00     Sequence
DRB3_0101  104  GEAYHAFSTPEEVEA  HAFSTPEEV        0.1740       7607.4                  50.00     Sequence
DRB3_0101  417  TSVTDWTAPLIEAAL  SVTDWTAPL        0.1740       7611.9                  50.00     Sequence
DRB3_0101  146  YLAEGRQPVVRLRMP  YLAEGRQPV        0.1730       7690.3                  50.00     Sequence
DRB3_0101   35  HTGGTFVFRIEDTDA  FVFRIEDTD        0.1730       7693.0                  50.00     Sequence
DRB3_0101  102  AAGEAYHAFSTPEEV  HAFSTPEEV        0.1705       7906.0                  50.00     Sequence
DRB3_0101   32  YARHTGGTFVFRIED  YARHTGGTF        0.1694       7998.5                  50.00     Sequence
DRB3_0101  226  ALHQALIRIGVAERI  IRIGVAERI        0.1673       8183.3                  50.00     Sequence
DRB3_0101  405  GAAVLDAALAALTSV  AVLDAALAA        0.1671       8198.2                  50.00     Sequence
DRB3_0101  198  VNPCDDALMKITHVL  ALMKITHVL        0.1645       8430.9                  50.00     Sequence
DRB3_0101  418  SVTDWTAPLIEAALK  SVTDWTAPL        0.1644       8441.6                  50.00     Sequence
DRB3_0101  253  GTKKLSKRDPQSNLF  SKRDPQSNL        0.1639       8489.9                  50.00     Sequence
DRB3_0101   62  DALRWLGLDWDEGPE  LGLDWDEGP        0.1636       8518.0                  50.00     Sequence
DRB3_0101  182  PDFALTRASGDPLYT  FALTRASGD        0.1632       8554.0                  50.00     Sequence
DRB3_0101  180  SVPDFALTRASGDPL  FALTRASGD        0.1628       8591.6                  50.00     Sequence
DRB3_0101   52  DSEESYLALLDALRW  YLALLDALR        0.1626       8604.0                  50.00     Sequence
DRB3_0101  278  GLLNYLALLGWSIAD  YLALLGWSI        0.1622       8646.2                  50.00     Sequence
DRB3_0101  179  GSVPDFALTRASGDP  FALTRASGD        0.1619       8669.7                  50.00     Sequence
DRB3_0101  134  FDRHLTDAQRAAYLA  HLTDAQRAA        0.1606       8793.6                  50.00     Sequence
DRB3_0101  217  LLPSTPRQLALHQAL  LLPSTPRQL        0.1605       8805.7                  50.00     Sequence
DRB3_0101  254  TKKLSKRDPQSNLFA  SKRDPQSNL        0.1598       8874.7                  50.00     Sequence
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DRB3_0101  299  LDEMVAAFDVADVNS  AAFDVADVN        0.1587       8981.8                      50.00     Sequence
DRB3_0101  362  AAAAELVQTRIVVLG  LVQTRIVVL        0.1587       8984.1                      50.00     Sequence
DRB3_0101  227  LHQALIRIGVAERIP  IRIGVAERI        0.1585       9001.0                      50.00     Sequence
DRB3_0101  239  RIPKFAHLPTVLGEG  FAHLPTVLG        0.1577       9073.9                      50.00     Sequence
DRB3_0101  375  LGDAWELLKFFNDDQ  DAWELLKFF        0.1565       9195.5                      50.00     Sequence
DRB3_0101  255  KKLSKRDPQSNLFAH  SKRDPQSNL        0.1561       9235.5                      50.00     Sequence
DRB3_0101  161  DDDLAWNDLVRGPVT  DDLAWNDLV        0.1550       9341.1                      50.00     Sequence
DRB3_0101  124  GRNPKLGYDNFDRHL  LGYDNFDRH        0.1547       9372.6                      50.00     Sequence
DRB3_0101  163  DLAWNDLVRGPVTFA  LVRGPVTFA        0.1531       9535.6                      50.00     Sequence
DRB3_0101  229  QALIRIGVAERIPKF  IRIGVAERI        0.1530       9548.4                      50.00     Sequence
DRB3_0101  256  KLSKRDPQSNLFAHR  SKRDPQSNL        0.1526       9594.5                      50.00     Sequence
DRB3_0101   21  GLVRTALFNWAYARH  ALFNWAYAR        0.1520       9655.5                      50.00     Sequence
DRB3_0101  252  EGTKKLSKRDPQSNL  SKRDPQSNL        0.1517       9686.3                      50.00     Sequence
DRB3_0101  433  DALIEGLALKPRKAF  LALKPRKAF        0.1513       9732.7                      50.00     Sequence
DRB3_0101  363  AAAELVQTRIVVLGD  LVQTRIVVL        0.1510       9761.8                      50.00     Sequence
DRB3_0101  472  RDRSMQRLRAARQLV  RLRAARQLV        0.1492       9952.4                      50.00     Sequence
DRB3_0101  257  LSKRDPQSNLFAHRD  SKRDPQSNL        0.1488       9993.3                      50.00     Sequence
DRB3_0101  406  AAVLDAALAALTSVT  AVLDAALAA        0.1480      10086.3                      50.00     Sequence
DRB3_0101  425  PLIEAALKDALIEGL  IEAALKDAL        0.1474      10149.9                      50.00     Sequence
DRB3_0101  105  EAYHAFSTPEEVEAR  HAFSTPEEV        0.1474      10150.3                      50.00     Sequence
DRB3_0101  162  DDLAWNDLVRGPVTF  DDLAWNDLV        0.1471      10181.4                      50.00     Sequence
DRB3_0101  230  ALIRIGVAERIPKFA  IRIGVAERI        0.1467      10227.8                      50.00     Sequence
DRB3_0101  365  AELVQTRIVVLGDAW  LVQTRIVVL        0.1463      10271.1                      50.00     Sequence
DRB3_0101   33  ARHTGGTFVFRIEDT  TGGTFVFRI        0.1449      10423.4                      50.00     Sequence
DRB3_0101  103  AGEAYHAFSTPEEVE  HAFSTPEEV        0.1447      10453.0                      50.00     Sequence
DRB3_0101  123  AGRNPKLGYDNFDRH  LGYDNFDRH        0.1435      10587.8                      50.00     Sequence
DRB3_0101  200  PCDDALMKITHVLRG  ALMKITHVL        0.1430      10646.0                      50.00     Sequence
DRB3_0101  444  RKAFSPIRVAATGTT  IRVAATGTT        0.1425      10698.2                      50.00     Sequence
DRB3_0101  240  IPKFAHLPTVLGEGT  FAHLPTVLG        0.1424      10705.6                      50.00     Sequence
DRB3_0101  364  AAELVQTRIVVLGDA  LVQTRIVVL        0.1423      10724.8                      50.00     Sequence
DRB3_0101  135  DRHLTDAQRAAYLAE  HLTDAQRAA        0.1420      10757.6                      50.00     Sequence
DRB3_0101  228  HQALIRIGVAERIPK  IRIGVAERI        0.1419      10769.7                      50.00     Sequence
DRB3_0101  136  RHLTDAQRAAYLAEG  HLTDAQRAA        0.1417      10791.5                      50.00     Sequence
DRB3_0101  231  LIRIGVAERIPKFAH  IRIGVAERI        0.1416      10803.1                      50.00     Sequence
DRB3_0101  204  ALMKITHVLRGEDLL  HVLRGEDLL        0.1408      10893.3                      50.00     Sequence
DRB3_0101  279  LLNYLALLGWSIADD  YLALLGWSI        0.1408      10893.7                      50.00     Sequence
DRB3_0101  366  ELVQTRIVVLGDAWE  LVQTRIVVL        0.1407      10905.3                      50.00     Sequence
DRB3_0101  258  SKRDPQSNLFAHRDR  SKRDPQSNL        0.1403      10955.0                      50.00     Sequence
DRB3_0101  151  RQPVVRLRMPDDDLA  LRMPDDDLA        0.1403      10962.4                      50.00     Sequence
DRB3_0101  426  LIEAALKDALIEGLA  IEAALKDAL        0.1402      10963.5                      50.00     Sequence
DRB3_0101  427  IEAALKDALIEGLAL  LKDALIEGL        0.1401      10978.6                      50.00     Sequence
DRB3_0101  347  LDTHGHHIALDEAAF  HIALDEAAF        0.1400      10997.8                      50.00     Sequence
DRB3_0101  106  AYHAFSTPEEVEARH  HAFSTPEEV        0.1392      11088.6                      50.00     Sequence
DRB3_0101  199  NPCDDALMKITHVLR  ALMKITHVL        0.1391      11095.5                      50.00     Sequence
DRB3_0101  207  KITHVLRGEDLLPST  HVLRGEDLL        0.1368      11385.9                      50.00     Sequence
DRB3_0101  473  DRSMQRLRAARQLVG  RLRAARQLV        0.1352      11577.6                      50.00     Sequence
DRB3_0101  434  ALIEGLALKPRKAFS  LALKPRKAF        0.1346      11652.0                      50.00     Sequence
DRB3_0101  164  LAWNDLVRGPVTFAA  LVRGPVTFA        0.1341      11720.3                      50.00     Sequence
DRB3_0101  241  PKFAHLPTVLGEGTK  FAHLPTVLG        0.1340      11733.6                      50.00     Sequence
DRB3_0101  445  KAFSPIRVAATGTTV  IRVAATGTT        0.1337      11772.5                      50.00     Sequence
DRB3_0101  206  MKITHVLRGEDLLPS  HVLRGEDLL        0.1323      11953.1                      50.00     Sequence
DRB3_0101  243  FAHLPTVLGEGTKKL  FAHLPTVLG        0.1312      12093.4                      50.00     Sequence
DRB3_0101  424  APLIEAALKDALIEG  IEAALKDAL        0.1304      12195.3                      50.00     Sequence
DRB3_0101  232  IRIGVAERIPKFAHL  IRIGVAERI        0.1303      12213.1                      50.00     Sequence
DRB3_0101  208  ITHVLRGEDLLPSTP  HVLRGEDLL        0.1302      12219.7                      50.00     Sequence
DRB3_0101  107  YHAFSTPEEVEARHV  HAFSTPEEV        0.1294      12324.1                      50.00     Sequence
DRB3_0101  409  LDAALAALTSVTDWT  ALTSVTDWT        0.1289      12392.7                      50.00     Sequence
DRB3_0101  242  KFAHLPTVLGEGTKK  FAHLPTVLG        0.1287      12427.2                      50.00     Sequence
DRB3_0101   96  VLARLLAAGEAYHAF  AAGEAYHAF        0.1273      12607.2                      50.00     Sequence
DRB3_0101   85  RQSQRAEIYRDVLAR  RQSQRAEIY        0.1272      12625.2                      50.00     Sequence
DRB3_0101  441  LKPRKAFSPIRVAAT  FSPIRVAAT        0.1271      12636.5                      50.00     Sequence
DRB3_0101  474  RSMQRLRAARQLVGH  RLRAARQLV        0.1270      12652.7                      50.00     Sequence
DRB3_0101   98  ARLLAAGEAYHAFST  AAGEAYHAF        0.1269      12663.8                      50.00     Sequence
DRB3_0101  205  LMKITHVLRGEDLLP  HVLRGEDLL        0.1266      12708.2                      50.00     Sequence
DRB3_0101   60  LLDALRWLGLDWDEG  LRWLGLDWD        0.1263      12755.8                      50.00     Sequence
DRB3_0101  108  HAFSTPEEVEARHVA  HAFSTPEEV        0.1260      12788.4                      50.00     Sequence
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DRB3_0101	407	AVLDAALAALTSVTD	AVLDAALAA	0.1257	12826.9	50.00	Sequence
DRB3_0101	275	IPEGLLNYLALLGWS	GLLNYLALL	0.1249	12947.4	50.00	Sequence
DRB3_0101	137	HLTDAQRAAYLAEGR	HLTDAQRAA	0.1232	13180.2	50.00	Sequence
DRB3_0101	446	AFSPIRVAATGTTVS	IRVAATGTT	0.1222	13326.3	50.00	Sequence
DRB3_0101	97	LARLLAAGEAYHAFS	AAGEAYHAF	0.1211	13487.6	50.00	Sequence
DRB3_0101	435	LIEGLALKPRKAFSP	LALKPRKAF	0.1208	13538.2	50.00	Sequence
DRB3_0101	209	THVLRGEDLLPSTPR	HVLRGEDLL	0.1206	13563.7	50.00	Sequence
DRB3_0101	99	RLLAAGEAYHAFSTP	AAGEAYHAF	0.1205	13581.0	50.00	Sequence
DRB3_0101	201	CDDALMKITHVLRGE	ALMKITHVL	0.1186	13859.0	50.00	Sequence
DRB3_0101	410	DAALAALTSVTDWTA	ALTSVTDWT	0.1171	14080.6	50.00	Sequence
DRB3_0101	456	GTTVSPPLFESLELL	GTTVSPPLF	0.1150	14406.6	50.00	Sequence
DRB3_0101	442	KPRKAFSPIRVAATG	FSPIRVAAT	0.1145	14487.5	50.00	Sequence
DRB3_0101	475	SMQRLRAARQLVGHA	RLRAARQLV	0.1141	14546.1	50.00	Sequence
DRB3_0101	360	AFAAAAELVQTRIVV	AELVQTRIV	0.1141	14554.8	50.00	Sequence
DRB3_0101	411	AALAALTSVTDWTAP	ALTSVTDWT	0.1133	14679.6	50.00	Sequence
DRB3_0101	428	EAALKDALIEGLALK	LKDALIEGL	0.1130	14721.4	50.00	Sequence
DRB3_0101	436	IEGLALKPRKAFSPI	LALKPRKAF	0.1123	14826.7	50.00	Sequence
DRB3_0101	408	VLDAALAALTSVTDW	LDAALAALT	0.1117	14933.8	50.00	Sequence
DRB3_0101	443	PRKAFSPIRVAATGT	FSPIRVAAT	0.1099	15218.9	50.00	Sequence
DRB3_0101	177	AAGSVPDFALTRASG	SVPDFALTR	0.1099	15230.8	50.00	Sequence
DRB3_0101	429	AALKDALIEGLALKP	LKDALIEGL	0.1094	15304.8	50.00	Sequence
DRB3_0101	447	FSPIRVAATGTTVSP	IRVAATGTT	0.1090	15369.7	50.00	Sequence
DRB3_0101	210	HVLRGEDLLPSTPRQ	HVLRGEDLL	0.1086	15447.5	50.00	Sequence
DRB3_0101	203	DALMKITHVLRGEDL	ALMKITHVL	0.1074	15634.2	50.00	Sequence
DRB3_0101	260	RDPQSNLFAHRDRGF	LFAHRDRGF	0.1070	15705.1	50.00	Sequence
DRB3_0101	202	DDALMKITHVLRGED	ALMKITHVL	0.1067	15756.6	50.00	Sequence
DRB3_0101	437	EGLALKPRKAFSPIR	LALKPRKAF	0.1055	15966.0	50.00	Sequence
DRB3_0101	222	PRQLALHQALIRIGV	HQALIRIGV	0.1050	16056.4	50.00	Sequence
DRB3_0101	423	TAPLIEAALKDALIE	IEAALKDAL	0.1047	16110.5	50.00	Sequence
DRB3_0101	450	IRVAATGTTVSPPLF	GTTVSPPLF	0.1044	16154.4	50.00	Sequence
DRB3_0101	100	LLAAGEAYHAFSTPE	AAGEAYHAF	0.1040	16226.2	50.00	Sequence
DRB3_0101	101	LAAGEAYHAFSTPEE	AAGEAYHAF	0.1037	16278.8	50.00	Sequence
DRB3_0101	458	TVSPPLFESLELLGR	PLFESLELL	0.1037	16286.7	50.00	Sequence
DRB3_0101	422	WTAPLIEAALKDALI	IEAALKDAL	0.1026	16479.9	50.00	Sequence
DRB3_0101	438	GLALKPRKAFSPIRV	LALKPRKAF	0.1021	16566.6	50.00	Sequence
DRB3_0101	451	RVAATGTTVSPPLFE	GTTVSPPLF	0.1017	16645.5	50.00	Sequence
DRB3_0101	459	VSPPLFESLELLGRD	FESLELLGR	0.1016	16649.8	50.00	Sequence
DRB3_0101	421	DWTAPLIEAALKDAL	IEAALKDAL	0.1016	16656.5	50.00	Sequence
DRB3_0101	430	ALKDALIEGLALKPR	LKDALIEGL	0.1002	16901.2	50.00	Sequence
DRB3_0101	453	AATGTTVSPPLFESL	GTTVSPPLF	0.1001	16933.0	50.00	Sequence
DRB3_0101	452	VAATGTTVSPPLFES	GTTVSPPLF	0.0996	17025.3	50.00	Sequence
DRB3_0101	343	LRDHLDTHGHHIALD	HLDTHGHHI	0.0992	17085.6	50.00	Sequence
DRB3_0101	439	LALKPRKAFSPIRVA	LALKPRKAF	0.0988	17170.3	50.00	Sequence
DRB3_0101	455	TGTTVSPPLFESLEL	GTTVSPPLF	0.0977	17370.2	50.00	Sequence
DRB3_0101	165	AWNDLVRGPVTFAAG	LVRGPVTFA	0.0976	17387.0	50.00	Sequence
DRB3_0101	223	RQLALHQALIRIGVA	HQALIRIGV	0.0970	17514.4	50.00	Sequence
DRB3_0101	457	TTVSPPLFESLELLG	PLFESLELL	0.0969	17522.2	50.00	Sequence
DRB3_0101	233	RIGVAERIPKFAHLP	GVAERIPKF	0.0958	17735.0	50.00	Sequence
DRB3_0101	221	TPRQLALHQALIRIG	ALHQALIRI	0.0957	17749.8	50.00	Sequence
DRB3_0101	109	AFSTPEEVEARHVAA	FSTPEEVEA	0.0953	17833.2	50.00	Sequence
DRB3_0101	460	SPPLFESLELLGRDR	FESLELLGR	0.0951	17876.2	50.00	Sequence
DRB3_0101	220	STPRQLALHQALIRI	LALHQALIR	0.0950	17891.9	50.00	Sequence
DRB3_0101	454	ATGTTVSPPLFESLE	GTTVSPPLF	0.0946	17973.4	50.00	Sequence
DRB3_0101	344	RDHLDTHGHHIALDE	HLDTHGHHI	0.0938	18115.6	50.00	Sequence
DRB3_0101	346	HLDTHGHHIALDEAA	HLDTHGHHI	0.0936	18151.6	50.00	Sequence
DRB3_0101	235	GVAERIPKFAHLPTV	GVAERIPKF	0.0922	18437.1	50.00	Sequence
DRB3_0101	166	WNDLVRGPVTFAAGS	LVRGPVTFA	0.0884	19209.3	50.00	Sequence
DRB3_0101	9	RFCPSPTGTPHVGLV	TGTPHVGLV	0.0881	19278.4	50.00	Sequence
DRB3_0101	234	IGVAERIPKFAHLPT	GVAERIPKF	0.0880	19285.7	50.00	Sequence
DRB3_0101	224	QLALHQALIRIGVAE	HQALIRIGV	0.0871	19491.7	50.00	Sequence
DRB3_0101	461	PPLFESLELLGRDRS	PLFESLELL	0.0868	19547.4	50.00	Sequence
DRB3_0101	345	DHLDTHGHHIALDEA	HLDTHGHHI	0.0846	20011.2	50.00	Sequence
DRB3_0101	225	LALHQALIRIGVAER	LALHQALIR	0.0832	20332.0	50.00	Sequence
DRB3_0101	167	NDLVRGPVTFAAGSV	LVRGPVTFA	0.0829	20383.5	50.00	Sequence
DRB3_0101	219	PSTPRQLALHQALIR	LALHQALIR	0.0818	20629.2	50.00	Sequence
DRB3_0101	150	GRQPVVRLRMPDDDL	VRLRMPDDD	0.0815	20701.4	50.00	Sequence

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DRB3_0101   95  DVLARLLAAGEAYHA  RLLAAGEAY        0.0814      20729.4              50.00     Sequence
DRB3_0101  462  PLFESLELLGRDRSM  FESLELLGR        0.0810      20807.6              50.00     Sequence
DRB3_0101  307  DVADVNSSPARFDQK  VNSSPARFD        0.0809      20832.6              50.00     Sequence
DRB3_0101  168  DLVRGPVTFAAGSVP  LVRGPVTFA        0.0808      20854.3              50.00     Sequence
DRB3_0101  110  FSTPEEVEARHVAAG  FSTPEEVEA        0.0804      20958.8              50.00     Sequence
DRB3_0101   10  FCPSPTGTPHVGLVR  TGTPHVGLV        0.0797      21112.6              50.00     Sequence
DRB3_0101  169  LVRGPVTFAAGSVPD  LVRGPVTFA        0.0781      21488.3              50.00     Sequence
DRB3_0101  244  AHLPTVLGEGTKKLS  VLGEGTKKL        0.0771      21718.5              50.00     Sequence
DRB3_0101  463  LFESLELLGRDRSMQ  FESLELLGR        0.0755      22098.5              50.00     Sequence
DRB3_0101  359  AAFAAAAELVQTRIV  AELVQTRIV        0.0749      22236.1              50.00     Sequence
DRB3_0101  310  DVNSSPARFDQKKAD  VNSSPARFD        0.0729      22725.5              50.00     Sequence
DRB3_0101   13  SPTGTPHVGLVRTAL  TGTPHVGLV        0.0718      22985.2              50.00     Sequence
DRB3_0101  308  VADVNSSPARFDQKK  VNSSPARFD        0.0716      23036.2              50.00     Sequence
DRB3_0101  431  LKDALIEGLALKPRK  LKDALIEGL        0.0716      23041.4              50.00     Sequence
DRB3_0101  449  PIRVAATGTTVSPPL  IRVAATGTT        0.0706      23297.1              50.00     Sequence
DRB3_0101  121  VAAGRNPKLGYDNFD  AGRNPKLGY        0.0704      23348.6              50.00     Sequence
DRB3_0101  149  EGRQPVVRLRMPDDD  VRLRMPDDD        0.0703      23367.1              50.00     Sequence
DRB3_0101  138  LTDAQRAAYLAEGRQ  LTDAQRAAY        0.0696      23534.8              50.00     Sequence
DRB3_0101  448  SPIRVAATGTTVSPP  IRVAATGTT        0.0694      23600.3              50.00     Sequence
DRB3_0101   94  RDVLARLLAAGEAYH  RLLAAGEAY        0.0690      23705.0              50.00     Sequence
DRB3_0101  355  ALDEAAFAAAAELVQ  FAAAAELVQ        0.0686      23797.5              50.00     Sequence
DRB3_0101  309  ADVNSSPARFDQKKA  VNSSPARFD        0.0685      23820.9              50.00     Sequence
DRB3_0101  245  HLPTVLGEGTKKLSK  VLGEGTKKL        0.0683      23880.3              50.00     Sequence
DRB3_0101  259  KRDPQSNLFAHRDRG  KRDPQSNLF        0.0681      23922.4              50.00     Sequence
DRB3_0101  122  AAGRNPKLGYDNFDR  AGRNPKLGY        0.0677      24047.3              50.00     Sequence
DRB3_0101  147  LAEGRQPVVRLRMPD  LAEGRQPVV        0.0668      24272.9              50.00     Sequence
DRB3_0101  319  DQKKADALNAEHIRM  KKADALNAE        0.0659      24511.7              50.00     Sequence
DRB3_0101   11  CPSPTGTPHVGLVRT  TGTPHVGLV        0.0651      24714.6              50.00     Sequence
DRB3_0101  120  HVAAGRNPKLGYDNF  AGRNPKLGY        0.0640      25008.6              50.00     Sequence
DRB3_0101  356  LDEAAFAAAAELVQT  FAAAAELVQ        0.0631      25272.2              50.00     Sequence
DRB3_0101  119  RHVAAGRNPKLGYDN  AGRNPKLGY        0.0629      25329.7              50.00     Sequence
DRB3_0101  311  VNSSPARFDQKKADA  VNSSPARFD        0.0621      25544.7              50.00     Sequence
DRB3_0101  419  VTDWTAPLIEAALKD  VTDWTAPLI        0.0617      25636.3              50.00     Sequence
DRB3_0101  218  LPSTPRQLALHQALI  RQLALHQAL        0.0615      25702.7              50.00     Sequence
DRB3_0101   12  PSPTGTPHVGLVRTA  TGTPHVGLV        0.0612      25778.5              50.00     Sequence
DRB3_0101  246  LPTVLGEGTKKLSKR  VLGEGTKKL        0.0598      26188.6              50.00     Sequence
DRB3_0101  357  DEAAFAAAAELVQTR  FAAAAELVQ        0.0596      26236.3              50.00     Sequence
DRB3_0101  117  EARHVAAGRNPKLGY  AGRNPKLGY        0.0592      26342.9              50.00     Sequence
DRB3_0101  236  VAERIPKFAHLPTVL  PKFAHLPTV        0.0583      26598.7              50.00     Sequence
DRB3_0101    0  VTATETVRVRFCPSP  VTATETVRV        0.0576      26804.4              50.00     Sequence
DRB3_0101    4  ETVRVRFCPSPTGTP  FCPSPTGTP        0.0575      26847.9              50.00     Sequence
DRB3_0101  118  ARHVAAGRNPKLGYD  AGRNPKLGY        0.0569      27019.0              50.00     Sequence
DRB3_0101  139  TDAQRAAYLAEGRQP  TDAQRAAYL        0.0567      27080.4              50.00     Sequence
DRB3_0101  420  TDWTAPLIEAALKDA  LIEAALKDA        0.0565      27119.5              50.00     Sequence
DRB3_0101    5  TVRVRFCPSPTGTPH  FCPSPTGTP        0.0549      27599.9              50.00     Sequence
DRB3_0101  358  EAAFAAAAELVQTRI  FAAAAELVQ        0.0529      28210.7              50.00     Sequence
DRB3_0101  148  AEGRQPVVRLRMPDD  VVRLRMPDD        0.0524      28376.9              50.00     Sequence
DRB3_0101   75  PEVGGPYGPYRQSQR  YGPYRQSQR        0.0514      28664.2              50.00     Sequence
DRB3_0101   76  EVGGPYGPYRQSQRA  YGPYRQSQR        0.0493      29321.7              50.00     Sequence
DRB3_0101    2  ATETVRVRFCPSPTG  VRFCPSPTG        0.0482      29693.6              50.00     Sequence
DRB3_0101    1  TATETVRVRFCPSPT  TATETVRVR        0.0476      29888.0              50.00     Sequence
DRB3_0101  247  PTVLGEGTKKLSKRD  VLGEGTKKL        0.0471      30049.8              50.00     Sequence
DRB3_0101    6  VRVRFCPSPTGTPHV  FCPSPTGTP        0.0463      30295.6              50.00     Sequence
DRB3_0101   77  VGGPYGPYRQSQRAE  YGPYRQSQR        0.0460      30399.0              50.00     Sequence
DRB3_0101  248  TVLGEGTKKLSKRDP  VLGEGTKKL        0.0456      30540.8              50.00     Sequence
DRB3_0101    3  TETVRVRFCPSPTGT  VRFCPSPTG        0.0452      30676.2              50.00     Sequence
DRB3_0101  471  GRDRSMQRLRAARQL  QRLRAARQL        0.0449      30758.7              50.00     Sequence
DRB3_0101  249  VLGEGTKKLSKRDPQ  VLGEGTKKL        0.0437      31155.6              50.00     Sequence
DRB3_0101   70  DWDEGPEVGGPYGPY  EGPEVGGPY        0.0419      31784.8              50.00     Sequence
DRB3_0101    7  RVRFCPSPTGTPHVG  FCPSPTGTP        0.0419      31787.2              50.00     Sequence
DRB3_0101    8  VRFCPSPTGTPHVGL  FCPSPTGTP        0.0409      32124.0              50.00     Sequence
DRB3_0101  440  ALKPRKAFSPIRVAA  KAFSPIRVA        0.0388      32851.6              50.00     Sequence
DRB3_0101   71  WDEGPEVGGPYGPYR  EGPEVGGPY        0.0386      32926.6              50.00     Sequence
DRB3_0101  111  STPEEVEARHVAAGR  EEVEARHVA        0.0386      32927.7              50.00     Sequence
DRB3_0101  251  GEGTKKLSKRDPQSN  LSKRDPQSN        0.0377      33261.4              50.00     Sequence
DRB3_0101  432  KDALIEGLALKPRKA  ALIEGLALK        0.0360      33865.7              50.00     Sequence
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   DRB3_0101  112  TPEEVEARHVAAGRN  EEVEARHVA        0.0355      34047.9              50.00    Sequence
   DRB3_0101  113  PEEVEARHVAAGRNP  EEVEARHVA        0.0344      34476.1              50.00    Sequence
   DRB3_0101  114  EEVEARHVAAGRNPK  EEVEARHVA        0.0323      35255.8              50.00    Sequence
   DRB3_0101   72  DEGPEVGGPYGPYRQ  EGPEVGGPY        0.0316      35507.3              50.00    Sequence
   DRB3_0101   73  EGPEVGGPYGPYRQS  EGPEVGGPY        0.0296      36302.1              50.00    Sequence
   DRB3_0101  115  EVEARHVAAGRNPKL  VAAGRNPKL        0.0291      36503.8              50.00    Sequence
   DRB3_0101  394  PKAAAKELGPDGAAV  ELGPDGAAV        0.0279      36978.4              50.00    Sequence
   DRB3_0101  116  VEARHVAAGRNPKLG  VAAGRNPKL        0.0266      37514.8              50.00    Sequence
   DRB3_0101  250  LGEGTKKLSKRDPQS  LGEGTKKLS        0.0236      38749.2              50.00    Sequence
   DRB3_0101   74  GPEVGGPYGPYRQSQ  EVGGPYGPY        0.0212      39766.0              50.00    Sequence
   DRB3_0101  393  DPKAAAKELGPDGAA  KELGPDGAA        0.0201      40209.0              50.00    Sequence
   DRB3_0101  392  IDPKAAAKELGPDGA  AAKELGPDG        0.0157      42178.2              50.00    Sequence
   DRB3_0101  391  VIDPKAAAKELGPDG  AAKELGPDG        0.0157      42187.3              50.00    Sequence
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Allele: DRB3_0101. Number of high binders 9. Number of weak binders 19. Number of peptides 476

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB4_0101  151  RQPVVRLRMPDDDLA  PVVRLRMPD        0.7452         15.7         SB     0.80    Sequence
   DRB4_0101  150  GRQPVVRLRMPDDDL  VRLRMPDDD        0.7356         17.5         SB     0.80    Sequence
   DRB4_0101  149  EGRQPVVRLRMPDDD  PVVRLRMPD        0.7285         18.9         SB     0.80    Sequence
   DRB4_0101  152  QPVVRLRMPDDDLAW  VRLRMPDDD        0.7082         23.5         SB     2.00    Sequence
   DRB4_0101  153  PVVRLRMPDDDLAWN  PVVRLRMPD        0.6767         33.0         SB     2.00    Sequence
   DRB4_0101   58  LALLDALRWLGLDWD  LALLDALRW        0.6388         49.8         SB     4.00    Sequence
   DRB4_0101  148  AEGRQPVVRLRMPDD  QPVVRLRMP        0.6340         52.5         WB     4.00    Sequence
   DRB4_0101  337  GDFTVRLRDHLDTHG  FTVRLRDHL        0.6217         59.9         WB     8.00    Sequence
   DRB4_0101  325  ALNAEHIRMLDVGDF  EHIRMLDVG        0.6202         60.9         WB     8.00    Sequence
   DRB4_0101  338  DFTVRLRDHLDTHGH  FTVRLRDHL        0.6187         61.9         WB     8.00    Sequence
   DRB4_0101  327  NAEHIRMLDVGDFTV  EHIRMLDVG        0.6186         62.0         WB     8.00    Sequence
   DRB4_0101  278  GLLNYLALLGWSIAD  LNYLALLGW        0.6137         65.3         WB     8.00    Sequence
   DRB4_0101  280  LNYLALLGWSIADDH  LNYLALLGW        0.6128         66.0         WB     8.00    Sequence
   DRB4_0101  336  VGDFTVRLRDHLDTH  FTVRLRDHL        0.6127         66.0         WB     8.00    Sequence
   DRB4_0101  328  AEHIRMLDVGDFTVR  EHIRMLDVG        0.6121         66.5         WB     8.00    Sequence
   DRB4_0101  326  LNAEHIRMLDVGDFT  AEHIRMLDV        0.6109         67.3         WB     8.00    Sequence
   DRB4_0101  147  LAEGRQPVVRLRMPD  QPVVRLRMP        0.6095         68.4         WB     8.00    Sequence
   DRB4_0101  277  EGLLNYLALLGWSIA  LNYLALLGW        0.6053         71.6         WB     8.00    Sequence
   DRB4_0101   60  LLDALRWLGLDWDEG  LRWLGLDWD        0.5989         76.7         WB     8.00    Sequence
   DRB4_0101  335  DVGDFTVRLRDHLDT  FTVRLRDHL        0.5976         77.8         WB     8.00    Sequence
   DRB4_0101   17  TPHVGLVRTALFNWA  VGLVRTALF        0.5971         78.2         WB     8.00    Sequence
   DRB4_0101  279  LLNYLALLGWSIADD  LNYLALLGW        0.5966         78.6         WB     8.00    Sequence
   DRB4_0101   59  ALLDALRWLGLDWDE  LRWLGLDWD        0.5921         82.5         WB     8.00    Sequence
   DRB4_0101   15  TGTPHVGLVRTALFN  VGLVRTALF        0.5917         82.9         WB     8.00    Sequence
   DRB4_0101   57  YLALLDALRWLGLDW  LALLDALRW        0.5886         85.7         WB     8.00    Sequence
   DRB4_0101  474  RSMQRLRAARQLVGH  MQRLRAARQ        0.5864         87.8         WB     8.00    Sequence
   DRB4_0101   16  GTPHVGLVRTALFNW  VGLVRTALF        0.5864         87.8         WB     8.00    Sequence
   DRB4_0101  471  GRDRSMQRLRAARQL  QRLRAARQL        0.5855         88.7         WB     8.00    Sequence
   DRB4_0101  275  IPEGLLNYLALLGWS  LNYLALLGW        0.5846         89.6         WB     8.00    Sequence
   DRB4_0101  274  FIPEGLLNYLALLGW  LNYLALLGW        0.5843         89.8         WB     8.00    Sequence
   DRB4_0101  473  DRSMQRLRAARQLVG  QRLRAARQL        0.5839         90.2         WB     8.00    Sequence
   DRB4_0101  475  SMQRLRAARQLVGHA  MQRLRAARQ        0.5791         95.0         WB     8.00    Sequence
   DRB4_0101  276  PEGLLNYLALLGWSI  LNYLALLGW        0.5790         95.1         WB     8.00    Sequence
   DRB4_0101  204  ALMKITHVLRGEDLL  MKITHVLRG        0.5767         97.5         WB     8.00    Sequence
   DRB4_0101  472  RDRSMQRLRAARQLV  QRLRAARQL        0.5754         98.9         WB     8.00    Sequence
   DRB4_0101  203  DALMKITHVLRGEDL  MKITHVLRG        0.5751         99.2         WB     8.00    Sequence
   DRB4_0101  467  LELLGRDRSMQRLRA  LELLGRDRS        0.5750         99.3         WB     8.00    Sequence
   DRB4_0101  339  FTVRLRDHLDTHGHH  VRLRDHLDT        0.5748         99.6         WB     8.00    Sequence
   DRB4_0101   19  HVGLVRTALFNWAYA  VGLVRTALF        0.5745         99.8         WB     8.00    Sequence
   DRB4_0101  466  SLELLGRDRSMQRLR  LELLGRDRS        0.5716        103.0         WB     8.00    Sequence
   DRB4_0101   18  PHVGLVRTALFNWAY  VGLVRTALF        0.5700        104.9         WB    16.00    Sequence
   DRB4_0101  470  LGRDRSMQRLRAARQ  RSMQRLRAA        0.5631        113.0         WB    16.00    Sequence
   DRB4_0101  324  DALNAEHIRMLDVGD  EHIRMLDVG        0.5630        113.2         WB    16.00    Sequence
   DRB4_0101   61  LDALRWLGLDWDEGP  LRWLGLDWD        0.5609        115.7         WB    16.00    Sequence
   DRB4_0101  465  ESLELLGRDRSMQRL  LELLGRDRS        0.5570        120.7         WB    16.00    Sequence
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DRB4_0101  201  CDDALMKITHVLRGE  MKITHVLRG        0.5569        120.8         WB    16.00     Sequence
DRB4_0101  154  VVRLRMPDDDLAWND  VRLRMPDDD        0.5561        121.9         WB    16.00     Sequence
DRB4_0101   55  ESYLALLDALRWLGL  ESYLALLDA        0.5547        123.7         WB    16.00     Sequence
DRB4_0101   14  PTGTPHVGLVRTALF  VGLVRTALF        0.5537        125.1         WB    16.00     Sequence
DRB4_0101  468  ELLGRDRSMQRLRAA  ELLGRDRSM        0.5536        125.2         WB    16.00     Sequence
DRB4_0101  218  LPSTPRQLALHQALI  RQLALHQAL        0.5529        126.1         WB    16.00     Sequence
DRB4_0101  205  LMKITHVLRGEDLLP  HVLRGEDLL        0.5503        129.8         WB    16.00     Sequence
DRB4_0101  202  DDALMKITHVLRGED  MKITHVLRG        0.5483        132.6         WB    16.00     Sequence
DRB4_0101   54  EESYLALLDALRWLG  ESYLALLDA        0.5469        134.7         WB    16.00     Sequence
DRB4_0101  221  TPRQLALHQALIRIG  RQLALHQAL        0.5454        136.8         WB    16.00     Sequence
DRB4_0101   20  VGLVRTALFNWAYAR  VGLVRTALF        0.5451        137.2         WB    16.00     Sequence
DRB4_0101  281  NYLALLGWSIADDHD  LGWSIADDH        0.5449        137.5         WB    16.00     Sequence
DRB4_0101   56  SYLALLDALRWLGLD  LALLDALRW        0.5447        137.9         WB    16.00     Sequence
DRB4_0101  206  MKITHVLRGEDLLPS  MKITHVLRG        0.5417        142.4         WB    16.00     Sequence
DRB4_0101  282  YLALLGWSIADDHDL  ALLGWSIAD        0.5413        143.0         WB    16.00     Sequence
DRB4_0101  200  PCDDALMKITHVLRG  LMKITHVLR        0.5408        143.8         WB    16.00     Sequence
DRB4_0101  226  ALHQALIRIGVAERI  IRIGVAERI        0.5398        145.3         WB    16.00     Sequence
DRB4_0101  329  EHIRMLDVGDFTVRL  IRMLDVGDF        0.5386        147.2         WB    16.00     Sequence
DRB4_0101  217  LLPSTPRQLALHQAL  RQLALHQAL        0.5315        159.0         WB    16.00     Sequence
DRB4_0101  227  LHQALIRIGVAERIP  IRIGVAERI        0.5306        160.6         WB    16.00     Sequence
DRB4_0101   62  DALRWLGLDWDEGPE  LRWLGLDWD        0.5284        164.5         WB    16.00     Sequence
DRB4_0101  230  ALIRIGVAERIPKFA  IRIGVAERI        0.5279        165.3         WB    16.00     Sequence
DRB4_0101  469  LLGRDRSMQRLRAAR  GRDRSMQRL        0.5273        166.5         WB    16.00     Sequence
DRB4_0101  220  STPRQLALHQALIRI  RQLALHQAL        0.5271        166.8         WB    16.00     Sequence
DRB4_0101  229  QALIRIGVAERIPKF  IRIGVAERI        0.5255        169.7         WB    16.00     Sequence
DRB4_0101  219  PSTPRQLALHQALIR  RQLALHQAL        0.5247        171.1         WB    16.00     Sequence
DRB4_0101  222  PRQLALHQALIRIGV  RQLALHQAL        0.5228        174.8         WB    16.00     Sequence
DRB4_0101  283  LALLGWSIADDHDLF  LGWSIADDH        0.5197        180.7         WB    16.00     Sequence
DRB4_0101  228  HQALIRIGVAERIPK  IRIGVAERI        0.5159        188.2         WB    16.00     Sequence
DRB4_0101  223  RQLALHQALIRIGVA  RQLALHQAL        0.5094        202.1         WB    16.00     Sequence
DRB4_0101   53  SEESYLALLDALRWL  ESYLALLDA        0.5037        214.8         WB    16.00     Sequence
DRB4_0101  207  KITHVLRGEDLLPST  THVLRGEDL        0.5030        216.6         WB    16.00     Sequence
DRB4_0101   93  YRDVLARLLAAGEAY  YRDVLARLL        0.5002        223.2         WB    16.00     Sequence
DRB4_0101  323  ADALNAEHIRMLDVG  EHIRMLDVG        0.4992        225.5         WB    16.00     Sequence
DRB4_0101   92  IYRDVLARLLAAGEA  YRDVLARLL        0.4983        227.8         WB    32.00     Sequence
DRB4_0101  340  TVRLRDHLDTHGHHI  VRLRDHLDT        0.4970        231.0         WB    32.00     Sequence
DRB4_0101  464  FESLELLGRDRSMQR  LELLGRDRS        0.4966        231.9         WB    32.00     Sequence
DRB4_0101  208  ITHVLRGEDLLPSTP  THVLRGEDL        0.4961        233.2         WB    32.00     Sequence
DRB4_0101  334  LDVGDFTVRLRDHLD  FTVRLRDHL        0.4941        238.4         WB    32.00     Sequence
DRB4_0101  146  YLAEGRQPVVRLRMP  QPVVRLRMP        0.4916        244.9         WB    32.00     Sequence
DRB4_0101  209  THVLRGEDLLPSTPR  THVLRGEDL        0.4877        255.6         WB    32.00     Sequence
DRB4_0101  284  ALLGWSIADDHDLFG  LGWSIADDH        0.4841        265.5         WB    32.00     Sequence
DRB4_0101   52  DSEESYLALLDALRW  ESYLALLDA        0.4836        267.0         WB    32.00     Sequence
DRB4_0101  155  VRLRMPDDDLAWNDL  VRLRMPDDD        0.4804        276.5         WB    32.00     Sequence
DRB4_0101  333  MLDVGDFTVRLRDHL  FTVRLRDHL        0.4785        282.0         WB    32.00     Sequence
DRB4_0101  462  PLFESLELLGRDRSM  LELLGRDRS        0.4772        286.3         WB    32.00     Sequence
DRB4_0101  463  LFESLELLGRDRSMQ  LELLGRDRS        0.4758        290.5         WB    32.00     Sequence
DRB4_0101   91  EIYRDVLARLLAAGE  YRDVLARLL        0.4734        298.3         WB    32.00     Sequence
DRB4_0101  272  RGFIPEGLLNYLALL  RGFIPEGLL        0.4689        313.0         WB    32.00     Sequence
DRB4_0101   63  ALRWLGLDWDEGPEV  LRWLGLDWD        0.4680        316.1         WB    32.00     Sequence
DRB4_0101   90  AEIYRDVLARLLAAG  YRDVLARLL        0.4678        316.8         WB    32.00     Sequence
DRB4_0101  461  PPLFESLELLGRDRS  LELLGRDRS        0.4662        322.3         WB    32.00     Sequence
DRB4_0101  378  AWELLKFFNDDQYVI  LKFFNDDQY        0.4660        323.0         WB    32.00     Sequence
DRB4_0101  341  VRLRDHLDTHGHHIA  VRLRDHLDT        0.4653        325.5         WB    32.00     Sequence
DRB4_0101  231  LIRIGVAERIPKFAH  IRIGVAERI        0.4640        329.9         WB    32.00     Sequence
DRB4_0101   24  RTALFNWAYARHTGG  RTALFNWAY        0.4631        333.2         WB    32.00     Sequence
DRB4_0101  330  HIRMLDVGDFTVRLR  IRMLDVGDF        0.4615        339.1         WB    32.00     Sequence
DRB4_0101  370  TRIVVLGDAWELLKF  TRIVVLGDA        0.4613        339.9         WB    32.00     Sequence
DRB4_0101  273  GFIPEGLLNYLALLG  EGLLNYLAL        0.4613        340.0         WB    32.00     Sequence
DRB4_0101   23  VRTALFNWAYARHTG  TALFNWAYA        0.4603        343.7         WB    32.00     Sequence
DRB4_0101   22  LVRTALFNWAYARHT  TALFNWAYA        0.4601        344.4         WB    32.00     Sequence
DRB4_0101  199  NPCDDALMKITHVLR  LMKITHVLR        0.4600        344.8         WB    32.00     Sequence
DRB4_0101   21  GLVRTALFNWAYARH  GLVRTALFN        0.4575        354.3         WB    32.00     Sequence
DRB4_0101  377  DAWELLKFFNDDQYV  LKFFNDDQY        0.4567        357.1         WB    32.00     Sequence
DRB4_0101   89  RAEIYRDVLARLLAA  YRDVLARLL        0.4566        357.6         WB    32.00     Sequence
DRB4_0101  369  QTRIVVLGDAWELLK  TRIVVLGDA        0.4560        359.9         WB    32.00     Sequence
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DRB4_0101  376  GDAWELLKFFNDDQY  LKFFNDDQY         0.4550        363.9          WB    32.00      Sequence
DRB4_0101  379  WELLKFFNDDQYVID  LKFFNDDQY         0.4535        370.0          WB    32.00      Sequence
DRB4_0101  380  ELLKFFNDDQYVIDP  LKFFNDDQY         0.4506        381.5          WB    32.00      Sequence
DRB4_0101   94  RDVLARLLAAGEAYH  RDVLARLLA         0.4465        398.9          WB    32.00      Sequence
DRB4_0101  368  VQTRIVVLGDAWELL  TRIVVLGDA         0.4447        406.8          WB    32.00      Sequence
DRB4_0101  126  NPKLGYDNFDRHLTD  LGYDNFDRH         0.4422        417.8          WB    32.00      Sequence
DRB4_0101  125  RNPKLGYDNFDRHLT  LGYDNFDRH         0.4413        422.1          WB    32.00      Sequence
DRB4_0101  322  KADALNAEHIRMLDV  AEHIRMLDV         0.4412        422.5          WB    32.00      Sequence
DRB4_0101    3  TETVRVRFCPSPTGT  VRVRFCPSP         0.4342        455.7          WB    32.00      Sequence
DRB4_0101  232  IRIGVAERIPKFAHL  IRIGVAERI         0.4332        460.6          WB    32.00      Sequence
DRB4_0101  365  AELVQTRIVVLGDAW  TRIVVLGDA         0.4328        462.6          WB    32.00      Sequence
DRB4_0101  124  GRNPKLGYDNFDRHL  LGYDNFDRH         0.4327        463.3          WB    32.00      Sequence
DRB4_0101  127  PKLGYDNFDRHLTDA  LGYDNFDRH         0.4324        464.7          WB    32.00      Sequence
DRB4_0101    2  ATETVRVRFCPSPTG  VRVRFCPSP         0.4323        465.0          WB    32.00      Sequence
DRB4_0101  216  DLLPSTPRQLALHQA  LPSTPRQLA         0.4313        470.1          WB    32.00      Sequence
DRB4_0101  367  LVQTRIVVLGDAWEL  TRIVVLGDA         0.4283        485.6          WB    32.00      Sequence
DRB4_0101  123  AGRNPKLGYDNFDRH  LGYDNFDRH         0.4275        489.8          WB    32.00      Sequence
DRB4_0101  366  ELVQTRIVVLGDAWE  TRIVVLGDA         0.4221        519.4                32.00      Sequence
DRB4_0101   51  RDSEESYLALLDALR  ESYLALLDA         0.4196        533.5                32.00      Sequence
DRB4_0101  225  LALHQALIRIGVAER  LHQALIRIG         0.4191        536.7                32.00      Sequence
DRB4_0101   88  QRAEIYRDVLARLLA  YRDVLARLL         0.4167        550.8                32.00      Sequence
DRB4_0101  381  LLKFFNDDQYVIDPK  LKFFNDDQY         0.4166        551.4                32.00      Sequence
DRB4_0101  224  QLALHQALIRIGVAE  QLALHQALI         0.4160        554.7                32.00      Sequence
DRB4_0101    4  ETVRVRFCPSPTGTP  VRVRFCPSP         0.4126        575.9                32.00      Sequence
DRB4_0101  128  KLGYDNFDRHLTDAQ  LGYDNFDRH         0.4123        577.8                32.00      Sequence
DRB4_0101  271  DRGFIPEGLLNYLAL  RGFIPEGLL         0.4117        581.5                32.00      Sequence
DRB4_0101   25  TALFNWAYARHTGGT  TALFNWAYA         0.4087        600.7                32.00      Sequence
DRB4_0101  364  AAELVQTRIVVLGDA  TRIVVLGDA         0.4068        613.2                32.00      Sequence
DRB4_0101    1  TATETVRVRFCPSPT  VRVRFCPSP         0.4065        615.1                32.00      Sequence
DRB4_0101  237  AERIPKFAHLPTVLG  IPKFAHLPT         0.4043        629.8                32.00      Sequence
DRB4_0101  129  LGYDNFDRHLTDAQR  LGYDNFDRH         0.4011        651.6                50.00      Sequence
DRB4_0101  382  LKFFNDDQYVIDPKA  LKFFNDDQY         0.3987        669.1                50.00      Sequence
DRB4_0101  236  VAERIPKFAHLPTVL  IPKFAHLPT         0.3985        670.4                50.00      Sequence
DRB4_0101  238  ERIPKFAHLPTVLGE  IPKFAHLPT         0.3926        715.0                50.00      Sequence
DRB4_0101   87  SQRAEIYRDVLARLL  YRDVLARLL         0.3911        726.8                50.00      Sequence
DRB4_0101   64  LRWLGLDWDEGPEVG  LRWLGLDWD         0.3890        743.2                50.00      Sequence
DRB4_0101   50  QRDSEESYLALLDAL  ESYLALLDA         0.3881        750.1                50.00      Sequence
DRB4_0101  331  IRMLDVGDFTVRLRD  IRMLDVGDF         0.3832        790.9                50.00      Sequence
DRB4_0101  181  VPDFALTRASGDPLY  VPDFALTRA         0.3821        800.6                50.00      Sequence
DRB4_0101  371  RIVVLGDAWELLKFF  RIVVLGDAW         0.3819        802.8                50.00      Sequence
DRB4_0101  235  GVAERIPKFAHLPTV  IPKFAHLPT         0.3808        811.9                50.00      Sequence
DRB4_0101  215  EDLLPSTPRQLALHQ  LPSTPRQLA         0.3798        820.9                50.00      Sequence
DRB4_0101   82  GPYRQSQRAEIYRDV  GPYRQSQRA         0.3783        834.1                50.00      Sequence
DRB4_0101  444  RKAFSPIRVAATGTT  RKAFSPIRV         0.3764        851.7                50.00      Sequence
DRB4_0101  270  RDRGFIPEGLLNYLA  RGFIPEGLL         0.3760        855.3                50.00      Sequence
DRB4_0101  180  SVPDFALTRASGDPL  VPDFALTRA         0.3749        865.6                50.00      Sequence
DRB4_0101  210  HVLRGEDLLPSTPRQ  HVLRGEDLL         0.3747        867.7                50.00      Sequence
DRB4_0101  294  HDLFGLDEMVAAFDV  DLFGLDEMV         0.3735        878.6                50.00      Sequence
DRB4_0101  234  IGVAERIPKFAHLPT  IPKFAHLPT         0.3723        890.3                50.00      Sequence
DRB4_0101  423  TAPLIEAALKDALIE  APLIEAALK         0.3711        902.3                50.00      Sequence
DRB4_0101  198  VNPCDDALMKITHVL  ALMKITHVL         0.3697        915.6                50.00      Sequence
DRB4_0101    5  TVRVRFCPSPTGTPH  VRVRFCPSP         0.3696        916.5                50.00      Sequence
DRB4_0101  240  IPKFAHLPTVLGEGT  IPKFAHLPT         0.3694        918.4                50.00      Sequence
DRB4_0101  349  THGHHIALDEAAFAA  GHHIALDEA         0.3686        926.7                50.00      Sequence
DRB4_0101  442  KPRKAFSPIRVAATG  RKAFSPIRV         0.3668        945.1                50.00      Sequence
DRB4_0101  285  LLGWSIADDHDLFGL  LGWSIADDH         0.3664        948.8                50.00      Sequence
DRB4_0101  422  WTAPLIEAALKDALI  APLIEAALK         0.3663        950.5                50.00      Sequence
DRB4_0101    0  VTATETVRVRFCPSP  VRVRFCPSP         0.3650        963.9                50.00      Sequence
DRB4_0101   13  SPTGTPHVGLVRTAL  TPHVGLVRT         0.3647        966.2                50.00      Sequence
DRB4_0101  269  HRDRGFIPEGLLNYL  RGFIPEGLL         0.3643        970.7                50.00      Sequence
DRB4_0101  350  HGHHIALDEAAFAAA  GHHIALDEA         0.3633        981.3                50.00      Sequence
DRB4_0101  348  DTHGHHIALDEAAFA  GHHIALDEA         0.3627        988.2                50.00      Sequence
DRB4_0101  351  GHHIALDEAAFAAAA  GHHIALDEA         0.3624        990.8                50.00      Sequence
DRB4_0101  332  RMLDVGDFTVRLRDH  DFTVRLRDH         0.3612       1004.1                50.00      Sequence
DRB4_0101  363  AAAELVQTRIVVLGD  AELVQTRIV         0.3596       1020.9                50.00      Sequence
DRB4_0101  443  PRKAFSPIRVAATGT  RKAFSPIRV         0.3587       1031.2                50.00      Sequence
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DRB4_0101  434  ALIEGLALKPRKAFS  ALIEGLALK        0.3574       1046.4                50.00     Sequence
DRB4_0101  321  KKADALNAEHIRMLD  LNAEHIRML        0.3554       1068.6                50.00     Sequence
DRB4_0101  239  RIPKFAHLPTVLGEG  IPKFAHLPT        0.3554       1068.8                50.00     Sequence
DRB4_0101  295  DLFGLDEMVAAFDVA  DLFGLDEMV        0.3542       1082.6                50.00     Sequence
DRB4_0101  433  DALIEGLALKPRKAF  ALIEGLALK        0.3539       1086.5                50.00     Sequence
DRB4_0101   81  YGPYRQSQRAEIYRD  GPYRQSQRA        0.3532       1094.5                50.00     Sequence
DRB4_0101  424  APLIEAALKDALIEG  APLIEAALK        0.3530       1096.6                50.00     Sequence
DRB4_0101  293  DHDLFGLDEMVAAFD  DLFGLDEMV        0.3530       1097.3                50.00     Sequence
DRB4_0101  214  GEDLLPSTPRQLALH  LPSTPRQLA        0.3514       1116.2                50.00     Sequence
DRB4_0101   95  DVLARLLAAGEAYHA  DVLARLLAA        0.3504       1128.8                50.00     Sequence
DRB4_0101  421  DWTAPLIEAALKDAL  APLIEAALK        0.3495       1139.9                50.00     Sequence
DRB4_0101  145  AYLAEGRQPVVRLRM  RQPVVRLRM        0.3492       1142.8                50.00     Sequence
DRB4_0101   37  GGTFVFRIEDTDAQR  TFVFRIEDT        0.3485       1152.2                50.00     Sequence
DRB4_0101  445  KAFSPIRVAATGTTV  FSPIRVAAT        0.3475       1164.6                50.00     Sequence
DRB4_0101   80  PYGPYRQSQRAEIYR  GPYRQSQRA        0.3474       1165.5                50.00     Sequence
DRB4_0101  268  AHRDRGFIPEGLLNY  RGFIPEGLL        0.3459       1184.2                50.00     Sequence
DRB4_0101   79  GPYGPYRQSQRAEIY  GPYRQSQRA        0.3453       1192.3                50.00     Sequence
DRB4_0101   38  GTFVFRIEDTDAQRD  TFVFRIEDT        0.3431       1220.9                50.00     Sequence
DRB4_0101  446  AFSPIRVAATGTTVS  FSPIRVAAT        0.3430       1221.9                50.00     Sequence
DRB4_0101  254  TKKLSKRDPQSNLFA  LSKRDPQSN        0.3427       1226.9                50.00     Sequence
DRB4_0101  431  LKDALIEGLALKPRK  ALIEGLALK        0.3423       1232.2                50.00     Sequence
DRB4_0101    6  VRVRFCPSPTGTPHV  VRVRFCPSP        0.3422       1233.1                50.00     Sequence
DRB4_0101  156  RLRMPDDDLAWNDLV  LRMPDDDLA        0.3421       1234.1                50.00     Sequence
DRB4_0101  345  DHLDTHGHHIALDEA  GHHIALDEA        0.3419       1236.4                50.00     Sequence
DRB4_0101  292  DDHDLFGLDEMVAAF  DLFGLDEMV        0.3419       1236.9                50.00     Sequence
DRB4_0101   36  TGGTFVFRIEDTDAQ  TFVFRIEDT        0.3410       1248.8                50.00     Sequence
DRB4_0101  346  HLDTHGHHIALDEAA  GHHIALDEA        0.3390       1275.8                50.00     Sequence
DRB4_0101  362  AAAAELVQTRIVVLG  AELVQTRIV        0.3388       1279.3                50.00     Sequence
DRB4_0101  347  LDTHGHHIALDEAAF  GHHIALDEA        0.3362       1315.8                50.00     Sequence
DRB4_0101  320  QKKADALNAEHIRML  LNAEHIRML        0.3355       1326.1                50.00     Sequence
DRB4_0101  459  VSPPLFESLELLGRD  PLFESLELL        0.3351       1331.0                50.00     Sequence
DRB4_0101   39  TFVFRIEDTDAQRDS  TFVFRIEDT        0.3344       1341.5                50.00     Sequence
DRB4_0101   49  AQRDSEESYLALLDA  ESYLALLDA        0.3342       1344.0                50.00     Sequence
DRB4_0101   78  GGPYGPYRQSQRAEI  GPYRQSQRA        0.3312       1388.9                50.00     Sequence
DRB4_0101  253  GTKKLSKRDPQSNLF  LSKRDPQSN        0.3300       1407.5                50.00     Sequence
DRB4_0101  432  KDALIEGLALKPRKA  ALIEGLALK        0.3293       1417.8                50.00     Sequence
DRB4_0101  420  TDWTAPLIEAALKDA  APLIEAALK        0.3286       1428.9                50.00     Sequence
DRB4_0101  435  LIEGLALKPRKAFSP  IEGLALKPR        0.3283       1433.2                50.00     Sequence
DRB4_0101   26  ALFNWAYARHTGGTF  LFNWAYARH        0.3282       1434.7                50.00     Sequence
DRB4_0101  430  ALKDALIEGLALKPR  IEGLALKPR        0.3278       1440.4                50.00     Sequence
DRB4_0101  460  SPPLFESLELLGRDR  PLFESLELL        0.3273       1449.1                50.00     Sequence
DRB4_0101  447  FSPIRVAATGTTVSP  SPIRVAATG        0.3260       1469.3                50.00     Sequence
DRB4_0101  458  TVSPPLFESLELLGR  PLFESLELL        0.3252       1482.4                50.00     Sequence
DRB4_0101  373  VVLGDAWELLKFFND  VVLGDAWEL        0.3251       1483.0                50.00     Sequence
DRB4_0101  441  LKPRKAFSPIRVAAT  FSPIRVAAT        0.3236       1508.5                50.00     Sequence
DRB4_0101  179  GSVPDFALTRASGDP  VPDFALTRA        0.3227       1522.9                50.00     Sequence
DRB4_0101   77  VGGPYGPYRQSQRAE  GPYRQSQRA        0.3225       1526.0                50.00     Sequence
DRB4_0101  436  IEGLALKPRKAFSPI  EGLALKPRK        0.3211       1549.0                50.00     Sequence
DRB4_0101  213  RGEDLLPSTPRQLAL  LPSTPRQLA        0.3204       1561.7                50.00     Sequence
DRB4_0101   35  HTGGTFVFRIEDTDA  TFVFRIEDT        0.3197       1572.3                50.00     Sequence
DRB4_0101  419  VTDWTAPLIEAALKD  APLIEAALK        0.3159       1638.8                50.00     Sequence
DRB4_0101  130  GYDNFDRHLTDAQRA  RHLTDAQRA        0.3157       1642.1                50.00     Sequence
DRB4_0101  457  TTVSPPLFESLELLG  PLFESLELL        0.3155       1646.8                50.00     Sequence
DRB4_0101  286  LGWSIADDHDLFGLD  LGWSIADDH        0.3139       1674.7                50.00     Sequence
DRB4_0101  438  GLALKPRKAFSPIRV  LALKPRKAF        0.3128       1695.1                50.00     Sequence
DRB4_0101  439  LALKPRKAFSPIRVA  LALKPRKAF        0.3120       1709.0                50.00     Sequence
DRB4_0101  291  ADDHDLFGLDEMVAA  DLFGLDEMV        0.3117       1715.3                50.00     Sequence
DRB4_0101  405  GAAVLDAALAALTSV  AAVLDAALA        0.3116       1717.5                50.00     Sequence
DRB4_0101  437  EGLALKPRKAFSPIR  LALKPRKAF        0.3113       1722.6                50.00     Sequence
DRB4_0101  134  FDRHLTDAQRAAYLA  RHLTDAQRA        0.3094       1758.6                50.00     Sequence
DRB4_0101  157  LRMPDDDLAWNDLVR  LRMPDDDLA        0.3088       1769.7                50.00     Sequence
DRB4_0101  135  DRHLTDAQRAAYLAE  RHLTDAQRA        0.3054       1835.4                50.00     Sequence
DRB4_0101  418  SVTDWTAPLIEAALK  APLIEAALK        0.3049       1845.7                50.00     Sequence
DRB4_0101  212  LRGEDLLPSTPRQLA  LPSTPRQLA        0.3046       1852.7                50.00     Sequence
DRB4_0101   76  EVGGPYGPYRQSQRA  GPYRQSQRA        0.3038       1868.9                50.00     Sequence
DRB4_0101  267  FAHRDRGFIPEGLLN  RGFIPEGLL        0.3037       1870.0                50.00     Sequence
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DRB4_0101  372  IVVLGDAWELLKFFN  VVLGDAWEL        0.3036       1871.7                  50.00     Sequence
DRB4_0101  404  DGAAVLDAALAALTS  AAVLDAALA        0.3029       1887.2                  50.00     Sequence
DRB4_0101  252  EGTKKLSKRDPQSNL  LSKRDPQSN        0.3028       1889.4                  50.00     Sequence
DRB4_0101  245  HLPTVLGEGTKKLSK  LPTVLGEGT        0.3024       1896.3                  50.00     Sequence
DRB4_0101  266  LFAHRDRGFIPEGLL  RGFIPEGLL        0.3020       1905.1                  50.00     Sequence
DRB4_0101  290  IADDHDLFGLDEMVA  HDLFGLDEM        0.3018       1908.8                  50.00     Sequence
DRB4_0101  298  GLDEMVAAFDVADVN  DEMVAAFDV        0.3018       1909.7                  50.00     Sequence
DRB4_0101  264  SNLFAHRDRGFIPEG  SNLFAHRDR        0.3013       1919.9                  50.00     Sequence
DRB4_0101  361  FAAAAELVQTRIVVL  AELVQTRIV        0.3013       1920.4                  50.00     Sequence
DRB4_0101  131  YDNFDRHLTDAQRAA  RHLTDAQRA        0.3009       1927.5                  50.00     Sequence
DRB4_0101  182  PDFALTRASGDPLYT  LTRASGDPL        0.2995       1956.8                  50.00     Sequence
DRB4_0101  178  AGSVPDFALTRASGD  VPDFALTRA        0.2994       1958.5                  50.00     Sequence
DRB4_0101  297  FGLDEMVAAFDVADV  DEMVAAFDV        0.2992       1963.3                  50.00     Sequence
DRB4_0101  246  LPTVLGEGTKKLSKR  LPTVLGEGT        0.2980       1988.3                  50.00     Sequence
DRB4_0101  429  AALKDALIEGLALKP  ALIEGLALK        0.2974       2001.8                  50.00     Sequence
DRB4_0101  255  KKLSKRDPQSNLFAH  LSKRDPQSN        0.2964       2024.6                  50.00     Sequence
DRB4_0101  403  PDGAAVLDAALAALT  AAVLDAALA        0.2962       2029.2                  50.00     Sequence
DRB4_0101  456  GTTVSPPLFESLELL  PLFESLELL        0.2959       2034.0                  50.00     Sequence
DRB4_0101  244  AHLPTVLGEGTKKLS  LPTVLGEGT        0.2959       2034.9                  50.00     Sequence
DRB4_0101  296  LFGLDEMVAAFDVAD  DEMVAAFDV        0.2951       2052.1                  50.00     Sequence
DRB4_0101  133  NFDRHLTDAQRAAYL  RHLTDAQRA        0.2949       2057.0                  50.00     Sequence
DRB4_0101  132  DNFDRHLTDAQRAAY  RHLTDAQRA        0.2947       2061.9                  50.00     Sequence
DRB4_0101  192  DPLYTLVNPCDDALM  DPLYTLVNP        0.2937       2083.9                  50.00     Sequence
DRB4_0101  375  LGDAWELLKFFNDDQ  LLKFFNDDQ        0.2932       2094.1                  50.00     Sequence
DRB4_0101  440  ALKPRKAFSPIRVAA  KAFSPIRVA        0.2929       2101.8                  50.00     Sequence
DRB4_0101  416  LTSVTDWTAPLIEAA  LTSVTDWTA        0.2928       2104.3                  50.00     Sequence
DRB4_0101  263  QSNLFAHRDRGFIPE  SNLFAHRDR        0.2920       2121.8                  50.00     Sequence
DRB4_0101  177  AAGSVPDFALTRASG  VPDFALTRA        0.2915       2133.1                  50.00     Sequence
DRB4_0101  415  ALTSVTDWTAPLIEA  LTSVTDWTA        0.2905       2157.8                  50.00     Sequence
DRB4_0101  136  RHLTDAQRAAYLAEG  RHLTDAQRA        0.2903       2160.9                  50.00     Sequence
DRB4_0101  289  SIADDHDLFGLDEMV  HDLFGLDEM        0.2899       2171.6                  50.00     Sequence
DRB4_0101  414  AALTSVTDWTAPLIE  LTSVTDWTA        0.2897       2176.1                  50.00     Sequence
DRB4_0101  448  SPIRVAATGTTVSPP  SPIRVAATG        0.2886       2201.5                  50.00     Sequence
DRB4_0101   34  RHTGGTFVFRIEDTD  TFVFRIEDT        0.2858       2270.6                  50.00     Sequence
DRB4_0101  360  AFAAAAELVQTRIVV  AELVQTRIV        0.2852       2285.8                  50.00     Sequence
DRB4_0101  402  GPDGAAVLDAALAAL  AAVLDAALA        0.2816       2376.3                  50.00     Sequence
DRB4_0101  241  PKFAHLPTVLGEGTK  LPTVLGEGT        0.2815       2377.6                  50.00     Sequence
DRB4_0101  176  FAAGSVPDFALTRAS  VPDFALTRA        0.2814       2380.3                  50.00     Sequence
DRB4_0101  191  GDPLYTLVNPCDDAL  DPLYTLVNP        0.2808       2396.2                  50.00     Sequence
DRB4_0101  197  LVNPCDDALMKITHV  DALMKITHV        0.2797       2424.0                  50.00     Sequence
DRB4_0101  243  FAHLPTVLGEGTKKL  LPTVLGEGT        0.2794       2433.4                  50.00     Sequence
DRB4_0101  262  PQSNLFAHRDRGFIP  SNLFAHRDR        0.2785       2456.0                  50.00     Sequence
DRB4_0101  374  VLGDAWELLKFFNDD  WELLKFFND        0.2782       2465.3                  50.00     Sequence
DRB4_0101  299  LDEMVAAFDVADVNS  EMVAAFDVA        0.2776       2480.7                  50.00     Sequence
DRB4_0101  251  GEGTKKLSKRDPQSN  LSKRDPQSN        0.2764       2513.8                  50.00     Sequence
DRB4_0101  256  KLSKRDPQSNLFAHR  LSKRDPQSN        0.2755       2536.6                  50.00     Sequence
DRB4_0101   12  PSPTGTPHVGLVRTA  PHVGLVRTA        0.2755       2538.1                  50.00     Sequence
DRB4_0101  211  VLRGEDLLPSTPRQL  LRGEDLLPS        0.2751       2548.3                  50.00     Sequence
DRB4_0101   96  VLARLLAAGEAYHAF  ARLLAAGEA        0.2748       2556.9                  50.00     Sequence
DRB4_0101  413  LAALTSVTDWTAPLI  LTSVTDWTA        0.2742       2572.6                  50.00     Sequence
DRB4_0101   40  FVFRIEDTDAQRDSE  VFRIEDTDA        0.2740       2579.2                  50.00     Sequence
DRB4_0101   86  QSQRAEIYRDVLARL  RAEIYRDVL        0.2735       2592.7                  50.00     Sequence
DRB4_0101  342  RLRDHLDTHGHHIAL  RLRDHLDTH        0.2712       2658.2                  50.00     Sequence
DRB4_0101  406  AAVLDAALAALTSVT  AAVLDAALA        0.2705       2679.5                  50.00     Sequence
DRB4_0101  168  DLVRGPVTFAAGSVP  DLVRGPVTF        0.2702       2688.1                  50.00     Sequence
DRB4_0101  233  RIGVAERIPKFAHLP  ERIPKFAHL        0.2698       2698.6                  50.00     Sequence
DRB4_0101  300  DEMVAAFDVADVNSS  DEMVAAFDV        0.2692       2716.8                  50.00     Sequence
DRB4_0101  242  KFAHLPTVLGEGTKK  LPTVLGEGT        0.2690       2721.5                  50.00     Sequence
DRB4_0101  190  SGDPLYTLVNPCDDA  YTLVNPCDD        0.2679       2755.1                  50.00     Sequence
DRB4_0101  166  WNDLVRGPVTFAAGS  DLVRGPVTF        0.2660       2813.4                  50.00     Sequence
DRB4_0101  261  DPQSNLFAHRDRGFI  SNLFAHRDR        0.2646       2856.1                  50.00     Sequence
DRB4_0101  160  PDDDLAWNDLVRGPV  DDLAWNDLV        0.2645       2857.4                  50.00     Sequence
DRB4_0101  425  PLIEAALKDALIEGL  LKDALIEGL        0.2625       2919.6                  50.00     Sequence
DRB4_0101   85  RQSQRAEIYRDVLAR  RAEIYRDVL        0.2610       2967.6                  50.00     Sequence
DRB4_0101   98  ARLLAAGEAYHAFST  ARLLAAGEA        0.2609       2973.1                  50.00     Sequence
DRB4_0101  193  PLYTLVNPCDDALMK  YTLVNPCDD        0.2604       2987.6                  50.00     Sequence
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DRB4_0101	189	ASGDPLYTLVNPCDD	DPLYTLVNP	0.2597	3012.0	50.00	Sequence
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DRB4_0101	352	HHIALDEAAFAAAAE	HHIALDEAA	0.2584	3053.5	50.00	Sequence
DRB4_0101	260	RDPQSNLFAHRDRGF	SNLFAHRDR	0.2573	3088.4	50.00	Sequence
DRB4_0101	183	DFALTRASGDPLYTL	LTRASGDPL	0.2566	3114.9	50.00	Sequence
DRB4_0101	165	AWNDLVRGPVTFAAG	DLVRGPVTF	0.2554	3152.3	50.00	Sequence
DRB4_0101	97	LARLLAAGEAYHAFS	ARLLAAGEA	0.2551	3165.0	50.00	Sequence
DRB4_0101	401	LGPDGAAVLDAALAA	AAVLDAALA	0.2549	3172.4	50.00	Sequence
DRB4_0101	167	NDLVRGPVTFAAGSV	DLVRGPVTF	0.2549	3172.5	50.00	Sequence
DRB4_0101	288	WSIADDHDLFGLDEM	HDLFGLDEM	0.2542	3195.5	50.00	Sequence
DRB4_0101	412	ALAALTSVTDWTAPL	LTSVTDWTA	0.2530	3235.8	50.00	Sequence
DRB4_0101	122	AAGRNPKLGYDNFDR	RNPKLGYDN	0.2529	3239.2	50.00	Sequence
DRB4_0101	250	LGEGTKKLSKRDPQS	LGEGTKKLS	0.2523	3262.5	50.00	Sequence
DRB4_0101	258	SKRDPQSNLFAHRDR	SNLFAHRDR	0.2522	3263.8	50.00	Sequence
DRB4_0101	259	KRDPQSNLFAHRDRG	SNLFAHRDR	0.2521	3267.0	50.00	Sequence
DRB4_0101	27	LFNWAYARHTGGTFV	LFNWAYARH	0.2511	3302.6	50.00	Sequence
DRB4_0101	184	FALTRASGDPLYTLV	ALTRASGDP	0.2510	3308.3	50.00	Sequence
DRB4_0101	388	DQYVIDPKAAAKELG	DQYVIDPKA	0.2500	3343.7	50.00	Sequence
DRB4_0101	386	NDDQYVIDPKAAAKE	DQYVIDPKA	0.2498	3349.4	50.00	Sequence
DRB4_0101	257	LSKRDPQSNLFAHRD	LSKRDPQSN	0.2491	3375.9	50.00	Sequence
DRB4_0101	164	LAWNDLVRGPVTFAA	DLVRGPVTF	0.2478	3422.7	50.00	Sequence
DRB4_0101	83	PYRQSQRAEIYRDVL	QRAEIYRDV	0.2462	3482.3	50.00	Sequence
DRB4_0101	185	ALTRASGDPLYTLVN	LTRASGDPL	0.2459	3493.6	50.00	Sequence
DRB4_0101	428	EAALKDALIEGLALK	ALIEGLALK	0.2453	3516.7	50.00	Sequence
DRB4_0101	169	LVRGPVTFAAGSVPD	PVTFAAGSV	0.2452	3520.8	50.00	Sequence
DRB4_0101	343	LRDHLDTHGHHIALD	LRDHLDTHG	0.2440	3567.9	50.00	Sequence
DRB4_0101	319	DQKKADALNAEHIRM	ADALNAEHI	0.2431	3602.2	50.00	Sequence
DRB4_0101	455	TGTTVSPPLFESLEL	PPLFESLEL	0.2425	3625.4	50.00	Sequence
DRB4_0101	265	NLFAHRDRGFIPEGL	DRGFIPEGL	0.2415	3666.8	50.00	Sequence
DRB4_0101	344	RDHLDTHGHHIALDE	DHLDTHGHH	0.2412	3676.8	50.00	Sequence
DRB4_0101	162	DDLAWNDLVRGPVTF	DLVRGPVTF	0.2394	3750.2	50.00	Sequence
DRB4_0101	302	MVAAFDVADVNSSPA	VAAFDVADV	0.2386	3784.2	50.00	Sequence
DRB4_0101	33	ARHTGGTFVFRIEDT	TFVFRIEDT	0.2360	3890.1	50.00	Sequence
DRB4_0101	159	MPDDDLAWNDLVRGP	LAWNDLVRG	0.2357	3903.6	50.00	Sequence
DRB4_0101	65	RWLGLDWDEGPEVGG	WLGLDWDEG	0.2344	3957.1	50.00	Sequence
DRB4_0101	301	EMVAAFDVADVNSSP	EMVAAFDVA	0.2320	4061.3	50.00	Sequence
DRB4_0101	249	VLGEGTKKLSKRDPQ	LGEGTKKLS	0.2320	4061.9	50.00	Sequence
DRB4_0101	158	RMPDDDLAWNDLVRG	LAWNDLVRG	0.2319	4068.1	50.00	Sequence
DRB4_0101	161	DDDLAWNDLVRGPVT	DDLAWNDLV	0.2316	4079.4	50.00	Sequence
DRB4_0101	400	ELGPDGAAVLDAALA	AAVLDAALA	0.2314	4090.8	50.00	Sequence
DRB4_0101	170	VRGPVTFAAGSVPDF	GPVTFAAGS	0.2307	4121.8	50.00	Sequence
DRB4_0101	385	FNDDQYVIDPKAAAK	DQYVIDPKA	0.2300	4150.4	50.00	Sequence
DRB4_0101	384	FFNDDQYVIDPKAAA	DQYVIDPKA	0.2270	4288.3	50.00	Sequence
DRB4_0101	195	YTLVNPCDDALMKIT	YTLVNPCDD	0.2253	4366.5	50.00	Sequence
DRB4_0101	175	TFAAGSVPDFALTRA	VPDFALTRA	0.2253	4369.4	50.00	Sequence
DRB4_0101	411	AALAALTSVTDWTAP	LTSVTDWTA	0.2250	4384.2	50.00	Sequence
DRB4_0101	359	AAFAAAAELVQTRIV	AELVQTRIV	0.2225	4502.1	50.00	Sequence
DRB4_0101	303	VAAFDVADVNSSPAR	VAAFDVADV	0.2221	4519.9	50.00	Sequence
DRB4_0101	186	LTRASGDPLYTLVNP	LTRASGDPL	0.2218	4535.8	50.00	Sequence
DRB4_0101	410	DAALAALTSVTDWTA	LTSVTDWTA	0.2211	4569.1	50.00	Sequence
DRB4_0101	163	DLAWNDLVRGPVTFA	DLVRGPVTF	0.2202	4616.2	50.00	Sequence
DRB4_0101	417	TSVTDWTAPLIEAAL	VTDWTAPLI	0.2197	4641.2	50.00	Sequence
DRB4_0101	84	YRQSQRAEIYRDVLA	RAEIYRDVL	0.2193	4663.2	50.00	Sequence
DRB4_0101	407	AVLDAALAALTSVTD	LDAALAALT	0.2192	4665.4	50.00	Sequence
DRB4_0101	383	KFFNDDQYVIDPKAA	DQYVIDPKA	0.2190	4677.1	50.00	Sequence
DRB4_0101	144	AAYLAEGRQPVVRLR	YLAEGRQPV	0.2189	4682.3	50.00	Sequence
DRB4_0101	194	LYTLVNPCDDALMKI	YTLVNPCDD	0.2156	4849.6	50.00	Sequence
DRB4_0101	307	DVADVNSSPARFDQK	VADVNSSPA	0.2142	4925.1	50.00	Sequence
DRB4_0101	188	RASGDPLYTLVNPCD	DPLYTLVNP	0.2132	4979.4	50.00	Sequence
DRB4_0101	408	VLDAALAALTSVTDW	LDAALAALT	0.2128	4998.6	50.00	Sequence
DRB4_0101	138	LTDAQRAAYLAEGRQ	LTDAQRAAY	0.2123	5027.9	50.00	Sequence
DRB4_0101	121	VAAGRNPKLGYDNFD	NPKLGYDNF	0.2114	5078.6	50.00	Sequence
DRB4_0101	304	AAFDVADVNSSPARF	VADVNSSPA	0.2112	5088.7	50.00	Sequence
DRB4_0101	137	HLTDAQRAAYLAEGR	LTDAQRAAY	0.2105	5126.1	50.00	Sequence
DRB4_0101	11	CPSPTGTPHVGLVRT	TPHVGLVRT	0.2092	5198.2	50.00	Sequence
DRB4_0101	120	HVAAGRNPKLGYDNF	NPKLGYDNF	0.2085	5236.9	50.00	Sequence

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DRB4_0101  314  SPARFDQKKADALNA  ARFDQKKAD        0.2074       5299.0                         50.00     Sequence
DRB4_0101  427  IEAALKDALIEGLAL  LKDALIEGL        0.2069       5327.6                         50.00     Sequence
DRB4_0101  308  VADVNSSPARFDQKK  VADVNSSPA        0.2056       5407.4                         50.00     Sequence
DRB4_0101  306  FDVADVNSSPARFDQ  VADVNSSPA        0.2044       5476.2                         50.00     Sequence
DRB4_0101   41  VFRIEDTDAQRDSEE  VFRIEDTDA        0.2039       5504.7                         50.00     Sequence
DRB4_0101  171  RGPVTFAAGSVPDFA  VTFAAGSVP        0.2035       5529.4                         50.00     Sequence
DRB4_0101  426  LIEAALKDALIEGLA  LKDALIEGL        0.2006       5705.8                         50.00     Sequence
DRB4_0101  196  TLVNPCDDALMKITH  LVNPCDDAL        0.2003       5724.8                         50.00     Sequence
DRB4_0101  313  SSPARFDQKKADALN  ARFDQKKAD        0.1997       5764.8                         50.00     Sequence
DRB4_0101  305  AFDVADVNSSPARFD  VADVNSSPA        0.1992       5795.3                         50.00     Sequence
DRB4_0101  187  TRASGDPLYTLVNPC  DPLYTLVNP        0.1990       5802.9                         50.00     Sequence
DRB4_0101  315  PARFDQKKADALNAE  ARFDQKKAD        0.1949       6070.3                         50.00     Sequence
DRB4_0101  317  RFDQKKADALNAEHI  ADALNAEHI        0.1926       6219.0                         50.00     Sequence
DRB4_0101  143  RAAYLAEGRQPVVRL  AAYLAEGRQ        0.1926       6220.9                         50.00     Sequence
DRB4_0101    7  RVRFCPSPTGTPHVG  RVRFCPSPT        0.1901       6389.8                         50.00     Sequence
DRB4_0101  454  ATGTTVSPPLFESLE  GTTVSPPLF        0.1901       6393.8                         50.00     Sequence
DRB4_0101  453  AATGTTVSPPLFESL  VSPPLFESL        0.1896       6424.3                         50.00     Sequence
DRB4_0101  312  NSSPARFDQKKADAL  ARFDQKKAD        0.1892       6455.1                         50.00     Sequence
DRB4_0101  389  QYVIDPKAAAKELGP  QYVIDPKAA        0.1886       6498.5                         50.00     Sequence
DRB4_0101  248  TVLGEGTKKLSKRDP  LGEGTKKLS        0.1869       6619.6                         50.00     Sequence
DRB4_0101  449  PIRVAATGTTVSPPL  PIRVAATGT        0.1866       6641.6                         50.00     Sequence
DRB4_0101  172  GPVTFAAGSVPDFAL  VTFAAGSVP        0.1864       6656.6                         50.00     Sequence
DRB4_0101  119  RHVAAGRNPKLGYDN  RHVAAGRNP        0.1862       6670.8                         50.00     Sequence
DRB4_0101   99  RLLAAGEAYHAFSTP  RLLAAGEAY        0.1857       6703.8                         50.00     Sequence
DRB4_0101  115  EVEARHVAAGRNPKL  EVEARHVAA        0.1847       6780.3                         50.00     Sequence
DRB4_0101  118  ARHVAAGRNPKLGYD  ARHVAAGRN        0.1825       6938.2                         50.00     Sequence
DRB4_0101  113  PEEVEARHVAAGRNP  EVEARHVAA        0.1810       7054.3                         50.00     Sequence
DRB4_0101  142  QRAAYLAEGRQPVVR  AAYLAEGRQ        0.1797       7154.7                         50.00     Sequence
DRB4_0101  117  EARHVAAGRNPKLGY  ARHVAAGRN        0.1783       7261.7                         50.00     Sequence
DRB4_0101  353  HIALDEAAFAAAAEL  IALDEAAFA        0.1772       7352.6                         50.00     Sequence
DRB4_0101  409  LDAALAALTSVTDWT  LDAALAALT        0.1772       7354.2                         50.00     Sequence
DRB4_0101  316  ARFDQKKADALNAEH  ARFDQKKAD        0.1766       7397.8                         50.00     Sequence
DRB4_0101  114  EEVEARHVAAGRNPK  EVEARHVAA        0.1761       7440.5                         50.00     Sequence
DRB4_0101  139  TDAQRAAYLAEGRQP  DAQRAAYLA        0.1748       7540.5                         50.00     Sequence
DRB4_0101  450  IRVAATGTTVSPPLF  IRVAATGTT        0.1742       7594.6                         50.00     Sequence
DRB4_0101  311  VNSSPARFDQKKADA  ARFDQKKAD        0.1738       7622.7                         50.00     Sequence
DRB4_0101  318  FDQKKADALNAEHIR  ADALNAEHI        0.1737       7637.5                         50.00     Sequence
DRB4_0101  140  DAQRAAYLAEGRQPV  DAQRAAYLA        0.1728       7711.6                         50.00     Sequence
DRB4_0101  112  TPEEVEARHVAAGRN  ARHVAAGRN        0.1719       7782.0                         50.00     Sequence
DRB4_0101   28  FNWAYARHTGGTFVF  FNWAYARHT        0.1697       7975.6                         50.00     Sequence
DRB4_0101  116  VEARHVAAGRNPKLG  ARHVAAGRN        0.1655       8338.8                         50.00     Sequence
DRB4_0101   66  WLGLDWDEGPEVGGP  LGLDWDEGP        0.1649       8395.5                         50.00     Sequence
DRB4_0101   75  PEVGGPYGPYRQSQR  GPYGPYRQS        0.1630       8573.7                         50.00     Sequence
DRB4_0101  141  AQRAAYLAEGRQPVV  AAYLAEGRQ        0.1622       8645.0                         50.00     Sequence
DRB4_0101  287  GWSIADDHDLFGLDE  WSIADDHDL        0.1581       9035.7                         50.00     Sequence
DRB4_0101  358  EAAFAAAAELVQTRI  AAELVQTRI        0.1566       9183.8                         50.00     Sequence
DRB4_0101  173  PVTFAAGSVPDFALT  VTFAAGSVP        0.1545       9398.8                         50.00     Sequence
DRB4_0101  397  AAKELGPDGAAVLDA  AKELGPDGA        0.1532       9526.4                         50.00     Sequence
DRB4_0101  247  PTVLGEGTKKLSKRD  LGEGTKKLS        0.1525       9601.5                         50.00     Sequence
DRB4_0101   74  GPEVGGPYGPYRQSQ  GGPYGPYRQ        0.1519       9663.5                         50.00     Sequence
DRB4_0101   48  DAQRDSEESYLALLD  EESYLALLD        0.1514       9716.3                         50.00     Sequence
DRB4_0101  398  AKELGPDGAAVLDAA  AKELGPDGA        0.1496       9904.6                         50.00     Sequence
DRB4_0101  354  IALDEAAFAAAAELV  IALDEAAFA        0.1476      10121.9                         50.00     Sequence
DRB4_0101   32  YARHTGGTFVFRIED  GTFVFRIED        0.1472      10167.1                         50.00     Sequence
DRB4_0101  399  KELGPDGAAVLDAAL  GAAVLDAAL        0.1469      10197.5                         50.00     Sequence
DRB4_0101  396  AAAKELGPDGAAVLD  AKELGPDGA        0.1442      10508.8                         50.00     Sequence
DRB4_0101  310  DVNSSPARFDQKKAD  ARFDQKKAD        0.1407      10913.3                         50.00     Sequence
DRB4_0101  395  KAAAKELGPDGAAVL  AKELGPDGA        0.1401      10976.2                         50.00     Sequence
DRB4_0101  390  YVIDPKAAAKELGPD  YVIDPKAAA        0.1396      11038.1                         50.00     Sequence
DRB4_0101  309  ADVNSSPARFDQKKA  SSPARFDQK        0.1385      11168.0                         50.00     Sequence
DRB4_0101   29  NWAYARHTGGTFVFR  WAYARHTGG        0.1383      11199.4                         50.00     Sequence
DRB4_0101  111  STPEEVEARHVAAGR  EVEARHVAA        0.1380      11228.0                         50.00     Sequence
DRB4_0101   73  EGPEVGGPYGPYRQS  GPYGPYRQS        0.1368      11382.1                         50.00     Sequence
DRB4_0101  174  VTFAAGSVPDFALTR  VTFAAGSVP        0.1343      11693.5                         50.00     Sequence
DRB4_0101  452  VAATGTTVSPPLFES  GTTVSPPLF        0.1335      11797.0                         50.00     Sequence
DRB4_0101  392  IDPKAAAKELGPDGA  AKELGPDGA        0.1325      11926.5                         50.00     Sequence
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   DRB4_0101  394  PKAAAKELGPDGAAV  AKELGPDGA        0.1254      12868.7               50.00     Sequence
   DRB4_0101    8  VRFCPSPTGTPHVGL  VRFCPSPTG        0.1233      13163.8               50.00     Sequence
   DRB4_0101   30  WAYARHTGGTFVFRI  WAYARHTGG        0.1229      13226.6               50.00     Sequence
   DRB4_0101  393  DPKAAAKELGPDGAA  AKELGPDGA        0.1215      13424.0               50.00     Sequence
   DRB4_0101  110  FSTPEEVEARHVAAG  EVEARHVAA        0.1199      13664.7               50.00     Sequence
   DRB4_0101  451  RVAATGTTVSPPLFE  GTTVSPPLF        0.1197      13686.3               50.00     Sequence
   DRB4_0101   42  FRIEDTDAQRDSEES  FRIEDTDAQ        0.1175      14023.8               50.00     Sequence
   DRB4_0101   72  DEGPEVGGPYGPYRQ  GGPYGPYRQ        0.1169      14108.4               50.00     Sequence
   DRB4_0101   47  TDAQRDSEESYLALL  AQRDSEESY        0.1143      14517.8               50.00     Sequence
   DRB4_0101   67  LGLDWDEGPEVGGPY  GLDWDEGPE        0.1125      14801.1               50.00     Sequence
   DRB4_0101  102  AAGEAYHAFSTPEEV  HAFSTPEEV        0.1099      15216.8               50.00     Sequence
   DRB4_0101  109  AFSTPEEVEARHVAA  EVEARHVAA        0.1042      16196.2               50.00     Sequence
   DRB4_0101   10  FCPSPTGTPHVGLVR  CPSPTGTPH        0.1041      16217.4               50.00     Sequence
   DRB4_0101   31  AYARHTGGTFVFRIE  RHTGGTFVF        0.1024      16511.5               50.00     Sequence
   DRB4_0101   68  GLDWDEGPEVGGPYG  GLDWDEGPE        0.1006      16845.5               50.00     Sequence
   DRB4_0101  103  AGEAYHAFSTPEEVE  HAFSTPEEV        0.0996      17028.9               50.00     Sequence
   DRB4_0101  101  LAAGEAYHAFSTPEE  LAAGEAYHA        0.0984      17235.8               50.00     Sequence
   DRB4_0101   46  DTDAQRDSEESYLAL  AQRDSEESY        0.0984      17248.3               50.00     Sequence
   DRB4_0101   44  IEDTDAQRDSEESYL  EDTDAQRDS        0.0959      17716.6               50.00     Sequence
   DRB4_0101  391  VIDPKAAAKELGPDG  IDPKAAAKE        0.0943      18028.3               50.00     Sequence
   DRB4_0101  104  GEAYHAFSTPEEVEA  HAFSTPEEV        0.0925      18377.9               50.00     Sequence
   DRB4_0101   43  RIEDTDAQRDSEESY  IEDTDAQRD        0.0913      18626.4               50.00     Sequence
   DRB4_0101  355  ALDEAAFAAAAELVQ  AAFAAAAEL        0.0910      18689.3               50.00     Sequence
   DRB4_0101    9  RFCPSPTGTPHVGLV  CPSPTGTPH        0.0898      18923.8               50.00     Sequence
   DRB4_0101   45  EDTDAQRDSEESYLA  EDTDAQRDS        0.0894      19000.1               50.00     Sequence
   DRB4_0101  105  EAYHAFSTPEEVEAR  HAFSTPEEV        0.0880      19295.3               50.00     Sequence
   DRB4_0101  108  HAFSTPEEVEARHVA  HAFSTPEEV        0.0866      19593.4               50.00     Sequence
   DRB4_0101  106  AYHAFSTPEEVEARH  HAFSTPEEV        0.0844      20063.4               50.00     Sequence
   DRB4_0101  357  DEAAFAAAAELVQTR  AAFAAAAEL        0.0815      20710.1               50.00     Sequence
   DRB4_0101   71  WDEGPEVGGPYGPYR  GPEVGGPYG        0.0813      20744.2               50.00     Sequence
   DRB4_0101  107  YHAFSTPEEVEARHV  HAFSTPEEV        0.0805      20933.6               50.00     Sequence
   DRB4_0101  356  LDEAAFAAAAELVQT  AAFAAAAEL        0.0802      20993.9               50.00     Sequence
   DRB4_0101   69  LDWDEGPEVGGPYGP  LDWDEGPEV        0.0721      22923.3               50.00     Sequence
   DRB4_0101   70  DWDEGPEVGGPYGPY  GPEVGGPYG        0.0674      24122.6               50.00     Sequence
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Allele: DRB4_0101. Number of high binders 6. Number of weak binders 122. Number of peptides 476

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB5_0101   24  RTALFNWAYARHTGG  FNWAYARHT        0.7884          9.9         SB     0.80     Sequence
   DRB5_0101   25  TALFNWAYARHTGGT  FNWAYARHT        0.7861         10.1         SB     0.80     Sequence
   DRB5_0101   26  ALFNWAYARHTGGTF  FNWAYARHT        0.7833         10.4         SB     0.80     Sequence
   DRB5_0101   27  LFNWAYARHTGGTFV  FNWAYARHT        0.7708         11.9         SB     1.00     Sequence
   DRB5_0101   23  VRTALFNWAYARHTG  FNWAYARHT        0.7682         12.3         SB     1.00     Sequence
   DRB5_0101   22  LVRTALFNWAYARHT  FNWAYARHT        0.7481         15.3         SB     2.00     Sequence
   DRB5_0101  474  RSMQRLRAARQLVGH  MQRLRAARQ        0.6953         27.0         SB     4.00     Sequence
   DRB5_0101  473  DRSMQRLRAARQLVG  MQRLRAARQ        0.6912         28.3         SB     4.00     Sequence
   DRB5_0101   54  EESYLALLDALRWLG  YLALLDALR        0.6890         28.9         SB     4.00     Sequence
   DRB5_0101   55  ESYLALLDALRWLGL  YLALLDALR        0.6855         30.0         SB     4.00     Sequence
   DRB5_0101  475  SMQRLRAARQLVGHA  LRAARQLVG        0.6827         31.0         SB     4.00     Sequence
   DRB5_0101   53  SEESYLALLDALRWL  YLALLDALR        0.6774         32.8         SB     4.00     Sequence
   DRB5_0101   28  FNWAYARHTGGTFVF  FNWAYARHT        0.6746         33.8         SB     4.00     Sequence
   DRB5_0101  472  RDRSMQRLRAARQLV  MQRLRAARQ        0.6716         34.9         SB     4.00     Sequence
   DRB5_0101  223  RQLALHQALIRIGVA  LALHQALIR        0.6655         37.3         SB     8.00     Sequence
   DRB5_0101   56  SYLALLDALRWLGLD  YLALLDALR        0.6611         39.1         SB     8.00     Sequence
   DRB5_0101  222  PRQLALHQALIRIGV  LALHQALIR        0.6594         39.9         SB     8.00     Sequence
   DRB5_0101   90  AEIYRDVLARLLAAG  YRDVLARLL        0.6468         45.7         SB     8.00     Sequence
   DRB5_0101   89  RAEIYRDVLARLLAA  YRDVLARLL        0.6422         48.0         SB     8.00     Sequence
   DRB5_0101   52  DSEESYLALLDALRW  YLALLDALR        0.6378         50.3         WB     8.00     Sequence
   DRB5_0101  221  TPRQLALHQALIRIG  LALHQALIR        0.6374         50.5         WB     8.00     Sequence
   DRB5_0101  224  QLALHQALIRIGVAE  LALHQALIR        0.6320         53.6         WB     8.00     Sequence
   DRB5_0101  225  LALHQALIRIGVAER  ALHQALIRI        0.6309         54.2         WB     8.00     Sequence
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DRB5_0101   91  EIYRDVLARLLAAGE  YRDVLARLL        0.6295          55.1          WB     8.00     Sequence
DRB5_0101  471  GRDRSMQRLRAARQL  MQRLRAARQ        0.6284          55.8          WB     8.00     Sequence
DRB5_0101   88  QRAEIYRDVLARLLA  YRDVLARLL        0.6108          67.4          WB     8.00     Sequence
DRB5_0101  220  STPRQLALHQALIRI  LALHQALIR        0.6009          75.1          WB    16.00     Sequence
DRB5_0101  470  LGRDRSMQRLRAARQ  RDRSMQRLR        0.5911          83.4          WB    16.00     Sequence
DRB5_0101   92  IYRDVLARLLAAGEA  YRDVLARLL        0.5854          88.7          WB    16.00     Sequence
DRB5_0101   57  YLALLDALRWLGLDW  YLALLDALR        0.5690         106.0          WB    16.00     Sequence
DRB5_0101  461  PPLFESLELLGRDRS  FESLELLGR        0.5631         113.0          WB    16.00     Sequence
DRB5_0101  462  PLFESLELLGRDRSM  FESLELLGR        0.5565         121.3          WB    16.00     Sequence
DRB5_0101  463  LFESLELLGRDRSMQ  FESLELLGR        0.5545         124.0          WB    16.00     Sequence
DRB5_0101  229  QALIRIGVAERIPKF  LIRIGVAER        0.5491         131.5          WB    16.00     Sequence
DRB5_0101  439  LALKPRKAFSPIRVA  ALKPRKAFS        0.5486         132.2          WB    16.00     Sequence
DRB5_0101  460  SPPLFESLELLGRDR  FESLELLGR        0.5439         139.1          WB    16.00     Sequence
DRB5_0101  438  GLALKPRKAFSPIRV  PRKAFSPIR        0.5390         146.7          WB    16.00     Sequence
DRB5_0101  230  ALIRIGVAERIPKFA  LIRIGVAER        0.5381         148.1          WB    16.00     Sequence
DRB5_0101   87  SQRAEIYRDVLARLL  YRDVLARLL        0.5357         152.0          WB    16.00     Sequence
DRB5_0101  226  ALHQALIRIGVAERI  LIRIGVAER        0.5337         155.3          WB    16.00     Sequence
DRB5_0101  228  HQALIRIGVAERIPK  LIRIGVAER        0.5330         156.5          WB    16.00     Sequence
DRB5_0101  464  FESLELLGRDRSMQR  FESLELLGR        0.5329         156.7          WB    16.00     Sequence
DRB5_0101   51  RDSEESYLALLDALR  YLALLDALR        0.5323         157.7          WB    16.00     Sequence
DRB5_0101  433  DALIEGLALKPRKAF  LIEGLALKP        0.5306         160.6          WB    16.00     Sequence
DRB5_0101  434  ALIEGLALKPRKAFS  LIEGLALKP        0.5305         160.7          WB    16.00     Sequence
DRB5_0101  469  LLGRDRSMQRLRAAR  RDRSMQRLR        0.5285         164.2          WB    16.00     Sequence
DRB5_0101  432  KDALIEGLALKPRKA  LIEGLALKP        0.5268         167.3          WB    16.00     Sequence
DRB5_0101  231  LIRIGVAERIPKFAH  LIRIGVAER        0.5240         172.5          WB    16.00     Sequence
DRB5_0101   21  GLVRTALFNWAYARH  GLVRTALFN        0.5207         178.8          WB    32.00     Sequence
DRB5_0101  440  ALKPRKAFSPIRVAA  RKAFSPIRV        0.5129         194.5          WB    32.00     Sequence
DRB5_0101  431  LKDALIEGLALKPRK  LIEGLALKP        0.5099         201.0          WB    32.00     Sequence
DRB5_0101   93  YRDVLARLLAAGEAY  YRDVLARLL        0.5097         201.4          WB    32.00     Sequence
DRB5_0101  435  LIEGLALKPRKAFSP  LIEGLALKP        0.5035         215.4          WB    32.00     Sequence
DRB5_0101  437  EGLALKPRKAFSPIR  ALKPRKAFS        0.5022         218.3          WB    32.00     Sequence
DRB5_0101  116  VEARHVAAGRNPKLG  ARHVAAGRN        0.4958         234.0          WB    32.00     Sequence
DRB5_0101  436  IEGLALKPRKAFSPI  GLALKPRKA        0.4955         234.9          WB    32.00     Sequence
DRB5_0101  468  ELLGRDRSMQRLRAA  RDRSMQRLR        0.4937         239.4          WB    32.00     Sequence
DRB5_0101  459  VSPPLFESLELLGRD  FESLELLGR        0.4918         244.3          WB    32.00     Sequence
DRB5_0101  117  EARHVAAGRNPKLGY  ARHVAAGRN        0.4918         244.4          WB    32.00     Sequence
DRB5_0101   20  VGLVRTALFNWAYAR  GLVRTALFN        0.4909         246.9          WB    32.00     Sequence
DRB5_0101    6  VRVRFCPSPTGTPHV  VRFCPSPTG        0.4905         247.9          WB    32.00     Sequence
DRB5_0101  441  LKPRKAFSPIRVAAT  RKAFSPIRV        0.4900         249.1          WB    32.00     Sequence
DRB5_0101  430  ALKDALIEGLALKPR  LIEGLALKP        0.4858         260.8          WB    32.00     Sequence
DRB5_0101  115  EVEARHVAAGRNPKL  ARHVAAGRN        0.4842         265.4          WB    32.00     Sequence
DRB5_0101  227  LHQALIRIGVAERIP  LIRIGVAER        0.4838         266.4          WB    32.00     Sequence
DRB5_0101    7  RVRFCPSPTGTPHVG  VRFCPSPTG        0.4825         270.2          WB    32.00     Sequence
DRB5_0101  467  LELLGRDRSMQRLRA  RDRSMQRLR        0.4774         285.7          WB    32.00     Sequence
DRB5_0101    5  TVRVRFCPSPTGTPH  VRFCPSPTG        0.4768         287.5          WB    32.00     Sequence
DRB5_0101  202  DDALMKITHVLRGED  LMKITHVLR        0.4764         288.7          WB    32.00     Sequence
DRB5_0101   17  TPHVGLVRTALFNWA  GLVRTALFN        0.4745         294.6          WB    32.00     Sequence
DRB5_0101  219  PSTPRQLALHQALIR  LALHQALIR        0.4741         295.9          WB    32.00     Sequence
DRB5_0101  203  DALMKITHVLRGEDL  LMKITHVLR        0.4739         296.7          WB    32.00     Sequence
DRB5_0101  201  CDDALMKITHVLRGE  LMKITHVLR        0.4736         297.6          WB    32.00     Sequence
DRB5_0101  214  GEDLLPSTPRQLALH  LLPSTPRQL        0.4729         299.6          WB    32.00     Sequence
DRB5_0101  213  RGEDLLPSTPRQLAL  LLPSTPRQL        0.4714         304.7          WB    32.00     Sequence
DRB5_0101  215  EDLLPSTPRQLALHQ  LLPSTPRQL        0.4681         315.6          WB    32.00     Sequence
DRB5_0101  458  TVSPPLFESLELLGR  FESLELLGR        0.4653         325.6          WB    32.00     Sequence
DRB5_0101  442  KPRKAFSPIRVAATG  RKAFSPIRV        0.4620         337.3          WB    32.00     Sequence
DRB5_0101  118  ARHVAAGRNPKLGYD  ARHVAAGRN        0.4619         337.5          WB    32.00     Sequence
DRB5_0101   16  GTPHVGLVRTALFNW  GLVRTALFN        0.4609         341.4          WB    32.00     Sequence
DRB5_0101   19  HVGLVRTALFNWAYA  GLVRTALFN        0.4579         352.7          WB    32.00     Sequence
DRB5_0101  145  AYLAEGRQPVVRLRM  AEGRQPVVR        0.4554         362.5          WB    32.00     Sequence
DRB5_0101  200  PCDDALMKITHVLRG  LMKITHVLR        0.4544         366.4          WB    32.00     Sequence
DRB5_0101  278  GLLNYLALLGWSIAD  YLALLGWSI        0.4536         369.5          WB    32.00     Sequence
DRB5_0101  277  EGLLNYLALLGWSIA  YLALLGWSI        0.4516         377.6          WB    32.00     Sequence
DRB5_0101  148  AEGRQPVVRLRMPDD  AEGRQPVVR        0.4507         381.0          WB    32.00     Sequence
DRB5_0101   18  PHVGLVRTALFNWAY  GLVRTALFN        0.4495         386.3          WB    32.00     Sequence
DRB5_0101  181  VPDFALTRASGDPLY  FALTRASGD        0.4482         391.5          WB    32.00     Sequence
DRB5_0101    4  ETVRVRFCPSPTGTP  RVRFCPSPT        0.4478         393.3          WB    32.00     Sequence
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DRB5_0101  279  LLNYLALLGWSIADD  YLALLGWSI        0.4451          404.8           WB    32.00     Sequence
DRB5_0101  270  RDRGFIPEGLLNYLA  GFIPEGLLN        0.4440          410.1           WB    32.00     Sequence
DRB5_0101   96  VLARLLAAGEAYHAF  RLLAAGEAY        0.4427          415.9           WB    32.00     Sequence
DRB5_0101  212  LRGEDLLPSTPRQLA  LLPSTPRQL        0.4426          416.0           WB    32.00     Sequence
DRB5_0101  271  DRGFIPEGLLNYLAL  GFIPEGLLN        0.4424          417.1           WB    32.00     Sequence
DRB5_0101  466  SLELLGRDRSMQRLR  RDRSMQRLR        0.4407          424.6           WB    32.00     Sequence
DRB5_0101  146  YLAEGRQPVVRLRMP  AEGRQPVVR        0.4376          439.1           WB    32.00     Sequence
DRB5_0101  429  AALKDALIEGLALKP  LIEGLALKP        0.4374          440.0           WB    32.00     Sequence
DRB5_0101  114  EEVEARHVAAGRNPK  ARHVAAGRN        0.4374          440.3           WB    32.00     Sequence
DRB5_0101  144  AAYLAEGRQPVVRLR  AEGRQPVVR        0.4368          443.2           WB    32.00     Sequence
DRB5_0101   95  DVLARLLAAGEAYHA  RLLAAGEAY        0.4362          446.1           WB    32.00     Sequence
DRB5_0101  143  RAAYLAEGRQPVVRL  AYLAEGRQP        0.4354          449.6           WB    32.00     Sequence
DRB5_0101  276  PEGLLNYLALLGWSI  YLALLGWSI        0.4342          455.5           WB    32.00     Sequence
DRB5_0101  204  ALMKITHVLRGEDLL  MKITHVLRG        0.4329          462.1           WB    32.00     Sequence
DRB5_0101   94  RDVLARLLAAGEAYH  RLLAAGEAY        0.4325          464.2           WB    32.00     Sequence
DRB5_0101  269  HRDRGFIPEGLLNYL  GFIPEGLLN        0.4322          465.4           WB    32.00     Sequence
DRB5_0101  147  LAEGRQPVVRLRMPD  AEGRQPVVR        0.4302          476.0           WB    32.00     Sequence
DRB5_0101  322  KADALNAEHIRMLDV  ALNAEHIRM        0.4299          477.2           WB    32.00     Sequence
DRB5_0101   15  TGTPHVGLVRTALFN  GLVRTALFN        0.4282          486.2           WB    32.00     Sequence
DRB5_0101  444  RKAFSPIRVAATGTT  RKAFSPIRV        0.4278          488.5           WB    32.00     Sequence
DRB5_0101  180  SVPDFALTRASGDPL  FALTRASGD        0.4258          498.9           WB    32.00     Sequence
DRB5_0101  182  PDFALTRASGDPLYT  FALTRASGD        0.4256          500.1                 32.00     Sequence
DRB5_0101  272  RGFIPEGLLNYLALL  FIPEGLLNY        0.4235          511.7                 32.00     Sequence
DRB5_0101  205  LMKITHVLRGEDLLP  MKITHVLRG        0.4235          511.7                 32.00     Sequence
DRB5_0101  142  QRAAYLAEGRQPVVR  AYLAEGRQP        0.4218          521.0                 32.00     Sequence
DRB5_0101  408  VLDAALAALTSVTDW  LDAALAALT        0.4207          527.5                 32.00     Sequence
DRB5_0101    8  VRFCPSPTGTPHVGL  RFCPSPTGT        0.4200          531.6                 32.00     Sequence
DRB5_0101  216  DLLPSTPRQLALHQA  LLPSTPRQL        0.4185          539.9                 32.00     Sequence
DRB5_0101  443  PRKAFSPIRVAATGT  RKAFSPIRV        0.4179          543.5                 32.00     Sequence
DRB5_0101  407  AVLDAALAALTSVTD  LDAALAALT        0.4170          548.8                 32.00     Sequence
DRB5_0101  211  VLRGEDLLPSTPRQL  LLPSTPRQL        0.4167          550.6                 32.00     Sequence
DRB5_0101   97  LARLLAAGEAYHAFS  RLLAAGEAY        0.4165          551.8                 32.00     Sequence
DRB5_0101  183  DFALTRASGDPLYTL  FALTRASGD        0.4153          558.9                 32.00     Sequence
DRB5_0101  323  ADALNAEHIRMLDVG  ALNAEHIRM        0.4153          559.4                 32.00     Sequence
DRB5_0101    0  VTATETVRVRFCPSP  VTATETVRV        0.4124          576.9                 32.00     Sequence
DRB5_0101  149  EGRQPVVRLRMPDDD  RQPVVRLRM        0.4093          596.3                 50.00     Sequence
DRB5_0101  232  IRIGVAERIPKFAHL  IRIGVAERI        0.4073          609.4                 50.00     Sequence
DRB5_0101   98  ARLLAAGEAYHAFST  RLLAAGEAY        0.4065          614.8                 50.00     Sequence
DRB5_0101  280  LNYLALLGWSIADDH  YLALLGWSI        0.4055          621.5                 50.00     Sequence
DRB5_0101  273  GFIPEGLLNYLALLG  FIPEGLLNY        0.4050          624.9                 50.00     Sequence
DRB5_0101   86  QSQRAEIYRDVLARL  IYRDVLARL        0.4048          626.2                 50.00     Sequence
DRB5_0101  133  NFDRHLTDAQRAAYL  RHLTDAQRA        0.4047          627.3                 50.00     Sequence
DRB5_0101  406  AAVLDAALAALTSVT  VLDAALAAL        0.4011          652.1                 50.00     Sequence
DRB5_0101  324  DALNAEHIRMLDVGD  ALNAEHIRM        0.3997          661.8                 50.00     Sequence
DRB5_0101  268  AHRDRGFIPEGLLNY  GFIPEGLLN        0.3960          688.8                 50.00     Sequence
DRB5_0101  321  KKADALNAEHIRMLD  ALNAEHIRM        0.3917          721.6                 50.00     Sequence
DRB5_0101  150  GRQPVVRLRMPDDDL  RQPVVRLRM        0.3910          727.2                 50.00     Sequence
DRB5_0101  141  AQRAAYLAEGRQPVV  AAYLAEGRQ        0.3895          739.3                 50.00     Sequence
DRB5_0101    3  TETVRVRFCPSPTGT  VRFCPSPTG        0.3889          744.1                 50.00     Sequence
DRB5_0101  134  FDRHLTDAQRAAYLA  RHLTDAQRA        0.3887          745.9                 50.00     Sequence
DRB5_0101  409  LDAALAALTSVTDWT  AALAALTSV        0.3882          749.7                 50.00     Sequence
DRB5_0101  135  DRHLTDAQRAAYLAE  RHLTDAQRA        0.3866          762.7                 50.00     Sequence
DRB5_0101  446  AFSPIRVAATGTTVS  IRVAATGTT        0.3820          801.5                 50.00     Sequence
DRB5_0101  445  KAFSPIRVAATGTTV  IRVAATGTT        0.3814          806.8                 50.00     Sequence
DRB5_0101   58  LALLDALRWLGLDWD  LALLDALRW        0.3808          812.0                 50.00     Sequence
DRB5_0101  306  FDVADVNSSPARFDQ  DVNSSPARF        0.3800          818.8                 50.00     Sequence
DRB5_0101  307  DVADVNSSPARFDQK  DVNSSPARF        0.3797          821.9                 50.00     Sequence
DRB5_0101  179  GSVPDFALTRASGDP  FALTRASGD        0.3796          822.8                 50.00     Sequence
DRB5_0101  113  PEEVEARHVAAGRNP  ARHVAAGRN        0.3782          835.5                 50.00     Sequence
DRB5_0101  308  VADVNSSPARFDQKK  DVNSSPARF        0.3753          861.6                 50.00     Sequence
DRB5_0101  325  ALNAEHIRMLDVGDF  ALNAEHIRM        0.3752          863.2                 50.00     Sequence
DRB5_0101  336  VGDFTVRLRDHLDTH  FTVRLRDHL        0.3744          869.9                 50.00     Sequence
DRB5_0101  422  WTAPLIEAALKDALI  PLIEAALKD        0.3738          876.0                 50.00     Sequence
DRB5_0101  405  GAAVLDAALAALTSV  VLDAALAAL        0.3713          899.8                 50.00     Sequence
DRB5_0101  320  QKKADALNAEHIRML  ALNAEHIRM        0.3702          910.9                 50.00     Sequence
DRB5_0101  423  TAPLIEAALKDALIE  PLIEAALKD        0.3699          914.0                 50.00     Sequence
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DRB5_0101	465	ESLELLGRDRSMQRL	LGRDRSMQR	0.3697	915.7	50.00	Sequence
DRB5_0101	199	NPCDDALMKITHVLR	LMKITHVLR	0.3696	916.9	50.00	Sequence
DRB5_0101	447	FSPIRVAATGTTVSP	IRVAATGTT	0.3689	923.3	50.00	Sequence
DRB5_0101	281	NYLALLGWSIADDHD	YLALLGWSI	0.3687	925.5	50.00	Sequence
DRB5_0101	99	RLLAAGEAYHAFSTP	RLLAAGEAY	0.3680	932.5	50.00	Sequence
DRB5_0101	309	ADVNSSPARFDQKKA	DVNSSPARF	0.3631	984.0	50.00	Sequence
DRB5_0101	136	RHLTDAQRAAYLAEG	RHLTDAQRA	0.3628	986.9	50.00	Sequence
DRB5_0101	2	ATETVRVRFCPSPTG	VRFCPSPTG	0.3619	996.1	50.00	Sequence
DRB5_0101	132	DNFDRHLTDAQRAAY	RHLTDAQRA	0.3605	1011.8	50.00	Sequence
DRB5_0101	243	FAHLPTVLGEGTKKL	FAHLPTVLG	0.3604	1012.5	50.00	Sequence
DRB5_0101	140	DAQRAAYLAEGRQPV	AAYLAEGRQ	0.3602	1015.1	50.00	Sequence
DRB5_0101	305	AFDVADVNSSPARFD	DVNSSPARF	0.3592	1026.3	50.00	Sequence
DRB5_0101	410	DAALAALTSVTDWTA	AALAALTSV	0.3585	1033.5	50.00	Sequence
DRB5_0101	424	APLIEAALKDALIEG	PLIEAALKD	0.3584	1035.3	50.00	Sequence
DRB5_0101	81	YGPYRQSQRAEIYRD	YRQSQRAEI	0.3576	1043.9	50.00	Sequence
DRB5_0101	29	NWAYARHTGGTFVFR	YARHTGGTF	0.3573	1046.7	50.00	Sequence
DRB5_0101	337	GDFTVRLRDHLDTHG	FTVRLRDHL	0.3572	1048.8	50.00	Sequence
DRB5_0101	421	DWTAPLIEAALKDAL	APLIEAALK	0.3564	1057.0	50.00	Sequence
DRB5_0101	178	AGSVPDFALTRASGD	FALTRASGD	0.3543	1081.7	50.00	Sequence
DRB5_0101	335	DVGDFTVRLRDHLDT	FTVRLRDHL	0.3532	1095.2	50.00	Sequence
DRB5_0101	14	PTGTPHVGLVRTALF	VGLVRTALF	0.3521	1108.1	50.00	Sequence
DRB5_0101	246	LPTVLGEGTKKLSKR	VLGEGTKKL	0.3515	1115.0	50.00	Sequence
DRB5_0101	448	SPIRVAATGTTVSPP	IRVAATGTT	0.3491	1144.2	50.00	Sequence
DRB5_0101	206	MKITHVLRGEDLLPS	MKITHVLRG	0.3473	1167.1	50.00	Sequence
DRB5_0101	248	TVLGEGTKKLSKRDP	VLGEGTKKL	0.3468	1173.8	50.00	Sequence
DRB5_0101	274	FIPEGLLNYLALLGW	FIPEGLLNY	0.3458	1186.3	50.00	Sequence
DRB5_0101	217	LLPSTPRQLALHQAL	LLPSTPRQL	0.3457	1187.2	50.00	Sequence
DRB5_0101	247	PTVLGEGTKKLSKRD	VLGEGTKKL	0.3455	1190.1	50.00	Sequence
DRB5_0101	338	DFTVRLRDHLDTHGH	FTVRLRDHL	0.3452	1193.2	50.00	Sequence
DRB5_0101	151	RQPVVRLRMPDDDLA	RQPVVRLRM	0.3430	1222.9	50.00	Sequence
DRB5_0101	334	LDVGDFTVRLRDHLD	FTVRLRDHL	0.3383	1286.0	50.00	Sequence
DRB5_0101	245	HLPTVLGEGTKKLSK	VLGEGTKKL	0.3364	1312.4	50.00	Sequence
DRB5_0101	164	LAWNDLVRGPVTFAA	LAWNDLVRG	0.3363	1315.0	50.00	Sequence
DRB5_0101	275	IPEGLLNYLALLGWS	LLNYLALLG	0.3356	1325.0	50.00	Sequence
DRB5_0101	242	KFAHLPTVLGEGTKK	FAHLPTVLG	0.3355	1325.2	50.00	Sequence
DRB5_0101	82	GPYRQSQRAEIYRDV	YRQSQRAEI	0.3345	1340.5	50.00	Sequence
DRB5_0101	428	EAALKDALIEGLALK	LKDALIEGL	0.3341	1346.0	50.00	Sequence
DRB5_0101	30	WAYARHTGGTFVFRI	YARHTGGTF	0.3325	1369.1	50.00	Sequence
DRB5_0101	80	PYGPYRQSQRAEIYR	YRQSQRAEI	0.3319	1378.9	50.00	Sequence
DRB5_0101	411	AALAALTSVTDWTAP	LAALTSVTD	0.3294	1415.9	50.00	Sequence
DRB5_0101	404	DGAAVLDAALAALTS	VLDAALAAL	0.3285	1429.3	50.00	Sequence
DRB5_0101	241	PKFAHLPTVLGEGTK	FAHLPTVLG	0.3278	1440.3	50.00	Sequence
DRB5_0101	240	IPKFAHLPTVLGEGT	FAHLPTVLG	0.3257	1473.6	50.00	Sequence
DRB5_0101	449	PIRVAATGTTVSPPL	IRVAATGTT	0.3243	1496.3	50.00	Sequence
DRB5_0101	388	DQYVIDPKAAAKELG	VIDPKAAAK	0.3242	1498.0	50.00	Sequence
DRB5_0101	420	TDWTAPLIEAALKDA	APLIEAALK	0.3234	1510.4	50.00	Sequence
DRB5_0101	184	FALTRASGDPLYTLV	FALTRASGD	0.3230	1517.8	50.00	Sequence
DRB5_0101	163	DLAWNDLVRGPVTFA	LAWNDLVRG	0.3225	1526.4	50.00	Sequence
DRB5_0101	79	GPYGPYRQSQRAEIY	YRQSQRAEI	0.3225	1526.7	50.00	Sequence
DRB5_0101	239	RIPKFAHLPTVLGEG	FAHLPTVLG	0.3215	1543.1	50.00	Sequence
DRB5_0101	192	DPLYTLVNPCDDALM	YTLVNPCDD	0.3210	1551.3	50.00	Sequence
DRB5_0101	361	FAAAAELVQTRIVVL	FAAAAELVQ	0.3171	1618.1	50.00	Sequence
DRB5_0101	130	GYDNFDRHLTDAQRA	RHLTDAQRA	0.3168	1622.5	50.00	Sequence
DRB5_0101	131	YDNFDRHLTDAQRAA	RHLTDAQRA	0.3154	1647.8	50.00	Sequence
DRB5_0101	304	AAFDVADVNSSPARF	DVNSSPARF	0.3142	1669.8	50.00	Sequence
DRB5_0101	333	MLDVGDFTVRLRDHL	FTVRLRDHL	0.3141	1671.0	50.00	Sequence
DRB5_0101	389	QYVIDPKAAAKELGP	VIDPKAAAK	0.3136	1679.5	50.00	Sequence
DRB5_0101	373	VVLGDAWELLKFFND	DAWELLKFF	0.3134	1683.0	50.00	Sequence
DRB5_0101	372	IVVLGDAWELLKFFN	DAWELLKFF	0.3125	1699.5	50.00	Sequence
DRB5_0101	310	DVNSSPARFDQKKAD	DVNSSPARF	0.3114	1720.8	50.00	Sequence
DRB5_0101	387	DDQYVIDPKAAAKEL	VIDPKAAAK	0.3111	1725.5	50.00	Sequence
DRB5_0101	105	EAYHAFSTPEEVEAR	YHAFSTPEE	0.3106	1735.1	50.00	Sequence
DRB5_0101	112	TPEEVEARHVAAGRN	ARHVAAGRN	0.3102	1742.4	50.00	Sequence
DRB5_0101	360	AFAAAAELVQTRIVV	FAAAAELVQ	0.3101	1746.0	50.00	Sequence
DRB5_0101	238	ERIPKFAHLPTVLGE	FAHLPTVLG	0.3084	1777.4	50.00	Sequence
DRB5_0101	244	AHLPTVLGEGTKKLS	TVLGEGTKK	0.3080	1784.9	50.00	Sequence

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DRB5_0101  374  VLGDAWELLKFFNDD  DAWELLKFF        0.3078       1789.1              50.00     Sequence
DRB5_0101  371  RIVVLGDAWELLKFF  RIVVLGDAW        0.3071       1803.6              50.00     Sequence
DRB5_0101  191  GDPLYTLVNPCDDAL  YTLVNPCDD        0.3062       1820.2              50.00     Sequence
DRB5_0101  359  AAFAAAAELVQTRIV  FAAAAELVQ        0.3057       1830.8              50.00     Sequence
DRB5_0101  450  IRVAATGTTVSPPLF  IRVAATGTT        0.3024       1897.5              50.00     Sequence
DRB5_0101  425  PLIEAALKDALIEGL  PLIEAALKD        0.3019       1907.8              50.00     Sequence
DRB5_0101  104  GEAYHAFSTPEEVEA  YHAFSTPEE        0.3014       1916.8              50.00     Sequence
DRB5_0101  375  LGDAWELLKFFNDDQ  DAWELLKFF        0.2997       1953.7              50.00     Sequence
DRB5_0101  233  RIGVAERIPKFAHLP  IGVAERIPK        0.2996       1954.0              50.00     Sequence
DRB5_0101   78  GGPYGPYRQSQRAEI  YRQSQRAEI        0.2986       1977.1              50.00     Sequence
DRB5_0101  162  DDLAWNDLVRGPVTF  LAWNDLVRG        0.2977       1994.6              50.00     Sequence
DRB5_0101  319  DQKKADALNAEHIRM  ALNAEHIRM        0.2973       2004.3              50.00     Sequence
DRB5_0101  267  FAHRDRGFIPEGLLN  GFIPEGLLN        0.2971       2009.3              50.00     Sequence
DRB5_0101  295  DLFGLDEMVAAFDVA  GLDEMVAAF        0.2959       2035.7              50.00     Sequence
DRB5_0101  419  VTDWTAPLIEAALKD  PLIEAALKD        0.2939       2080.4              50.00     Sequence
DRB5_0101  376  GDAWELLKFFNDDQY  DAWELLKFF        0.2931       2096.9              50.00     Sequence
DRB5_0101  139  TDAQRAAYLAEGRQP  RAAYLAEGR        0.2931       2097.8              50.00     Sequence
DRB5_0101   13  SPTGTPHVGLVRTAL  GTPHVGLVR        0.2929       2102.2              50.00     Sequence
DRB5_0101  296  LFGLDEMVAAFDVAD  GLDEMVAAF        0.2913       2138.5              50.00     Sequence
DRB5_0101  412  ALAALTSVTDWTAPL  ALAALTSVT        0.2912       2140.2              50.00     Sequence
DRB5_0101  358  EAAFAAAAELVQTRI  FAAAAELVQ        0.2908       2150.5              50.00     Sequence
DRB5_0101  106  AYHAFSTPEEVEARH  YHAFSTPEE        0.2903       2163.0              50.00     Sequence
DRB5_0101  339  FTVRLRDHLDTHGHH  FTVRLRDHL        0.2888       2196.7              50.00     Sequence
DRB5_0101  237  AERIPKFAHLPTVLG  FAHLPTVLG        0.2860       2265.6              50.00     Sequence
DRB5_0101  119  RHVAAGRNPKLGYDN  RHVAAGRNP        0.2856       2273.9              50.00     Sequence
DRB5_0101    9  RFCPSPTGTPHVGLV  RFCPSPTGT        0.2847       2297.8              50.00     Sequence
DRB5_0101   31  AYARHTGGTFVFRIE  YARHTGGTF        0.2840       2315.0              50.00     Sequence
DRB5_0101  377  DAWELLKFFNDDQYV  DAWELLKFF        0.2835       2327.6              50.00     Sequence
DRB5_0101   83  PYRQSQRAEIYRDVL  YRQSQRAEI        0.2828       2344.3              50.00     Sequence
DRB5_0101  390  YVIDPKAAAKELGPD  VIDPKAAAK        0.2811       2387.3              50.00     Sequence
DRB5_0101  249  VLGEGTKKLSKRDPQ  VLGEGTKKL        0.2803       2410.1              50.00     Sequence
DRB5_0101  294  HDLFGLDEMVAAFDV  GLDEMVAAF        0.2802       2410.9              50.00     Sequence
DRB5_0101  297  FGLDEMVAAFDVADV  GLDEMVAAF        0.2796       2428.0              50.00     Sequence
DRB5_0101  357  DEAAFAAAAELVQTR  FAAAAELVQ        0.2774       2485.6              50.00     Sequence
DRB5_0101  190  SGDPLYTLVNPCDDA  YTLVNPCDD        0.2759       2527.2              50.00     Sequence
DRB5_0101  161  DDDLAWNDLVRGPVT  LAWNDLVRG        0.2758       2529.4              50.00     Sequence
DRB5_0101   32  YARHTGGTFVFRIED  YARHTGGTF        0.2748       2555.7              50.00     Sequence
DRB5_0101   59  ALLDALRWLGLDWDE  LLDALRWLG        0.2745       2564.7              50.00     Sequence
DRB5_0101  403  PDGAAVLDAALAALT  LDAALAALT        0.2744       2566.9              50.00     Sequence
DRB5_0101  103  AGEAYHAFSTPEEVE  YHAFSTPEE        0.2733       2597.8              50.00     Sequence
DRB5_0101  165  AWNDLVRGPVTFAAG  DLVRGPVTF        0.2719       2637.0              50.00     Sequence
DRB5_0101  282  YLALLGWSIADDHDL  YLALLGWSI        0.2709       2668.0              50.00     Sequence
DRB5_0101  193  PLYTLVNPCDDALMK  YTLVNPCDD        0.2707       2673.1              50.00     Sequence
DRB5_0101  427  IEAALKDALIEGLAL  LKDALIEGL        0.2699       2696.5              50.00     Sequence
DRB5_0101    1  TATETVRVRFCPSPT  ATETVRVRF        0.2697       2702.2              50.00     Sequence
DRB5_0101  362  AAAAELVQTRIVVLG  AELVQTRIV        0.2684       2740.0              50.00     Sequence
DRB5_0101  262  PQSNLFAHRDRGFIP  LFAHRDRGF        0.2683       2742.9              50.00     Sequence
DRB5_0101  370  TRIVVLGDAWELLKF  RIVVLGDAW        0.2673       2771.6              50.00     Sequence
DRB5_0101  413  LAALTSVTDWTAPLI  LTSVTDWTA        0.2660       2811.4              50.00     Sequence
DRB5_0101   85  RQSQRAEIYRDVLAR  EIYRDVLAR        0.2650       2844.0              50.00     Sequence
DRB5_0101  138  LTDAQRAAYLAEGRQ  LTDAQRAAY        0.2647       2851.7              50.00     Sequence
DRB5_0101  234  IGVAERIPKFAHLPT  IGVAERIPK        0.2634       2892.5              50.00     Sequence
DRB5_0101  386  NDDQYVIDPKAAAKE  VIDPKAAAK        0.2630       2905.8              50.00     Sequence
DRB5_0101  261  DPQSNLFAHRDRGFI  SNLFAHRDR        0.2627       2914.8              50.00     Sequence
DRB5_0101  100  LLAAGEAYHAFSTPE  LLAAGEAYH        0.2626       2916.7              50.00     Sequence
DRB5_0101  107  YHAFSTPEEVEARHV  YHAFSTPEE        0.2625       2921.6              50.00     Sequence
DRB5_0101  166  WNDLVRGPVTFAAGS  DLVRGPVTF        0.2621       2932.4              50.00     Sequence
DRB5_0101  369  QTRIVVLGDAWELLK  RIVVLGDAW        0.2565       3115.5              50.00     Sequence
DRB5_0101   84  YRQSQRAEIYRDVLA  YRQSQRAEI        0.2555       3152.0              50.00     Sequence
DRB5_0101  363  AAAELVQTRIVVLGD  LVQTRIVVL        0.2551       3163.7              50.00     Sequence
DRB5_0101  194  LYTLVNPCDDALMKI  YTLVNPCDD        0.2535       3218.3              50.00     Sequence
DRB5_0101  263  QSNLFAHRDRGFIPE  LFAHRDRGF        0.2520       3272.4              50.00     Sequence
DRB5_0101  210  HVLRGEDLLPSTPRQ  DLLPSTPRQ        0.2518       3280.0              50.00     Sequence
DRB5_0101  264  SNLFAHRDRGFIPEG  LFAHRDRGF        0.2512       3299.1              50.00     Sequence
DRB5_0101  293  DHDLFGLDEMVAAFD  GLDEMVAAF        0.2512       3300.1              50.00     Sequence
DRB5_0101  160  PDDDLAWNDLVRGPV  LAWNDLVRG        0.2499       3346.2              50.00     Sequence
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DRB5_0101	168	DLVRGPVTFAAGSVP	DLVRGPVTF	0.2487	3389.5	50.00	Sequence
DRB5_0101	137	HLTDAQRAAYLAEGR	LTDAQRAAY	0.2487	3391.6	50.00	Sequence
DRB5_0101	189	ASGDPLYTLVNPCDD	YTLVNPCDD	0.2477	3427.8	50.00	Sequence
DRB5_0101	198	VNPCDDALMKITHVL	ALMKITHVL	0.2458	3499.5	50.00	Sequence
DRB5_0101	457	TTVSPPLFESLELLG	LFESLELLG	0.2443	3555.5	50.00	Sequence
DRB5_0101	102	AAGEAYHAFSTPEEV	YHAFSTPEE	0.2422	3636.7	50.00	Sequence
DRB5_0101	12	PSPTGTPHVGLVRTA	GTPHVGLVR	0.2418	3654.7	50.00	Sequence
DRB5_0101	152	QPVVRLRMPDDDLAW	PVVRLRMPD	0.2400	3726.7	50.00	Sequence
DRB5_0101	414	AALTSVTDWTAPLIE	LTSVTDWTA	0.2394	3750.8	50.00	Sequence
DRB5_0101	167	NDLVRGPVTFAAGSV	DLVRGPVTF	0.2386	3784.4	50.00	Sequence
DRB5_0101	39	TFVFRIEDTDAQRDS	FRIEDTDAQ	0.2352	3924.4	50.00	Sequence
DRB5_0101	40	FVFRIEDTDAQRDSE	FRIEDTDAQ	0.2347	3946.7	50.00	Sequence
DRB5_0101	177	AAGSVPDFALTRASG	SVPDFALTR	0.2347	3947.0	50.00	Sequence
DRB5_0101	378	AWELLKFFNDDQYVI	AWELLKFFN	0.2337	3989.6	50.00	Sequence
DRB5_0101	356	LDEAAFAAAAELVQT	FAAAAELVQ	0.2333	4006.6	50.00	Sequence
DRB5_0101	418	SVTDWTAPLIEAALK	APLIEAALK	0.2318	4073.5	50.00	Sequence
DRB5_0101	368	VQTRIVVLGDAWELL	RIVVLGDAW	0.2306	4124.5	50.00	Sequence
DRB5_0101	50	QRDSEESYLALLDAL	SYLALLDAL	0.2283	4229.1	50.00	Sequence
DRB5_0101	188	RASGDPLYTLVNPCD	LYTLVNPCD	0.2266	4308.1	50.00	Sequence
DRB5_0101	379	WELLKFFNDDQYVID	LKFFNDDQY	0.2257	4348.0	50.00	Sequence
DRB5_0101	38	GTFVFRIEDTDAQRD	FRIEDTDAQ	0.2254	4362.3	50.00	Sequence
DRB5_0101	298	GLDEMVAAFDVADVN	GLDEMVAAF	0.2252	4374.4	50.00	Sequence
DRB5_0101	207	KITHVLRGEDLLPST	ITHVLRGED	0.2234	4460.5	50.00	Sequence
DRB5_0101	60	LLDALRWLGLDWDEG	LLDALRWLG	0.2231	4471.3	50.00	Sequence
DRB5_0101	77	VGGPYGPYRQSQRAE	YGPYRQSQR	0.2230	4477.0	50.00	Sequence
DRB5_0101	385	FNDDQYVIDPKAAAK	VIDPKAAAK	0.2213	4560.6	50.00	Sequence
DRB5_0101	380	ELLKFFNDDQYVIDP	LKFFNDDQY	0.2210	4575.2	50.00	Sequence
DRB5_0101	426	LIEAALKDALIEGLA	AALKDALIE	0.2209	4582.2	50.00	Sequence
DRB5_0101	101	LAAGEAYHAFSTPEE	LAAGEAYHA	0.2193	4659.7	50.00	Sequence
DRB5_0101	159	MPDDDLAWNDLVRGP	LAWNDLVRG	0.2164	4811.3	50.00	Sequence
DRB5_0101	260	RDPQSNLFAHRDRGF	PQSNLFAHR	0.2160	4830.2	50.00	Sequence
DRB5_0101	355	ALDEAAFAAAAELVQ	FAAAAELVQ	0.2158	4842.4	50.00	Sequence
DRB5_0101	364	AAELVQTRIVVLGDA	AELVQTRIV	0.2152	4873.9	50.00	Sequence
DRB5_0101	265	NLFAHRDRGFIPEGL	FAHRDRGFI	0.2150	4881.7	50.00	Sequence
DRB5_0101	381	LLKFFNDDQYVIDPK	LKFFNDDQY	0.2149	4890.2	50.00	Sequence
DRB5_0101	391	VIDPKAAAKELGPDG	VIDPKAAAK	0.2134	4968.1	50.00	Sequence
DRB5_0101	33	ARHTGGTFVFRIEDT	HTGGTFVFR	0.2129	4993.4	50.00	Sequence
DRB5_0101	327	NAEHIRMLDVGDFTV	HIRMLDVGD	0.2121	5038.4	50.00	Sequence
DRB5_0101	108	HAFSTPEEVEARHVA	FSTPEEVEA	0.2115	5072.2	50.00	Sequence
DRB5_0101	326	LNAEHIRMLDVGDFT	IRMLDVGDF	0.2107	5113.1	50.00	Sequence
DRB5_0101	11	CPSPTGTPHVGLVRT	GTPHVGLVR	0.2100	5153.3	50.00	Sequence
DRB5_0101	292	DDHDLFGLDEMVAAF	GLDEMVAAF	0.2100	5154.3	50.00	Sequence
DRB5_0101	195	YTLVNPCDDALMKIT	YTLVNPCDD	0.2099	5162.7	50.00	Sequence
DRB5_0101	169	LVRGPVTFAAGSVPD	VTFAAGSVP	0.2089	5213.6	50.00	Sequence
DRB5_0101	174	VTFAAGSVPDFALTR	VTFAAGSVP	0.2087	5228.1	50.00	Sequence
DRB5_0101	328	AEHIRMLDVGDFTVR	HIRMLDVGD	0.2084	5245.5	50.00	Sequence
DRB5_0101	34	RHTGGTFVFRIEDTD	HTGGTFVFR	0.2081	5259.4	50.00	Sequence
DRB5_0101	37	GGTFVFRIEDTDAQR	FVFRIEDTD	0.2077	5283.3	50.00	Sequence
DRB5_0101	415	ALTSVTDWTAPLIEA	LTSVTDWTA	0.2075	5296.3	50.00	Sequence
DRB5_0101	256	KLSKRDPQSNLFAHR	LSKRDPQSN	0.2042	5491.2	50.00	Sequence
DRB5_0101	208	ITHVLRGEDLLPSTP	ITHVLRGED	0.2031	5552.8	50.00	Sequence
DRB5_0101	365	AELVQTRIVVLGDAW	ELVQTRIVV	0.2020	5618.3	50.00	Sequence
DRB5_0101	455	TGTTVSPPLFESLEL	GTTVSPPLF	0.2018	5632.9	50.00	Sequence
DRB5_0101	76	EVGGPYGPYRQSQRA	YGPYRQSQR	0.2017	5637.2	50.00	Sequence
DRB5_0101	209	THVLRGEDLLPSTPR	VLRGEDLLP	0.2002	5728.2	50.00	Sequence
DRB5_0101	236	VAERIPKFAHLPTVL	RIPKFAHLP	0.1991	5796.7	50.00	Sequence
DRB5_0101	170	VRGPVTFAAGSVPDF	VTFAAGSVP	0.1991	5797.5	50.00	Sequence
DRB5_0101	257	LSKRDPQSNLFAHRD	LSKRDPQSN	0.1991	5801.4	50.00	Sequence
DRB5_0101	235	GVAERIPKFAHLPTV	GVAERIPKF	0.1988	5815.9	50.00	Sequence
DRB5_0101	158	RMPDDDLAWNDLVRG	LAWNDLVRG	0.1988	5820.2	50.00	Sequence
DRB5_0101	36	TGGTFVFRIEDTDAQ	FVFRIEDTD	0.1983	5851.7	50.00	Sequence
DRB5_0101	259	KRDPQSNLFAHRDRG	PQSNLFAHR	0.1974	5905.8	50.00	Sequence
DRB5_0101	332	RMLDVGDFTVRLRDH	DFTVRLRDH	0.1960	6000.6	50.00	Sequence
DRB5_0101	255	KKLSKRDPQSNLFAH	LSKRDPQSN	0.1952	6051.2	50.00	Sequence
DRB5_0101	367	LVQTRIVVLGDAWEL	RIVVLGDAW	0.1948	6075.6	50.00	Sequence
DRB5_0101	382	LKFFNDDQYVIDPKA	LKFFNDDQY	0.1948	6077.1	50.00	Sequence

DRB5_0101	10	FCPSPTGTPHVGLVR	FCPSPTGTP	0.1947	6084.5	50.00	Sequence
DRB5_0101	456	GTTVSPPLFESLELL	GTTVSPPLF	0.1938	6144.5	50.00	Sequence
DRB5_0101	129	LGYDNFDRHLTDAQR	DRHLTDAQR	0.1927	6213.7	50.00	Sequence
DRB5_0101	451	RVAATGTTVSPPLFE	RVAATGTTV	0.1922	6251.8	50.00	Sequence
DRB5_0101	315	PARFDQKKADALNAE	FDQKKADAL	0.1920	6260.8	50.00	Sequence
DRB5_0101	153	PVVRLRMPDDDLAWN	VVRLRMPDD	0.1916	6291.1	50.00	Sequence
DRB5_0101	266	LFAHRDRGFIPEGLL	FAHRDRGFI	0.1897	6423.5	50.00	Sequence
DRB5_0101	316	ARFDQKKADALNAEH	FDQKKADAL	0.1894	6440.7	50.00	Sequence
DRB5_0101	35	HTGGTFVFRIEDTDA	FVFRIEDTD	0.1894	6442.2	50.00	Sequence
DRB5_0101	366	ELVQTRIVVLGDAWE	ELVQTRIVV	0.1887	6491.4	50.00	Sequence
DRB5_0101	303	VAAFDVADVNSSPAR	ADVNSSPAR	0.1875	6576.2	50.00	Sequence
DRB5_0101	453	AATGTTVSPPLFESL	GTTVSPPLF	0.1856	6709.5	50.00	Sequence
DRB5_0101	329	EHIRMLDVGDFTVRL	HIRMLDVGD	0.1856	6713.8	50.00	Sequence
DRB5_0101	176	FAAGSVPDFALTRAS	SVPDFALTR	0.1847	6777.8	50.00	Sequence
DRB5_0101	258	SKRDPQSNLFAHRDR	RDPQSNLFA	0.1845	6789.5	50.00	Sequence
DRB5_0101	314	SPARFDQKKADALNA	FDQKKADAL	0.1841	6818.3	50.00	Sequence
DRB5_0101	128	KLGYDNFDRHLTDAQ	KLGYDNFDR	0.1834	6876.1	50.00	Sequence
DRB5_0101	186	LTRASGDPLYTLVNP	RASGDPLYT	0.1829	6908.1	50.00	Sequence
DRB5_0101	172	GPVTFAAGSVPDFAL	VTFAAGSVP	0.1821	6973.4	50.00	Sequence
DRB5_0101	197	LVNPCDDALMKITHV	DALMKITHV	0.1818	6993.7	50.00	Sequence
DRB5_0101	171	RGPVTFAAGSVPDFA	VTFAAGSVP	0.1813	7031.4	50.00	Sequence
DRB5_0101	61	LDALRWLGLDWDEGP	LRWLGLDWD	0.1809	7063.5	50.00	Sequence
DRB5_0101	41	VFRIEDTDAQRDSEE	FRIEDTDAQ	0.1808	7066.0	50.00	Sequence
DRB5_0101	330	HIRMLDVGDFTVRLR	IRMLDVGDF	0.1806	7084.2	50.00	Sequence
DRB5_0101	120	HVAAGRNPKLGYDNF	HVAAGRNPK	0.1801	7124.1	50.00	Sequence
DRB5_0101	254	TKKLSKRDPQSNLFA	LSKRDPQSN	0.1798	7145.3	50.00	Sequence
DRB5_0101	218	LPSTPRQLALHQALI	TPRQLALHQ	0.1794	7175.8	50.00	Sequence
DRB5_0101	187	TRASGDPLYTLVNPC	RASGDPLYT	0.1785	7250.2	50.00	Sequence
DRB5_0101	251	GEGTKKLSKRDPQSN	GTKKLSKRD	0.1782	7273.1	50.00	Sequence
DRB5_0101	185	ALTRASGDPLYTLVN	LTRASGDPL	0.1778	7301.0	50.00	Sequence
DRB5_0101	252	EGTKKLSKRDPQSNL	GTKKLSKRD	0.1766	7397.0	50.00	Sequence
DRB5_0101	175	TFAAGSVPDFALTRA	SVPDFALTR	0.1765	7405.1	50.00	Sequence
DRB5_0101	173	PVTFAAGSVPDFALT	VTFAAGSVP	0.1754	7491.3	50.00	Sequence
DRB5_0101	416	LTSVTDWTAPLIEAA	VTDWTAPLI	0.1752	7512.4	50.00	Sequence
DRB5_0101	454	ATGTTVSPPLFESLE	GTTVSPPLF	0.1752	7512.5	50.00	Sequence
DRB5_0101	402	GPDGAAVLDAALAAL	VLDAALAAL	0.1739	7614.2	50.00	Sequence
DRB5_0101	331	IRMLDVGDFTVRLRD	IRMLDVGDF	0.1735	7650.7	50.00	Sequence
DRB5_0101	63	ALRWLGLDWDEGPEV	LRWLGLDWD	0.1710	7861.6	50.00	Sequence
DRB5_0101	253	GTKKLSKRDPQSNLF	LSKRDPQSN	0.1703	7924.1	50.00	Sequence
DRB5_0101	452	VAATGTTVSPPLFES	GTTVSPPLF	0.1677	8144.7	50.00	Sequence
DRB5_0101	417	TSVTDWTAPLIEAAL	TDWTAPLIE	0.1674	8176.8	50.00	Sequence
DRB5_0101	62	DALRWLGLDWDEGPE	LRWLGLDWD	0.1665	8255.1	50.00	Sequence
DRB5_0101	313	SSPARFDQKKADALN	FDQKKADAL	0.1652	8371.1	50.00	Sequence
DRB5_0101	127	PKLGYDNFDRHLTDA	KLGYDNFDR	0.1636	8517.7	50.00	Sequence
DRB5_0101	154	VVRLRMPDDDLAWND	VRLRMPDDD	0.1613	8727.2	50.00	Sequence
DRB5_0101	109	AFSTPEEVEARHVAA	FSTPEEVEA	0.1607	8784.2	50.00	Sequence
DRB5_0101	317	RFDQKKADALNAEHI	FDQKKADAL	0.1607	8787.0	50.00	Sequence
DRB5_0101	64	LRWLGLDWDEGPEVG	LRWLGLDWD	0.1603	8824.7	50.00	Sequence
DRB5_0101	111	STPEEVEARHVAAGR	PEEVEARHV	0.1600	8851.0	50.00	Sequence
DRB5_0101	342	RLRDHLDTHGHHIAL	HLDTHGHHI	0.1588	8971.1	50.00	Sequence
DRB5_0101	110	FSTPEEVEARHVAAG	FSTPEEVEA	0.1579	9055.2	50.00	Sequence
DRB5_0101	318	FDQKKADALNAEHIR	FDQKKADAL	0.1528	9570.7	50.00	Sequence
DRB5_0101	350	HGHHIALDEAAFAAA	IALDEAAFA	0.1520	9650.7	50.00	Sequence
DRB5_0101	42	FRIEDTDAQRDSEES	FRIEDTDAQ	0.1513	9726.7	50.00	Sequence
DRB5_0101	250	LGEGTKKLSKRDPQS	GTKKLSKRD	0.1509	9767.8	50.00	Sequence
DRB5_0101	341	VRLRDHLDTHGHHIA	HLDTHGHHI	0.1501	9859.8	50.00	Sequence
DRB5_0101	349	THGHHIALDEAAFAA	IALDEAAFA	0.1494	9931.6	50.00	Sequence
DRB5_0101	311	VNSSPARFDQKKADA	VNSSPARFD	0.1491	9960.9	50.00	Sequence
DRB5_0101	291	ADDHDLFGLDEMVAA	LFGLDEMVA	0.1467	10222.4	50.00	Sequence
DRB5_0101	351	GHHIALDEAAFAAAA	IALDEAAFA	0.1467	10224.6	50.00	Sequence
DRB5_0101	121	VAAGRNPKLGYDNFD	VAAGRNPKL	0.1466	10230.4	50.00	Sequence
DRB5_0101	75	PEVGGPYGPYRQSQR	YGPYRQSQR	0.1458	10324.3	50.00	Sequence
DRB5_0101	126	NPKLGYDNFDRHLTD	KLGYDNFDR	0.1450	10417.5	50.00	Sequence
DRB5_0101	383	KFFNDDQYVIDPKAA	QYVIDPKAA	0.1449	10421.6	50.00	Sequence
DRB5_0101	384	FFNDDQYVIDPKAAA	QYVIDPKAA	0.1436	10576.1	50.00	Sequence
DRB5_0101	354	IALDEAAFAAAAELV	AAFAAAAEL	0.1429	10653.4	50.00	Sequence

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   DRB5_0101  343  LRDHLDTHGHHIALD  HLDTHGHHI        0.1413      10837.7                50.00     Sequence
   DRB5_0101  283  LALLGWSIADDHDLF  LGWSIADDH        0.1407      10906.8                50.00     Sequence
   DRB5_0101  312  NSSPARFDQKKADAL  FDQKKADAL        0.1386      11160.6                50.00     Sequence
   DRB5_0101  340  TVRLRDHLDTHGHHI  HLDTHGHHI        0.1385      11177.4                50.00     Sequence
   DRB5_0101  125  RNPKLGYDNFDRHLT  KLGYDNFDR        0.1383      11203.0                50.00     Sequence
   DRB5_0101  348  DTHGHHIALDEAAFA  IALDEAAFA        0.1356      11533.4                50.00     Sequence
   DRB5_0101  196  TLVNPCDDALMKITH  PCDDALMKI        0.1311      12105.3                50.00     Sequence
   DRB5_0101  302  MVAAFDVADVNSSPA  FDVADVNSS        0.1308      12141.9                50.00     Sequence
   DRB5_0101  299  LDEMVAAFDVADVNS  LDEMVAAFD        0.1293      12348.2                50.00     Sequence
   DRB5_0101  124  GRNPKLGYDNFDRHL  KLGYDNFDR        0.1286      12442.6                50.00     Sequence
   DRB5_0101  344  RDHLDTHGHHIALDE  HLDTHGHHI        0.1285      12455.4                50.00     Sequence
   DRB5_0101  122  AAGRNPKLGYDNFDR  RNPKLGYDN        0.1284      12469.5                50.00     Sequence
   DRB5_0101  353  HIALDEAAFAAAAEL  ALDEAAFAA        0.1276      12569.7                50.00     Sequence
   DRB5_0101  284  ALLGWSIADDHDLFG  LGWSIADDH        0.1274      12596.8                50.00     Sequence
   DRB5_0101   65  RWLGLDWDEGPEVGG  LDWDEGPEV        0.1250      12923.3                50.00     Sequence
   DRB5_0101  352  HHIALDEAAFAAAAE  IALDEAAFA        0.1237      13106.9                50.00     Sequence
   DRB5_0101  301  EMVAAFDVADVNSSP  FDVADVNSS        0.1231      13191.4                50.00     Sequence
   DRB5_0101  345  DHLDTHGHHIALDEA  HLDTHGHHI        0.1209      13519.9                50.00     Sequence
   DRB5_0101  123  AGRNPKLGYDNFDRH  RNPKLGYDN        0.1206      13567.1                50.00     Sequence
   DRB5_0101  300  DEMVAAFDVADVNSS  FDVADVNSS        0.1168      14136.6                50.00     Sequence
   DRB5_0101   74  GPEVGGPYGPYRQSQ  VGGPYGPYR        0.1158      14288.7                50.00     Sequence
   DRB5_0101  155  VRLRMPDDDLAWNDL  VRLRMPDDD        0.1106      15111.6                50.00     Sequence
   DRB5_0101  346  HLDTHGHHIALDEAA  HLDTHGHHI        0.1087      15429.7                50.00     Sequence
   DRB5_0101   49  AQRDSEESYLALLDA  RDSEESYLA        0.1084      15471.8                50.00     Sequence
   DRB5_0101   66  WLGLDWDEGPEVGGP  LDWDEGPEV        0.1078      15578.1                50.00     Sequence
   DRB5_0101  285  LLGWSIADDHDLFGL  LGWSIADDH        0.1066      15781.9                50.00     Sequence
   DRB5_0101  347  LDTHGHHIALDEAAF  HGHHIALDE        0.1058      15909.1                50.00     Sequence
   DRB5_0101   48  DAQRDSEESYLALLD  RDSEESYLA        0.1038      16264.3                50.00     Sequence
   DRB5_0101   73  EGPEVGGPYGPYRQS  VGGPYGPYR        0.1037      16274.5                50.00     Sequence
   DRB5_0101  157  LRMPDDDLAWNDLVR  DLAWNDLVR        0.0995      17033.4                50.00     Sequence
   DRB5_0101   72  DEGPEVGGPYGPYRQ  VGGPYGPYR        0.0991      17118.2                50.00     Sequence
   DRB5_0101  401  LGPDGAAVLDAALAA  AVLDAALAA        0.0983      17259.9                50.00     Sequence
   DRB5_0101   68  GLDWDEGPEVGGPYG  LDWDEGPEV        0.0969      17522.0                50.00     Sequence
   DRB5_0101   71  WDEGPEVGGPYGPYR  VGGPYGPYR        0.0962      17658.3                50.00     Sequence
   DRB5_0101   67  LGLDWDEGPEVGGPY  LDWDEGPEV        0.0950      17896.0                50.00     Sequence
   DRB5_0101  290  IADDHDLFGLDEMVA  LFGLDEMVA        0.0927      18339.2                50.00     Sequence
   DRB5_0101  392  IDPKAAAKELGPDGA  IDPKAAAKE        0.0917      18534.1                50.00     Sequence
   DRB5_0101   43  RIEDTDAQRDSEESY  IEDTDAQRD        0.0893      19016.3                50.00     Sequence
   DRB5_0101   47  TDAQRDSEESYLALL  RDSEESYLA        0.0853      19870.1                50.00     Sequence
   DRB5_0101  286  LGWSIADDHDLFGLD  LGWSIADDH        0.0832      20334.2                50.00     Sequence
   DRB5_0101   69  LDWDEGPEVGGPYGP  LDWDEGPEV        0.0817      20660.0                50.00     Sequence
   DRB5_0101  393  DPKAAAKELGPDGAA  PKAAAKELG        0.0788      21322.2                50.00     Sequence
   DRB5_0101  400  ELGPDGAAVLDAALA  AAVLDAALA        0.0787      21346.0                50.00     Sequence
   DRB5_0101  395  KAAAKELGPDGAAVL  AAKELGPDG        0.0767      21810.6                50.00     Sequence
   DRB5_0101   46  DTDAQRDSEESYLAL  QRDSEESYL        0.0741      22436.7                50.00     Sequence
   DRB5_0101  394  PKAAAKELGPDGAAV  AAKELGPDG        0.0735      22569.7                50.00     Sequence
   DRB5_0101  396  AAAKELGPDGAAVLD  AAKELGPDG        0.0701      23422.5                50.00     Sequence
   DRB5_0101  397  AAKELGPDGAAVLDA  AAKELGPDG        0.0679      23984.9                50.00     Sequence
   DRB5_0101   45  EDTDAQRDSEESYLA  RDSEESYLA        0.0647      24825.9                50.00     Sequence
   DRB5_0101   44  IEDTDAQRDSEESYL  IEDTDAQRD        0.0645      24892.3                50.00     Sequence
   DRB5_0101   70  DWDEGPEVGGPYGPY  GPEVGGPYG        0.0578      26755.1                50.00     Sequence
   DRB5_0101  288  WSIADDHDLFGLDEM  WSIADDHDL        0.0557      27357.3                50.00     Sequence
   DRB5_0101  289  SIADDHDLFGLDEMV  HDLFGLDEM        0.0554      27451.9                50.00     Sequence
   DRB5_0101  156  RLRMPDDDLAWNDLV  LRMPDDDLA        0.0551      27545.6                50.00     Sequence
   DRB5_0101  399  KELGPDGAAVLDAAL  ELGPDGAAV        0.0502      29035.6                50.00     Sequence
   DRB5_0101  287  GWSIADDHDLFGLDE  WSIADDHDL        0.0491      29386.1                50.00     Sequence
   DRB5_0101  398  AKELGPDGAAVLDAA  ELGPDGAAV        0.0425      31558.3                50.00     Sequence
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Allele: DRB5_0101. Number of high binders 19. Number of weak binders 91. Number of peptides 476

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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         IAb   26  ALFNWAYARHTGGTF  FNWAYARHT        0.7051         24.3          SB     0.30     Sequence
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IAb  356  LDEAAFAAAAELVQT  AAFAAAAEL        0.7034        24.8         SB     0.30     Sequence
IAb  357  DEAAFAAAAELVQTR  AAFAAAAEL        0.7014        25.3         SB     0.40     Sequence
IAb   25  TALFNWAYARHTGGT  FNWAYARHT        0.6969        26.6         SB     0.40     Sequence
IAb  358  EAAFAAAAELVQTRI  AAFAAAAEL        0.6861        29.8         SB     0.80     Sequence
IAb  355  ALDEAAFAAAAELVQ  AAFAAAAEL        0.6861        29.8         SB     0.80     Sequence
IAb   24  RTALFNWAYARHTGG  FNWAYARHT        0.6734        34.2         SB     0.80     Sequence
IAb   27  LFNWAYARHTGGTFV  FNWAYARHT        0.6691        35.9         SB     0.80     Sequence
IAb  354  IALDEAAFAAAAELV  AAFAAAAEL        0.6467        45.7         SB     0.80     Sequence
IAb   23  VRTALFNWAYARHTG  FNWAYARHT        0.6357        51.5         WB     1.00     Sequence
IAb  443  PRKAFSPIRVAATGT  RKAFSPIRV        0.6316        53.8         WB     1.00     Sequence
IAb  442  KPRKAFSPIRVAATG  RKAFSPIRV        0.6310        54.2         WB     1.00     Sequence
IAb  105  EAYHAFSTPEEVEAR  HAFSTPEEV        0.6300        54.8         WB     1.00     Sequence
IAb  359  AAFAAAAELVQTRIV  AAFAAAAEL        0.6261        57.1         WB     2.00     Sequence
IAb  441  LKPRKAFSPIRVAAT  RKAFSPIRV        0.6206        60.6         WB     2.00     Sequence
IAb  104  GEAYHAFSTPEEVEA  HAFSTPEEV        0.6179        62.4         WB     2.00     Sequence
IAb  444  RKAFSPIRVAATGTT  RKAFSPIRV        0.6129        65.9         WB     2.00     Sequence
IAb  106  AYHAFSTPEEVEARH  HAFSTPEEV        0.6076        69.8         WB     2.00     Sequence
IAb  107  YHAFSTPEEVEARHV  HAFSTPEEV        0.6025        73.8         WB     2.00     Sequence
IAb   28  FNWAYARHTGGTFVF  FNWAYARHT        0.6014        74.7         WB     2.00     Sequence
IAb  173  PVTFAAGSVPDFALT  VTFAAGSVP        0.5979        77.5         WB     2.00     Sequence
IAb  172  GPVTFAAGSVPDFAL  VTFAAGSVP        0.5854        88.7         WB     2.00     Sequence
IAb   22  LVRTALFNWAYARHT  FNWAYARHT        0.5840        90.1         WB     2.00     Sequence
IAb  103  AGEAYHAFSTPEEVE  HAFSTPEEV        0.5824        91.7         WB     2.00     Sequence
IAb  353  HIALDEAAFAAAAEL  AAFAAAAEL        0.5813        92.8         WB     2.00     Sequence
IAb  450  IRVAATGTTVSPPLF  IRVAATGTT        0.5743       100.0         WB     4.00     Sequence
IAb  171  RGPVTFAAGSVPDFA  VTFAAGSVP        0.5673       107.9         WB     4.00     Sequence
IAb  174  VTFAAGSVPDFALTR  VTFAAGSVP        0.5649       110.8         WB     4.00     Sequence
IAb    6  VRVRFCPSPTGTPHV  VRFCPSPTG        0.5634       112.6         WB     4.00     Sequence
IAb    7  RVRFCPSPTGTPHVG  RVRFCPSPT        0.5582       119.1         WB     4.00     Sequence
IAb  449  PIRVAATGTTVSPPL  IRVAATGTT        0.5531       125.9         WB     4.00     Sequence
IAb  440  ALKPRKAFSPIRVAA  KAFSPIRVA        0.5524       126.8         WB     4.00     Sequence
IAb  102  AAGEAYHAFSTPEEV  HAFSTPEEV        0.5518       127.7         WB     4.00     Sequence
IAb  406  AAVLDAALAALTSVT  AVLDAALAA        0.5450       137.5         WB     4.00     Sequence
IAb  445  KAFSPIRVAATGTTV  KAFSPIRVA        0.5443       138.4         WB     4.00     Sequence
IAb    5  TVRVRFCPSPTGTPH  RVRFCPSPT        0.5376       148.9         WB     4.00     Sequence
IAb  170  VRGPVTFAAGSVPDF  VTFAAGSVP        0.5347       153.6         WB     4.00     Sequence
IAb  447  FSPIRVAATGTTVSP  IRVAATGTT        0.5285       164.2         WB     4.00     Sequence
IAb  405  GAAVLDAALAALTSV  AVLDAALAA        0.5259       168.9         WB     4.00     Sequence
IAb  419  VTDWTAPLIEAALKD  TDWTAPLIE        0.5245       171.6         WB     4.00     Sequence
IAb  448  SPIRVAATGTTVSPP  IRVAATGTT        0.5232       173.9         WB     4.00     Sequence
IAb  451  RVAATGTTVSPPLFE  VAATGTTVS        0.5205       179.0         WB     4.00     Sequence
IAb  439  LALKPRKAFSPIRVA  RKAFSPIRV        0.5177       184.7         WB     4.00     Sequence
IAb  418  SVTDWTAPLIEAALK  TDWTAPLIE        0.5167       186.6         WB     4.00     Sequence
IAb    4  ETVRVRFCPSPTGTP  RVRFCPSPT        0.5140       192.2         WB     4.00     Sequence
IAb  417  TSVTDWTAPLIEAAL  TDWTAPLIE        0.5065       208.5         WB     8.00     Sequence
IAb  446  AFSPIRVAATGTTVS  IRVAATGTT        0.5058       210.0         WB     8.00     Sequence
IAb  407  AVLDAALAALTSVTD  AVLDAALAA        0.4976       229.6         WB     8.00     Sequence
IAb  420  TDWTAPLIEAALKDA  TDWTAPLIE        0.4942       238.0         WB     8.00     Sequence
IAb   97  LARLLAAGEAYHAFS  ARLLAAGEA        0.4840       265.9         WB     8.00     Sequence
IAb  169  LVRGPVTFAAGSVPD  VTFAAGSVP        0.4797       278.4         WB     8.00     Sequence
IAb  389  QYVIDPKAAAKELGP  QYVIDPKAA        0.4795       279.2         WB     8.00     Sequence
IAb  404  DGAAVLDAALAALTS  AVLDAALAA        0.4789       280.8         WB     8.00     Sequence
IAb  168  DLVRGPVTFAAGSVP  VTFAAGSVP        0.4749       293.5         WB     8.00     Sequence
IAb   96  VLARLLAAGEAYHAF  ARLLAAGEA        0.4737       297.2         WB     8.00     Sequence
IAb  416  LTSVTDWTAPLIEAA  TDWTAPLIE        0.4727       300.6         WB     8.00     Sequence
IAb  452  VAATGTTVSPPLFES  VAATGTTVS        0.4710       306.0         WB     8.00     Sequence
IAb   98  ARLLAAGEAYHAFST  ARLLAAGEA        0.4689       313.0         WB     8.00     Sequence
IAb  108  HAFSTPEEVEARHVA  HAFSTPEEV        0.4676       317.4         WB     8.00     Sequence
IAb  388  DQYVIDPKAAAKELG  QYVIDPKAA        0.4670       319.4         WB     8.00     Sequence
IAb  387  DDQYVIDPKAAAKEL  QYVIDPKAA        0.4559       360.5         WB     8.00     Sequence
IAb  438  GLALKPRKAFSPIRV  RKAFSPIRV        0.4519       376.2         WB     8.00     Sequence
IAb   95  DVLARLLAAGEAYHA  ARLLAAGEA        0.4477       393.9         WB     8.00     Sequence
IAb    8  VRFCPSPTGTPHVGL  VRFCPSPTG        0.4473       395.4         WB     8.00     Sequence
IAb  237  AERIPKFAHLPTVLG  RIPKFAHLP        0.4433       413.2         WB     8.00     Sequence
IAb  239  RIPKFAHLPTVLGEG  KFAHLPTVL        0.4423       417.6         WB     8.00     Sequence
IAb  302  MVAAFDVADVNSSPA  AAFDVADVN        0.4411       422.8         WB     8.00     Sequence
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IAb	403	PDGAAVLDAALAALT	AVLDAALAA	0.4409	423.8	WB	8.00	Sequence
IAb	386	NDDQYVIDPKAAAKE	QYVIDPKAA	0.4343	455.3	WB	16.00	Sequence
IAb	101	LAAGEAYHAFSTPEE	AYHAFSTPE	0.4337	458.1	WB	16.00	Sequence
IAb	238	ERIPKFAHLPTVLGE	KFAHLPTVL	0.4323	465.3	WB	16.00	Sequence
IAb	236	VAERIPKFAHLPTVL	RIPKFAHLP	0.4222	519.0		16.00	Sequence
IAb	303	VAAFDVADVNSSPAR	FDVADVNSS	0.4220	520.2		16.00	Sequence
IAb	352	HHIALDEAAFAAAAE	EAAFAAAAE	0.4204	529.3		16.00	Sequence
IAb	454	ATGTTVSPPLFESLE	GTTVSPPLF	0.4166	551.5		16.00	Sequence
IAb	408	VLDAALAALTSVTDW	LDAALAALT	0.4154	558.3		16.00	Sequence
IAb	301	EMVAAFDVADVNSSP	AAFDVADVN	0.4146	563.3		16.00	Sequence
IAb	175	TFAAGSVPDFALTRA	TFAAGSVPD	0.4142	565.8		16.00	Sequence
IAb	304	AAFDVADVNSSPARF	FDVADVNSS	0.4118	580.8		16.00	Sequence
IAb	455	TGTTVSPPLFESLEL	GTTVSPPLF	0.4108	586.8		16.00	Sequence
IAb	240	IPKFAHLPTVLGEGT	PKFAHLPTV	0.4101	591.8		16.00	Sequence
IAb	453	AATGTTVSPPLFESL	GTTVSPPLF	0.4093	596.6		16.00	Sequence
IAb	360	AFAAAAELVQTRIVV	FAAAAELVQ	0.4059	618.8		16.00	Sequence
IAb	409	LDAALAALTSVTDWT	DAALAALTS	0.4056	621.0		16.00	Sequence
IAb	3	TETVRVRFCPSPTGT	RVRFCPSPT	0.4048	626.6		16.00	Sequence
IAb	99	RLLAAGEAYHAFSTP	RLLAAGEAY	0.3990	666.9		16.00	Sequence
IAb	167	NDLVRGPVTFAAGSV	LVRGPVTFA	0.3974	678.4		16.00	Sequence
IAb	385	FNDDQYVIDPKAAAK	QYVIDPKAA	0.3921	718.6		16.00	Sequence
IAb	214	GEDLLPSTPRQLALH	LLPSTPRQL	0.3915	723.4		16.00	Sequence
IAb	456	GTTVSPPLFESLELL	GTTVSPPLF	0.3890	743.2		16.00	Sequence
IAb	300	DEMVAAFDVADVNSS	AAFDVADVN	0.3854	773.0		16.00	Sequence
IAb	213	RGEDLLPSTPRQLAL	LLPSTPRQL	0.3803	816.9		16.00	Sequence
IAb	180	SVPDFALTRASGDPL	PDFALTRAS	0.3792	826.0		16.00	Sequence
IAb	235	GVAERIPKFAHLPTV	RIPKFAHLP	0.3774	842.9		16.00	Sequence
IAb	215	EDLLPSTPRQLALHQ	LLPSTPRQL	0.3746	868.5		16.00	Sequence
IAb	415	ALTSVTDWTAPLIEA	TDWTAPLIE	0.3734	879.9		16.00	Sequence
IAb	181	VPDFALTRASGDPLY	PDFALTRAS	0.3703	909.6		16.00	Sequence
IAb	179	GSVPDFALTRASGDP	PDFALTRAS	0.3657	956.7		16.00	Sequence
IAb	212	LRGEDLLPSTPRQLA	LLPSTPRQL	0.3649	964.4		16.00	Sequence
IAb	94	RDVLARLLAAGEAYH	ARLLAAGEA	0.3645	969.1		16.00	Sequence
IAb	241	PKFAHLPTVLGEGTK	KFAHLPTVL	0.3638	976.3		16.00	Sequence
IAb	390	YVIDPKAAAKELGPD	YVIDPKAAA	0.3571	1049.4		16.00	Sequence
IAb	182	PDFALTRASGDPLYT	FALTRASGD	0.3569	1051.4		16.00	Sequence
IAb	410	DAALAALTSVTDWTA	DAALAALTS	0.3562	1060.2		16.00	Sequence
IAb	306	FDVADVNSSPARFDQ	ADVNSSPAR	0.3555	1067.3		16.00	Sequence
IAb	176	FAAGSVPDFALTRAS	PDFALTRAS	0.3499	1134.7		16.00	Sequence
IAb	100	LLAAGEAYHAFSTPE	AYHAFSTPE	0.3446	1201.1		32.00	Sequence
IAb	141	AQRAAYLAEGRQPVV	AAYLAEGRQ	0.3432	1220.0		32.00	Sequence
IAb	305	AFDVADVNSSPARFD	ADVNSSPAR	0.3428	1224.7		32.00	Sequence
IAb	475	SMQRLRAARQLVGHA	QRLRAARQL	0.3418	1237.8		32.00	Sequence
IAb	9	RFCPSPTGTPHVGLV	FCPSPTGTP	0.3416	1240.5		32.00	Sequence
IAb	178	AGSVPDFALTRASGD	PDFALTRAS	0.3410	1248.7		32.00	Sequence
IAb	2	ATETVRVRFCPSPTG	RVRFCPSPT	0.3387	1281.2		32.00	Sequence
IAb	384	FFNDDQYVIDPKAAA	QYVIDPKAA	0.3367	1309.4		32.00	Sequence
IAb	437	EGLALKPRKAFSPIR	GLALKPRKA	0.3358	1322.1		32.00	Sequence
IAb	166	WNDLVRGPVTFAAGS	DLVRGPVTF	0.3335	1355.3		32.00	Sequence
IAb	308	VADVNSSPARFDQKK	ADVNSSPAR	0.3328	1365.1		32.00	Sequence
IAb	211	VLRGEDLLPSTPRQL	LLPSTPRQL	0.3316	1383.7		32.00	Sequence
IAb	474	RSMQRLRAARQLVGH	QRLRAARQL	0.3288	1425.3		32.00	Sequence
IAb	402	GPDGAAVLDAALAAL	AVLDAALAA	0.3284	1432.2		32.00	Sequence
IAb	307	DVADVNSSPARFDQK	ADVNSSPAR	0.3267	1458.7		32.00	Sequence
IAb	436	IEGLALKPRKAFSPI	GLALKPRKA	0.3255	1478.0		32.00	Sequence
IAb	93	YRDVLARLLAAGEAY	ARLLAAGEA	0.3231	1515.7		32.00	Sequence
IAb	421	DWTAPLIEAALKDAL	WTAPLIEAA	0.3214	1543.8		32.00	Sequence
IAb	435	LIEGLALKPRKAFSP	GLALKPRKA	0.3199	1569.3		32.00	Sequence
IAb	414	AALTSVTDWTAPLIE	TDWTAPLIE	0.3160	1636.5		32.00	Sequence
IAb	165	AWNDLVRGPVTFAAG	DLVRGPVTF	0.3155	1645.9		32.00	Sequence
IAb	216	DLLPSTPRQLALHQA	LLPSTPRQL	0.3105	1738.2		32.00	Sequence
IAb	140	DAQRAAYLAEGRQPV	AQRAAYLAE	0.3097	1752.1		32.00	Sequence
IAb	457	TTVSPPLFESLELLG	TTVSPPLFE	0.3097	1753.1		32.00	Sequence
IAb	177	AAGSVPDFALTRASG	PDFALTRAS	0.3090	1765.8		32.00	Sequence
IAb	142	QRAAYLAEGRQPVVR	AAYLAEGRQ	0.3075	1795.6		32.00	Sequence
IAb	194	LYTLVNPCDDALMKI	YTLVNPCDD	0.3050	1844.1		32.00	Sequence

IAb	29	NWAYARHTGGTFVFR	YARHTGGTF	0.3036	1872.0	32.00	Sequence
IAb	143	RAAYLAEGRQPVVRL	AAYLAEGRQ	0.3028	1888.8	32.00	Sequence
IAb	193	PLYTLVNPCDDALMK	YTLVNPCDD	0.3024	1896.4	32.00	Sequence
IAb	10	FCPSPTGTPHVGLVR	FCPSPTGTP	0.3020	1904.3	32.00	Sequence
IAb	217	LLPSTPRQLALHQAL	LLPSTPRQL	0.2999	1948.6	32.00	Sequence
IAb	21	GLVRTALFNWAYARH	ALFNWAYAR	0.2999	1949.7	32.00	Sequence
IAb	191	GDPLYTLVNPCDDAL	YTLVNPCDD	0.2983	1982.2	32.00	Sequence
IAb	422	WTAPLIEAALKDALI	WTAPLIEAA	0.2978	1993.2	32.00	Sequence
IAb	118	ARHVAAGRNPKLGYD	ARHVAAGRN	0.2968	2015.1	32.00	Sequence
IAb	411	AALAALTSVTDWTAP	AALAALTSV	0.2959	2034.1	32.00	Sequence
IAb	234	IGVAERIPKFAHLPT	RIPKFAHLP	0.2947	2061.7	32.00	Sequence
IAb	164	LAWNDLVRGPVTFAA	DLVRGPVTF	0.2935	2089.2	32.00	Sequence
IAb	473	DRSMQRLRAARQLVG	QRLRAARQL	0.2932	2096.1	32.00	Sequence
IAb	192	DPLYTLVNPCDDALM	YTLVNPCDD	0.2928	2103.3	32.00	Sequence
IAb	30	WAYARHTGGTFVFRI	WAYARHTGG	0.2893	2185.8	32.00	Sequence
IAb	351	GHHIALDEAAFAAAA	DEAAFAAAA	0.2882	2212.7	32.00	Sequence
IAb	78	GGPYGPYRQSQRAEI	GGPYGPYRQ	0.2874	2231.4	32.00	Sequence
IAb	117	EARHVAAGRNPKLGY	ARHVAAGRN	0.2873	2233.9	32.00	Sequence
IAb	401	LGPDGAAVLDAALAA	AVLDAALAA	0.2858	2271.0	32.00	Sequence
IAb	434	ALIEGLALKPRKAFS	GLALKPRKA	0.2857	2271.4	32.00	Sequence
IAb	299	LDEMVAAFDVADVNS	MVAAFDVAD	0.2857	2272.3	32.00	Sequence
IAb	309	ADVNSSPARFDQKKA	ADVNSSPAR	0.2854	2278.6	32.00	Sequence
IAb	183	DFALTRASGDPLYTL	FALTRASGD	0.2829	2341.0	32.00	Sequence
IAb	271	DRGFIPEGLLNYLAL	DRGFIPEGL	0.2808	2395.4	32.00	Sequence
IAb	184	FALTRASGDPLYTLV	FALTRASGD	0.2801	2415.1	32.00	Sequence
IAb	116	VEARHVAAGRNPKLG	ARHVAAGRN	0.2773	2488.0	32.00	Sequence
IAb	90	AEIYRDVLARLLAAG	EIYRDVLAR	0.2771	2493.2	32.00	Sequence
IAb	144	AAYLAEGRQPVVRLR	AAYLAEGRQ	0.2759	2527.5	32.00	Sequence
IAb	139	TDAQRAAYLAEGRQP	AQRAAYLAE	0.2757	2532.7	32.00	Sequence
IAb	89	RAEIYRDVLARLLAA	EIYRDVLAR	0.2737	2588.8	32.00	Sequence
IAb	270	RDRGFIPEGLLNYLA	DRGFIPEGL	0.2715	2649.1	32.00	Sequence
IAb	190	SGDPLYTLVNPCDDA	YTLVNPCDD	0.2708	2668.6	32.00	Sequence
IAb	77	VGGPYGPYRQSQRAE	GGPYGPYRQ	0.2707	2672.8	32.00	Sequence
IAb	433	DALIEGLALKPRKAF	GLALKPRKA	0.2704	2681.1	32.00	Sequence
IAb	79	GPYGPYRQSQRAEIY	GPYRQSQRA	0.2687	2732.2	32.00	Sequence
IAb	163	DLAWNDLVRGPVTFA	LVRGPVTFA	0.2644	2861.5	32.00	Sequence
IAb	242	KFAHLPTVLGEGTKK	KFAHLPTVL	0.2641	2871.3	32.00	Sequence
IAb	119	RHVAAGRNPKLGYDN	RHVAAGRNP	0.2639	2877.0	32.00	Sequence
IAb	92	IYRDVLARLLAAGEA	ARLLAAGEA	0.2632	2898.7	32.00	Sequence
IAb	269	HRDRGFIPEGLLNYL	DRGFIPEGL	0.2614	2956.9	32.00	Sequence
IAb	361	FAAAAELVQTRIVVL	FAAAAELVQ	0.2585	3048.6	32.00	Sequence
IAb	186	LTRASGDPLYTLVNP	RASGDPLYT	0.2571	3097.8	32.00	Sequence
IAb	91	EIYRDVLARLLAAGE	EIYRDVLAR	0.2561	3129.2	32.00	Sequence
IAb	88	QRAEIYRDVLARLLA	EIYRDVLAR	0.2560	3132.5	32.00	Sequence
IAb	233	RIGVAERIPKFAHLP	RIPKFAHLP	0.2559	3137.5	32.00	Sequence
IAb	185	ALTRASGDPLYTLVN	RASGDPLYT	0.2527	3246.4	32.00	Sequence
IAb	115	EVEARHVAAGRNPKL	ARHVAAGRN	0.2521	3267.2	32.00	Sequence
IAb	81	YGPYRQSQRAEIYRD	GPYRQSQRA	0.2521	3267.3	32.00	Sequence
IAb	80	PYGPYRQSQRAEIYR	GPYRQSQRA	0.2517	3283.0	32.00	Sequence
IAb	298	GLDEMVAAFDVADVN	MVAAFDVAD	0.2509	3312.8	32.00	Sequence
IAb	31	AYARHTGGTFVFRIE	YARHTGGTF	0.2498	3349.4	32.00	Sequence
IAb	1	TATETVRVRFCPSPT	RVRFCPSPT	0.2496	3358.7	32.00	Sequence
IAb	20	VGLVRTALFNWAYAR	ALFNWAYAR	0.2471	3449.0	32.00	Sequence
IAb	398	AKELGPDGAAVLDAA	LGPDGAAVL	0.2469	3459.6	32.00	Sequence
IAb	138	LTDAQRAAYLAEGRQ	AQRAAYLAE	0.2465	3472.4	32.00	Sequence
IAb	268	AHRDRGFIPEGLLNY	DRGFIPEGL	0.2462	3482.3	32.00	Sequence
IAb	76	EVGGPYGPYRQSQRA	GGPYGPYRQ	0.2445	3549.3	32.00	Sequence
IAb	189	ASGDPLYTLVNPCDD	YTLVNPCDD	0.2444	3553.3	32.00	Sequence
IAb	432	KDALIEGLALKPRKA	GLALKPRKA	0.2402	3718.0	50.00	Sequence
IAb	195	YTLVNPCDDALMKIT	YTLVNPCDD	0.2358	3899.0	50.00	Sequence
IAb	383	KFFNDDQYVIDPKAA	QYVIDPKAA	0.2333	4005.5	50.00	Sequence
IAb	137	HLTDAQRAAYLAEGR	AQRAAYLAE	0.2333	4005.9	50.00	Sequence
IAb	391	VIDPKAAAKELGPDG	IDPKAAAKE	0.2330	4018.1	50.00	Sequence
IAb	75	PEVGGPYGPYRQSQR	GGPYGPYRQ	0.2330	4018.3	50.00	Sequence
IAb	87	SQRAEIYRDVLARLL	EIYRDVLAR	0.2314	4090.7	50.00	Sequence
IAb	12	PSPTGTPHVGLVRTA	PSPTGTPHV	0.2289	4202.5	50.00	Sequence

IAb	400	ELGPDGAAVLDAALA	LGPDGAAVL	0.2282	4233.8	50.00	Sequence
IAb	188	RASGDPLYTLVNPCD	RASGDPLYT	0.2277	4257.3	50.00	Sequence
IAb	397	AAKELGPDGAAVLDA	LGPDGAAVL	0.2269	4294.6	50.00	Sequence
IAb	120	HVAAGRNPKLGYDNF	HVAAGRNPK	0.2253	4368.1	50.00	Sequence
IAb	423	TAPLIEAALKDALIE	PLIEAALKD	0.2251	4376.3	50.00	Sequence
IAb	392	IDPKAAAKELGPDGA	IDPKAAAKE	0.2243	4415.7	50.00	Sequence
IAb	472	RDRSMQRLRAARQLV	QRLRAARQL	0.2240	4429.5	50.00	Sequence
IAb	282	YLALLGWSIADDHDL	ALLGWSIAD	0.2223	4511.2	50.00	Sequence
IAb	399	KELGPDGAAVLDAAL	LGPDGAAVL	0.2221	4524.3	50.00	Sequence
IAb	230	ALIRIGVAERIPKFA	ALIRIGVAE	0.2213	4560.6	50.00	Sequence
IAb	272	RGFIPEGLLNYLALL	RGFIPEGLL	0.2206	4595.2	50.00	Sequence
IAb	187	TRASGDPLYTLVNPC	RASGDPLYT	0.2205	4599.2	50.00	Sequence
IAb	413	LAALTSVTDWTAPLI	LAALTSVTD	0.2190	4678.5	50.00	Sequence
IAb	232	IRIGVAERIPKFAHL	VAERIPKFA	0.2184	4707.3	50.00	Sequence
IAb	82	GPYRQSQRAEIYRDV	GPYRQSQRA	0.2175	4755.3	50.00	Sequence
IAb	283	LALLGWSIADDHDLF	ALLGWSIAD	0.2148	4892.6	50.00	Sequence
IAb	281	NYLALLGWSIADDHD	ALLGWSIAD	0.2139	4943.8	50.00	Sequence
IAb	32	YARHTGGTFVFRIED	YARHTGGTF	0.2135	4964.1	50.00	Sequence
IAb	145	AYLAEGRQPVVRLRM	YLAEGRQPV	0.2132	4976.4	50.00	Sequence
IAb	114	EEVEARHVAAGRNPK	ARHVAAGRN	0.2111	5091.9	50.00	Sequence
IAb	74	GPEVGGPYGPYRQSQ	GGPYGPYRQ	0.2105	5127.6	50.00	Sequence
IAb	277	EGLLNYLALLGWSIA	YLALLGWSI	0.2099	5158.2	50.00	Sequence
IAb	412	ALAALTSVTDWTAPL	ALAALTSVT	0.2084	5245.5	50.00	Sequence
IAb	280	LNYLALLGWSIADDH	LALLGWSIA	0.2064	5360.5	50.00	Sequence
IAb	458	TVSPPLFESLELLGR	TVSPPLFES	0.2045	5472.3	50.00	Sequence
IAb	121	VAAGRNPKLGYDNFD	AAGRNPKLG	0.2041	5496.1	50.00	Sequence
IAb	231	LIRIGVAERIPKFAH	VAERIPKFA	0.2039	5504.0	50.00	Sequence
IAb	221	TPRQLALHQALIRIG	RQLALHQAL	0.2035	5531.6	50.00	Sequence
IAb	297	FGLDEMVAAFDVADV	MVAAFDVAD	0.2024	5595.4	50.00	Sequence
IAb	396	AAAKELGPDGAAVLD	LGPDGAAVL	0.2015	5653.2	50.00	Sequence
IAb	73	EGPEVGGPYGPYRQS	PEVGGPYGP	0.1989	5814.9	50.00	Sequence
IAb	146	YLAEGRQPVVRLRMP	YLAEGRQPV	0.1977	5888.0	50.00	Sequence
IAb	222	PRQLALHQALIRIGV	RQLALHQAL	0.1960	5995.0	50.00	Sequence
IAb	223	RQLALHQALIRIGVA	RQLALHQAL	0.1955	6027.8	50.00	Sequence
IAb	431	LKDALIEGLALKPRK	DALIEGLAL	0.1955	6028.5	50.00	Sequence
IAb	395	KAAAKELGPDGAAVL	LGPDGAAVL	0.1953	6042.3	50.00	Sequence
IAb	278	GLLNYLALLGWSIAD	YLALLGWSI	0.1948	6078.0	50.00	Sequence
IAb	429	AALKDALIEGLALKP	AALKDALIE	0.1944	6100.0	50.00	Sequence
IAb	314	SPARFDQKKADALNA	ARFDQKKAD	0.1942	6113.4	50.00	Sequence
IAb	11	CPSPTGTPHVGLVRT	PSPTGTPHV	0.1941	6120.8	50.00	Sequence
IAb	315	PARFDQKKADALNAE	FDQKKADAL	0.1929	6199.1	50.00	Sequence
IAb	229	QALIRIGVAERIPKF	IRIGVAERI	0.1920	6261.4	50.00	Sequence
IAb	279	LLNYLALLGWSIADD	ALLGWSIAD	0.1918	6278.6	50.00	Sequence
IAb	224	QLALHQALIRIGVAE	LALHQALIR	0.1917	6282.5	50.00	Sequence
IAb	276	PEGLLNYLALLGWSI	YLALLGWSI	0.1915	6300.1	50.00	Sequence
IAb	424	APLIEAALKDALIEG	PLIEAALKD	0.1899	6409.9	50.00	Sequence
IAb	430	ALKDALIEGLALKPR	DALIEGLAL	0.1896	6427.3	50.00	Sequence
IAb	113	PEEVEARHVAAGRNP	ARHVAAGRN	0.1879	6543.5	50.00	Sequence
IAb	136	RHLTDAQRAAYLAEG	AQRAAYLAE	0.1878	6555.7	50.00	Sequence
IAb	284	ALLGWSIADDHDLFG	ALLGWSIAD	0.1876	6566.8	50.00	Sequence
IAb	267	FAHRDRGFIPEGLLN	RGFIPEGLL	0.1872	6594.4	50.00	Sequence
IAb	220	STPRQLALHQALIRI	RQLALHQAL	0.1866	6642.5	50.00	Sequence
IAb	19	HVGLVRTALFNWAYA	GLVRTALFN	0.1865	6649.2	50.00	Sequence
IAb	13	SPTGTPHVGLVRTAL	GTPHVGLVR	0.1864	6656.0	50.00	Sequence
IAb	210	HVLRGEDLLPSTPRQ	EDLLPSTPR	0.1860	6681.6	50.00	Sequence
IAb	16	GTPHVGLVRTALFNW	GTPHVGLVR	0.1860	6685.7	50.00	Sequence
IAb	273	GFIPEGLLNYLALLG	FIPEGLLNY	0.1844	6797.5	50.00	Sequence
IAb	313	SSPARFDQKKADALN	ARFDQKKAD	0.1836	6855.7	50.00	Sequence
IAb	225	LALHQALIRIGVAER	LALHQALIR	0.1835	6864.2	50.00	Sequence
IAb	15	TGTPHVGLVRTALFN	GTPHVGLVR	0.1835	6864.7	50.00	Sequence
IAb	310	DVNSSPARFDQKKAD	VNSSPARFD	0.1795	7172.6	50.00	Sequence
IAb	228	HQALIRIGVAERIPK	IRIGVAERI	0.1794	7180.9	50.00	Sequence
IAb	18	PHVGLVRTALFNWAY	GLVRTALFN	0.1787	7230.5	50.00	Sequence
IAb	274	FIPEGLLNYLALLGW	FIPEGLLNY	0.1783	7266.0	50.00	Sequence
IAb	459	VSPPLFESLELLGRD	PLFESLELL	0.1763	7420.5	50.00	Sequence
IAb	393	DPKAAAKELGPDGAA	AKELGPDGA	0.1757	7469.8	50.00	Sequence

IAb	227	LHQALIRIGVAERIP	ALIRIGVAE	0.1750	7526.9	50.00	Sequence
IAb	350	HGHHIALDEAAFAAA	HHIALDEAA	0.1748	7546.4	50.00	Sequence
IAb	317	RFDQKKADALNAEHI	FDQKKADAL	0.1739	7620.4	50.00	Sequence
IAb	316	ARFDQKKADALNAEH	FDQKKADAL	0.1738	7624.6	50.00	Sequence
IAb	14	PTGTPHVGLVRTALF	GTPHVGLVR	0.1735	7652.2	50.00	Sequence
IAb	312	NSSPARFDQKKADAL	ARFDQKKAD	0.1732	7677.6	50.00	Sequence
IAb	54	EESYLALLDALRWLG	ESYLALLDA	0.1724	7740.6	50.00	Sequence
IAb	53	SEESYLALLDALRWL	ESYLALLDA	0.1714	7825.0	50.00	Sequence
IAb	72	DEGPEVGGPYGPYRQ	PEVGGPYGP	0.1704	7911.5	50.00	Sequence
IAb	318	FDQKKADALNAEHIR	FDQKKADAL	0.1698	7961.3	50.00	Sequence
IAb	349	THGHHIALDEAAFAA	HHIALDEAA	0.1696	7982.1	50.00	Sequence
IAb	460	SPPLFESLELLGRDR	PLFESLELL	0.1686	8070.6	50.00	Sequence
IAb	135	DRHLTDAQRAAYLAE	AQRAAYLAE	0.1685	8072.0	50.00	Sequence
IAb	425	PLIEAALKDALIEGL	PLIEAALKD	0.1681	8115.3	50.00	Sequence
IAb	394	PKAAAKELGPDGAAV	AKELGPDGA	0.1665	8254.4	50.00	Sequence
IAb	52	DSEESYLALLDALRW	ESYLALLDA	0.1647	8411.5	50.00	Sequence
IAb	311	VNSSPARFDQKKADA	VNSSPARFD	0.1647	8411.5	50.00	Sequence
IAb	471	GRDRSMQRLRAARQL	QRLRAARQL	0.1644	8445.3	50.00	Sequence
IAb	219	PSTPRQLALHQALIR	RQLALHQAL	0.1635	8527.6	50.00	Sequence
IAb	122	AAGRNPKLGYDNFDR	AAGRNPKLG	0.1631	8558.0	50.00	Sequence
IAb	209	THVLRGEDLLPSTPR	EDLLPSTPR	0.1625	8614.4	50.00	Sequence
IAb	226	ALHQALIRIGVAERI	IRIGVAERI	0.1622	8645.1	50.00	Sequence
IAb	320	QKKADALNAEHIRML	ADALNAEHI	0.1617	8692.1	50.00	Sequence
IAb	296	LFGLDEMVAAFDVAD	MVAAFDVAD	0.1609	8764.8	50.00	Sequence
IAb	33	ARHTGGTFVFRIEDT	ARHTGGTFV	0.1606	8796.3	50.00	Sequence
IAb	428	EAALKDALIEGLALK	AALKDALIE	0.1598	8871.4	50.00	Sequence
IAb	134	FDRHLTDAQRAAYLA	HLTDAQRAA	0.1594	8907.3	50.00	Sequence
IAb	17	TPHVGLVRTALFNWA	GLVRTALFN	0.1589	8957.7	50.00	Sequence
IAb	257	LSKRDPQSNLFAHRD	LSKRDPQSN	0.1586	8993.4	50.00	Sequence
IAb	319	DQKKADALNAEHIRM	ADALNAEHI	0.1571	9132.8	50.00	Sequence
IAb	275	IPEGLLNYLALLGWS	GLLNYLALL	0.1538	9472.8	50.00	Sequence
IAb	266	LFAHRDRGFIPEGLL	RGFIPEGLL	0.1536	9485.3	50.00	Sequence
IAb	109	AFSTPEEVEARHVAA	FSTPEEVEA	0.1527	9584.8	50.00	Sequence
IAb	427	IEAALKDALIEGLAL	AALKDALIE	0.1520	9653.9	50.00	Sequence
IAb	218	LPSTPRQLALHQALI	RQLALHQAL	0.1519	9660.4	50.00	Sequence
IAb	86	QSQRAEIYRDVLARL	EIYRDVLAR	0.1496	9907.5	50.00	Sequence
IAb	162	DDLAWNDLVRGPVTF	DLVRGPVTF	0.1493	9937.5	50.00	Sequence
IAb	256	KLSKRDPQSNLFAHR	LSKRDPQSN	0.1483	10050.4	50.00	Sequence
IAb	321	KKADALNAEHIRMLD	ADALNAEHI	0.1481	10070.1	50.00	Sequence
IAb	133	NFDRHLTDAQRAAYL	HLTDAQRAA	0.1475	10140.3	50.00	Sequence
IAb	51	RDSEESYLALLDALR	ESYLALLDA	0.1466	10239.4	50.00	Sequence
IAb	426	LIEAALKDALIEGLA	AALKDALIE	0.1458	10321.4	50.00	Sequence
IAb	37	GGTFVFRIEDTDAQR	FVFRIEDTD	0.1458	10322.2	50.00	Sequence
IAb	243	FAHLPTVLGEGTKKL	FAHLPTVLG	0.1457	10331.2	50.00	Sequence
IAb	348	DTHGHHIALDEAAFA	HHIALDEAA	0.1444	10481.8	50.00	Sequence
IAb	36	TGGTFVFRIEDTDAQ	FVFRIEDTD	0.1441	10513.4	50.00	Sequence
IAb	255	KKLSKRDPQSNLFAH	LSKRDPQSN	0.1407	10908.8	50.00	Sequence
IAb	38	GTFVFRIEDTDAQRD	FVFRIEDTD	0.1402	10964.2	50.00	Sequence
IAb	55	ESYLALLDALRWLGL	ESYLALLDA	0.1399	11000.3	50.00	Sequence
IAb	147	LAEGRQPVVRLRMPD	AEGRQPVVR	0.1375	11293.3	50.00	Sequence
IAb	34	RHTGGTFVFRIEDTD	RHTGGTFVF	0.1368	11379.7	50.00	Sequence
IAb	83	PYRQSQRAEIYRDVL	PYRQSQRAE	0.1340	11731.0	50.00	Sequence
IAb	254	TKKLSKRDPQSNLFA	LSKRDPQSN	0.1330	11861.6	50.00	Sequence
IAb	372	IVVLGDAWELLKFFN	VVLGDAWEL	0.1312	12095.9	50.00	Sequence
IAb	294	HDLFGLDEMVAAFDV	FGLDEMVAA	0.1304	12198.3	50.00	Sequence
IAb	295	DLFGLDEMVAAFDVA	FGLDEMVAA	0.1301	12230.3	50.00	Sequence
IAb	110	FSTPEEVEARHVAAG	FSTPEEVEA	0.1293	12344.9	50.00	Sequence
IAb	461	PPLFESLELLGRDRS	PLFESLELL	0.1285	12451.4	50.00	Sequence
IAb	112	TPEEVEARHVAAGRN	ARHVAAGRN	0.1266	12702.6	50.00	Sequence
IAb	371	RIVVLGDAWELLKFF	VVLGDAWEL	0.1261	12780.8	50.00	Sequence
IAb	322	KADALNAEHIRMLDV	ADALNAEHI	0.1260	12793.9	50.00	Sequence
IAb	39	TFVFRIEDTDAQRDS	FRIEDTDAQ	0.1259	12798.1	50.00	Sequence
IAb	35	HTGGTFVFRIEDTDA	FVFRIEDTD	0.1253	12890.5	50.00	Sequence
IAb	148	AEGRQPVVRLRMPDD	AEGRQPVVR	0.1248	12963.6	50.00	Sequence
IAb	347	LDTHGHHIALDEAAF	HHIALDEAA	0.1241	13059.5	50.00	Sequence
IAb	71	WDEGPEVGGPYGPYR	PEVGGPYGP	0.1220	13350.8	50.00	Sequence

IAb	323	ADALNAEHIRMLDVG	ADALNAEHI	0.1217	13404.5	50.00	Sequence
IAb	246	LPTVLGEGTKKLSKR	VLGEGTKKL	0.1196	13707.4	50.00	Sequence
IAb	132	DNFDRHLTDAQRAAY	RHLTDAQRA	0.1196	13710.9	50.00	Sequence
IAb	370	TRIVVLGDAWELLKF	VVLGDAWEL	0.1181	13925.6	50.00	Sequence
IAb	293	DHDLFGLDEMVAAFD	FGLDEMVAA	0.1177	13992.1	50.00	Sequence
IAb	346	HLDTHGHHIALDEAA	HHIALDEAA	0.1172	14071.6	50.00	Sequence
IAb	69	LDWDEGPEVGGPYGP	LDWDEGPEV	0.1163	14202.4	50.00	Sequence
IAb	247	PTVLGEGTKKLSKRD	VLGEGTKKL	0.1160	14246.9	50.00	Sequence
IAb	50	QRDSEESYLALLDAL	EESYLALLD	0.1160	14256.2	50.00	Sequence
IAb	245	HLPTVLGEGTKKLSK	PTVLGEGTK	0.1149	14423.7	50.00	Sequence
IAb	152	QPVVRLRMPDDDLAW	VRLRMPDDD	0.1143	14519.7	50.00	Sequence
IAb	244	AHLPTVLGEGTKKLS	PTVLGEGTK	0.1138	14600.8	50.00	Sequence
IAb	153	PVVRLRMPDDDLAWN	VRLRMPDDD	0.1132	14695.8	50.00	Sequence
IAb	161	DDDLAWNDLVRGPVT	LAWNDLVRG	0.1130	14716.3	50.00	Sequence
IAb	131	YDNFDRHLTDAQRAA	RHLTDAQRA	0.1130	14725.2	50.00	Sequence
IAb	40	FVFRIEDTDAQRDSE	FRIEDTDAQ	0.1130	14729.0	50.00	Sequence
IAb	260	RDPQSNLFAHRDRGF	RDPQSNLFA	0.1128	14756.3	50.00	Sequence
IAb	292	DDHDLFGLDEMVAAF	FGLDEMVAA	0.1107	15099.5	50.00	Sequence
IAb	85	RQSQRAEIYRDVLAR	EIYRDVLAR	0.1104	15138.1	50.00	Sequence
IAb	151	RQPVVRLRMPDDDLA	VRLRMPDDD	0.1095	15288.7	50.00	Sequence
IAb	0	VTATETVRVRFCPSP	VRVRFCPSP	0.1093	15330.3	50.00	Sequence
IAb	208	ITHVLRGEDLLPSTP	GEDLLPSTP	0.1092	15333.1	50.00	Sequence
IAb	285	LLGWSIADDHDLFGL	LGWSIADDH	0.1084	15479.2	50.00	Sequence
IAb	470	LGRDRSMQRLRAARQ	RSMQRLRAA	0.1078	15571.7	50.00	Sequence
IAb	259	KRDPQSNLFAHRDRG	RDPQSNLFA	0.1064	15804.1	50.00	Sequence
IAb	373	VVLGDAWELLKFFND	VVLGDAWEL	0.1063	15825.5	50.00	Sequence
IAb	253	GTKKLSKRDPQSNLF	LSKRDPQSN	0.1063	15830.6	50.00	Sequence
IAb	265	NLFAHRDRGFIPEGL	DRGFIPEGL	0.1052	16012.7	50.00	Sequence
IAb	70	DWDEGPEVGGPYGPY	PEVGGPYGP	0.1027	16451.2	50.00	Sequence
IAb	369	QTRIVVLGDAWELLK	VVLGDAWEL	0.1023	16536.9	50.00	Sequence
IAb	258	SKRDPQSNLFAHRDR	RDPQSNLFA	0.1009	16790.9	50.00	Sequence
IAb	362	AAAAELVQTRIVVLG	AAAAELVQT	0.1003	16891.5	50.00	Sequence
IAb	160	PDDDLAWNDLVRGPV	LAWNDLVRG	0.0995	17032.8	50.00	Sequence
IAb	56	SYLALLDALRWLGLD	SYLALLDAL	0.0988	17159.0	50.00	Sequence
IAb	462	PLFESLELLGRDRSM	PLFESLELL	0.0985	17225.6	50.00	Sequence
IAb	154	VVRLRMPDDDLAWND	VRLRMPDDD	0.0964	17614.2	50.00	Sequence
IAb	261	DPQSNLFAHRDRGFI	DPQSNLFAH	0.0939	18095.4	50.00	Sequence
IAb	84	YRQSQRAEIYRDVLA	YRQSQRAEI	0.0932	18243.8	50.00	Sequence
IAb	150	GRQPVVRLRMPDDDL	VVRLRMPDD	0.0931	18260.8	50.00	Sequence
IAb	68	GLDWDEGPEVGGPYG	LDWDEGPEV	0.0929	18296.0	50.00	Sequence
IAb	128	KLGYDNFDRHLTDAQ	FDRHLTDAQ	0.0922	18432.1	50.00	Sequence
IAb	291	ADDHDLFGLDEMVAA	FGLDEMVAA	0.0918	18510.2	50.00	Sequence
IAb	67	LGLDWDEGPEVGGPY	LDWDEGPEV	0.0913	18614.3	50.00	Sequence
IAb	41	VFRIEDTDAQRDSEE	FRIEDTDAQ	0.0911	18653.8	50.00	Sequence
IAb	149	EGRQPVVRLRMPDDD	VRLRMPDDD	0.0902	18835.3	50.00	Sequence
IAb	130	GYDNFDRHLTDAQRA	RHLTDAQRA	0.0900	18874.9	50.00	Sequence
IAb	368	VQTRIVVLGDAWELL	VVLGDAWEL	0.0898	18922.9	50.00	Sequence
IAb	252	EGTKKLSKRDPQSNL	LSKRDPQSN	0.0884	19207.0	50.00	Sequence
IAb	111	STPEEVEARHVAAGR	VEARHVAAG	0.0867	19561.8	50.00	Sequence
IAb	129	LGYDNFDRHLTDAQR	FDRHLTDAQ	0.0847	19993.9	50.00	Sequence
IAb	49	AQRDSEESYLALLDA	ESYLALLDA	0.0842	20101.0	50.00	Sequence
IAb	363	AAAELVQTRIVVLGD	AELVQTRIV	0.0842	20110.6	50.00	Sequence
IAb	66	WLGLDWDEGPEVGGP	LDWDEGPEV	0.0840	20140.9	50.00	Sequence
IAb	207	KITHVLRGEDLLPST	HVLRGEDLL	0.0836	20246.4	50.00	Sequence
IAb	248	TVLGEGTKKLSKRDP	VLGEGTKKL	0.0821	20561.4	50.00	Sequence
IAb	57	YLALLDALRWLGLDW	YLALLDALR	0.0794	21186.5	50.00	Sequence
IAb	345	DHLDTHGHHIALDEA	GHHIALDEA	0.0788	21305.8	50.00	Sequence
IAb	367	LVQTRIVVLGDAWEL	VVLGDAWEL	0.0788	21321.5	50.00	Sequence
IAb	64	LRWLGLDWDEGPEVG	LDWDEGPEV	0.0769	21746.7	50.00	Sequence
IAb	42	FRIEDTDAQRDSEES	FRIEDTDAQ	0.0768	21783.0	50.00	Sequence
IAb	65	RWLGLDWDEGPEVGG	LDWDEGPEV	0.0767	21796.2	50.00	Sequence
IAb	364	AAELVQTRIVVLGDA	AELVQTRIV	0.0767	21803.7	50.00	Sequence
IAb	196	TLVNPCDDALMKITH	VNPCDDALM	0.0767	21815.8	50.00	Sequence
IAb	206	MKITHVLRGEDLLPS	HVLRGEDLL	0.0760	21981.4	50.00	Sequence
IAb	286	LGWSIADDHDLFGLD	LGWSIADDH	0.0755	22085.1	50.00	Sequence
IAb	251	GEGTKKLSKRDPQSN	LSKRDPQSN	0.0753	22126.9	50.00	Sequence

IAb	159	MPDDDLAWNDLVRGP	LAWNDLVRG	0.0748	22269.4	50.00	Sequence
IAb	262	PQSNLFAHRDRGFIP	QSNLFAHRD	0.0740	22458.1	50.00	Sequence
IAb	469	LLGRDRSMQRLRAAR	RSMQRLRAA	0.0739	22476.6	50.00	Sequence
IAb	365	AELVQTRIVVLGDAW	AELVQTRIV	0.0738	22509.7	50.00	Sequence
IAb	63	ALRWLGLDWDEGPEV	LDWDEGPEV	0.0734	22587.0	50.00	Sequence
IAb	58	LALLDALRWLGLDWD	LALLDALRW	0.0734	22594.8	50.00	Sequence
IAb	155	VRLRMPDDDLAWNDL	VRLRMPDDD	0.0730	22689.9	50.00	Sequence
IAb	264	SNLFAHRDRGFIPEG	SNLFAHRDR	0.0717	23021.0	50.00	Sequence
IAb	249	VLGEGTKKLSKRDPQ	VLGEGTKKL	0.0707	23270.7	50.00	Sequence
IAb	468	ELLGRDRSMQRLRAA	RSMQRLRAA	0.0698	23495.1	50.00	Sequence
IAb	61	LDALRWLGLDWDEGP	LRWLGLDWD	0.0695	23569.7	50.00	Sequence
IAb	263	QSNLFAHRDRGFIPE	QSNLFAHRD	0.0690	23711.9	50.00	Sequence
IAb	127	PKLGYDNFDRHLTDA	LGYDNFDRH	0.0685	23815.3	50.00	Sequence
IAb	204	ALMKITHVLRGEDLL	MKITHVLRG	0.0678	24006.2	50.00	Sequence
IAb	60	LLDALRWLGLDWDEG	DALRWLGLD	0.0676	24056.4	50.00	Sequence
IAb	62	DALRWLGLDWDEGPE	LRWLGLDWD	0.0675	24086.6	50.00	Sequence
IAb	344	RDHLDTHGHHIALDE	LDTHGHHIA	0.0665	24341.5	50.00	Sequence
IAb	382	LKFFNDDQYVIDPKA	DQYVIDPKA	0.0661	24447.6	50.00	Sequence
IAb	203	DALMKITHVLRGEDL	MKITHVLRG	0.0645	24881.5	50.00	Sequence
IAb	59	ALLDALRWLGLDWDE	LRWLGLDWD	0.0633	25211.3	50.00	Sequence
IAb	205	LMKITHVLRGEDLLP	MKITHVLRG	0.0627	25368.1	50.00	Sequence
IAb	202	DDALMKITHVLRGED	MKITHVLRG	0.0615	25693.8	50.00	Sequence
IAb	126	NPKLGYDNFDRHLTD	LGYDNFDRH	0.0612	25777.3	50.00	Sequence
IAb	158	RMPDDDLAWNDLVRG	LAWNDLVRG	0.0593	26324.4	50.00	Sequence
IAb	48	DAQRDSEESYLALLD	EESYLALLD	0.0588	26470.6	50.00	Sequence
IAb	198	VNPCDDALMKITHVL	VNPCDDALM	0.0577	26773.4	50.00	Sequence
IAb	341	VRLRDHLDTHGHHIA	VRLRDHLDT	0.0574	26863.3	50.00	Sequence
IAb	340	TVRLRDHLDTHGHHI	TVRLRDHLD	0.0573	26896.2	50.00	Sequence
IAb	125	RNPKLGYDNFDRHLT	LGYDNFDRH	0.0567	27079.6	50.00	Sequence
IAb	324	DALNAEHIRMLDVGD	LNAEHIRML	0.0566	27109.5	50.00	Sequence
IAb	201	CDDALMKITHVLRGE	ALMKITHVL	0.0563	27197.9	50.00	Sequence
IAb	379	WELLKFFNDDQYVID	WELLKFFND	0.0562	27229.1	50.00	Sequence
IAb	343	LRDHLDTHGHHIALD	HLDTHGHHI	0.0561	27241.5	50.00	Sequence
IAb	197	LVNPCDDALMKITHV	VNPCDDALM	0.0548	27642.3	50.00	Sequence
IAb	366	ELVQTRIVVLGDAWE	LVQTRIVVL	0.0547	27665.7	50.00	Sequence
IAb	123	AGRNPKLGYDNFDRH	AGRNPKLGY	0.0533	28079.1	50.00	Sequence
IAb	378	AWELLKFFNDDQYVI	WELLKFFND	0.0506	28930.9	50.00	Sequence
IAb	200	PCDDALMKITHVLRG	ALMKITHVL	0.0504	28992.9	50.00	Sequence
IAb	380	ELLKFFNDDQYVIDP	ELLKFFNDD	0.0490	29415.1	50.00	Sequence
IAb	342	RLRDHLDTHGHHIAL	LDTHGHHIA	0.0490	29422.4	50.00	Sequence
IAb	467	LELLGRDRSMQRLRA	LELLGRDRS	0.0486	29563.1	50.00	Sequence
IAb	381	LLKFFNDDQYVIDPK	LKFFNDDQY	0.0478	29814.3	50.00	Sequence
IAb	325	ALNAEHIRMLDVGDF	LNAEHIRML	0.0477	29829.8	50.00	Sequence
IAb	339	FTVRLRDHLDTHGHH	TVRLRDHLD	0.0471	30039.4	50.00	Sequence
IAb	333	MLDVGDFTVRLRDHL	DVGDFTVRL	0.0454	30592.4	50.00	Sequence
IAb	47	TDAQRDSEESYLALL	DAQRDSEES	0.0454	30593.4	50.00	Sequence
IAb	124	GRNPKLGYDNFDRHL	LGYDNFDRH	0.0451	30692.2	50.00	Sequence
IAb	290	IADDHDLFGLDEMVA	HDLFGLDEM	0.0449	30763.0	50.00	Sequence
IAb	157	LRMPDDDLAWNDLVR	DLAWNDLVR	0.0447	30828.3	50.00	Sequence
IAb	377	DAWELLKFFNDDQYV	WELLKFFND	0.0443	30949.6	50.00	Sequence
IAb	326	LNAEHIRMLDVGDFT	LNAEHIRML	0.0441	31035.5	50.00	Sequence
IAb	334	LDVGDFTVRLRDHLD	LDVGDFTVR	0.0436	31200.1	50.00	Sequence
IAb	250	LGEGTKKLSKRDPQS	KLSKRDPQS	0.0434	31256.9	50.00	Sequence
IAb	463	LFESLELLGRDRSMQ	FESLELLGR	0.0427	31490.8	50.00	Sequence
IAb	338	DFTVRLRDHLDTHGH	TVRLRDHLD	0.0423	31647.2	50.00	Sequence
IAb	466	SLELLGRDRSMQRLR	LELLGRDRS	0.0419	31760.0	50.00	Sequence
IAb	332	RMLDVGDFTVRLRDH	LDVGDFTVR	0.0417	31844.4	50.00	Sequence
IAb	331	IRMLDVGDFTVRLRD	LDVGDFTVR	0.0417	31852.3	50.00	Sequence
IAb	330	HIRMLDVGDFTVRLR	MLDVGDFTV	0.0411	32045.2	50.00	Sequence
IAb	46	DTDAQRDSEESYLAL	DAQRDSEES	0.0411	32051.4	50.00	Sequence
IAb	374	VLGDAWELLKFFNDD	VLGDAWELL	0.0410	32077.8	50.00	Sequence
IAb	336	VGDFTVRLRDHLDTH	GDFTVRLRD	0.0409	32133.0	50.00	Sequence
IAb	337	GDFTVRLRDHLDTHG	TVRLRDHLD	0.0407	32201.6	50.00	Sequence
IAb	199	NPCDDALMKITHVLR	ALMKITHVL	0.0404	32308.4	50.00	Sequence
IAb	376	GDAWELLKFFNDDQY	WELLKFFND	0.0403	32313.3	50.00	Sequence
IAb	335	DVGDFTVRLRDHLDT	VGDFTVRLR	0.0403	32330.4	50.00	Sequence

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         IAb  465  ESLELLGRDRSMQRL  LELLGRDRS       0.0393      32677.5               50.00     Sequence
         IAb  464  FESLELLGRDRSMQR  LELLGRDRS       0.0384      32989.4               50.00     Sequence
         IAb  375  LGDAWELLKFFNDDQ  WELLKFFND       0.0374      33377.5               50.00     Sequence
         IAb   45  EDTDAQRDSEESYLA  DAQRDSEES       0.0369      33535.3               50.00     Sequence
         IAb   44  IEDTDAQRDSEESYL  DAQRDSEES       0.0356      34032.5               50.00     Sequence
         IAb  156  RLRMPDDDLAWNDLV  RLRMPDDDL       0.0303      36012.2               50.00     Sequence
         IAb  329  EHIRMLDVGDFTVRL  MLDVGDFTV       0.0295      36325.3               50.00     Sequence
         IAb  328  AEHIRMLDVGDFTVR  AEHIRMLDV       0.0286      36711.7               50.00     Sequence
         IAb   43  RIEDTDAQRDSEESY  DAQRDSEES       0.0284      36769.4               50.00     Sequence
         IAb  327  NAEHIRMLDVGDFTV  AEHIRMLDV       0.0272      37265.6               50.00     Sequence
         IAb  288  WSIADDHDLFGLDEM  HDLFGLDEM       0.0268      37429.3               50.00     Sequence
         IAb  289  SIADDHDLFGLDEMV  HDLFGLDEM       0.0256      37891.8               50.00     Sequence
         IAb  287  GWSIADDHDLFGLDE  WSIADDHDL       0.0254      37993.2               50.00     Sequence
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Allele: IAb. Number of high binders 9. Number of weak binders 62. Number of peptides 476

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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         IAd  470  LGRDRSMQRLRAARQ  RSMQRLRAA       0.5321        158.0         WB     0.30     Sequence
         IAd  471  GRDRSMQRLRAARQL  RSMQRLRAA       0.5198        180.4         WB     0.40     Sequence
         IAd  405  GAAVLDAALAALTSV  AALAALTSV       0.5116        197.3         WB     0.40     Sequence
         IAd  406  AAVLDAALAALTSVT  AALAALTSV       0.5041        213.9         WB     0.40     Sequence
         IAd  407  AVLDAALAALTSVTD  AALAALTSV       0.4940        238.5         WB     0.80     Sequence
         IAd  472  RDRSMQRLRAARQLV  RSMQRLRAA       0.4903        248.4         WB     0.80     Sequence
         IAd  408  VLDAALAALTSVTDW  AALAALTSV       0.4877        255.5         WB     0.80     Sequence
         IAd  409  LDAALAALTSVTDWT  AALAALTSV       0.4873        256.6         WB     0.80     Sequence
         IAd  404  DGAAVLDAALAALTS  DAALAALTS       0.4859        260.4         WB     0.80     Sequence
         IAd  473  DRSMQRLRAARQLVG  RSMQRLRAA       0.4846        264.0         WB     0.80     Sequence
         IAd  469  LLGRDRSMQRLRAAR  RSMQRLRAA       0.4737        297.2         WB     0.80     Sequence
         IAd  220  STPRQLALHQALIRI  PRQLALHQA       0.4667        320.5         WB     0.80     Sequence
         IAd  226  ALHQALIRIGVAERI  QALIRIGVA       0.4625        335.4         WB     0.80     Sequence
         IAd  219  PSTPRQLALHQALIR  PRQLALHQA       0.4576        353.9         WB     1.00     Sequence
         IAd  221  TPRQLALHQALIRIG  PRQLALHQA       0.4564        358.3         WB     1.00     Sequence
         IAd  222  PRQLALHQALIRIGV  PRQLALHQA       0.4501        383.8         WB     1.00     Sequence
         IAd  218  LPSTPRQLALHQALI  PRQLALHQA       0.4499        384.3         WB     1.00     Sequence
         IAd  227  LHQALIRIGVAERIP  QALIRIGVA       0.4479        392.9         WB     2.00     Sequence
         IAd  410  DAALAALTSVTDWTA  AALAALTSV       0.4466        398.4         WB     2.00     Sequence
         IAd  217  LLPSTPRQLALHQAL  PRQLALHQA       0.4465        398.9         WB     2.00     Sequence
         IAd  474  RSMQRLRAARQLVGH  RSMQRLRAA       0.4362        445.8         WB     2.00     Sequence
         IAd  468  ELLGRDRSMQRLRAA  RSMQRLRAA       0.4218        521.0                2.00     Sequence
         IAd  225  LALHQALIRIGVAER  QALIRIGVA       0.4150        560.8                2.00     Sequence
         IAd  216  DLLPSTPRQLALHQA  PRQLALHQA       0.4091        597.9                2.00     Sequence
         IAd  403  PDGAAVLDAALAALT  AVLDAALAA       0.4067        613.9                2.00     Sequence
         IAd  441  LKPRKAFSPIRVAAT  RKAFSPIRV       0.4053        622.9                2.00     Sequence
         IAd   95  DVLARLLAAGEAYHA  LAAGEAYHA       0.4023        643.7                4.00     Sequence
         IAd   55  ESYLALLDALRWLGL  SYLALLDAL       0.4008        654.4                4.00     Sequence
         IAd   92  IYRDVLARLLAAGEA  RDVLARLLA       0.3967        683.6                4.00     Sequence
         IAd  442  KPRKAFSPIRVAATG  RKAFSPIRV       0.3967        683.7                4.00     Sequence
         IAd  411  AALAALTSVTDWTAP  AALAALTSV       0.3949        697.3                4.00     Sequence
         IAd   53  SEESYLALLDALRWL  SYLALLDAL       0.3921        718.7                4.00     Sequence
         IAd  228  HQALIRIGVAERIPK  QALIRIGVA       0.3917        721.8                4.00     Sequence
         IAd   54  EESYLALLDALRWLG  SYLALLDAL       0.3907        729.6                4.00     Sequence
         IAd  440  ALKPRKAFSPIRVAA  RKAFSPIRV       0.3894        740.3                4.00     Sequence
         IAd  439  LALKPRKAFSPIRVA  RKAFSPIRV       0.3859        768.7                4.00     Sequence
         IAd   52  DSEESYLALLDALRW  LALLDALRW       0.3859        768.9                4.00     Sequence
         IAd  136  RHLTDAQRAAYLAEG  RHLTDAQRA       0.3824        797.8                4.00     Sequence
         IAd   93  YRDVLARLLAAGEAY  ARLLAAGEA       0.3815        806.2                4.00     Sequence
         IAd  444  RKAFSPIRVAATGTT  IRVAATGTT       0.3810        810.0                4.00     Sequence
         IAd  350  HGHHIALDEAAFAAA  HHIALDEAA       0.3781        835.9                4.00     Sequence
         IAd  351  GHHIALDEAAFAAAA  HHIALDEAA       0.3763        852.1                4.00     Sequence
         IAd  224  QLALHQALIRIGVAE  QALIRIGVA       0.3748        866.6                4.00     Sequence
         IAd  223  RQLALHQALIRIGVA  QALIRIGVA       0.3742        871.9                4.00     Sequence
         IAd  135  DRHLTDAQRAAYLAE  RHLTDAQRA       0.3734        879.9                4.00     Sequence
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IAd	443	PRKAFSPIRVAATGT	RKAFSPIRV	0.3682	930.6	4.00	Sequence
IAd	96	VLARLLAAGEAYHAF	ARLLAAGEA	0.3647	966.9	4.00	Sequence
IAd	97	LARLLAAGEAYHAFS	ARLLAAGEA	0.3592	1026.4	4.00	Sequence
IAd	94	RDVLARLLAAGEAYH	ARLLAAGEA	0.3559	1062.6	4.00	Sequence
IAd	134	FDRHLTDAQRAAYLA	RHLTDAQRA	0.3548	1076.4	4.00	Sequence
IAd	51	RDSEESYLALLDALR	ESYLALLDA	0.3527	1101.2	8.00	Sequence
IAd	98	ARLLAAGEAYHAFST	ARLLAAGEA	0.3511	1120.3	8.00	Sequence
IAd	402	GPDGAAVLDAALAAL	AAVLDAALA	0.3505	1127.0	8.00	Sequence
IAd	56	SYLALLDALRWLGLD	SYLALLDAL	0.3433	1218.7	8.00	Sequence
IAd	401	LGPDGAAVLDAALAA	AAVLDAALA	0.3380	1289.8	8.00	Sequence
IAd	475	SMQRLRAARQLVGHA	MQRLRAARQ	0.3374	1298.3	8.00	Sequence
IAd	349	THGHHIALDEAAFAA	GHHIALDEA	0.3368	1306.9	8.00	Sequence
IAd	89	RAEIYRDVLARLLAA	RDVLARLLA	0.3365	1310.8	8.00	Sequence
IAd	86	QSQRAEIYRDVLARL	QRAEIYRDV	0.3355	1325.3	8.00	Sequence
IAd	90	AEIYRDVLARLLAAG	RDVLARLLA	0.3249	1486.9	8.00	Sequence
IAd	229	QALIRIGVAERIPKF	QALIRIGVA	0.3205	1559.6	8.00	Sequence
IAd	131	YDNFDRHLTDAQRAA	RHLTDAQRA	0.3196	1575.1	8.00	Sequence
IAd	367	LVQTRIVVLGDAWEL	VQTRIVVLG	0.3193	1580.5	8.00	Sequence
IAd	88	QRAEIYRDVLARLLA	RDVLARLLA	0.3187	1589.9	8.00	Sequence
IAd	87	SQRAEIYRDVLARLL	SQRAEIYRD	0.3186	1591.5	8.00	Sequence
IAd	130	GYDNFDRHLTDAQRA	RHLTDAQRA	0.3144	1665.7	8.00	Sequence
IAd	352	HHIALDEAAFAAAAE	HHIALDEAA	0.3141	1671.3	8.00	Sequence
IAd	91	EIYRDVLARLLAAGE	RDVLARLLA	0.3139	1675.0	8.00	Sequence
IAd	133	NFDRHLTDAQRAAYL	RHLTDAQRA	0.3120	1708.9	8.00	Sequence
IAd	132	DNFDRHLTDAQRAAY	RHLTDAQRA	0.3099	1748.4	8.00	Sequence
IAd	315	PARFDQKKADALNAE	QKKADALNA	0.3059	1826.1	8.00	Sequence
IAd	50	QRDSEESYLALLDAL	ESYLALLDA	0.3049	1846.8	8.00	Sequence
IAd	366	ELVQTRIVVLGDAWE	VQTRIVVLG	0.3029	1886.5	8.00	Sequence
IAd	318	FDQKKADALNAEHIR	QKKADALNA	0.3018	1908.7	8.00	Sequence
IAd	84	YRQSQRAEIYRDVLA	QRAEIYRDV	0.2997	1952.4	16.00	Sequence
IAd	317	RFDQKKADALNAEHI	QKKADALNA	0.2984	1979.6	16.00	Sequence
IAd	365	AELVQTRIVVLGDAW	VQTRIVVLG	0.2945	2066.9	16.00	Sequence
IAd	201	CDDALMKITHVLRGE	MKITHVLRG	0.2938	2080.6	16.00	Sequence
IAd	314	SPARFDQKKADALNA	QKKADALNA	0.2933	2093.4	16.00	Sequence
IAd	348	DTHGHHIALDEAAFA	GHHIALDEA	0.2913	2139.0	16.00	Sequence
IAd	200	PCDDALMKITHVLRG	MKITHVLRG	0.2888	2196.2	16.00	Sequence
IAd	359	AAFAAAAELVQTRIV	AAAAELVQT	0.2876	2227.1	16.00	Sequence
IAd	82	GPYRQSQRAEIYRDV	QRAEIYRDV	0.2850	2290.1	16.00	Sequence
IAd	358	EAAFAAAAELVQTRI	AAAAELVQT	0.2842	2309.2	16.00	Sequence
IAd	316	ARFDQKKADALNAEH	QKKADALNA	0.2838	2318.8	16.00	Sequence
IAd	425	PLIEAALKDALIEGL	LIEAALKDA	0.2837	2322.2	16.00	Sequence
IAd	203	DALMKITHVLRGEDL	MKITHVLRG	0.2829	2341.8	16.00	Sequence
IAd	83	PYRQSQRAEIYRDVL	QRAEIYRDV	0.2829	2342.6	16.00	Sequence
IAd	364	AAELVQTRIVVLGDA	VQTRIVVLG	0.2823	2357.0	16.00	Sequence
IAd	400	ELGPDGAAVLDAALA	AAVLDAALA	0.2823	2357.6	16.00	Sequence
IAd	426	LIEAALKDALIEGLA	LIEAALKDA	0.2806	2400.7	16.00	Sequence
IAd	319	DQKKADALNAEHIRM	QKKADALNA	0.2802	2410.8	16.00	Sequence
IAd	85	RQSQRAEIYRDVLAR	QRAEIYRDV	0.2796	2428.2	16.00	Sequence
IAd	297	FGLDEMVAAFDVADV	EMVAAFDVA	0.2795	2429.2	16.00	Sequence
IAd	438	GLALKPRKAFSPIRV	RKAFSPIRV	0.2795	2430.7	16.00	Sequence
IAd	368	VQTRIVVLGDAWELL	VQTRIVVLG	0.2747	2560.2	16.00	Sequence
IAd	353	HIALDEAAFAAAAEL	LDEAAFAAA	0.2742	2574.2	16.00	Sequence
IAd	423	TAPLIEAALKDALIE	LIEAALKDA	0.2691	2719.1	16.00	Sequence
IAd	357	DEAAFAAAAELVQTR	AAAAELVQT	0.2681	2749.4	16.00	Sequence
IAd	424	APLIEAALKDALIEG	LIEAALKDA	0.2673	2774.2	16.00	Sequence
IAd	360	AFAAAAELVQTRIVV	AAAAELVQT	0.2662	2805.3	16.00	Sequence
IAd	356	LDEAAFAAAAELVQT	AAAAELVQT	0.2637	2882.4	16.00	Sequence
IAd	300	DEMVAAFDVADVNSS	VAAFDVADV	0.2635	2890.8	16.00	Sequence
IAd	146	YLAEGRQPVVRLRMP	RQPVVRLRM	0.2630	2904.3	16.00	Sequence
IAd	202	DDALMKITHVLRGED	MKITHVLRG	0.2630	2905.4	16.00	Sequence
IAd	320	QKKADALNAEHIRML	QKKADALNA	0.2628	2910.6	16.00	Sequence
IAd	467	LELLGRDRSMQRLRA	DRSMQRLRA	0.2621	2934.0	16.00	Sequence
IAd	328	AEHIRMLDVGDFTVR	IRMLDVGDF	0.2611	2965.8	16.00	Sequence
IAd	445	KAFSPIRVAATGTTV	IRVAATGTT	0.2603	2990.8	16.00	Sequence
IAd	145	AYLAEGRQPVVRLRM	RQPVVRLRM	0.2602	2995.2	16.00	Sequence
IAd	361	FAAAAELVQTRIVVL	AAAAELVQT	0.2577	3077.5	16.00	Sequence

IAd	298	GLDEMVAAFDVADVN	VAAFDVADV	0.2568	3106.1	16.00	Sequence
IAd	420	TDWTAPLIEAALKDA	WTAPLIEAA	0.2563	3123.0	16.00	Sequence
IAd	431	LKDALIEGLALKPRK	LKDALIEGL	0.2538	3210.3	16.00	Sequence
IAd	301	EMVAAFDVADVNSSP	VAAFDVADV	0.2535	3219.7	16.00	Sequence
IAd	430	ALKDALIEGLALKPR	LKDALIEGL	0.2531	3235.0	16.00	Sequence
IAd	421	DWTAPLIEAALKDAL	WTAPLIEAA	0.2505	3324.8	16.00	Sequence
IAd	422	WTAPLIEAALKDALI	LIEAALKDA	0.2504	3330.8	16.00	Sequence
IAd	362	AAAAELVQTRIVVLG	AAAAELVQT	0.2502	3338.2	16.00	Sequence
IAd	355	ALDEAAFAAAAELVQ	LDEAAFAAA	0.2494	3365.9	16.00	Sequence
IAd	412	ALAALTSVTDWTAPL	LAALTSVTD	0.2487	3390.1	16.00	Sequence
IAd	327	NAEHIRMLDVGDFTV	IRMLDVGDF	0.2478	3423.8	16.00	Sequence
IAd	369	QTRIVVLGDAWELLK	TRIVVLGDA	0.2438	3574.6	32.00	Sequence
IAd	428	EAALKDALIEGLALK	LKDALIEGL	0.2426	3624.3	32.00	Sequence
IAd	148	AEGRQPVVRLRMPDD	RQPVVRLRM	0.2424	3630.5	32.00	Sequence
IAd	99	RLLAAGEAYHAFSTP	LAAGEAYHA	0.2413	3671.8	32.00	Sequence
IAd	81	YGPYRQSQRAEIYRD	QSQRAEIYR	0.2412	3677.9	32.00	Sequence
IAd	17	TPHVGLVRTALFNWA	PHVGLVRTA	0.2402	3716.8	32.00	Sequence
IAd	207	KITHVLRGEDLLPST	LRGEDLLPS	0.2400	3724.4	32.00	Sequence
IAd	354	IALDEAAFAAAAELV	LDEAAFAAA	0.2387	3777.5	32.00	Sequence
IAd	429	AALKDALIEGLALKP	LKDALIEGL	0.2386	3782.4	32.00	Sequence
IAd	329	EHIRMLDVGDFTVRL	IRMLDVGDF	0.2382	3797.9	32.00	Sequence
IAd	147	LAEGRQPVVRLRMPD	RQPVVRLRM	0.2371	3844.7	32.00	Sequence
IAd	299	LDEMVAAFDVADVNS	VAAFDVADV	0.2367	3862.7	32.00	Sequence
IAd	370	TRIVVLGDAWELLKF	TRIVVLGDA	0.2364	3873.5	32.00	Sequence
IAd	427	IEAALKDALIEGLAL	LKDALIEGL	0.2355	3913.5	32.00	Sequence
IAd	413	LAALTSVTDWTAPLI	LAALTSVTD	0.2335	3996.4	32.00	Sequence
IAd	432	KDALIEGLALKPRKA	IEGLALKPR	0.2316	4081.4	32.00	Sequence
IAd	363	AAAELVQTRIVVLGD	AAAELVQTR	0.2312	4096.2	32.00	Sequence
IAd	326	LNAEHIRMLDVGDFT	IRMLDVGDF	0.2312	4097.7	32.00	Sequence
IAd	57	YLALLDDALRWLGLDW	LALLDALRW	0.2311	4104.2	32.00	Sequence
IAd	18	PHVGLVRTALFNWAY	PHVGLVRTA	0.2305	4129.6	32.00	Sequence
IAd	240	IPKFAHLPTVLGEGT	PKFAHLPTV	0.2294	4180.4	32.00	Sequence
IAd	347	LDTHGHHIALDEAAF	GHHIALDEA	0.2273	4274.5	32.00	Sequence
IAd	137	HLTDAQRAAYLAEGR	DAQRAAYLA	0.2271	4283.2	32.00	Sequence
IAd	208	ITHVLRGEDLLPSTP	LRGEDLLPS	0.2271	4285.5	32.00	Sequence
IAd	149	EGRQPVVRLRMPDDD	RQPVVRLRM	0.2263	4321.9	32.00	Sequence
IAd	209	THVLRGEDLLPSTPR	LRGEDLLPS	0.2251	4377.2	32.00	Sequence
IAd	325	ALNAEHIRMLDVGDF	IRMLDVGDF	0.2240	4430.1	32.00	Sequence
IAd	206	MKITHVLRGEDLLPS	LRGEDLLPS	0.2210	4576.3	32.00	Sequence
IAd	346	HLDTHGHHIALDEAA	GHHIALDEA	0.2206	4596.5	32.00	Sequence
IAd	296	LFGLDEMVAAFDVAD	EMVAAFDVA	0.2202	4614.2	32.00	Sequence
IAd	165	AWNDLVRGPVTFAAG	VRGPVTFAA	0.2202	4616.0	32.00	Sequence
IAd	49	AQRDSEESYLALLDA	ESYLALLDA	0.2181	4721.4	32.00	Sequence
IAd	138	LTDAQRAAYLAEGRQ	QRAAYLAEG	0.2137	4952.0	32.00	Sequence
IAd	164	LAWNDLVRGPVTFAA	VRGPVTFAA	0.2131	4986.3	32.00	Sequence
IAd	199	NPCDDALMKITHVLR	LMKITHVLR	0.2117	5058.6	32.00	Sequence
IAd	433	DALIEGLALKPRKAF	IEGLALKPR	0.2106	5119.3	32.00	Sequence
IAd	239	RIPKFAHLPTVLGEG	PKFAHLPTV	0.2104	5130.5	32.00	Sequence
IAd	241	PKFAHLPTVLGEGTK	PKFAHLPTV	0.2081	5259.6	32.00	Sequence
IAd	212	LRGEDLLPSTPRQLA	LRGEDLLPS	0.2076	5288.7	32.00	Sequence
IAd	447	FSPIRVAATGTTVSP	IRVAATGTT	0.2065	5352.3	32.00	Sequence
IAd	101	LAAGEAYHAFSTPEE	LAAGEAYHA	0.2064	5360.9	32.00	Sequence
IAd	58	LALLDALRWLGLDWD	LALLDALRW	0.2047	5460.3	32.00	Sequence
IAd	210	HVLRGEDLLPSTPRQ	LRGEDLLPS	0.2046	5463.7	32.00	Sequence
IAd	211	VLRGEDLLPSTPRQL	LRGEDLLPS	0.2035	5531.7	32.00	Sequence
IAd	13	SPTGTPHVGLVRTAL	PHVGLVRTA	0.2029	5568.8	32.00	Sequence
IAd	139	TDAQRAAYLAEGRQP	AQRAAYLAE	0.2025	5592.7	32.00	Sequence
IAd	144	AAYLAEGRQPVVRLR	GRQPVVRLR	0.2024	5594.8	32.00	Sequence
IAd	100	LLAAGEAYHAFSTPE	LAAGEAYHA	0.2011	5676.0	32.00	Sequence
IAd	23	VRTALFNWAYARHTG	VRTALFNWA	0.2006	5708.5	32.00	Sequence
IAd	204	ALMKITHVLRGEDLL	MKITHVLRG	0.2005	5709.9	32.00	Sequence
IAd	113	PEEVEARHVAAGRNP	ARHVAAGRN	0.2000	5745.9	32.00	Sequence
IAd	16	GTPHVGLVRTALFNW	PHVGLVRTA	0.1999	5752.3	32.00	Sequence
IAd	12	PSPTGTPHVGLVRTA	PHVGLVRTA	0.1995	5777.0	32.00	Sequence
IAd	465	ESLELLGRDRSMQRL	GRDRSMQRL	0.1969	5936.6	32.00	Sequence
IAd	14	PTGTPHVGLVRTALF	PHVGLVRTA	0.1969	5937.0	32.00	Sequence

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IAd  166  WNDLVRGPVTFAAGS  VRGPVTFAA         0.1952        6048.5                 32.00     Sequence
IAd   15  TGTPHVGLVRTALFN  PHVGLVRTA         0.1946        6087.0                 32.00     Sequence
IAd  302  MVAAFDVADVNSSPA  VAAFDVADV         0.1943        6105.8                 32.00     Sequence
IAd  414  AALTSVTDWTAPLIE  LTSVTDWTA         0.1934        6169.1                 32.00     Sequence
IAd  295  DLFGLDEMVAAFDVA  FGLDEMVAA         0.1930        6192.2                 32.00     Sequence
IAd   22  LVRTALFNWAYARHT  VRTALFNWA         0.1928        6206.6                 32.00     Sequence
IAd  275  IPEGLLNYLALLGWS  NYLALLGWS         0.1918        6277.9                 32.00     Sequence
IAd  140  DAQRAAYLAEGRQPV  QRAAYLAEG         0.1915        6293.5                 32.00     Sequence
IAd  114  EEVEARHVAAGRNPK  ARHVAAGRN         0.1911        6326.4                 32.00     Sequence
IAd  150  GRQPVVRLRMPDDDL  RQPVVRLRM         0.1905        6366.6                 32.00     Sequence
IAd  276  PEGLLNYLALLGWSI  NYLALLGWS         0.1902        6383.1                 32.00     Sequence
IAd  176  FAAGSVPDFALTRAS  VPDFALTRA         0.1893        6446.6                 32.00     Sequence
IAd  446  AFSPIRVAATGTTVS  IRVAATGTT         0.1882        6528.1                 32.00     Sequence
IAd  399  KELGPDGAAVLDAAL  PDGAAVLDA         0.1872        6597.0                 32.00     Sequence
IAd  230  ALIRIGVAERIPKFA  IRIGVAERI         0.1850        6758.5                 32.00     Sequence
IAd  466  SLELLGRDRSMQRLR  GRDRSMQRL         0.1842        6813.2                 32.00     Sequence
IAd  115  EVEARHVAAGRNPKL  ARHVAAGRN         0.1842        6815.5                 32.00     Sequence
IAd  112  TPEEVEARHVAAGRN  ARHVAAGRN         0.1837        6852.8                 32.00     Sequence
IAd  303  VAAFDVADVNSSPAR  VAAFDVADV         0.1829        6908.9                 32.00     Sequence
IAd  419  VTDWTAPLIEAALKD  WTAPLIEAA         0.1821        6971.4                 32.00     Sequence
IAd  393  DPKAAAKELGPDGAA  AKELGPDGA         0.1819        6987.0                 32.00     Sequence
IAd  116  VEARHVAAGRNPKLG  ARHVAAGRN         0.1815        7012.8                 32.00     Sequence
IAd  175  TFAAGSVPDFALTRA  VPDFALTRA         0.1798        7149.6                 32.00     Sequence
IAd  238  ERIPKFAHLPTVLGE  PKFAHLPTV         0.1791        7197.4                 32.00     Sequence
IAd  448  SPIRVAATGTTVSPP  IRVAATGTT         0.1781        7279.5                 50.00     Sequence
IAd  330  HIRMLDVGDFTVRLR  IRMLDVGDF         0.1771        7355.0                 50.00     Sequence
IAd  434  ALIEGLALKPRKAFS  IEGLALKPR         0.1765        7409.3                 50.00     Sequence
IAd  277  EGLLNYLALLGWSIA  NYLALLGWS         0.1760        7444.2                 50.00     Sequence
IAd  436  IEGLALKPRKAFSPI  IEGLALKPR         0.1760        7449.5                 50.00     Sequence
IAd  415  ALTSVTDWTAPLIEA  LTSVTDWTA         0.1758        7463.3                 50.00     Sequence
IAd  170  VRGPVTFAAGSVPDF  VRGPVTFAA         0.1752        7510.9                 50.00     Sequence
IAd  231  LIRIGVAERIPKFAH  IRIGVAERI         0.1752        7511.1                 50.00     Sequence
IAd  182  PDFALTRASGDPLYT  RASGDPLYT         0.1749        7537.5                 50.00     Sequence
IAd  181  VPDFALTRASGDPLY  VPDFALTRA         0.1737        7631.1                 50.00     Sequence
IAd  416  LTSVTDWTAPLIEAA  LTSVTDWTA         0.1727        7718.3                 50.00     Sequence
IAd  237  AERIPKFAHLPTVLG  PKFAHLPTV         0.1726        7722.7                 50.00     Sequence
IAd  331  IRMLDVGDFTVRLRD  IRMLDVGDF         0.1720        7772.4                 50.00     Sequence
IAd  279  LLNYLALLGWSIADD  NYLALLGWS         0.1712        7845.3                 50.00     Sequence
IAd  394  PKAAAKELGPDGAAV  PKAAAKELG         0.1709        7871.7                 50.00     Sequence
IAd  243  FAHLPTVLGEGTKKL  FAHLPTVLG         0.1697        7969.0                 50.00     Sequence
IAd  280  LNYLALLGWSIADDH  YLALLGWSI         0.1697        7973.7                 50.00     Sequence
IAd  323  ADALNAEHIRMLDVG  EHIRMLDVG         0.1689        8040.6                 50.00     Sequence
IAd    0  VTATETVRVRFCPSP  VTATETVRV         0.1688        8053.4                 50.00     Sequence
IAd  242  KFAHLPTVLGEGTKK  AHLPTVLGE         0.1685        8076.5                 50.00     Sequence
IAd  274  FIPEGLLNYLALLGW  PEGLLNYLA         0.1673        8184.7                 50.00     Sequence
IAd  371  RIVVLGDAWELLKFF  VVLGDAWEL         0.1673        8184.8                 50.00     Sequence
IAd  392  IDPKAAAKELGPDGA  IDPKAAAKE         0.1672        8187.4                 50.00     Sequence
IAd  278  GLLNYLALLGWSIAD  LNYLALLGW         0.1672        8191.3                 50.00     Sequence
IAd   24  RTALFNWAYARHTGG  FNWAYARHT         0.1666        8241.0                 50.00     Sequence
IAd  324  DALNAEHIRMLDVGD  AEHIRMLDV         0.1654        8352.9                 50.00     Sequence
IAd  141  AQRAAYLAEGRQPVV  QRAAYLAEG         0.1650        8387.6                 50.00     Sequence
IAd  449  PIRVAATGTTVSPPL  IRVAATGTT         0.1648        8405.0                 50.00     Sequence
IAd  167  NDLVRGPVTFAAGSV  VRGPVTFAA         0.1647        8418.9                 50.00     Sequence
IAd  142  QRAAYLAEGRQPVVR  QRAAYLAEG         0.1646        8427.3                 50.00     Sequence
IAd  180  SVPDFALTRASGDPL  VPDFALTRA         0.1645        8436.5                 50.00     Sequence
IAd  198  VNPCDDALMKITHVL  PCDDALMKI         0.1640        8483.1                 50.00     Sequence
IAd  168  DLVRGPVTFAAGSVP  VRGPVTFAA         0.1636        8512.4                 50.00     Sequence
IAd  386  NDDQYVIDPKAAAKE  QYVIDPKAA         0.1632        8550.8                 50.00     Sequence
IAd  387  DDQYVIDPKAAAKEL  QYVIDPKAA         0.1631        8558.9                 50.00     Sequence
IAd  205  LMKITHVLRGEDLLP  MKITHVLRG         0.1607        8791.1                 50.00     Sequence
IAd   48  DAQRDSEESYLALLD  RDSEESYLA         0.1601        8844.4                 50.00     Sequence
IAd  435  LIEGLALKPRKAFSP  IEGLALKPR         0.1597        8880.0                 50.00     Sequence
IAd   47  TDAQRDSEESYLALL  RDSEESYLA         0.1595        8903.1                 50.00     Sequence
IAd  169  LVRGPVTFAAGSVPD  VRGPVTFAA         0.1586        8990.9                 50.00     Sequence
IAd   21  GLVRTALFNWAYARH  VRTALFNWA         0.1578        9065.7                 50.00     Sequence
IAd  235  GVAERIPKFAHLPTV  IPKFAHLPT         0.1576        9090.9                 50.00     Sequence
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IAd	395	KAAAKELGPDGAAVL	AKELGPDGA	0.1575	9098.8	50.00	Sequence
IAd	388	DQYVIDPKAAAKELG	QYVIDPKAA	0.1573	9113.6	50.00	Sequence
IAd	450	IRVAATGTTVSPPLF	IRVAATGTT	0.1569	9154.1	50.00	Sequence
IAd	464	FESLELLGRDRSMQR	FESLELLGR	0.1569	9155.1	50.00	Sequence
IAd	80	PYGPYRQSQRAEIYR	YRQSQRAEI	0.1568	9169.8	50.00	Sequence
IAd	117	EARHVAAGRNPKLGY	ARHVAAGRN	0.1563	9218.3	50.00	Sequence
IAd	177	AAGSVPDFALTRASG	VPDFALTRA	0.1558	9263.8	50.00	Sequence
IAd	232	IRIGVAERIPKFAHL	IRIGVAERI	0.1555	9297.3	50.00	Sequence
IAd	398	AKELGPDGAAVLDAA	PDGAAVLDA	0.1548	9367.5	50.00	Sequence
IAd	183	DFALTRASGDPLYTL	RASGDPLYT	0.1543	9420.0	50.00	Sequence
IAd	418	SVTDWTAPLIEAALK	WTAPLIEAA	0.1541	9441.3	50.00	Sequence
IAd	46	DTDAQRDSEESYLAL	RDSEESYLA	0.1537	9476.9	50.00	Sequence
IAd	437	EGLALKPRKAFSPIR	GLALKPRKA	0.1536	9486.4	50.00	Sequence
IAd	45	EDTDAQRDSEESYLA	RDSEESYLA	0.1514	9719.0	50.00	Sequence
IAd	108	HAFSTPEEVEARHVA	PEEVEARHV	0.1514	9720.0	50.00	Sequence
IAd	236	VAERIPKFAHLPTVL	IPKFAHLPT	0.1504	9818.9	50.00	Sequence
IAd	417	TSVTDWTAPLIEAAL	WTAPLIEAA	0.1489	9983.1	50.00	Sequence
IAd	178	AGSVPDFALTRASGD	VPDFALTRA	0.1485	10029.1	50.00	Sequence
IAd	19	HVGLVRTALFNWAYA	VRTALFNWA	0.1480	10081.8	50.00	Sequence
IAd	376	GDAWELLKFFNDDQY	GDAWELLKF	0.1478	10104.8	50.00	Sequence
IAd	294	HDLFGLDEMVAAFDV	FGLDEMVAA	0.1453	10381.3	50.00	Sequence
IAd	107	YHAFSTPEEVEARHV	FSTPEEVEA	0.1449	10430.6	50.00	Sequence
IAd	396	AAAKELGPDGAAVLD	AKELGPDGA	0.1439	10535.0	50.00	Sequence
IAd	163	DLAWNDLVRGPVTFA	LAWNDLVRG	0.1432	10617.4	50.00	Sequence
IAd	143	RAAYLAEGRQPVVRL	RAAYLAEGR	0.1429	10653.7	50.00	Sequence
IAd	215	EDLLPSTPRQLALHQ	TPRQLALHQ	0.1417	10792.4	50.00	Sequence
IAd	20	VGLVRTALFNWAYAR	VRTALFNWA	0.1415	10816.0	50.00	Sequence
IAd	184	FALTRASGDPLYTLV	RASGDPLYT	0.1407	10914.0	50.00	Sequence
IAd	345	DHLDTHGHHIALDEA	GHHIALDEA	0.1403	10956.5	50.00	Sequence
IAd	322	KADALNAEHIRMLDV	AEHIRMLDV	0.1393	11081.0	50.00	Sequence
IAd	385	FNDDQYVIDPKAAAK	QYVIDPKAA	0.1390	11110.4	50.00	Sequence
IAd	384	FFNDDQYVIDPKAAA	QYVIDPKAA	0.1388	11134.4	50.00	Sequence
IAd	281	NYLALLGWSIADDHD	NYLALLGWS	0.1387	11147.6	50.00	Sequence
IAd	389	QYVIDPKAAAKELGP	QYVIDPKAA	0.1384	11180.1	50.00	Sequence
IAd	375	LGDAWELLKFFNDDQ	GDAWELLKF	0.1383	11192.9	50.00	Sequence
IAd	185	ALTRASGDPLYTLVN	RASGDPLYT	0.1347	11637.6	50.00	Sequence
IAd	179	GSVPDFALTRASGDP	VPDFALTRA	0.1338	11753.6	50.00	Sequence
IAd	197	LVNPCDDALMKITHV	PCDDALMKI	0.1334	11804.4	50.00	Sequence
IAd	244	AHLPTVLGEGTKKLS	AHLPTVLGE	0.1332	11831.9	50.00	Sequence
IAd	373	VVLGDAWELLKFFND	GDAWELLKF	0.1331	11846.7	50.00	Sequence
IAd	109	AFSTPEEVEARHVAA	FSTPEEVEA	0.1317	12020.0	50.00	Sequence
IAd	186	LTRASGDPLYTLVNP	RASGDPLYT	0.1311	12110.3	50.00	Sequence
IAd	105	EAYHAFSTPEEVEAR	FSTPEEVEA	0.1310	12121.3	50.00	Sequence
IAd	234	IGVAERIPKFAHLPT	GVAERIPKF	0.1300	12242.9	50.00	Sequence
IAd	374	VLGDAWELLKFFNDD	GDAWELLKF	0.1288	12410.1	50.00	Sequence
IAd	161	DDDLAWNDLVRGPVT	LAWNDLVRG	0.1275	12590.0	50.00	Sequence
IAd	391	VIDPKAAAKELGPDG	PKAAAKELG	0.1252	12906.7	50.00	Sequence
IAd	111	STPEEVEARHVAAGR	PEEVEARHV	0.1249	12940.1	50.00	Sequence
IAd	390	YVIDPKAAAKELGPD	PKAAAKELG	0.1219	13365.1	50.00	Sequence
IAd	273	GFIPEGLLNYLALLG	PEGLLNYLA	0.1214	13436.8	50.00	Sequence
IAd	162	DDLAWNDLVRGPVTF	LAWNDLVRG	0.1210	13507.3	50.00	Sequence
IAd	160	PDDDLAWNDLVRGPV	LAWNDLVRG	0.1209	13514.5	50.00	Sequence
IAd	304	AAFDVADVNSSPARF	FDVADVNSS	0.1208	13531.3	50.00	Sequence
IAd	383	KFFNDDQYVIDPKAA	QYVIDPKAA	0.1197	13688.9	50.00	Sequence
IAd	270	RDRGFIPEGLLNYLA	PEGLLNYLA	0.1191	13774.9	50.00	Sequence
IAd	282	YLALLGWSIADDHDL	YLALLGWSI	0.1183	13904.1	50.00	Sequence
IAd	451	RVAATGTTVSPPLFE	VAATGTTVS	0.1181	13925.3	50.00	Sequence
IAd	104	GEAYHAFSTPEEVEA	FSTPEEVEA	0.1175	14028.3	50.00	Sequence
IAd	151	RQPVVRLRMPDDDLA	RQPVVRLRM	0.1173	14050.0	50.00	Sequence
IAd	110	FSTPEEVEARHVAAG	PEEVEARHV	0.1167	14152.0	50.00	Sequence
IAd	28	FNWAYARHTGGTFVF	RHTGGTFVF	0.1154	14347.3	50.00	Sequence
IAd	372	IVVLGDAWELLKFFN	GDAWELLKF	0.1148	14442.1	50.00	Sequence
IAd	1	TATETVRVRFCPSPT	TATETVRVR	0.1146	14469.8	50.00	Sequence
IAd	397	AAKELGPDGAAVLDA	PDGAAVLDA	0.1145	14482.5	50.00	Sequence
IAd	321	KKADALNAEHIRMLD	ADALNAEHI	0.1139	14583.6	50.00	Sequence
IAd	25	TALFNWAYARHTGGT	FNWAYARHT	0.1109	15055.6	50.00	Sequence

IAd	106	AYHAFSTPEEVEARH	FSTPEEVEA	0.1102	15168.0	50.00	Sequence
IAd	152	QPVVRLRMPDDDLAW	QPVVRLRMP	0.1085	15456.7	50.00	Sequence
IAd	118	ARHVAAGRNPKLGYD	ARHVAAGRN	0.1083	15487.0	50.00	Sequence
IAd	288	WSIADDHDLFGLDEM	WSIADDHDL	0.1081	15522.3	50.00	Sequence
IAd	293	DHDLFGLDEMVAAFD	FGLDEMVAA	0.1072	15670.8	50.00	Sequence
IAd	286	LGWSIADDHDLFGLD	WSIADDHDL	0.1062	15849.0	50.00	Sequence
IAd	61	LDALRWLGLDWDEGP	LDALRWLGL	0.1057	15932.0	50.00	Sequence
IAd	158	RMPDDDLAWNDLVRG	LAWNDLVRG	0.1053	15997.8	50.00	Sequence
IAd	11	CPSPTGTPHVGLVRT	TPHVGLVRT	0.1050	16055.7	50.00	Sequence
IAd	264	SNLFAHRDRGFIPEG	AHRDRGFIP	0.1034	16330.6	50.00	Sequence
IAd	305	AFDVADVNSSPARFD	VADVNSSPA	0.1029	16415.1	50.00	Sequence
IAd	257	LSKRDPQSNLFAHRD	RDPQSNLFA	0.1028	16435.9	50.00	Sequence
IAd	266	LFAHRDRGFIPEGLL	HRDRGFIPE	0.1028	16446.8	50.00	Sequence
IAd	265	NLFAHRDRGFIPEGL	AHRDRGFIP	0.1021	16559.8	50.00	Sequence
IAd	60	LLDALRWLGLDWDEG	LDALRWLGL	0.1019	16608.1	50.00	Sequence
IAd	155	VRLRMPDDDLAWNDL	LRMPDDDLA	0.1012	16725.8	50.00	Sequence
IAd	285	LLGWSIADDHDLFGL	WSIADDHDL	0.1007	16821.1	50.00	Sequence
IAd	306	FDVADVNSSPARFDQ	VADVNSSPA	0.1006	16837.1	50.00	Sequence
IAd	154	VVRLRMPDDDLAWND	LRMPDDDLA	0.1003	16883.5	50.00	Sequence
IAd	268	AHRDRGFIPEGLLNY	HRDRGFIPE	0.1000	16937.2	50.00	Sequence
IAd	272	RGFIPEGLLNYLALL	PEGLLNYLA	0.1000	16940.5	50.00	Sequence
IAd	271	DRGFIPEGLLNYLAL	PEGLLNYLA	0.0996	17026.9	50.00	Sequence
IAd	267	FAHRDRGFIPEGLLN	HRDRGFIPE	0.0993	17076.0	50.00	Sequence
IAd	258	SKRDPQSNLFAHRDR	RDPQSNLFA	0.0991	17110.4	50.00	Sequence
IAd	195	YTLVNPCDDALMKIT	PCDDALMKI	0.0989	17142.1	50.00	Sequence
IAd	196	TLVNPCDDALMKITH	PCDDALMKI	0.0984	17248.5	50.00	Sequence
IAd	313	SSPARFDQKKADALN	PARFDQKKA	0.0982	17285.5	50.00	Sequence
IAd	159	MPDDDLAWNDLVRGP	LAWNDLVRG	0.0980	17319.9	50.00	Sequence
IAd	187	TRASGDPLYTLVNPC	RASGDPLYT	0.0973	17455.9	50.00	Sequence
IAd	79	GPYGPYRQSQRAEIY	YRQSQRAEI	0.0973	17456.3	50.00	Sequence
IAd	153	PVVRLRMPDDDLAWN	LRMPDDDLA	0.0970	17506.8	50.00	Sequence
IAd	291	ADDHDLFGLDEMVAA	FGLDEMVAA	0.0970	17512.7	50.00	Sequence
IAd	156	RLRMPDDDLAWNDLV	LRMPDDDLA	0.0966	17590.2	50.00	Sequence
IAd	30	WAYARHTGGTFVFRI	RHTGGTFVF	0.0956	17775.4	50.00	Sequence
IAd	233	RIGVAERIPKFAHLP	IGVAERIPK	0.0950	17894.1	50.00	Sequence
IAd	245	HLPTVLGEGTKKLSK	HLPTVLGEG	0.0944	18012.0	50.00	Sequence
IAd	171	RGPVTFAAGSVPDFA	TFAAGSVPD	0.0938	18125.3	50.00	Sequence
IAd	283	LALLGWSIADDHDLF	LALLGWSIA	0.0935	18187.6	50.00	Sequence
IAd	59	ALLDALRWLGLDWDE	LDALRWLGL	0.0931	18251.3	50.00	Sequence
IAd	259	KRDPQSNLFAHRDRG	RDPQSNLFA	0.0930	18277.2	50.00	Sequence
IAd	102	AAGEAYHAFSTPEEV	AAGEAYHAF	0.0927	18345.1	50.00	Sequence
IAd	292	DDHDLFGLDEMVAAF	FGLDEMVAA	0.0918	18526.1	50.00	Sequence
IAd	29	NWAYARHTGGTFVFR	RHTGGTFVF	0.0917	18546.7	50.00	Sequence
IAd	256	KLSKRDPQSNLFAHR	RDPQSNLFA	0.0916	18560.8	50.00	Sequence
IAd	157	LRMPDDDLAWNDLVR	LRMPDDDLA	0.0894	18997.0	50.00	Sequence
IAd	2	ATETVRVRFCPSPTG	RVRFCPSPT	0.0889	19114.3	50.00	Sequence
IAd	269	HRDRGFIPEGLLNYL	HRDRGFIPE	0.0888	19131.5	50.00	Sequence
IAd	287	GWSIADDHDLFGLDE	WSIADDHDL	0.0886	19162.1	50.00	Sequence
IAd	26	ALFNWAYARHTGGTF	FNWAYARHT	0.0871	19491.5	50.00	Sequence
IAd	31	AYARHTGGTFVFRIE	RHTGGTFVF	0.0863	19647.1	50.00	Sequence
IAd	103	AGEAYHAFSTPEEVE	EAYHAFSTP	0.0857	19792.2	50.00	Sequence
IAd	461	PPLFESLELLGRDRS	FESLELLGR	0.0856	19803.3	50.00	Sequence
IAd	260	RDPQSNLFAHRDRGF	RDPQSNLFA	0.0850	19943.1	50.00	Sequence
IAd	462	PLFESLELLGRDRSM	FESLELLGR	0.0833	20297.7	50.00	Sequence
IAd	174	VTFAAGSVPDFALTR	FAAGSVPDF	0.0833	20304.1	50.00	Sequence
IAd	213	RGEDLLPSTPRQLAL	RGEDLLPST	0.0819	20612.4	50.00	Sequence
IAd	188	RASGDPLYTLVNPCD	RASGDPLYT	0.0809	20844.3	50.00	Sequence
IAd	27	LFNWAYARHTGGTFV	FNWAYARHT	0.0808	20867.3	50.00	Sequence
IAd	62	DALRWLGLDWDEGPE	WLGLDWDEG	0.0806	20901.0	50.00	Sequence
IAd	463	LFESLELLGRDRSMQ	FESLELLGR	0.0803	20962.4	50.00	Sequence
IAd	214	GEDLLPSTPRQLALH	LPSTPRQLA	0.0792	21231.7	50.00	Sequence
IAd	452	VAATGTTVSPPLFES	VAATGTTVS	0.0790	21268.3	50.00	Sequence
IAd	459	VSPPLFESLELLGRD	FESLELLGR	0.0788	21319.2	50.00	Sequence
IAd	453	AATGTTVSPPLFESL	AATGTTVSP	0.0785	21373.7	50.00	Sequence
IAd	44	IEDTDAQRDSEESYL	IEDTDAQRD	0.0781	21481.1	50.00	Sequence
IAd	312	NSSPARFDQKKADAL	PARFDQKKA	0.0776	21586.4	50.00	Sequence

IAd	377	DAWELLKFFNDDQYV	WELLKFFND	0.0774	21641.3	50.00	Sequence
IAd	460	SPPLFESLELLGRDR	FESLELLGR	0.0772	21699.0	50.00	Sequence
IAd	255	KKLSKRDPQSNLFAH	RDPQSNLFA	0.0765	21852.4	50.00	Sequence
IAd	32	YARHTGGTFVFRIED	RHTGGTFVF	0.0754	22112.8	50.00	Sequence
IAd	458	TVSPPLFESLELLGR	FESLELLGR	0.0742	22390.9	50.00	Sequence
IAd	42	FRIEDTDAQRDSEES	FRIEDTDAQ	0.0741	22436.0	50.00	Sequence
IAd	284	ALLGWSIADDHDLFG	WSIADDHDL	0.0740	22446.4	50.00	Sequence
IAd	63	ALRWLGLDWDEGPEV	WLGLDWDEG	0.0726	22790.5	50.00	Sequence
IAd	338	DFTVRLRDHLDTHGH	RDHLDTHGH	0.0717	23020.8	50.00	Sequence
IAd	173	PVTFAAGSVPDFALT	FAAGSVPDF	0.0705	23327.2	50.00	Sequence
IAd	339	FTVRLRDHLDTHGHH	RDHLDTHGH	0.0688	23762.5	50.00	Sequence
IAd	261	DPQSNLFAHRDRGFI	DPQSNLFAH	0.0682	23912.1	50.00	Sequence
IAd	172	GPVTFAAGSVPDFAL	FAAGSVPDF	0.0675	24078.3	50.00	Sequence
IAd	43	RIEDTDAQRDSEESY	IEDTDAQRD	0.0667	24302.3	50.00	Sequence
IAd	454	ATGTTVSPPLFESLE	ATGTTVSPP	0.0666	24326.0	50.00	Sequence
IAd	3	TETVRVRFCPSPTGT	RVRFCPSPT	0.0662	24440.5	50.00	Sequence
IAd	41	VFRIEDTDAQRDSEE	FRIEDTDAQ	0.0660	24485.5	50.00	Sequence
IAd	39	TFVFRIEDTDAQRDS	FRIEDTDAQ	0.0658	24524.7	50.00	Sequence
IAd	254	TKKLSKRDPQSNLFA	RDPQSNLFA	0.0652	24692.7	50.00	Sequence
IAd	341	VRLRDHLDTHGHHIA	RDHLDTHGH	0.0643	24941.6	50.00	Sequence
IAd	38	GTFVFRIEDTDAQRD	VFRIEDTDA	0.0636	25123.7	50.00	Sequence
IAd	64	LRWLGLDWDEGPEVG	WLGLDWDEG	0.0634	25177.3	50.00	Sequence
IAd	40	FVFRIEDTDAQRDSE	FRIEDTDAQ	0.0633	25202.3	50.00	Sequence
IAd	332	RMLDVGDFTVRLRDH	MLDVGDFTV	0.0632	25245.7	50.00	Sequence
IAd	340	TVRLRDHLDTHGHHI	RDHLDTHGH	0.0625	25420.0	50.00	Sequence
IAd	382	LKFFNDDQYVIDPKA	DQYVIDPKA	0.0615	25695.2	50.00	Sequence
IAd	308	VADVNSSPARFDQKK	VADVNSSPA	0.0609	25874.9	50.00	Sequence
IAd	311	VNSSPARFDQKKADA	PARFDQKKA	0.0606	25962.1	50.00	Sequence
IAd	5	TVRVRFCPSPTGTPH	RVRFCPSPT	0.0603	26026.5	50.00	Sequence
IAd	307	DVADVNSSPARFDQK	VADVNSSPA	0.0599	26138.5	50.00	Sequence
IAd	119	RHVAAGRNPKLGYDN	RHVAAGRNP	0.0590	26395.1	50.00	Sequence
IAd	4	ETVRVRFCPSPTGTP	RVRFCPSPT	0.0579	26731.1	50.00	Sequence
IAd	309	ADVNSSPARFDQKKA	PARFDQKKA	0.0578	26763.2	50.00	Sequence
IAd	246	LPTVLGEGTKKLSKR	EGTKKLSKR	0.0574	26878.2	50.00	Sequence
IAd	310	DVNSSPARFDQKKAD	PARFDQKKA	0.0572	26930.0	50.00	Sequence
IAd	290	IADDHDLFGLDEMVA	LFGLDEMVA	0.0559	27319.7	50.00	Sequence
IAd	252	EGTKKLSKRDPQSNL	LSKRDPQSN	0.0558	27349.3	50.00	Sequence
IAd	78	GGPYGPYRQSQRAEI	YRQSQRAEI	0.0551	27542.3	50.00	Sequence
IAd	262	PQSNLFAHRDRGFIP	QSNLFAHRD	0.0547	27677.0	50.00	Sequence
IAd	69	LDWDEGPEVGGPYGP	LDWDEGPEV	0.0545	27726.5	50.00	Sequence
IAd	249	VLGEGTKKLSKRDPQ	LGEGTKKLS	0.0535	28032.1	50.00	Sequence
IAd	66	WLGLDWDEGPEVGGP	WLGLDWDEG	0.0529	28194.8	50.00	Sequence
IAd	333	MLDVGDFTVRLRDHL	MLDVGDFTV	0.0521	28444.2	50.00	Sequence
IAd	65	RWLGLDWDEGPEVGG	WDEGPEVGG	0.0514	28680.3	50.00	Sequence
IAd	193	PLYTLVNPCDDALMK	PLYTLVNPC	0.0513	28704.5	50.00	Sequence
IAd	251	GEGTKKLSKRDPQSN	LSKRDPQSN	0.0511	28769.8	50.00	Sequence
IAd	70	DWDEGPEVGGPYGPY	WDEGPEVGG	0.0510	28796.6	50.00	Sequence
IAd	7	RVRFCPSPTGTPHVG	RVRFCPSPT	0.0503	29012.4	50.00	Sequence
IAd	335	DVGDFTVRLRDHLDT	VGDFTVRLR	0.0499	29136.3	50.00	Sequence
IAd	6	VRVRFCPSPTGTPHV	RVRFCPSPT	0.0498	29173.6	50.00	Sequence
IAd	68	GLDWDEGPEVGGPYG	WDEGPEVGG	0.0497	29187.8	50.00	Sequence
IAd	37	GGTFVFRIEDTDAQR	VFRIEDTDA	0.0496	29228.8	50.00	Sequence
IAd	36	TGGTFVFRIEDTDAQ	FRIEDTDAQ	0.0493	29341.0	50.00	Sequence
IAd	342	RLRDHLDTHGHHIAL	RDHLDTHGH	0.0482	29692.6	50.00	Sequence
IAd	336	VGDFTVRLRDHLDTH	VRLRDHLDT	0.0473	29982.9	50.00	Sequence
IAd	253	GTKKLSKRDPQSNLF	LSKRDPQSN	0.0467	30175.2	50.00	Sequence
IAd	378	AWELLKFFNDDQYVI	WELLKFFND	0.0466	30202.7	50.00	Sequence
IAd	263	QSNLFAHRDRGFIPE	QSNLFAHRD	0.0463	30296.9	50.00	Sequence
IAd	250	LGEGTKKLSKRDPQS	LGEGTKKLS	0.0458	30448.7	50.00	Sequence
IAd	194	LYTLVNPCDDALMKI	PCDDALMKI	0.0454	30586.4	50.00	Sequence
IAd	33	ARHTGGTFVFRIEDT	RHTGGTFVF	0.0449	30769.3	50.00	Sequence
IAd	337	GDFTVRLRDHLDTHG	VRLRDHLDT	0.0447	30838.0	50.00	Sequence
IAd	248	TVLGEGTKKLSKRDP	EGTKKLSKR	0.0428	31472.0	50.00	Sequence
IAd	343	LRDHLDTHGHHIALD	RDHLDTHGH	0.0412	32010.5	50.00	Sequence
IAd	67	LGLDWDEGPEVGGPY	WDEGPEVGG	0.0410	32088.5	50.00	Sequence
IAd	71	WDEGPEVGGPYGPYR	WDEGPEVGG	0.0400	32420.8	50.00	Sequence

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        IAd  379  WELLKFFNDDQYVID  WELLKFFND       0.0400      32428.5                 50.00     Sequence
        IAd  289  SIADDHDLFGLDEMV  ADDHDLFGL       0.0397      32537.8                 50.00     Sequence
        IAd   10  FCPSPTGTPHVGLVR  GTPHVGLVR       0.0389      32810.0                 50.00     Sequence
        IAd  455  TGTTVSPPLFESLEL  PPLFESLEL       0.0387      32893.5                 50.00     Sequence
        IAd  192  DPLYTLVNPCDDALM  PLYTLVNPC       0.0380      33161.2                 50.00     Sequence
        IAd  247  PTVLGEGTKKLSKRD  LGEGTKKLS       0.0375      33331.7                 50.00     Sequence
        IAd  344  RDHLDTHGHHIALDE  RDHLDTHGH       0.0368      33567.6                 50.00     Sequence
        IAd  381  LLKFFNDDQYVIDPK  DDQYVIDPK       0.0367      33622.9                 50.00     Sequence
        IAd   73  EGPEVGGPYGPYRQS  GPYGPYRQS       0.0365      33681.9                 50.00     Sequence
        IAd    8  VRFCPSPTGTPHVGL  VRFCPSPTG       0.0362      33800.5                 50.00     Sequence
        IAd   34  RHTGGTFVFRIEDTD  RHTGGTFVF       0.0357      33978.4                 50.00     Sequence
        IAd  129  LGYDNFDRHLTDAQR  DRHLTDAQR       0.0334      34826.3                 50.00     Sequence
        IAd  189  ASGDPLYTLVNPCDD  ASGDPLYTL       0.0334      34844.7                 50.00     Sequence
        IAd   72  DEGPEVGGPYGPYRQ  GPEVGGPYG       0.0327      35097.1                 50.00     Sequence
        IAd   77  VGGPYGPYRQSQRAE  GPYRQSQRA       0.0324      35204.4                 50.00     Sequence
        IAd   74  GPEVGGPYGPYRQSQ  GPYGPYRQS       0.0312      35670.2                 50.00     Sequence
        IAd    9  RFCPSPTGTPHVGLV  PSPTGTPHV       0.0312      35692.6                 50.00     Sequence
        IAd  120  HVAAGRNPKLGYDNF  VAAGRNPKL       0.0307      35863.7                 50.00     Sequence
        IAd  121  VAAGRNPKLGYDNFD  VAAGRNPKL       0.0306      35900.2                 50.00     Sequence
        IAd   35  HTGGTFVFRIEDTDA  VFRIEDTDA       0.0284      36790.5                 50.00     Sequence
        IAd   76  EVGGPYGPYRQSQRA  GPYRQSQRA       0.0283      36808.0                 50.00     Sequence
        IAd  122  AAGRNPKLGYDNFDR  RNPKLGYDN       0.0257      37845.9                 50.00     Sequence
        IAd  457  TTVSPPLFESLELLG  VSPPLFESL       0.0254      37989.5                 50.00     Sequence
        IAd  456  GTTVSPPLFESLELL  VSPPLFESL       0.0250      38133.2                 50.00     Sequence
        IAd  124  GRNPKLGYDNFDRHL  RNPKLGYDN       0.0248      38217.9                 50.00     Sequence
        IAd  123  AGRNPKLGYDNFDRH  RNPKLGYDN       0.0247      38257.6                 50.00     Sequence
        IAd  334  LDVGDFTVRLRDHLD  VGDFTVRLR       0.0247      38276.6                 50.00     Sequence
        IAd   75  PEVGGPYGPYRQSQR  GPYGPYRQS       0.0234      38810.8                 50.00     Sequence
        IAd  125  RNPKLGYDNFDRHLT  RNPKLGYDN       0.0210      39844.8                 50.00     Sequence
        IAd  191  GDPLYTLVNPCDDAL  PLYTLVNPC       0.0207      39967.8                 50.00     Sequence
        IAd  380  ELLKFFNDDQYVIDP  NDDQYVIDP       0.0197      40381.2                 50.00     Sequence
        IAd  190  SGDPLYTLVNPCDDA  PLYTLVNPC       0.0193      40577.9                 50.00     Sequence
        IAd  126  NPKLGYDNFDRHLTD  YDNFDRHLT       0.0193      40591.1                 50.00     Sequence
        IAd  127  PKLGYDNFDRHLTDA  KLGYDNFDR       0.0190      40700.5                 50.00     Sequence
        IAd  128  KLGYDNFDRHLTDAQ  YDNFDRHLT       0.0175      41371.4                 50.00     Sequence
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Allele: IAd. Number of high binders 0. Number of weak binders 21. Number of peptides 476

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     Allele  pos           peptide      core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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        IAs  236  VAERIPKFAHLPTVL  KFAHLPTVL       0.4173        546.9                  0.80     Sequence
        IAs  237  AERIPKFAHLPTVLG  KFAHLPTVL       0.4035        635.5                  0.80     Sequence
        IAs  238  ERIPKFAHLPTVLGE  KFAHLPTVL       0.3902        733.9                  0.80     Sequence
        IAs  239  RIPKFAHLPTVLGEG  KFAHLPTVL       0.3783        834.0                  0.80     Sequence
        IAs  451  RVAATGTTVSPPLFE  ATGTTVSPP       0.3518       1111.8                  2.00     Sequence
        IAs  452  VAATGTTVSPPLFES  ATGTTVSPP       0.3439       1211.1                  2.00     Sequence
        IAs  453  AATGTTVSPPLFESL  ATGTTVSPP       0.3405       1255.4                  2.00     Sequence
        IAs  454  ATGTTVSPPLFESLE  ATGTTVSPP       0.3399       1264.8                  2.00     Sequence
        IAs  450  IRVAATGTTVSPPLF  ATGTTVSPP       0.3359       1320.5                  2.00     Sequence
        IAs  149  EGRQPVVRLRMPDDD  QPVVRLRMP       0.3333       1357.9                  2.00     Sequence
        IAs  152  QPVVRLRMPDDDLAW  QPVVRLRMP       0.3320       1376.9                  2.00     Sequence
        IAs  150  GRQPVVRLRMPDDDL  QPVVRLRMP       0.3307       1396.8                  2.00     Sequence
        IAs  151  RQPVVRLRMPDDDLA  QPVVRLRMP       0.3289       1424.3                  2.00     Sequence
        IAs  448  SPIRVAATGTTVSPP  ATGTTVSPP       0.3269       1455.4                  2.00     Sequence
        IAs  241  PKFAHLPTVLGEGTK  KFAHLPTVL       0.3175       1611.3                  2.00     Sequence
        IAs  449  PIRVAATGTTVSPPL  ATGTTVSPP       0.3113       1722.2                  4.00     Sequence
        IAs  240  IPKFAHLPTVLGEGT  KFAHLPTVL       0.3095       1756.7                  4.00     Sequence
        IAs  148  AEGRQPVVRLRMPDD  QPVVRLRMP       0.2875       2229.1                  4.00     Sequence
        IAs  114  EEVEARHVAAGRNPK  RHVAAGRNP       0.2522       3265.4                  8.00     Sequence
        IAs  115  EVEARHVAAGRNPKL  RHVAAGRNP       0.2473       3441.5                  8.00     Sequence
        IAs  249  VLGEGTKKLSKRDPQ  KKLSKRDPQ       0.2454       3515.1                  8.00     Sequence
        IAs  242  KFAHLPTVLGEGTKK  KFAHLPTVL       0.2443       3556.9                  8.00     Sequence
        IAs  116  VEARHVAAGRNPKLG  RHVAAGRNP       0.2440       3566.3                  8.00     Sequence
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IAs	146	YLAEGRQPVVRLRMP	QPVVRLRMP	0.2408	3692.9	8.00	Sequence
IAs	119	RHVAAGRNPKLGYDN	RHVAAGRNP	0.2405	3706.3	8.00	Sequence
IAs	147	LAEGRQPVVRLRMPD	QPVVRLRMP	0.2384	3789.4	8.00	Sequence
IAs	113	PEEVEARHVAAGRNP	RHVAAGRNP	0.2368	3855.1	8.00	Sequence
IAs	118	ARHVAAGRNPKLGYD	RHVAAGRNP	0.2351	3930.2	8.00	Sequence
IAs	250	LGEGTKKLSKRDPQS	KKLSKRDPQ	0.2313	4092.1	8.00	Sequence
IAs	117	EARHVAAGRNPKLGY	RHVAAGRNP	0.2293	4185.2	8.00	Sequence
IAs	139	TDAQRAAYLAEGRQP	AYLAEGRQP	0.2255	4360.1	8.00	Sequence
IAs	254	TKKLSKRDPQSNLFA	KKLSKRDPQ	0.2198	4637.6	8.00	Sequence
IAs	251	GEGTKKLSKRDPQSN	KKLSKRDPQ	0.2182	4718.6	8.00	Sequence
IAs	171	RGPVTFAAGSVPDFA	AAGSVPDFA	0.2161	4827.5	8.00	Sequence
IAs	142	QRAAYLAEGRQPVVR	AYLAEGRQP	0.2140	4936.6	8.00	Sequence
IAs	140	DAQRAAYLAEGRQPV	AYLAEGRQP	0.2137	4951.8	8.00	Sequence
IAs	253	GTKKLSKRDPQSNLF	KKLSKRDPQ	0.2132	4977.3	8.00	Sequence
IAs	141	AQRAAYLAEGRQPVV	AYLAEGRQP	0.2099	5160.0	16.00	Sequence
IAs	235	GVAERIPKFAHLPTV	RIPKFAHLP	0.2089	5214.7	16.00	Sequence
IAs	252	EGTKKLSKRDPQSNL	KKLSKRDPQ	0.2084	5243.8	16.00	Sequence
IAs	172	GPVTFAAGSVPDFAL	AAGSVPDFA	0.2065	5353.4	16.00	Sequence
IAs	326	LNAEHIRMLDVGDFT	RMLDVGDFT	0.2037	5516.9	16.00	Sequence
IAs	354	IALDEAAFAAAAELV	AFAAAAELV	0.2035	5531.1	16.00	Sequence
IAs	173	PVTFAAGSVPDFALT	AAGSVPDFA	0.2003	5725.5	16.00	Sequence
IAs	174	VTFAAGSVPDFALTR	AAGSVPDFA	0.1985	5836.1	16.00	Sequence
IAs	439	LALKPRKAFSPIRVA	KAFSPIRVA	0.1978	5884.6	16.00	Sequence
IAs	255	KKLSKRDPQSNLFAH	KKLSKRDPQ	0.1962	5982.0	16.00	Sequence
IAs	323	ADALNAEHIRMLDVG	EHIRMLDVG	0.1962	5982.6	16.00	Sequence
IAs	355	ALDEAAFAAAAELVQ	AFAAAAELV	0.1917	6282.8	16.00	Sequence
IAs	233	RIGVAERIPKFAHLP	RIGVAERIP	0.1900	6399.7	16.00	Sequence
IAs	440	ALKPRKAFSPIRVAA	KAFSPIRVA	0.1888	6480.3	16.00	Sequence
IAs	357	DEAAFAAAAELVQTR	AAFAAAAEL	0.1868	6623.8	16.00	Sequence
IAs	227	LHQALIRIGVAERIP	RIGVAERIP	0.1865	6648.4	16.00	Sequence
IAs	441	LKPRKAFSPIRVAAT	KAFSPIRVA	0.1854	6724.6	16.00	Sequence
IAs	327	NAEHIRMLDVGDFTV	RMLDVGDFT	0.1848	6773.1	16.00	Sequence
IAs	442	KPRKAFSPIRVAATG	KPRKAFSPI	0.1835	6863.0	16.00	Sequence
IAs	298	GLDEMVAAFDVADVN	AAFDVADVN	0.1828	6920.6	16.00	Sequence
IAs	356	LDEAAFAAAAELVQT	AFAAAAELV	0.1820	6982.0	16.00	Sequence
IAs	324	DALNAEHIRMLDVGD	EHIRMLDVG	0.1814	7024.3	16.00	Sequence
IAs	69	LDWDEGPEVGGPYGP	EGPEVGGPY	0.1798	7148.5	16.00	Sequence
IAs	419	VTDWTAPLIEAALKD	TDWTAPLIE	0.1795	7170.4	16.00	Sequence
IAs	328	AEHIRMLDVGDFTVR	RMLDVGDFT	0.1793	7183.2	16.00	Sequence
IAs	414	AALTSVTDWTAPLIE	TDWTAPLIE	0.1770	7365.2	16.00	Sequence
IAs	420	TDWTAPLIEAALKDA	TDWTAPLIE	0.1760	7447.7	16.00	Sequence
IAs	72	DEGPEVGGPYGPYRQ	EGPEVGGPY	0.1759	7453.7	16.00	Sequence
IAs	418	SVTDWTAPLIEAALK	TDWTAPLIE	0.1754	7496.8	16.00	Sequence
IAs	229	QALIRIGVAERIPKF	RIGVAERIP	0.1753	7501.6	16.00	Sequence
IAs	365	AELVQTRIVVLGDAW	RIVVLGDAW	0.1747	7550.7	16.00	Sequence
IAs	154	VVRLRMPDDDLAWND	VRLRMPDDD	0.1733	7666.3	16.00	Sequence
IAs	176	FAAGSVPDFALTRAS	AAGSVPDFA	0.1728	7704.7	16.00	Sequence
IAs	325	ALNAEHIRMLDVGDF	EHIRMLDVG	0.1719	7780.5	16.00	Sequence
IAs	299	LDEMVAAFDVADVNS	AAFDVADVN	0.1710	7858.6	16.00	Sequence
IAs	228	HQALIRIGVAERIPK	RIGVAERIP	0.1710	7861.8	16.00	Sequence
IAs	153	PVVRLRMPDDDLAWN	VRLRMPDDD	0.1706	7892.2	16.00	Sequence
IAs	71	WDEGPEVGGPYGPYR	EGPEVGGPY	0.1702	7929.1	16.00	Sequence
IAs	68	GLDWDEGPEVGGPYG	EGPEVGGPY	0.1701	7941.3	16.00	Sequence
IAs	232	IRIGVAERIPKFAHL	RIGVAERIP	0.1700	7947.2	16.00	Sequence
IAs	455	TGTTVSPPLFESLEL	TGTTVSPPL	0.1693	8003.2	16.00	Sequence
IAs	67	LGLDWDEGPEVGGPY	EGPEVGGPY	0.1682	8100.2	16.00	Sequence
IAs	175	TFAAGSVPDFALTRA	AAGSVPDFA	0.1669	8214.0	16.00	Sequence
IAs	143	RAAYLAEGRQPVVRL	AYLAEGRQP	0.1657	8321.3	16.00	Sequence
IAs	415	ALTSVTDWTAPLIEA	TDWTAPLIE	0.1657	8325.7	16.00	Sequence
IAs	390	YVIDPKAAAKELGPD	KAAAKELGP	0.1654	8349.3	16.00	Sequence
IAs	231	LIRIGVAERIPKFAH	RIGVAERIP	0.1650	8389.2	16.00	Sequence
IAs	230	ALIRIGVAERIPKFA	RIGVAERIP	0.1649	8394.8	16.00	Sequence
IAs	170	VRGPVTFAAGSVPDF	VTFAAGSVP	0.1642	8461.5	16.00	Sequence
IAs	70	DWDEGPEVGGPYGPY	EGPEVGGPY	0.1638	8498.3	16.00	Sequence
IAs	7	RVRFCPSPTGTPHVG	SPTGTPHVG	0.1622	8645.5	16.00	Sequence
IAs	366	ELVQTRIVVLGDAWE	RIVVLGDAW	0.1612	8736.3	16.00	Sequence

IAs	79	GPYGPYRQSQRAEIY	RQSQRAEIY	0.1592	8935.3	32.00	Sequence
IAs	391	VIDPKAAAKELGPDG	KAAAKELGP	0.1591	8939.6	32.00	Sequence
IAs	300	DEMVAAFDVADVNSS	AAFDVADVN	0.1587	8984.1	32.00	Sequence
IAs	436	IEGLALKPRKAFSPI	IEGLALKPR	0.1571	9135.2	32.00	Sequence
IAs	359	AAFAAAAELVQTRIV	AFAAAAELV	0.1559	9259.7	32.00	Sequence
IAs	303	VAAFDVADVNSSPAR	AAFDVADVN	0.1554	9308.5	32.00	Sequence
IAs	144	AAYLAEGRQPVVRLR	AYLAEGRQP	0.1553	9319.1	32.00	Sequence
IAs	145	AYLAEGRQPVVRLRM	AYLAEGRQP	0.1546	9387.3	32.00	Sequence
IAs	392	IDPKAAAKELGPDGA	KAAAKELGP	0.1543	9412.3	32.00	Sequence
IAs	301	EMVAAFDVADVNSSP	AAFDVADVN	0.1539	9457.8	32.00	Sequence
IAs	471	GRDRSMQRLRAARQL	QRLRAARQL	0.1521	9646.6	32.00	Sequence
IAs	302	MVAAFDVADVNSSPA	AAFDVADVN	0.1520	9656.3	32.00	Sequence
IAs	367	LVQTRIVVLGDAWEL	RIVVLGDAW	0.1510	9761.7	32.00	Sequence
IAs	8	VRFCPSPTGTPHVGL	SPTGTPHVG	0.1509	9769.9	32.00	Sequence
IAs	438	GLALKPRKAFSPIRV	RKAFSPIRV	0.1509	9773.7	32.00	Sequence
IAs	6	VRVRFCPSPTGTPHV	RVRFCPSPT	0.1508	9781.8	32.00	Sequence
IAs	234	IGVAERIPKFAHLPT	RIPKFAHLP	0.1506	9797.5	32.00	Sequence
IAs	93	YRDVLARLLAAGEAY	RLLAAGEAY	0.1504	9828.0	32.00	Sequence
IAs	102	AAGEAYHAFSTPEEV	HAFSTPEEV	0.1501	9858.4	32.00	Sequence
IAs	358	EAAFAAAAELVQTRI	AAFAAAAEL	0.1491	9960.1	32.00	Sequence
IAs	389	QYVIDPKAAAKELGP	KAAAKELGP	0.1488	9997.6	32.00	Sequence
IAs	416	LTSVTDWTAPLIEAA	TDWTAPLIE	0.1488	9998.2	32.00	Sequence
IAs	443	PRKAFSPIRVAATGT	KAFSPIRVA	0.1485	10027.2	32.00	Sequence
IAs	395	KAAAKELGPDGAAVL	AAAKELGPD	0.1485	10030.1	32.00	Sequence
IAs	370	TRIVVLGDAWELLKF	RIVVLGDAW	0.1479	10093.4	32.00	Sequence
IAs	5	TVRVRFCPSPTGTPH	RVRFCPSPT	0.1476	10128.3	32.00	Sequence
IAs	444	RKAFSPIRVAATGTT	KAFSPIRVA	0.1467	10227.8	32.00	Sequence
IAs	432	KDALIEGLALKPRKA	IEGLALKPR	0.1462	10284.7	32.00	Sequence
IAs	417	TSVTDWTAPLIEAAL	TDWTAPLIE	0.1458	10323.1	32.00	Sequence
IAs	369	QTRIVVLGDAWELLK	RIVVLGDAW	0.1448	10434.8	32.00	Sequence
IAs	80	PYGPYRQSQRAEIYR	RQSQRAEIY	0.1447	10448.4	32.00	Sequence
IAs	445	KAFSPIRVAATGTTV	KAFSPIRVA	0.1446	10459.9	32.00	Sequence
IAs	422	WTAPLIEAALKDALI	APLIEAALK	0.1442	10502.4	32.00	Sequence
IAs	9	RFCPSPTGTPHVGLV	SPTGTPHVG	0.1442	10509.2	32.00	Sequence
IAs	177	AAGSVPDFALTRASG	AAGSVPDFA	0.1435	10588.8	32.00	Sequence
IAs	353	HIALDEAAFAAAAEL	AAFAAAAEL	0.1432	10622.0	32.00	Sequence
IAs	368	VQTRIVVLGDAWELL	RIVVLGDAW	0.1431	10627.0	32.00	Sequence
IAs	10	FCPSPTGTPHVGLVR	SPTGTPHVG	0.1431	10628.6	32.00	Sequence
IAs	394	PKAAAKELGPDGAAV	AAAKELGPD	0.1425	10700.4	32.00	Sequence
IAs	103	AGEAYHAFSTPEEVE	HAFSTPEEV	0.1417	10797.0	32.00	Sequence
IAs	435	LIEGLALKPRKAFSP	IEGLALKPR	0.1416	10808.6	32.00	Sequence
IAs	304	AAFDVADVNSSPARF	AAFDVADVN	0.1414	10827.2	32.00	Sequence
IAs	472	RDRSMQRLRAARQLV	QRLRAARQL	0.1411	10867.7	32.00	Sequence
IAs	94	RDVLARLLAAGEAYH	RLLAAGEAY	0.1387	11149.5	32.00	Sequence
IAs	421	DWTAPLIEAALKDAL	APLIEAALK	0.1377	11274.6	32.00	Sequence
IAs	168	DLVRGPVTFAAGSVP	VTFAAGSVP	0.1375	11296.3	32.00	Sequence
IAs	4	ETVRVRFCPSPTGTP	RVRFCPSPT	0.1368	11374.7	32.00	Sequence
IAs	403	PDGAAVLDAALAALT	DGAAVLDAA	0.1365	11411.9	32.00	Sequence
IAs	474	RSMQRLRAARQLVGH	RSMQRLRAA	0.1363	11445.4	32.00	Sequence
IAs	169	LVRGPVTFAAGSVPD	VTFAAGSVP	0.1360	11475.3	32.00	Sequence
IAs	393	DPKAAAKELGPDGAA	AAAKELGPD	0.1356	11535.1	32.00	Sequence
IAs	473	DRSMQRLRAARQLVG	QRLRAARQL	0.1339	11737.6	32.00	Sequence
IAs	329	EHIRMLDVGDFTVRL	EHIRMLDVG	0.1336	11777.7	32.00	Sequence
IAs	433	DALIEGLALKPRKAF	IEGLALKPR	0.1314	12060.0	32.00	Sequence
IAs	104	GEAYHAFSTPEEVEA	HAFSTPEEV	0.1314	12064.2	32.00	Sequence
IAs	383	KFFNDDQYVIDPKAA	QYVIDPKAA	0.1313	12082.6	32.00	Sequence
IAs	434	ALIEGLALKPRKAFS	IEGLALKPR	0.1313	12084.3	32.00	Sequence
IAs	211	VLRGEDLLPSTPRQL	LLPSTPRQL	0.1305	12184.1	32.00	Sequence
IAs	85	RQSQRAEIYRDVLAR	RQSQRAEIY	0.1302	12217.3	32.00	Sequence
IAs	81	YGPYRQSQRAEIYRD	RQSQRAEIY	0.1301	12235.8	32.00	Sequence
IAs	404	DGAAVLDAALAALTS	DGAAVLDAA	0.1296	12298.0	32.00	Sequence
IAs	106	AYHAFSTPEEVEARH	HAFSTPEEV	0.1294	12331.0	32.00	Sequence
IAs	84	YRQSQRAEIYRDVLA	RQSQRAEIY	0.1294	12333.5	32.00	Sequence
IAs	401	LGPDGAAVLDAALAA	DGAAVLDAA	0.1290	12379.0	32.00	Sequence
IAs	95	DVLARLLAAGEAYHA	RLLAAGEAY	0.1282	12485.0	32.00	Sequence
IAs	456	GTTVSPPLFESLELL	TTVSPPLFE	0.1281	12508.4	32.00	Sequence

IAs	320	QKKADALNAEHIRML	KKADALNAE	0.1276	12565.6	32.00	Sequence
IAs	431	LKDALIEGLALKPRK	IEGLALKPR	0.1274	12600.6	32.00	Sequence
IAs	3	TETVRVRFCPSPTGT	RFCPSPTGT	0.1274	12601.4	32.00	Sequence
IAs	400	ELGPDGAAVLDAALA	AAVLDAALA	0.1258	12825.1	32.00	Sequence
IAs	423	TAPLIEAALKDALIE	APLIEAALK	0.1255	12867.2	32.00	Sequence
IAs	402	GPDGAAVLDAALAAL	DGAAVLDAA	0.1252	12905.0	32.00	Sequence
IAs	105	EAYHAFSTPEEVEAR	HAFSTPEEV	0.1247	12971.9	32.00	Sequence
IAs	83	PYRQSQRAEIYRDVL	RQSQRAEIY	0.1245	13004.4	32.00	Sequence
IAs	424	APLIEAALKDALIEG	APLIEAALK	0.1241	13052.9	32.00	Sequence
IAs	280	LNYLALLGWSIADDH	LGWSIADDH	0.1220	13351.8	32.00	Sequence
IAs	212	LRGEDLLPSTPRQLA	LLPSTPRQL	0.1213	13454.9	32.00	Sequence
IAs	384	FFNDDQYVIDPKAAA	QYVIDPKAA	0.1213	13458.0	32.00	Sequence
IAs	82	GPYRQSQRAEIYRDV	RQSQRAEIY	0.1210	13497.1	32.00	Sequence
IAs	447	FSPIRVAATGTTVSP	SPIRVAATG	0.1209	13511.1	32.00	Sequence
IAs	138	LTDAQRAAYLAEGRQ	RAAYLAEGR	0.1208	13534.1	32.00	Sequence
IAs	321	KKADALNAEHIRMLD	KKADALNAE	0.1194	13743.8	32.00	Sequence
IAs	385	FNDDQYVIDPKAAAK	QYVIDPKAA	0.1185	13873.4	32.00	Sequence
IAs	318	FDQKKADALNAEHIR	KKADALNAE	0.1183	13895.5	32.00	Sequence
IAs	120	HVAAGRNPKLGYDNF	AAGRNPKLG	0.1171	14081.7	32.00	Sequence
IAs	319	DQKKADALNAEHIRM	KKADALNAE	0.1166	14157.3	32.00	Sequence
IAs	386	NDDQYVIDPKAAAKE	QYVIDPKAA	0.1159	14267.9	32.00	Sequence
IAs	297	FGLDEMVAAFDVADV	EMVAAFDVA	0.1152	14374.6	32.00	Sequence
IAs	360	AFAAAAELVQTRIVV	AFAAAAELV	0.1149	14420.3	32.00	Sequence
IAs	437	EGLALKPRKAFSPIR	KPRKAFSPI	0.1142	14537.5	32.00	Sequence
IAs	13	SPTGTPHVGLVRTAL	SPTGTPHVG	0.1141	14545.5	32.00	Sequence
IAs	96	VLARLLAAGEAYHAF	RLLAAGEAY	0.1141	14554.3	32.00	Sequence
IAs	317	RFDQKKADALNAEHI	ADALNAEHI	0.1126	14791.8	32.00	Sequence
IAs	446	AFSPIRVAATGTTVS	SPIRVAATG	0.1117	14937.8	32.00	Sequence
IAs	281	NYLALLGWSIADDHD	LGWSIADDH	0.1112	15004.4	32.00	Sequence
IAs	2	ATETVRVRFCPSPTG	RVRFCPSPT	0.1110	15042.9	32.00	Sequence
IAs	73	EGPEVGGPYGPYRQS	EGPEVGGPY	0.1105	15128.1	50.00	Sequence
IAs	475	SMQRLRAARQLVGHA	QRLRAARQL	0.1088	15399.8	50.00	Sequence
IAs	315	PARFDQKKADALNAE	KKADALNAE	0.1088	15407.5	50.00	Sequence
IAs	396	AAAKELGPDGAAVLD	AAAKELGPD	0.1084	15477.3	50.00	Sequence
IAs	11	CPSPTGTPHVGLVRT	SPTGTPHVG	0.1077	15589.8	50.00	Sequence
IAs	107	YHAFSTPEEVEARHV	HAFSTPEEV	0.1070	15711.2	50.00	Sequence
IAs	98	ARLLAAGEAYHAFST	RLLAAGEAY	0.1068	15745.5	50.00	Sequence
IAs	155	VRLRMPDDDLAWNDL	VRLRMPDDD	0.1065	15801.4	50.00	Sequence
IAs	430	ALKDALIEGLALKPR	IEGLALKPR	0.1064	15816.6	50.00	Sequence
IAs	162	DDLAWNDLVRGPVTF	DLVRGPVTF	0.1063	15825.6	50.00	Sequence
IAs	137	HLTDAQRAAYLAEGR	RAAYLAEGR	0.1058	15923.0	50.00	Sequence
IAs	1	TATETVRVRFCPSPT	RVRFCPSPT	0.1054	15992.6	50.00	Sequence
IAs	165	AWNDLVRGPVTFAAG	AWNDLVRGP	0.1044	16162.9	50.00	Sequence
IAs	217	LLPSTPRQLALHQAL	LLPSTPRQL	0.1042	16194.8	50.00	Sequence
IAs	97	LARLLAAGEAYHAFS	RLLAAGEAY	0.1036	16301.0	50.00	Sequence
IAs	331	IRMLDVGDFTVRLRD	RMLDVGDFT	0.1030	16403.0	50.00	Sequence
IAs	371	RIVVLGDAWELLKFF	RIVVLGDAW	0.1027	16457.8	50.00	Sequence
IAs	316	ARFDQKKADALNAEH	KKADALNAE	0.1025	16490.4	50.00	Sequence
IAs	226	ALHQALIRIGVAERI	IRIGVAERI	0.1024	16505.1	50.00	Sequence
IAs	121	VAAGRNPKLGYDNFD	AAGRNPKLG	0.1024	16510.9	50.00	Sequence
IAs	322	KADALNAEHIRMLDV	ADALNAEHI	0.1023	16529.0	50.00	Sequence
IAs	163	DLAWNDLVRGPVTFA	DLVRGPVTF	0.1016	16663.1	50.00	Sequence
IAs	330	HIRMLDVGDFTVRLR	RMLDVGDFT	0.1011	16741.0	50.00	Sequence
IAs	164	LAWNDLVRGPVTFAA	DLVRGPVTF	0.1011	16754.1	50.00	Sequence
IAs	99	RLLAAGEAYHAFSTP	RLLAAGEAY	0.1010	16766.0	50.00	Sequence
IAs	19	HVGLVRTALFNWAYA	VGLVRTALF	0.1008	16791.4	50.00	Sequence
IAs	388	DQYVIDPKAAAKELG	QYVIDPKAA	0.0999	16973.0	50.00	Sequence
IAs	285	LLGWSIADDHDLFGL	LGWSIADDH	0.0992	17095.0	50.00	Sequence
IAs	387	DDQYVIDPKAAAKEL	QYVIDPKAA	0.0991	17112.1	50.00	Sequence
IAs	108	HAFSTPEEVEARHVA	HAFSTPEEV	0.0987	17182.4	50.00	Sequence
IAs	283	LALLGWSIADDHDLF	LGWSIADDH	0.0982	17287.0	50.00	Sequence
IAs	284	ALLGWSIADDHDLFG	LGWSIADDH	0.0977	17365.3	50.00	Sequence
IAs	282	YLALLGWSIADDHDL	LGWSIADDH	0.0976	17392.8	50.00	Sequence
IAs	307	DVADVNSSPARFDQK	ADVNSSPAR	0.0976	17397.3	50.00	Sequence
IAs	308	VADVNSSPARFDQKK	VADVNSSPA	0.0971	17479.0	50.00	Sequence
IAs	219	PSTPRQLALHQALIR	LALHQALIR	0.0968	17541.7	50.00	Sequence

IAs	20	VGLVRTALFNWAYAR	TALFNWAYA	0.0966	17590.8	50.00	Sequence
IAs	399	KELGPDGAAVLDAAL	DGAAVLDAA	0.0964	17612.1	50.00	Sequence
IAs	66	WLGLDWDEGPEVGGP	DEGPEVGGP	0.0940	18082.3	50.00	Sequence
IAs	130	GYDNFDRHLTDAQRA	RHLTDAQRA	0.0940	18083.2	50.00	Sequence
IAs	12	PSPTGTPHVGLVRTA	SPTGTPHVG	0.0938	18115.2	50.00	Sequence
IAs	213	RGEDLLPSTPRQLAL	LLPSTPRQL	0.0929	18299.7	50.00	Sequence
IAs	305	AFDVADVNSSPARFD	ADVNSSPAR	0.0927	18338.2	50.00	Sequence
IAs	306	FDVADVNSSPARFDQ	ADVNSSPAR	0.0926	18363.0	50.00	Sequence
IAs	214	GEDLLPSTPRQLALH	LLPSTPRQL	0.0921	18450.8	50.00	Sequence
IAs	266	LFAHRDRGFIPEGLL	RGFIPEGLL	0.0920	18483.0	50.00	Sequence
IAs	426	LIEAALKDALIEGLA	KDALIEGLA	0.0915	18575.6	50.00	Sequence
IAs	15	TGTPHVGLVRTALFN	VGLVRTALF	0.0912	18648.3	50.00	Sequence
IAs	225	LALHQALIRIGVAER	QALIRIGVA	0.0904	18793.0	50.00	Sequence
IAs	23	VRTALFNWAYARHTG	TALFNWAYA	0.0903	18825.9	50.00	Sequence
IAs	14	PTGTPHVGLVRTALF	VGLVRTALF	0.0902	18840.4	50.00	Sequence
IAs	224	QLALHQALIRIGVAE	QALIRIGVA	0.0901	18867.9	50.00	Sequence
IAs	332	RMLDVGDFTVRLRDH	RMLDVGDFT	0.0900	18874.5	50.00	Sequence
IAs	136	RHLTDAQRAAYLAEG	RHLTDAQRA	0.0891	19061.4	50.00	Sequence
IAs	220	STPRQLALHQALIRI	LALHQALIR	0.0891	19069.5	50.00	Sequence
IAs	457	TTVSPPLFESLELLG	TTVSPPLFE	0.0886	19178.5	50.00	Sequence
IAs	122	AAGRNPKLGYDNFDR	AAGRNPKLG	0.0886	19179.1	50.00	Sequence
IAs	215	EDLLPSTPRQLALHQ	LLPSTPRQL	0.0883	19235.3	50.00	Sequence
IAs	218	LPSTPRQLALHQALI	RQLALHQAL	0.0876	19372.5	50.00	Sequence
IAs	203	DALMKITHVLRGEDL	DALMKITHV	0.0875	19396.2	50.00	Sequence
IAs	382	LKFFNDDQYVIDPKA	KFFNDDQYV	0.0874	19414.0	50.00	Sequence
IAs	267	FAHRDRGFIPEGLLN	RGFIPEGLL	0.0873	19439.5	50.00	Sequence
IAs	17	TPHVGLVRTALFNWA	VGLVRTALF	0.0867	19576.4	50.00	Sequence
IAs	198	VNPCDDALMKITHVL	ALMKITHVL	0.0864	19642.9	50.00	Sequence
IAs	16	GTPHVGLVRTALFNW	VGLVRTALF	0.0861	19697.3	50.00	Sequence
IAs	22	LVRTALFNWAYARHT	TALFNWAYA	0.0861	19704.2	50.00	Sequence
IAs	216	DLLPSTPRQLALHQA	LLPSTPRQL	0.0854	19842.4	50.00	Sequence
IAs	201	CDDALMKITHVLRGE	DALMKITHV	0.0853	19864.3	50.00	Sequence
IAs	223	RQLALHQALIRIGVA	QALIRIGVA	0.0850	19942.4	50.00	Sequence
IAs	166	WNDLVRGPVTFAAGS	DLVRGPVTF	0.0844	20070.8	50.00	Sequence
IAs	221	TPRQLALHQALIRIG	RQLALHQAL	0.0840	20139.3	50.00	Sequence
IAs	248	TVLGEGTKKLSKRDP	EGTKKLSKR	0.0839	20167.2	50.00	Sequence
IAs	286	LGWSIADDHDLFGLD	LGWSIADDH	0.0839	20181.0	50.00	Sequence
IAs	131	YDNFDRHLTDAQRAA	RHLTDAQRA	0.0837	20206.6	50.00	Sequence
IAs	222	PRQLALHQALIRIGV	RQLALHQAL	0.0833	20299.9	50.00	Sequence
IAs	63	ALRWLGLDWDEGPEV	LRWLGLDWD	0.0833	20305.6	50.00	Sequence
IAs	21	GLVRTALFNWAYARH	TALFNWAYA	0.0829	20390.8	50.00	Sequence
IAs	209	THVLRGEDLLPSTPR	LRGEDLLPS	0.0825	20472.0	50.00	Sequence
IAs	18	PHVGLVRTALFNWAY	VGLVRTALF	0.0823	20516.8	50.00	Sequence
IAs	204	ALMKITHVLRGEDLL	HVLRGEDLL	0.0821	20571.4	50.00	Sequence
IAs	468	ELLGRDRSMQRLRAA	RSMQRLRAA	0.0816	20672.7	50.00	Sequence
IAs	133	NFDRHLTDAQRAAYL	RHLTDAQRA	0.0815	20704.1	50.00	Sequence
IAs	470	LGRDRSMQRLRAARQ	RSMQRLRAA	0.0814	20729.2	50.00	Sequence
IAs	161	DDDLAWNDLVRGPVT	NDLVRGPVT	0.0812	20773.0	50.00	Sequence
IAs	268	AHRDRGFIPEGLLNY	RGFIPEGLL	0.0811	20780.6	50.00	Sequence
IAs	135	DRHLTDAQRAAYLAE	RHLTDAQRA	0.0808	20866.4	50.00	Sequence
IAs	381	LLKFFNDDQYVIDPK	KFFNDDQYV	0.0805	20922.3	50.00	Sequence
IAs	210	HVLRGEDLLPSTPRQ	LRGEDLLPS	0.0804	20960.6	50.00	Sequence
IAs	199	NPCDDALMKITHVLR	ALMKITHVL	0.0799	21060.1	50.00	Sequence
IAs	425	PLIEAALKDALIEGL	AALKDALIE	0.0797	21104.4	50.00	Sequence
IAs	134	FDRHLTDAQRAAYLA	RHLTDAQRA	0.0792	21213.6	50.00	Sequence
IAs	192	DPLYTLVNPCDDALM	PLYTLVNPC	0.0792	21217.5	50.00	Sequence
IAs	405	GAAVLDAALAALTSV	LDAALAALT	0.0791	21235.6	50.00	Sequence
IAs	270	RDRGFIPEGLLNYLA	RGFIPEGLL	0.0789	21298.9	50.00	Sequence
IAs	64	LRWLGLDWDEGPEVG	LRWLGLDWD	0.0786	21362.4	50.00	Sequence
IAs	269	HRDRGFIPEGLLNYL	RGFIPEGLL	0.0783	21431.8	50.00	Sequence
IAs	202	DDALMKITHVLRGED	ALMKITHVL	0.0781	21482.7	50.00	Sequence
IAs	132	DNFDRHLTDAQRAAY	RHLTDAQRA	0.0780	21505.5	50.00	Sequence
IAs	191	GDPLYTLVNPCDDAL	YTLVNPCDD	0.0772	21680.0	50.00	Sequence
IAs	428	EAALKDALIEGLALK	LKDALIEGL	0.0771	21712.1	50.00	Sequence
IAs	245	HLPTVLGEGTKKLSK	TVLGEGTKK	0.0770	21723.4	50.00	Sequence
IAs	295	DLFGLDEMVAAFDVA	EMVAAFDVA	0.0769	21765.3	50.00	Sequence

IAs	469	LLGRDRSMQRLRAAR	RSMQRLRAA	0.0760	21969.3	50.00	Sequence
IAs	0	VTATETVRVRFCPSP	VRVRFCPSP	0.0759	21992.1	50.00	Sequence
IAs	187	TRASGDPLYTLVNPC	PLYTLVNPC	0.0750	22218.1	50.00	Sequence
IAs	190	SGDPLYTLVNPCDDA	YTLVNPCDD	0.0749	22233.7	50.00	Sequence
IAs	377	DAWELLKFFNDDQYV	KFFNDDQYV	0.0749	22242.9	50.00	Sequence
IAs	427	IEAALKDALIEGLAL	AALKDALIE	0.0749	22243.6	50.00	Sequence
IAs	189	ASGDPLYTLVNPCDD	YTLVNPCDD	0.0746	22311.1	50.00	Sequence
IAs	74	GPEVGGPYGPYRQSQ	PEVGGPYGP	0.0742	22403.2	50.00	Sequence
IAs	167	NDLVRGPVTFAAGSV	DLVRGPVTF	0.0742	22412.5	50.00	Sequence
IAs	429	AALKDALIEGLALKP	LKDALIEGL	0.0741	22429.4	50.00	Sequence
IAs	413	LAALTSVTDWTAPLI	TSVTDWTAP	0.0738	22505.8	50.00	Sequence
IAs	200	PCDDALMKITHVLRG	ALMKITHVL	0.0736	22560.4	50.00	Sequence
IAs	34	RHTGGTFVFRIEDTD	TFVFRIEDT	0.0734	22585.8	50.00	Sequence
IAs	364	AAELVQTRIVVLGDA	AELVQTRIV	0.0733	22617.8	50.00	Sequence
IAs	361	FAAAAELVQTRIVVL	AAAAELVQT	0.0729	22712.0	50.00	Sequence
IAs	193	PLYTLVNPCDDALMK	PLYTLVNPC	0.0729	22728.5	50.00	Sequence
IAs	188	RASGDPLYTLVNPCD	PLYTLVNPC	0.0719	22973.0	50.00	Sequence
IAs	33	ARHTGGTFVFRIEDT	TFVFRIEDT	0.0716	23034.2	50.00	Sequence
IAs	182	PDFALTRASGDPLYT	RASGDPLYT	0.0714	23104.4	50.00	Sequence
IAs	362	AAAAELVQTRIVVLG	AAAAELVQT	0.0713	23123.4	50.00	Sequence
IAs	351	GHHIALDEAAFAAAA	IALDEAAFA	0.0700	23441.8	50.00	Sequence
IAs	206	MKITHVLRGEDLLPS	LRGEDLLPS	0.0698	23488.0	50.00	Sequence
IAs	352	HHIALDEAAFAAAAE	EAAFAAAAE	0.0690	23694.0	50.00	Sequence
IAs	411	AALAALTSVTDWTAP	AALAALTSV	0.0690	23708.3	50.00	Sequence
IAs	296	LFGLDEMVAAFDVAD	EMVAAFDVA	0.0684	23852.7	50.00	Sequence
IAs	406	AAVLDAALAALTSVT	AAVLDAALA	0.0681	23927.4	50.00	Sequence
IAs	183	DFALTRASGDPLYTL	RASGDPLYT	0.0676	24056.4	50.00	Sequence
IAs	348	DTHGHHIALDEAAFA	IALDEAAFA	0.0675	24087.9	50.00	Sequence
IAs	350	HGHHIALDEAAFAAA	IALDEAAFA	0.0671	24185.1	50.00	Sequence
IAs	184	FALTRASGDPLYTLV	ALTRASGDP	0.0667	24294.4	50.00	Sequence
IAs	349	THGHHIALDEAAFAA	IALDEAAFA	0.0666	24312.8	50.00	Sequence
IAs	412	ALAALTSVTDWTAPL	TSVTDWTAP	0.0666	24331.8	50.00	Sequence
IAs	65	RWLGLDWDEGPEVGG	GLDWDEGPE	0.0663	24412.5	50.00	Sequence
IAs	378	AWELLKFFNDDQYVI	KFFNDDQYV	0.0659	24516.0	50.00	Sequence
IAs	160	PDDDLAWNDLVRGPV	AWNDLVRGP	0.0654	24630.0	50.00	Sequence
IAs	409	LDAALAALTSVTDWT	AALTSVTDW	0.0647	24822.1	50.00	Sequence
IAs	35	HTGGTFVFRIEDTDA	FVFRIEDTD	0.0643	24936.2	50.00	Sequence
IAs	363	AAAELVQTRIVVLGD	AAAELVQTR	0.0638	25081.8	50.00	Sequence
IAs	208	ITHVLRGEDLLPSTP	LRGEDLLPS	0.0633	25213.2	50.00	Sequence
IAs	101	LAAGEAYHAFSTPEE	YHAFSTPEE	0.0628	25334.4	50.00	Sequence
IAs	92	IYRDVLARLLAAGEA	ARLLAAGEA	0.0624	25449.8	50.00	Sequence
IAs	75	PEVGGPYGPYRQSQR	EVGGPYGPY	0.0622	25514.0	50.00	Sequence
IAs	271	DRGFIPEGLLNYLAL	RGFIPEGLL	0.0616	25686.3	50.00	Sequence
IAs	246	LPTVLGEGTKKLSKR	EGTKKLSKR	0.0615	25690.5	50.00	Sequence
IAs	205	LMKITHVLRGEDLLP	THVLRGEDL	0.0615	25692.4	50.00	Sequence
IAs	53	SEESYLALLDALRWL	ESYLALLDA	0.0613	25763.9	50.00	Sequence
IAs	207	KITHVLRGEDLLPST	LRGEDLLPS	0.0612	25791.0	50.00	Sequence
IAs	380	ELLKFFNDDQYVIDP	KFFNDDQYV	0.0611	25810.3	50.00	Sequence
IAs	50	QRDSEESYLALLDAL	SYLALLDAL	0.0609	25876.8	50.00	Sequence
IAs	244	AHLPTVLGEGTKKLS	TVLGEGTKK	0.0598	26170.8	50.00	Sequence
IAs	408	VLDAALAALTSVTDW	AALTSVTDW	0.0597	26219.5	50.00	Sequence
IAs	62	DALRWLGLDWDEGPE	LRWLGLDWD	0.0595	26253.6	50.00	Sequence
IAs	25	TALFNWAYARHTGGT	TALFNWAYA	0.0592	26362.6	50.00	Sequence
IAs	185	ALTRASGDPLYTLVN	ALTRASGDP	0.0583	26605.9	50.00	Sequence
IAs	272	RGFIPEGLLNYLALL	RGFIPEGLL	0.0581	26654.9	50.00	Sequence
IAs	379	WELLKFFNDDQYVID	KFFNDDQYV	0.0581	26660.3	50.00	Sequence
IAs	112	TPEEVEARHVAAGRN	EEVEARHVA	0.0581	26660.3	50.00	Sequence
IAs	243	FAHLPTVLGEGTKKL	TVLGEGTKK	0.0579	26728.2	50.00	Sequence
IAs	54	EESYLALLDALRWLG	ESYLALLDA	0.0573	26899.1	50.00	Sequence
IAs	36	TGGTFVFRIEDTDAQ	GTFVFRIED	0.0569	27024.2	50.00	Sequence
IAs	398	AKELGPDGAAVLDAA	DGAAVLDAA	0.0566	27104.2	50.00	Sequence
IAs	24	RTALFNWAYARHTGG	FNWAYARHT	0.0563	27199.4	50.00	Sequence
IAs	247	PTVLGEGTKKLSKRD	EGTKKLSKR	0.0560	27275.1	50.00	Sequence
IAs	186	LTRASGDPLYTLVNP	LTRASGDPL	0.0556	27384.8	50.00	Sequence
IAs	55	ESYLALLDALRWLGL	SYLALLDAL	0.0553	27476.2	50.00	Sequence
IAs	88	QRAEIYRDVLARLLA	RDVLARLLA	0.0552	27514.3	50.00	Sequence

IAs	311	VNSSPARFDQKKADA	ARFDQKKAD	0.0551	27548.9	50.00	Sequence
IAs	124	GRNPKLGYDNFDRHL	GRNPKLGYD	0.0551	27555.7	50.00	Sequence
IAs	181	VPDFALTRASGDPLY	TRASGDPLY	0.0549	27596.3	50.00	Sequence
IAs	313	SSPARFDQKKADALN	SSPARFDQK	0.0545	27732.8	50.00	Sequence
IAs	100	LLAAGEAYHAFSTPE	AYHAFSTPE	0.0541	27842.2	50.00	Sequence
IAs	312	NSSPARFDQKKADAL	ARFDQKKAD	0.0539	27893.5	50.00	Sequence
IAs	310	DVNSSPARFDQKKAD	ARFDQKKAD	0.0539	27917.6	50.00	Sequence
IAs	123	AGRNPKLGYDNFDRH	GRNPKLGYD	0.0538	27934.0	50.00	Sequence
IAs	32	YARHTGGTFVFRIED	GGTFVFRIE	0.0537	27976.0	50.00	Sequence
IAs	258	SKRDPQSNLFAHRDR	SNLFAHRDR	0.0537	27976.9	50.00	Sequence
IAs	410	DAALAALTSVTDWTA	AALAALTSV	0.0534	28042.4	50.00	Sequence
IAs	76	EVGGPYGPYRQSQRA	EVGGPYGPY	0.0529	28215.2	50.00	Sequence
IAs	309	ADVNSSPARFDQKKA	ADVNSSPAR	0.0529	28222.0	50.00	Sequence
IAs	459	VSPPLFESLELLGRD	ESLELLGRD	0.0527	28266.6	50.00	Sequence
IAs	407	AVLDAALAALTSVTD	LDAALAALT	0.0524	28354.8	50.00	Sequence
IAs	314	SPARFDQKKADALNA	QKKADALNA	0.0522	28409.5	50.00	Sequence
IAs	56	SYLALLDALRWLGLD	SYLALLDAL	0.0517	28569.4	50.00	Sequence
IAs	52	DSEESYLALLDALRW	SYLALLDAL	0.0513	28704.5	50.00	Sequence
IAs	51	RDSEESYLALLDALR	SYLALLDAL	0.0506	28906.2	50.00	Sequence
IAs	180	SVPDFALTRASGDPL	ALTRASGDP	0.0506	28921.2	50.00	Sequence
IAs	259	KRDPQSNLFAHRDRG	SNLFAHRDR	0.0492	29351.8	50.00	Sequence
IAs	263	QSNLFAHRDRGFIPE	SNLFAHRDR	0.0483	29659.2	50.00	Sequence
IAs	347	LDTHGHHIALDEAAF	HHIALDEAA	0.0474	29947.5	50.00	Sequence
IAs	28	FNWAYARHTGGTFVF	RHTGGTFVF	0.0473	29959.2	50.00	Sequence
IAs	197	LVNPCDDALMKITHV	DALMKITHV	0.0461	30346.8	50.00	Sequence
IAs	87	SQRAEIYRDVLARLL	QRAEIYRDV	0.0460	30410.5	50.00	Sequence
IAs	195	YTLVNPCDDALMKIT	YTLVNPCDD	0.0459	30443.1	50.00	Sequence
IAs	194	LYTLVNPCDDALMKI	YTLVNPCDD	0.0458	30468.5	50.00	Sequence
IAs	466	SLELLGRDRSMQRLR	RDRSMQRLR	0.0455	30574.2	50.00	Sequence
IAs	109	AFSTPEEVEARHVAA	EEVEARHVA	0.0451	30699.2	50.00	Sequence
IAs	262	PQSNLFAHRDRGFIP	SNLFAHRDR	0.0451	30708.1	50.00	Sequence
IAs	458	TVSPPLFESLELLGR	PLFESLELL	0.0450	30736.0	50.00	Sequence
IAs	279	LLNYLALLGWSIADD	NYLALLGWS	0.0446	30844.0	50.00	Sequence
IAs	31	AYARHTGGTFVFRIE	GGTFVFRIE	0.0443	30948.9	50.00	Sequence
IAs	111	STPEEVEARHVAAGR	EEVEARHVA	0.0431	31354.8	50.00	Sequence
IAs	288	WSIADDHDLFGLDEM	SIADDHDLF	0.0430	31399.6	50.00	Sequence
IAs	261	DPQSNLFAHRDRGFI	SNLFAHRDR	0.0430	31399.9	50.00	Sequence
IAs	260	RDPQSNLFAHRDRGF	SNLFAHRDR	0.0426	31518.0	50.00	Sequence
IAs	179	GSVPDFALTRASGDP	ALTRASGDP	0.0425	31577.8	50.00	Sequence
IAs	467	LELLGRDRSMQRLRA	RDRSMQRLR	0.0423	31653.4	50.00	Sequence
IAs	91	EIYRDVLARLLAAGE	RDVLARLLA	0.0417	31839.9	50.00	Sequence
IAs	110	FSTPEEVEARHVAAG	EEVEARHVA	0.0415	31921.6	50.00	Sequence
IAs	37	GGTFVFRIEDTDAQR	TFVFRIEDT	0.0414	31950.0	50.00	Sequence
IAs	38	GTFVFRIEDTDAQRD	TFVFRIEDT	0.0413	31986.6	50.00	Sequence
IAs	89	RAEIYRDVLARLLAA	RDVLARLLA	0.0410	32100.3	50.00	Sequence
IAs	59	ALLDALRWLGLDWDE	LRWLGLDWD	0.0409	32120.1	50.00	Sequence
IAs	77	VGGPYGPYRQSQRAE	VGGPYGPYR	0.0407	32197.4	50.00	Sequence
IAs	372	IVVLGDAWELLKFFN	DAWELLKFF	0.0397	32545.2	50.00	Sequence
IAs	287	GWSIADDHDLFGLDE	SIADDHDLF	0.0391	32748.6	50.00	Sequence
IAs	159	MPDDDLAWNDLVRGP	AWNDLVRGP	0.0383	33039.8	50.00	Sequence
IAs	256	KLSKRDPQSNLFAHR	KLSKRDPQS	0.0380	33132.1	50.00	Sequence
IAs	346	HLDTHGHHIALDEAA	HHIALDEAA	0.0380	33144.7	50.00	Sequence
IAs	265	NLFAHRDRGFIPEGL	DRGFIPEGL	0.0379	33172.7	50.00	Sequence
IAs	397	AAKELGPDGAAVLDA	LGPDGAAVL	0.0379	33174.5	50.00	Sequence
IAs	86	QSQRAEIYRDVLARL	RAEIYRDVL	0.0378	33209.3	50.00	Sequence
IAs	30	WAYARHTGGTFVFRI	RHTGGTFVF	0.0377	33234.8	50.00	Sequence
IAs	289	SIADDHDLFGLDEMV	SIADDHDLF	0.0377	33240.6	50.00	Sequence
IAs	196	TLVNPCDDALMKITH	NPCDDALMK	0.0376	33294.2	50.00	Sequence
IAs	90	AEIYRDVLARLLAAG	RDVLARLLA	0.0373	33411.5	50.00	Sequence
IAs	39	TFVFRIEDTDAQRDS	TFVFRIEDT	0.0371	33455.2	50.00	Sequence
IAs	264	SNLFAHRDRGFIPEG	SNLFAHRDR	0.0367	33606.2	50.00	Sequence
IAs	58	LALLDALRWLGLDWD	ALLDALRWL	0.0367	33612.4	50.00	Sequence
IAs	61	LDALRWLGLDWDEGP	RWLGLDWDE	0.0367	33624.7	50.00	Sequence
IAs	277	EGLLNYLALLGWSIA	NYLALLGWS	0.0367	33627.6	50.00	Sequence
IAs	45	EDTDAQRDSEESYLA	RDSEESYLA	0.0363	33761.1	50.00	Sequence
IAs	460	SPPLFESLELLGRDR	PLFESLELL	0.0360	33859.8	50.00	Sequence

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         IAs   29  NWAYARHTGGTFVFR  RHTGGTFVF         0.0358      33930.6               50.00     Sequence
         IAs   78  GGPYGPYRQSQRAEI  GPYRQSQRA         0.0357      33989.1               50.00     Sequence
         IAs  373  VVLGDAWELLKFFND  VLGDAWELL         0.0355      34043.1               50.00     Sequence
         IAs  465  ESLELLGRDRSMQRL  ESLELLGRD         0.0351      34187.5               50.00     Sequence
         IAs  273  GFIPEGLLNYLALLG  GFIPEGLLN         0.0351      34200.0               50.00     Sequence
         IAs  257  LSKRDPQSNLFAHRD  KRDPQSNLF         0.0350      34247.8               50.00     Sequence
         IAs  275  IPEGLLNYLALLGWS  NYLALLGWS         0.0347      34339.1               50.00     Sequence
         IAs   57  YLALLDALRWLGLDW  ALLDALRWL         0.0343      34489.9               50.00     Sequence
         IAs   26  ALFNWAYARHTGGTF  FNWAYARHT         0.0339      34653.0               50.00     Sequence
         IAs   49  AQRDSEESYLALLDA  RDSEESYLA         0.0339      34656.4               50.00     Sequence
         IAs  278  GLLNYLALLGWSIAD  NYLALLGWS         0.0333      34884.0               50.00     Sequence
         IAs  178  AGSVPDFALTRASGD  FALTRASGD         0.0331      34937.6               50.00     Sequence
         IAs   46  DTDAQRDSEESYLAL  RDSEESYLA         0.0330      34989.4               50.00     Sequence
         IAs  125  RNPKLGYDNFDRHLT  RNPKLGYDN         0.0327      35084.2               50.00     Sequence
         IAs  461  PPLFESLELLGRDRS  PLFESLELL         0.0327      35085.0               50.00     Sequence
         IAs   48  DAQRDSEESYLALLD  QRDSEESYL         0.0327      35111.2               50.00     Sequence
         IAs  462  PLFESLELLGRDRSM  FESLELLGR         0.0323      35243.6               50.00     Sequence
         IAs   60  LLDALRWLGLDWDEG  RWLGLDWDE         0.0321      35310.8               50.00     Sequence
         IAs  333  MLDVGDFTVRLRDHL  FTVRLRDHL         0.0321      35324.9               50.00     Sequence
         IAs  374  VLGDAWELLKFFNDD  VLGDAWELL         0.0313      35650.2               50.00     Sequence
         IAs  376  GDAWELLKFFNDDQY  LKFFNDDQY         0.0308      35832.7               50.00     Sequence
         IAs   27  LFNWAYARHTGGTFV  FNWAYARHT         0.0307      35859.8               50.00     Sequence
         IAs  345  DHLDTHGHHIALDEA  GHHIALDEA         0.0306      35892.8               50.00     Sequence
         IAs  276  PEGLLNYLALLGWSI  NYLALLGWS         0.0305      35948.8               50.00     Sequence
         IAs   47  TDAQRDSEESYLALL  RDSEESYLA         0.0304      35998.6               50.00     Sequence
         IAs   44  IEDTDAQRDSEESYL  QRDSEESYL         0.0299      36195.5               50.00     Sequence
         IAs  463  LFESLELLGRDRSMQ  ESLELLGRD         0.0292      36463.1               50.00     Sequence
         IAs  274  FIPEGLLNYLALLGW  EGLLNYLAL         0.0288      36613.8               50.00     Sequence
         IAs  464  FESLELLGRDRSMQR  ESLELLGRD         0.0283      36817.6               50.00     Sequence
         IAs  334  LDVGDFTVRLRDHLD  FTVRLRDHL         0.0281      36881.8               50.00     Sequence
         IAs  375  LGDAWELLKFFNDDQ  DAWELLKFF         0.0274      37190.3               50.00     Sequence
         IAs   40  FVFRIEDTDAQRDSE  FVFRIEDTD         0.0268      37394.5               50.00     Sequence
         IAs   41  VFRIEDTDAQRDSEE  FRIEDTDAQ         0.0266      37494.1               50.00     Sequence
         IAs   42  FRIEDTDAQRDSEES  FRIEDTDAQ         0.0262      37638.0               50.00     Sequence
         IAs  335  DVGDFTVRLRDHLDT  FTVRLRDHL         0.0247      38294.9               50.00     Sequence
         IAs  339  FTVRLRDHLDTHGHH  FTVRLRDHL         0.0245      38375.7               50.00     Sequence
         IAs  294  HDLFGLDEMVAAFDV  HDLFGLDEM         0.0244      38411.5               50.00     Sequence
         IAs  156  RLRMPDDDLAWNDLV  LRMPDDDLA         0.0243      38421.0               50.00     Sequence
         IAs  338  DFTVRLRDHLDTHGH  FTVRLRDHL         0.0243      38441.4               50.00     Sequence
         IAs  337  GDFTVRLRDHLDTHG  FTVRLRDHL         0.0239      38594.8               50.00     Sequence
         IAs  336  VGDFTVRLRDHLDTH  FTVRLRDHL         0.0238      38659.5               50.00     Sequence
         IAs  291  ADDHDLFGLDEMVAA  FGLDEMVAA         0.0236      38735.3               50.00     Sequence
         IAs  292  DDHDLFGLDEMVAAF  HDLFGLDEM         0.0229      39023.1               50.00     Sequence
         IAs  343  LRDHLDTHGHHIALD  THGHHIALD         0.0226      39155.9               50.00     Sequence
         IAs  344  RDHLDTHGHHIALDE  THGHHIALD         0.0224      39254.3               50.00     Sequence
         IAs  126  NPKLGYDNFDRHLTD  NPKLGYDNF         0.0221      39378.9               50.00     Sequence
         IAs  157  LRMPDDDLAWNDLVR  LRMPDDDLA         0.0220      39426.2               50.00     Sequence
         IAs  290  IADDHDLFGLDEMVA  DLFGLDEMV         0.0219      39460.4               50.00     Sequence
         IAs  293  DHDLFGLDEMVAAFD  HDLFGLDEM         0.0213      39689.0               50.00     Sequence
         IAs  158  RMPDDDLAWNDLVRG  MPDDDLAWN         0.0211      39793.9               50.00     Sequence
         IAs  128  KLGYDNFDRHLTDAQ  LGYDNFDRH         0.0209      39865.5               50.00     Sequence
         IAs  129  LGYDNFDRHLTDAQR  LGYDNFDRH         0.0209      39890.1               50.00     Sequence
         IAs  127  PKLGYDNFDRHLTDA  LGYDNFDRH         0.0204      40117.3               50.00     Sequence
         IAs   43  RIEDTDAQRDSEESY  TDAQRDSEE         0.0187      40841.3               50.00     Sequence
         IAs  341  VRLRDHLDTHGHHIA  DHLDTHGHH         0.0183      41017.1               50.00     Sequence
         IAs  340  TVRLRDHLDTHGHHI  DHLDTHGHH         0.0176      41347.3               50.00     Sequence
         IAs  342  RLRDHLDTHGHHIAL  DHLDTHGHH         0.0170      41610.7               50.00     Sequence
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Allele: IAs. Number of high binders 0. Number of weak binders 0. Number of peptides 476

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Explain the output. Go **back**.