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  271  QRDFVAATGANLVTV  FVAATGANL        0.8890          3.3         SB     0.30     Sequence
   DRB1_0101   22  GAQYAQLIARRVREA  YAQLIARRV        0.8884          3.3         SB     0.30     Sequence
   DRB1_0101   21  FGAQYAQLIARRVRE  YAQLIARRV        0.8845          3.5         SB     0.40     Sequence
   DRB1_0101  365  DLKFTLVEPLRLLFK  FTLVEPLRL        0.8830          3.5         SB     0.40     Sequence
   DRB1_0101   20  DFGAQYAQLIARRVR  YAQLIARRV        0.8828          3.6         SB     0.40     Sequence
   DRB1_0101  270  VQRDFVAATGANLVT  FVAATGANL        0.8818          3.6         SB     0.80     Sequence
   DRB1_0101   23  AQYAQLIARRVREAR  YAQLIARRV        0.8805          3.6         SB     0.80     Sequence
   DRB1_0101  272  RDFVAATGANLVTVD  FVAATGANL        0.8775          3.8         SB     0.80     Sequence
   DRB1_0101   19  VDFGAQYAQLIARRV  YAQLIARRV        0.8775          3.8         SB     0.80     Sequence
   DRB1_0101  364  DDLKFTLVEPLRLLF  FTLVEPLRL        0.8772          3.8         SB     0.80     Sequence
   DRB1_0101  366  LKFTLVEPLRLLFKD  FTLVEPLRL        0.8728          4.0         SB     0.80     Sequence
   DRB1_0101  269  QVQRDFVAATGANLV  FVAATGANL        0.8720          4.0         SB     0.80     Sequence
   DRB1_0101  363  PDDLKFTLVEPLRLL  FTLVEPLRL        0.8700          4.1         SB     1.00     Sequence
   DRB1_0101   24  QYAQLIARRVREARV  YAQLIARRV        0.8699          4.1         SB     1.00     Sequence
   DRB1_0101   25  YAQLIARRVREARVF  YAQLIARRV        0.8551          4.8         SB     2.00     Sequence
   DRB1_0101  362  LPDDLKFTLVEPLRL  FTLVEPLRL        0.8546          4.8         SB     2.00     Sequence
   DRB1_0101  273  DFVAATGANLVTVDA  FVAATGANL        0.8515          5.0         SB     2.00     Sequence
   DRB1_0101  367  KFTLVEPLRLLFKDE  FTLVEPLRL        0.8504          5.0         SB     2.00     Sequence
   DRB1_0101  268  AQVQRDFVAATGANL  FVAATGANL        0.8504          5.0         SB     2.00     Sequence
   DRB1_0101   18  VVDFGAQYAQLIARR  FGAQYAQLI        0.8475          5.2         SB     4.00     Sequence
   DRB1_0101   92  CYGFQAMAQALGGIV  FQAMAQALG        0.8451          5.3         SB     4.00     Sequence
   DRB1_0101   36  ARVFSEVIPHTASIE  FSEVIPHTA        0.8430          5.5         SB     4.00     Sequence
   DRB1_0101   49  IEEIRARQPVALVLS  IRARQPVAL        0.8352          5.9         SB     4.00     Sequence
   DRB1_0101  274  FVAATGANLVTVDAA  FVAATGANL        0.8337          6.0         SB     4.00     Sequence
   DRB1_0101   17  LVVDFGAQYAQLIAR  FGAQYAQLI        0.8337          6.0         SB     4.00     Sequence
   DRB1_0101   35  EARVFSEVIPHTASI  FSEVIPHTA        0.8327          6.1         SB     4.00     Sequence
   DRB1_0101  289  ETFLEALSGVSAPEG  LEALSGVSA        0.8306          6.2         SB     4.00     Sequence
   DRB1_0101   91  ICYGFQAMAQALGGI  FQAMAQALG        0.8292          6.3         SB     4.00     Sequence
   DRB1_0101   57  PVALVLSGGPASVYA  VLSGGPASV        0.8278          6.4         SB     4.00     Sequence
   DRB1_0101   93  YGFQAMAQALGGIVA  FQAMAQALG        0.8261          6.6         SB     4.00     Sequence
   DRB1_0101   58  VALVLSGGPASVYAD  VLSGGPASV        0.8189          7.1         SB     8.00     Sequence
   DRB1_0101   16  VLVVDFGAQYAQLIA  FGAQYAQLI        0.8167          7.3         SB     8.00     Sequence
   DRB1_0101   37  RVFSEVIPHTASIEE  FSEVIPHTA        0.8153          7.4         SB     8.00     Sequence
   DRB1_0101  290  TFLEALSGVSAPEGK  LEALSGVSA        0.8132          7.5         SB     8.00     Sequence
   DRB1_0101  368  FTLVEPLRLLFKDEV  FTLVEPLRL        0.8128          7.6         SB     8.00     Sequence
   DRB1_0101   95  FQAMAQALGGIVAHT  MAQALGGIV        0.8115          7.7         SB     8.00     Sequence
   DRB1_0101  192  SRFLHDFAGLGAQWT  LHDFAGLGA        0.8110          7.7         SB     8.00     Sequence
   DRB1_0101   94  GFQAMAQALGGIVAH  FQAMAQALG        0.8106          7.8         SB     8.00     Sequence
   DRB1_0101   48  SIEEIRARQPVALVL  IRARQPVAL        0.8094          7.9         SB     8.00     Sequence
   DRB1_0101  444  QCPVVLLADVRSVGV  VVLLADVRS        0.8086          7.9         SB     8.00     Sequence
   DRB1_0101  288  AETFLEALSGVSAPE  LEALSGVSA        0.8077          8.0         SB     8.00     Sequence
   DRB1_0101  191  LSRFLHDFAGLGAQW  FLHDFAGLG        0.8023          8.5         SB     8.00     Sequence
   DRB1_0101   50  EEIRARQPVALVLSG  IRARQPVAL        0.8021          8.5         SB     8.00     Sequence
   DRB1_0101   56  QPVALVLSGGPASVY  VLSGGPASV        0.8012          8.6         SB     8.00     Sequence
   DRB1_0101   15  PVLVVDFGAQYAQLI  FGAQYAQLI        0.7963          9.1         SB     8.00     Sequence
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DRB1_0101   90  GICYGFQAMAQALGG  FQAMAQALG        0.7898          9.7          SB     8.00      Sequence
DRB1_0101  309  GRQFIRAFEGAVRDV  FIRAFEGAV        0.7897          9.7          SB     8.00      Sequence
DRB1_0101   34  REARVFSEVIPHTAS  FSEVIPHTA        0.7868         10.0          SB     8.00      Sequence
DRB1_0101  287  AAETFLEALSGVSAP  LEALSGVSA        0.7854         10.2          SB     8.00      Sequence
DRB1_0101  286  DAAETFLEALSGVSA  LEALSGVSA        0.7813         10.7          SB     8.00      Sequence
DRB1_0101  445  CPVVLLADVRSVGVQ  VVLLADVRS        0.7782         11.0          SB    16.00      Sequence
DRB1_0101   59  ALVLSGGPASVYADG  VLSGGPASV        0.7756         11.3          SB    16.00      Sequence
DRB1_0101   51  EIRARQPVALVLSGG  IRARQPVAL        0.7756         11.3          SB    16.00      Sequence
DRB1_0101  310  RQFIRAFEGAVRDVL  FIRAFEGAV        0.7742         11.5          SB    16.00      Sequence
DRB1_0101  193  RFLHDFAGLGAQWTP  LHDFAGLGA        0.7712         11.9          SB    16.00      Sequence
DRB1_0101   89  LGICYGFQAMAQALG  FQAMAQALG        0.7711         11.9          SB    16.00      Sequence
DRB1_0101  291  FLEALSGVSAPEGKR  LEALSGVSA        0.7679         12.3          SB    16.00      Sequence
DRB1_0101   96  QAMAQALGGIVAHTG  AQALGGIVA        0.7673         12.4          SB    16.00      Sequence
DRB1_0101  148  PDGFDVVASSAGAPV  FDVVASSAG        0.7658         12.6          SB    16.00      Sequence
DRB1_0101  232  SGGVDSAVAAALVQR  VDSAVAAAL        0.7658         12.6          SB    16.00      Sequence
DRB1_0101  233  GGVDSAVAAALVQRA  DSAVAAALV        0.7649         12.7          SB    16.00      Sequence
DRB1_0101  190  VLSRFLHDFAGLGAQ  FLHDFAGLG        0.7575         13.8          SB    16.00      Sequence
DRB1_0101   38  VFSEVIPHTASIEEI  FSEVIPHTA        0.7550         14.2          SB    16.00      Sequence
DRB1_0101  446  PVVLLADVRSVGVQG  VVLLADVRS        0.7521         14.6          SB    16.00      Sequence
DRB1_0101  279  GANLVTVDAAETFLE  LVTVDAAET        0.7519         14.6          SB    16.00      Sequence
DRB1_0101  150  GFDVVASSAGAPVAA  FDVVASSAG        0.7477         15.3          SB    16.00      Sequence
DRB1_0101  149  DGFDVVASSAGAPVA  FDVVASSAG        0.7468         15.5          SB    16.00      Sequence
DRB1_0101  241  AALVQRAIGDRLTCV  VQRAIGDRL        0.7435         16.0          SB    16.00      Sequence
DRB1_0101  151  FDVVASSAGAPVAAF  VASSAGAPV        0.7429         16.1          SB    16.00      Sequence
DRB1_0101  489  YEVLERISTRITNEV  LERISTRIT        0.7397         16.7          SB    16.00      Sequence
DRB1_0101  234  GVDSAVAAALVQRAI  DSAVAAALV        0.7393         16.8          SB    16.00      Sequence
DRB1_0101  195  LHDFAGLGAQWTPAN  FAGLGAQWT        0.7383         17.0          SB    16.00      Sequence
DRB1_0101   47  ASIEEIRARQPVALV  IRARQPVAL        0.7371         17.2          SB    16.00      Sequence
DRB1_0101   33  VREARVFSEVIPHTA  FSEVIPHTA        0.7370         17.2          SB    16.00      Sequence
DRB1_0101   52  IRARQPVALVLSGGP  IRARQPVAL        0.7365         17.3          SB    16.00      Sequence
DRB1_0101  443  WQCPVVLLADVRSVG  VVLLADVRS        0.7355         17.5          SB    16.00      Sequence
DRB1_0101  278  TGANLVTVDAAETFL  LVTVDAAET        0.7338         17.8          SB    16.00      Sequence
DRB1_0101  194  FLHDFAGLGAQWTPA  FAGLGAQWT        0.7326         18.1          SB    16.00      Sequence
DRB1_0101   55  RQPVALVLSGGPASV  ALVLSGGPA        0.7321         18.2          SB    16.00      Sequence
DRB1_0101  235  VDSAVAAALVQRAIG  VAAALVQRA        0.7316         18.3          SB    16.00      Sequence
DRB1_0101  231  LSGGVDSAVAAALVQ  VDSAVAAAL        0.7275         19.1          SB    16.00      Sequence
DRB1_0101  447  VVLLADVRSVGVQGD  VVLLADVRS        0.7229         20.0          SB    16.00      Sequence
DRB1_0101  405  GLGIRIVGEVTAKRL  IRIVGEVTA        0.7174         21.3          SB    16.00      Sequence
DRB1_0101   60  LVLSGGPASVYADGA  VLSGGPASV        0.7169         21.4          SB    16.00      Sequence
DRB1_0101  189  QVLSRFLHDFAGLGA  FLHDFAGLG        0.7150         21.8          SB    16.00      Sequence
DRB1_0101  153  VVASSAGAPVAAFEA  SSAGAPVAA        0.7114         22.7          SB    16.00      Sequence
DRB1_0101  236  DSAVAAALVQRAIGD  VAAALVQRA        0.7106         22.9          SB    16.00      Sequence
DRB1_0101  307  IIGRQFIRAFEGAVR  FIRAFEGAV        0.7073         23.7          SB    32.00      Sequence
DRB1_0101  416  AKRLDTLRHADSIVR  LDTLRHADS        0.7058         24.1          SB    32.00      Sequence
DRB1_0101   97  AMAQALGGIVAHTGT  MAQALGGIV        0.7038         24.6          SB    32.00      Sequence
DRB1_0101  242  ALVQRAIGDRLTCVF  VQRAIGDRL        0.7020         25.1          SB    32.00      Sequence
DRB1_0101  280  ANLVTVDAAETFLEA  LVTVDAAET        0.7017         25.2          SB    32.00      Sequence
DRB1_0101   88  VLGICYGFQAMAQAL  CYGFQAMAQ        0.7010         25.4          SB    32.00      Sequence
DRB1_0101  308  IGRQFIRAFEGAVRD  FIRAFEGAV        0.6996         25.8          SB    32.00      Sequence
DRB1_0101  442  IWQCPVVLLADVRSV  VVLLADVRS        0.6937         27.5          SB    32.00      Sequence
DRB1_0101  292  LEALSGVSAPEGKRK  LEALSGVSA        0.6933         27.6          SB    32.00      Sequence
DRB1_0101  230  GLSGGVDSAVAAALV  VDSAVAAAL        0.6931         27.7          SB    32.00      Sequence
DRB1_0101   39  FSEVIPHTASIEEIR  FSEVIPHTA        0.6888         29.0          SB    32.00      Sequence
DRB1_0101  311  QFIRAFEGAVRDVLD  FIRAFEGAV        0.6853         30.1          SB    32.00      Sequence
DRB1_0101  486  RVPYEVLERISTRIT  YEVLERIST        0.6762         33.2          SB    32.00      Sequence
DRB1_0101  468  PIVLRPVSSEDAMTA  LRPVSSEDA        0.6762         33.2          SB    32.00      Sequence
DRB1_0101  328  TAEFLVQGTLYPDVV  FLVQGTLYP        0.6761         33.3          SB    32.00      Sequence
DRB1_0101  116  RTELKVLGGKLHSDL  LKVLGGKLH        0.6745         33.8          SB    32.00      Sequence
DRB1_0101   46  TASIEEIRARQPVAL  IRARQPVAL        0.6738         34.1          SB    32.00      Sequence
DRB1_0101  237  SAVAAALVQRAIGDR  VAAALVQRA        0.6737         34.1          SB    32.00      Sequence
DRB1_0101  471  LRPVSSEDAMTADWT  VSSEDAMTA        0.6737         34.1          SB    32.00      Sequence
DRB1_0101  152  DVVASSAGAPVAAFE  SSAGAPVAA        0.6702         35.5          SB    32.00      Sequence
DRB1_0101  490  EVLERISTRITNEVA  LERISTRIT        0.6680         36.3          SB    32.00      Sequence
DRB1_0101  217  QVRTQIGDGHAICGL  TQIGDGHAI        0.6661         37.1          SB    32.00      Sequence
DRB1_0101  196  HDFAGLGAQWTPANI  FAGLGAQWT        0.6652         37.4          SB    32.00      Sequence
DRB1_0101  406  LGIRIVGEVTAKRLD  IRIVGEVTA        0.6624         38.6          SB    32.00      Sequence
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DRB1_0101  147  APDGFDVVASSAGAP  FDVVASSAG         0.6624         38.6          SB    32.00       Sequence
DRB1_0101   98  MAQALGGIVAHTGTR  LGGIVAHTG         0.6611         39.1          SB    32.00       Sequence
DRB1_0101  146  AAPDGFDVVASSAGA  FDVVASSAG         0.6556         41.5          SB    32.00       Sequence
DRB1_0101   77  LDPALLDLGVPVLGI  ALLDLGVPV         0.6531         42.7          SB    32.00       Sequence
DRB1_0101  488  PYEVLERISTRITNE  LERISTRIT         0.6526         42.9          SB    32.00       Sequence
DRB1_0101   79  PALLDLGVPVLGICY  LDLGVPVLG         0.6467         45.7          SB    32.00       Sequence
DRB1_0101  487  VPYEVLERISTRITN  LERISTRIT         0.6431         47.6          SB    32.00       Sequence
DRB1_0101   99  AQALGGIVAHTGTRE  LGGIVAHTG         0.6422         48.0          SB    32.00       Sequence
DRB1_0101  417  KRLDTLRHADSIVRE  LDTLRHADS         0.6406         48.9          SB    32.00       Sequence
DRB1_0101  469  IVLRPVSSEDAMTAD  LRPVSSEDA         0.6404         49.0          SB    32.00       Sequence
DRB1_0101  240  AAALVQRAIGDRLTC  VQRAIGDRL         0.6390         49.7          SB    32.00       Sequence
DRB1_0101   87  PVLGICYGFQAMAQA  CYGFQAMAQ         0.6387         49.9          SB    32.00       Sequence
DRB1_0101  154  VASSAGAPVAAFEAF  SSAGAPVAA         0.6336         52.7          WB    32.00       Sequence
DRB1_0101  275  VAATGANLVTVDAAE  VAATGANLV         0.6289         55.5          WB    32.00       Sequence
DRB1_0101   78  DPALLDLGVPVLGIC  LDLGVPVLG         0.6288         55.5          WB    32.00       Sequence
DRB1_0101  277  ATGANLVTVDAAETF  LVTVDAAET         0.6287         55.6          WB    32.00       Sequence
DRB1_0101  404  PGLGIRIVGEVTAKR  IRIVGEVTA         0.6286         55.6          WB    32.00       Sequence
DRB1_0101  281  NLVTVDAAETFLEAL  LVTVDAAET         0.6279         56.1          WB    32.00       Sequence
DRB1_0101  243  LVQRAIGDRLTCVFV  VQRAIGDRL         0.6274         56.3          WB    32.00       Sequence
DRB1_0101  373  PLRLLFKDEVRAVGR  LLFKDEVRA         0.6264         57.0          WB    32.00       Sequence
DRB1_0101  327  KTAEFLVQGTLYPDV  FLVQGTLYP         0.6261         57.1          WB    32.00       Sequence
DRB1_0101  415  TAKRLDTLRHADSIV  LDTLRHADS         0.6245         58.1          WB    32.00       Sequence
DRB1_0101   80  ALLDLGVPVLGICYG  LDLGVPVLG         0.6235         58.8          WB    32.00       Sequence
DRB1_0101  408  IRIVGEVTAKRLDTL  VGEVTAKRL         0.6220         59.7          WB    32.00       Sequence
DRB1_0101   26  AQLIARRVREARVFS  LIARRVREA         0.6182         62.2          WB    32.00       Sequence
DRB1_0101  329  AEFLVQGTLYPDVVE  FLVQGTLYP         0.6165         63.4          WB    32.00       Sequence
DRB1_0101  465  YGHPIVLRPVSSEDA  PIVLRPVSS         0.6160         63.8          WB    32.00       Sequence
DRB1_0101  470  VLRPVSSEDAMTADW  VSSEDAMTA         0.6154         64.2          WB    32.00       Sequence
DRB1_0101  162  VAAFEAFDRRLAGVQ  FEAFDRRLA         0.6152         64.3          WB    32.00       Sequence
DRB1_0101   86  VPVLGICYGFQAMAQ  CYGFQAMAQ         0.6141         65.1          WB    32.00       Sequence
DRB1_0101  491  VLERISTRITNEVAE  LERISTRIT         0.6141         65.1          WB    32.00       Sequence
DRB1_0101  285  VDAAETFLEALSGVS  FLEALSGVS         0.6128         66.0          WB    32.00       Sequence
DRB1_0101  441  QIWQCPVVLLADVRS  VVLLADVRS         0.6115         66.9          WB    32.00       Sequence
DRB1_0101  481  TADWTRVPYEVLERI  WTRVPYEVL         0.6115         66.9          WB    32.00       Sequence
DRB1_0101  197  DFAGLGAQWTPANIA  FAGLGAQWT         0.6109         67.4          WB    32.00       Sequence
DRB1_0101  188  QQVLSRFLHDFAGLG  FLHDFAGLG         0.6106         67.6          WB    32.00       Sequence
DRB1_0101  306  KIIGRQFIRAFEGAV  FIRAFEGAV         0.6084         69.2          WB    32.00       Sequence
DRB1_0101  229  CGLSGGVDSAVAAAL  VDSAVAAAL         0.6074         70.0          WB    32.00       Sequence
DRB1_0101   54  ARQPVALVLSGGPAS  LVLSGGPAS         0.6073         70.0          WB    32.00       Sequence
DRB1_0101  239  VAAALVQRAIGDRLT  VQRAIGDRL         0.6056         71.3          WB    32.00       Sequence
DRB1_0101  251  RLTCVFVDHGLLRAG  CVFVDHGLL         0.6050         71.8          WB    32.00       Sequence
DRB1_0101  238  AVAAALVQRAIGDRL  VAAALVQRA         0.5996         76.1          WB    50.00       Sequence
DRB1_0101  374  LRLLFKDEVRAVGRE  LLFKDEVRA         0.5984         77.1          WB    50.00       Sequence
DRB1_0101   14  RPVLVVDFGAQYAQL  VVDFGAQYA         0.5963         78.9          WB    50.00       Sequence
DRB1_0101  100  QALGGIVAHTGTREY  LGGIVAHTG         0.5954         79.7          WB    50.00       Sequence
DRB1_0101  218  VRTQIGDGHAICGLS  TQIGDGHAI         0.5947         80.2          WB    50.00       Sequence
DRB1_0101  312  FIRAFEGAVRDVLDG  FIRAFEGAV         0.5943         80.6          WB    50.00       Sequence
DRB1_0101  161  PVAAFEAFDRRLAGV  FEAFDRRLA         0.5941         80.8          WB    50.00       Sequence
DRB1_0101  253  TCVFVDHGLLRAGER  FVDHGLLRA         0.5925         82.2          WB    50.00       Sequence
DRB1_0101  250  DRLTCVFVDHGLLRA  CVFVDHGLL         0.5916         83.0          WB    50.00       Sequence
DRB1_0101  179  PEVMHTPHGQQVLSR  MHTPHGQQV         0.5904         84.1          WB    50.00       Sequence
DRB1_0101  467  HPIVLRPVSSEDAMT  LRPVSSEDA         0.5889         85.5          WB    50.00       Sequence
DRB1_0101  407  GIRIVGEVTAKRLDT  IRIVGEVTA         0.5881         86.2          WB    50.00       Sequence
DRB1_0101  448  VLLADVRSVGVQGDG  VLLADVRSV         0.5881         86.2          WB    50.00       Sequence
DRB1_0101   66  PASVYADGAPKLDPA  VYADGAPKL         0.5858         88.4          WB    50.00       Sequence
DRB1_0101  509  VVLDITSKPPATIEW  DITSKPPAT         0.5848         89.3          WB    50.00       Sequence
DRB1_0101  198  FAGLGAQWTPANIAN  FAGLGAQWT         0.5847         89.5          WB    50.00       Sequence
DRB1_0101  202  GAQWTPANIANALIE  WTPANIANA         0.5841         90.0          WB    50.00       Sequence
DRB1_0101   76  KLDPALLDLGVPVLG  ALLDLGVPV         0.5839         90.2          WB    50.00       Sequence
DRB1_0101   27  QLIARRVREARVFSE  ARRVREARV         0.5837         90.4          WB    50.00       Sequence
DRB1_0101   81  LLDLGVPVLGICYGF  LDLGVPVLG         0.5835         90.6          WB    50.00       Sequence
DRB1_0101  228  ICGLSGGVDSAVAAA  LSGGVDSAV         0.5831         91.0          WB    50.00       Sequence
DRB1_0101  485  TRVPYEVLERISTRI  YEVLERIST         0.5825         91.6          WB    50.00       Sequence
DRB1_0101  252  LTCVFVDHGLLRAGE  CVFVDHGLL         0.5800         94.1          WB    50.00       Sequence
DRB1_0101  114  YGRTELKVLGGKLHS  LKVLGGKLH         0.5784         95.7          WB    50.00       Sequence
DRB1_0101  115  GRTELKVLGGKLHSD  LKVLGGKLH         0.5764         97.9          WB    50.00       Sequence
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DRB1_0101  117  TELKVLGGKLHSDLP  LKVLGGKLH       0.5754       98.8       WB    50.00     Sequence
DRB1_0101  397  ARQPFPGPGLGIRIV  PFPGPGLGI       0.5750       99.3       WB    50.00     Sequence
DRB1_0101  463  RTYGHPIVLRPVSSE  PIVLRPVSS       0.5733      101.2       WB    50.00     Sequence
DRB1_0101  163  AAFEAFDRRLAGVQY  FEAFDRRLA       0.5712      103.5       WB    50.00     Sequence
DRB1_0101  466  GHPIVLRPVSSEDAM  PIVLRPVSS       0.5695      105.4       WB    50.00     Sequence
DRB1_0101  462  GRTYGHPIVLRPVSS  YGHPIVLRP       0.5690      106.0       WB    50.00     Sequence
DRB1_0101  440  NQIWQCPVVLLADVR  WQCPVVLLA       0.5684      106.7       WB    50.00     Sequence
DRB1_0101   61  VLSGGPASVYADGAP  VLSGGPASV       0.5638      112.1       WB    50.00     Sequence
DRB1_0101  499  ITNEVAEVNRVVLDI  EVAEVNRVV       0.5626      113.6       WB    50.00     Sequence
DRB1_0101  330  EFLVQGTLYPDVVES  FLVQGTLYP       0.5620      114.3       WB    50.00     Sequence
DRB1_0101  249  GDRLTCVFVDHGLLR  CVFVDHGLL       0.5594      117.6       WB    50.00     Sequence
DRB1_0101  282  LVTVDAAETFLEALS  LVTVDAAET       0.5589      118.2       WB    50.00     Sequence
DRB1_0101  145  TAAPDGFDVVASSAG  FDVVASSAG       0.5589      118.2       WB    50.00     Sequence
DRB1_0101   82  LDLGVPVLGICYGFQ  LDLGVPVLG       0.5589      118.3       WB    50.00     Sequence
DRB1_0101  201  LGAQWTPANIANALI  WTPANIANA       0.5586      118.6       WB    50.00     Sequence
DRB1_0101  472  RPVSSEDAMTADWTR  VSSEDAMTA       0.5583      119.1       WB    50.00     Sequence
DRB1_0101  439  DNQIWQCPVVLLADV  WQCPVVLLA       0.5557      122.4       WB    50.00     Sequence
DRB1_0101  180  EVMHTPHGQQVLSRF  MHTPHGQQV       0.5546      123.8       WB    50.00     Sequence
DRB1_0101  326  GKTAEFLVQGTLYPD  FLVQGTLYP       0.5545      124.0       WB    50.00     Sequence
DRB1_0101  325  DGKTAEFLVQGTLYP  FLVQGTLYP       0.5545      124.1       WB    50.00     Sequence
DRB1_0101  510  VLDITSKPPATIEWE  ITSKPPATI       0.5531      125.9       WB    50.00     Sequence
DRB1_0101  212  NALIEQVRTQIGDGH  IEQVRTQIG       0.5523      126.9       WB    50.00     Sequence
DRB1_0101  418  RLDTLRHADSIVREE  LDTLRHADS       0.5505      129.5       WB    50.00     Sequence
DRB1_0101  419  LDTLRHADSIVREEL  LRHADSIVR       0.5499      130.4       WB    50.00     Sequence
DRB1_0101   67  ASVYADGAPKLDPAL  VYADGAPKL       0.5491      131.4       WB    50.00     Sequence
DRB1_0101  164  AFEAFDRRLAGVQYH  FEAFDRRLA       0.5476      133.6       WB    50.00     Sequence
DRB1_0101  184  TPHGQQVLSRFLHDF  GQQVLSRFL       0.5465      135.2       WB    50.00     Sequence
DRB1_0101  464  TYGHPIVLRPVSSED  PIVLRPVSS       0.5460      135.9       WB    50.00     Sequence
DRB1_0101  101  ALGGIVAHTGTREYG  LGGIVAHTG       0.5459      136.1       WB    50.00     Sequence
DRB1_0101  403  GPGLGIRIVGEVTAK  GIRIVGEVT       0.5459      136.1       WB    50.00     Sequence
DRB1_0101    7  DVPETPARPVLVVDF  ETPARPVLV       0.5441      138.7       WB    50.00     Sequence
DRB1_0101  304  KRKIIGRQFIRAFEG  IIGRQFIRA       0.5439      139.1       WB    50.00     Sequence
DRB1_0101  160  APVAAFEAFDRRLAG  FEAFDRRLA       0.5419      142.1       WB    50.00     Sequence
DRB1_0101  482  ADWTRVPYEVLERIS  WTRVPYEVL       0.5417      142.3       WB    50.00     Sequence
DRB1_0101  203  AQWTPANIANALIEQ  WTPANIANA       0.5408      143.8       WB    50.00     Sequence
DRB1_0101  133  VQPVWMSHGDAVTAA  MSHGDAVTA       0.5377      148.8       WB    50.00     Sequence
DRB1_0101  254  CVFVDHGLLRAGERA  CVFVDHGLL       0.5372      149.5       WB    50.00     Sequence
DRB1_0101   85  GVPVLGICYGFQAMA  LGICYGFQA       0.5370      149.9       WB    50.00     Sequence
DRB1_0101  216  EQVRTQIGDGHAICG  TQIGDGHAI       0.5369      150.0       WB    50.00     Sequence
DRB1_0101  492  LERISTRITNEVAEV  LERISTRIT       0.5356      152.1       WB    50.00     Sequence
DRB1_0101  302  EGKRKIIGRQFIRAF  KRKIIGRQF       0.5348      153.4       WB    50.00     Sequence
DRB1_0101  437  GLDNQIWQCPVVLLA  QIWQCPVVL       0.5342      154.4       WB    50.00     Sequence
DRB1_0101  303  GKRKIIGRQFIRAFE  IIGRQFIRA       0.5332      156.1       WB    50.00     Sequence
DRB1_0101  480  MTADWTRVPYEVLER  WTRVPYEVL       0.5325      157.3       WB    50.00     Sequence
DRB1_0101  181  VMHTPHGQQVLSRFL  MHTPHGQQV       0.5314      159.3       WB    50.00     Sequence
DRB1_0101  200  GLGAQWTPANIANAL  AQWTPANIA       0.5313      159.4       WB    50.00     Sequence
DRB1_0101  398  RQPFPGPGLGIRIVG  PFPGPGLGI       0.5297      162.1       WB    50.00     Sequence
DRB1_0101  409  RIVGEVTAKRLDTLR  VGEVTAKRL       0.5295      162.5       WB    50.00     Sequence
DRB1_0101  372  EPLRLLFKDEVRAVG  LLFKDEVRA       0.5294      162.7       WB    50.00     Sequence
DRB1_0101  248  IGDRLTCVFVDHGLL  CVFVDHGLL       0.5288      163.7       WB    50.00     Sequence
DRB1_0101  438  LDNQIWQCPVVLLAD  QIWQCPVVL       0.5287      164.0       WB    50.00     Sequence
DRB1_0101   75  PKLDPALLDLGVPVL  LLDLGVPVL       0.5274      166.2       WB    50.00     Sequence
DRB1_0101  225  GHAICGLSGGVDSAV  ICGLSGGVD       0.5270      166.9       WB    50.00     Sequence
DRB1_0101   53  RARQPVALVLSGGPA  ARQPVALVL       0.5255      169.7       WB    50.00     Sequence
DRB1_0101  461  DGRTYGHPIVLRPVS  YGHPIVLRP       0.5254      169.9       WB    50.00     Sequence
DRB1_0101  204  QWTPANIANALIEQV  PANIANALI       0.5250      170.6       WB    50.00     Sequence
DRB1_0101    8  VPETPARPVLVVDFG  ETPARPVLV       0.5241      172.3       WB    50.00     Sequence
DRB1_0101  102  LGGIVAHTGTREYGR  LGGIVAHTG       0.5227      175.0       WB    50.00     Sequence
DRB1_0101  244  VQRAIGDRLTCVFVD  VQRAIGDRL       0.5223      175.7       WB    50.00     Sequence
DRB1_0101  155  ASSAGAPVAAFEAFD  SSAGAPVAA       0.5212      177.7       WB    50.00     Sequence
DRB1_0101  331  FLVQGTLYPDVVESG  FLVQGTLYP       0.5207      178.7       WB    50.00     Sequence
DRB1_0101  165  FEAFDRRLAGVQYHP  FEAFDRRLA       0.5196      180.9       WB    50.00     Sequence
DRB1_0101  301  PEGKRKIIGRQFIRA  KRKIIGRQF       0.5192      181.6       WB    50.00     Sequence
DRB1_0101  497  TRITNEVAEVNRVVL  EVAEVNRVV       0.5188      182.4       WB    50.00     Sequence
DRB1_0101  134  QPVWMSHGDAVTAAP  MSHGDAVTA       0.5148      190.6       WB    50.00     Sequence
DRB1_0101  159  GAPVAAFEAFDRRLA  FEAFDRRLA       0.5144      191.4       WB    50.00     Sequence
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DRB1_0101  219  RTQIGDGHAICGLSG  TQIGDGHAI         0.5143         191.6          WB    50.00      Sequence
DRB1_0101  182  MHTPHGQQVLSRFLH  GQQVLSRFL         0.5137         192.7          WB    50.00      Sequence
DRB1_0101   84  LGVPVLGICYGFQAM  PVLGICYGF         0.5133         193.6          WB    50.00      Sequence
DRB1_0101  498  RITNEVAEVNRVVLD  EVAEVNRVV         0.5120         196.5          WB    50.00      Sequence
DRB1_0101  375  RLLFKDEVRAVGREL  LFKDEVRAV         0.5117         197.0          WB    50.00      Sequence
DRB1_0101  113  EYGRTELKVLGGKLH  ELKVLGGKL         0.5101         200.4          WB    50.00      Sequence
DRB1_0101   83  DLGVPVLGICYGFQA  DLGVPVLGI         0.5082         204.7          WB    50.00      Sequence
DRB1_0101  496  STRITNEVAEVNRVV  ITNEVAEVN         0.5076         206.0          WB    50.00      Sequence
DRB1_0101  414  VTAKRLDTLRHADSI  LDTLRHADS         0.5072         206.9          WB    50.00      Sequence
DRB1_0101  507  NRVVLDITSKPPATI  VLDITSKPP         0.5067         208.0          WB    50.00      Sequence
DRB1_0101  305  RKIIGRQFIRAFEGA  IIGRQFIRA         0.5064         208.6          WB    50.00      Sequence
DRB1_0101  508  RVVLDITSKPPATIE  DITSKPPAT         0.5060         209.6          WB    50.00      Sequence
DRB1_0101  371  VEPLRLLFKDEVRAV  LRLLFKDEV         0.5056         210.4          WB    50.00      Sequence
DRB1_0101  276  AATGANLVTVDAAET  LVTVDAAET         0.5039         214.4          WB    50.00      Sequence
DRB1_0101  185  PHGQQVLSRFLHDFA  GQQVLSRFL         0.5021         218.7          WB    50.00      Sequence
DRB1_0101  227  AICGLSGGVDSAVAA  LSGGVDSAV         0.5009         221.4          WB    50.00      Sequence
DRB1_0101  402  PGPGLGIRIVGEVTA  GIRIVGEVT         0.5007         221.9          WB    50.00      Sequence
DRB1_0101  484  WTRVPYEVLERISTR  WTRVPYEVL         0.4989         226.2          WB    50.00      Sequence
DRB1_0101  500  TNEVAEVNRVVLDIT  EVAEVNRVV         0.4986         226.9          WB    50.00      Sequence
DRB1_0101  118  ELKVLGGKLHSDLPE  LKVLGGKLH         0.4981         228.1          WB    50.00      Sequence
DRB1_0101   13  ARPVLVVDFGAQYAQ  VVDFGAQYA         0.4978         228.9          WB    50.00      Sequence
DRB1_0101  135  PVWMSHGDAVTAAPD  MSHGDAVTA         0.4975         229.7          WB    50.00      Sequence
DRB1_0101  396  VARQPFPGPGLGIRI  PFPGPGLGI         0.4944         237.6          WB    50.00      Sequence
DRB1_0101   28  LIARRVREARVFSEV  ARRVREARV         0.4942         238.1          WB    50.00      Sequence
DRB1_0101  226  HAICGLSGGVDSAVA  ICGLSGGVD         0.4942         238.1          WB    50.00      Sequence
DRB1_0101  293  EALSGVSAPEGKRKI  LSGVSAPEG         0.4940         238.6          WB    50.00      Sequence
DRB1_0101  178  HPEVMHTPHGQQVLS  MHTPHGQQV         0.4929         241.4          WB    50.00      Sequence
DRB1_0101  361  GLPDDLKFTLVEPLR  LKFTLVEPL         0.4929         241.5          WB    50.00      Sequence
DRB1_0101  321  RDVLDGKTAEFLVQG  LDGKTAEFL         0.4925         242.6          WB    50.00      Sequence
DRB1_0101    5  DIDVPETPARPVLVV  ETPARPVLV         0.4922         243.3          WB    50.00      Sequence
DRB1_0101  460  GDGRTYGHPIVLRPV  YGHPIVLRP         0.4919         244.0          WB    50.00      Sequence
DRB1_0101  436  AGLDNQIWQCPVVLL  QIWQCPVVL         0.4919         244.1          WB    50.00      Sequence
DRB1_0101  399  QPFPGPGLGIRIVGE  PFPGPGLGI         0.4904         248.0          WB    50.00      Sequence
DRB1_0101  377  LFKDEVRAVGRELGL  EVRAVGREL         0.4901         248.8          WB    50.00      Sequence
DRB1_0101  483  DWTRVPYEVLERIST  WTRVPYEVL         0.4899         249.4          WB    50.00      Sequence
DRB1_0101  187  GQQVLSRFLHDFAGL  GQQVLSRFL         0.4887         252.6          WB    50.00      Sequence
DRB1_0101  378  FKDEVRAVGRELGLP  EVRAVGREL         0.4869         257.5          WB    50.00      Sequence
DRB1_0101    6  IDVPETPARPVLVVD  ETPARPVLV         0.4861         259.9          WB    50.00      Sequence
DRB1_0101  183  HTPHGQQVLSRFLHD  GQQVLSRFL         0.4857         260.9          WB    50.00      Sequence
DRB1_0101   65  GPASVYADGAPKLDP  VYADGAPKL         0.4853         262.3          WB    50.00      Sequence
DRB1_0101  400  PFPGPGLGIRIVGEV  GPGLGIRIV         0.4848         263.5          WB    50.00      Sequence
DRB1_0101   63  SGGPASVYADGAPKL  VYADGAPKL         0.4838         266.4          WB    50.00      Sequence
DRB1_0101  427  SIVREELTAAGLDNQ  REELTAAGL         0.4836         267.1          WB    50.00      Sequence
DRB1_0101  369  TLVEPLRLLFKDEVR  TLVEPLRLL         0.4828         269.4          WB    50.00      Sequence
DRB1_0101  424  HADSIVREELTAAGL  IVREELTAA         0.4823         270.8          WB    50.00      Sequence
DRB1_0101  186  HGQQVLSRFLHDFAG  GQQVLSRFL         0.4812         274.1          WB    50.00      Sequence
DRB1_0101   64  GGPASVYADGAPKLD  VYADGAPKL         0.4807         275.7          WB    50.00      Sequence
DRB1_0101  156  SSAGAPVAAFEAFDR  GAPVAAFEA         0.4788         281.3          WB    50.00      Sequence
DRB1_0101  401  FPGPGLGIRIVGEVT  GPGLGIRIV         0.4787         281.6          WB    50.00      Sequence
DRB1_0101  425  ADSIVREELTAAGLD  IVREELTAA         0.4777         284.5          WB    50.00      Sequence
DRB1_0101  215  IEQVRTQIGDGHAIC  TQIGDGHAI         0.4762         289.2          WB    50.00      Sequence
DRB1_0101  258  DHGLLRAGERAQVQR  LLRAGERAQ         0.4750         293.0          WB    50.00      Sequence
DRB1_0101   12  PARPVLVVDFGAQYA  PVLVVDFGA         0.4749         293.5          WB    50.00      Sequence
DRB1_0101  385  VGRELGLPEEIVARQ  ELGLPEEIV         0.4745         294.5          WB    50.00      Sequence
DRB1_0101  313  IRAFEGAVRDVLDGK  FEGAVRDVL         0.4744         295.0          WB    50.00      Sequence
DRB1_0101   45  HTASIEEIRARQPVA  IEEIRARQP         0.4737         297.2          WB    50.00      Sequence
DRB1_0101  384  AVGRELGLPEEIVAR  RELGLPEEI         0.4723         301.9          WB    50.00      Sequence
DRB1_0101  205  WTPANIANALIEQVR  PANIANALI         0.4685         314.4          WB    50.00      Sequence
DRB1_0101  132  EVQPVWMSHGDAVTA  MSHGDAVTA         0.4683         315.3          WB    50.00      Sequence
DRB1_0101  166  EAFDRRLAGVQYHPE  DRRLAGVQY         0.4677         317.2          WB    50.00      Sequence
DRB1_0101  395  IVARQPFPGPGLGIR  RQPFPGPGL         0.4673         318.4          WB    50.00      Sequence
DRB1_0101   68  SVYADGAPKLDPALL  VYADGAPKL         0.4650         326.6          WB    50.00      Sequence
DRB1_0101  473  PVSSEDAMTADWTRV  VSSEDAMTA         0.4647         327.7          WB    50.00      Sequence
DRB1_0101    9  PETPARPVLVVDFGA  ETPARPVLV         0.4638         330.9          WB    50.00      Sequence
DRB1_0101  493  ERISTRITNEVAEVN  STRITNEVA         0.4625         335.6          WB    50.00      Sequence
DRB1_0101  213  ALIEQVRTQIGDGHA  IEQVRTQIG         0.4617         338.3          WB    50.00      Sequence
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DRB1_0101  392  PEEIVARQPFPGPGL  IVARQPFPG       0.4610       341.1       WB    50.00     Sequence
DRB1_0101  211  ANALIEQVRTQIGDG  IEQVRTQIG       0.4609       341.5       WB    50.00     Sequence
DRB1_0101  318  GAVRDVLDGKTAEFL  RDVLDGKTA       0.4603       343.6       WB    50.00     Sequence
DRB1_0101  360  GGLPDDLKFTLVEPL  PDDLKFTLV       0.4600       344.8       WB    50.00     Sequence
DRB1_0101  255  VFVDHGLLRAGERAQ  FVDHGLLRA       0.4597       345.9       WB    50.00     Sequence
DRB1_0101  259  HGLLRAGERAQVQRD  LLRAGERAQ       0.4591       348.2       WB    50.00     Sequence
DRB1_0101  136  VWMSHGDAVTAAPDG  MSHGDAVTA       0.4591       348.2       WB    50.00     Sequence
DRB1_0101  479  AMTADWTRVPYEVLE  WTRVPYEVL       0.4578       352.9       WB    50.00     Sequence
DRB1_0101  376  LLFKDEVRAVGRELG  FKDEVRAVG       0.4575       354.1       WB    50.00     Sequence
DRB1_0101  300  APEGKRKIIGRQFIR  KRKIIGRQF       0.4573       354.8       WB    50.00     Sequence
DRB1_0101  112  REYGRTELKVLGGKL  GRTELKVLG       0.4566       357.6       WB    50.00     Sequence
DRB1_0101  324  LDGKTAEFLVQGTLY  EFLVQGTLY       0.4558       360.8       WB    50.00     Sequence
DRB1_0101  119  LKVLGGKLHSDLPEV  LKVLGGKLH       0.4557       361.3       WB    50.00     Sequence
DRB1_0101  320  VRDVLDGKTAEFLVQ  LDGKTAEFL       0.4542       367.2       WB    50.00     Sequence
DRB1_0101  111  TREYGRTELKVLGGK  YGRTELKVL       0.4533       370.6       WB    50.00     Sequence
DRB1_0101  199  AGLGAQWTPANIANA  AQWTPANIA       0.4526       373.3       WB    50.00     Sequence
DRB1_0101  256  FVDHGLLRAGERAQV  HGLLRAGER       0.4524       374.2       WB    50.00     Sequence
DRB1_0101  426  DSIVREELTAAGLDN  REELTAAGL       0.4505       382.2       WB    50.00     Sequence
DRB1_0101  174  GVQYHPEVMHTPHGQ  YHPEVMHTP       0.4497       385.2       WB    50.00     Sequence
DRB1_0101  267  RAQVQRDFVAATGAN  RDFVAATGA       0.4475       394.6       WB    50.00     Sequence
DRB1_0101  214  LIEQVRTQIGDGHAI  TQIGDGHAI       0.4473       395.4       WB    50.00     Sequence
DRB1_0101  257  VDHGLLRAGERAQVQ  GLLRAGERA       0.4472       396.1       WB    50.00     Sequence
DRB1_0101  207  PANIANALIEQVRTQ  IANALIEQV       0.4456       402.9       WB    50.00     Sequence
DRB1_0101  458  VQGDGRTYGHPIVLR  DGRTYGHPI       0.4450       405.3       WB    50.00     Sequence
DRB1_0101  224  DGHAICGLSGGVDSA  ICGLSGGVD       0.4446       407.3       WB    50.00     Sequence
DRB1_0101   10  ETPARPVLVVDFGAQ  ETPARPVLV       0.4440       409.9       WB    50.00     Sequence
DRB1_0101  294  ALSGVSAPEGKRKII  LSGVSAPEG       0.4437       411.2       WB    50.00     Sequence
DRB1_0101  206  TPANIANALIEQVRT  PANIANALI       0.4432       413.6       WB    50.00     Sequence
DRB1_0101  246  RAIGDRLTCVFVDHG  GDRLTCVFV       0.4428       415.4       WB    50.00     Sequence
DRB1_0101  449  LLADVRSVGVQGDGR  LADVRSVGV       0.4415       421.0       WB    50.00     Sequence
DRB1_0101  501  NEVAEVNRVVLDITS  EVAEVNRVV       0.4400       427.8       WB    50.00     Sequence
DRB1_0101  370  LVEPLRLLFKDEVRA  LVEPLRLLF       0.4395       430.1       WB    50.00     Sequence
DRB1_0101  177  YHPEVMHTPHGQQVL  MHTPHGQQV       0.4388       433.7       WB    50.00     Sequence
DRB1_0101  420  DTLRHADSIVREELT  LRHADSIVR       0.4376       439.4       WB    50.00     Sequence
DRB1_0101  209  NIANALIEQVRTQIG  IEQVRTQIG       0.4371       441.8       WB    50.00     Sequence
DRB1_0101   74  APKLDPALLDLGVPV  LDPALLDLG       0.4364       445.0       WB    50.00     Sequence
DRB1_0101  220  TQIGDGHAICGLSGG  TQIGDGHAI       0.4344       454.9       WB    50.00     Sequence
DRB1_0101  245  QRAIGDRLTCVFVDH  GDRLTCVFV       0.4333       460.4       WB    50.00     Sequence
DRB1_0101  247  AIGDRLTCVFVDHGL  DRLTCVFVD       0.4330       461.5       WB    50.00     Sequence
DRB1_0101  208  ANIANALIEQVRTQI  IANALIEQV       0.4327       463.4       WB    50.00     Sequence
DRB1_0101  459  QGDGRTYGHPIVLRP  TYGHPIVLR       0.4326       463.5       WB    50.00     Sequence
DRB1_0101  319  AVRDVLDGKTAEFLV  RDVLDGKTA       0.4293       480.7       WB    50.00     Sequence
DRB1_0101  410  IVGEVTAKRLDTLRH  VGEVTAKRL       0.4290       482.0       WB    50.00     Sequence
DRB1_0101  478  DAMTADWTRVPYEVL  WTRVPYEVL       0.4282       486.4       WB    50.00     Sequence
DRB1_0101  221  QIGDGHAICGLSGGV  GHAICGLSG       0.4264       496.0       WB    50.00     Sequence
DRB1_0101   71  ADGAPKLDPALLDLG  APKLDPALL       0.4256       500.2             50.00     Sequence
DRB1_0101  210  IANALIEQVRTQIGD  IEQVRTQIG       0.4255       500.7             50.00     Sequence
DRB1_0101  494  RISTRITNEVAEVNR  STRITNEVA       0.4255       500.7             50.00     Sequence
DRB1_0101  222  IGDGHAICGLSGGVD  GHAICGLSG       0.4238       510.2             50.00     Sequence
DRB1_0101  323  VLDGKTAEFLVQGTL  LDGKTAEFL       0.4237       510.5             50.00     Sequence
DRB1_0101  167  AFDRRLAGVQYHPEV  DRRLAGVQY       0.4233       512.9             50.00     Sequence
DRB1_0101  421  TLRHADSIVREELTA  LRHADSIVR       0.4228       515.5             50.00     Sequence
DRB1_0101  386  GRELGLPEEIVARQP  ELGLPEEIV       0.4216       522.1             50.00     Sequence
DRB1_0101  322  DVLDGKTAEFLVQGT  LDGKTAEFL       0.4203       529.8             50.00     Sequence
DRB1_0101  393  EEIVARQPFPGPGLG  IVARQPFPG       0.4200       531.2             50.00     Sequence
DRB1_0101  170  RRLAGVQYHPEVMHT  LAGVQYHPE       0.4200       531.4             50.00     Sequence
DRB1_0101  383  RAVGRELGLPEEIVA  RELGLPEEI       0.4182       541.6             50.00     Sequence
DRB1_0101  474  VSSEDAMTADWTRVP  VSSEDAMTA       0.4178       543.9             50.00     Sequence
DRB1_0101   72  DGAPKLDPALLDLGV  APKLDPALL       0.4176       545.1             50.00     Sequence
DRB1_0101   11  TPARPVLVVDFGAQY  PVLVVDFGA       0.4176       545.4             50.00     Sequence
DRB1_0101  284  TVDAAETFLEALSGV  ETFLEALSG       0.4156       557.2             50.00     Sequence
DRB1_0101  428  IVREELTAAGLDNQI  REELTAAGL       0.4154       558.7             50.00     Sequence
DRB1_0101  394  EIVARQPFPGPGLGI  IVARQPFPG       0.4142       565.7             50.00     Sequence
DRB1_0101  422  LRHADSIVREELTAA  ADSIVREEL       0.4134       570.5             50.00     Sequence
DRB1_0101  260  GLLRAGERAQVQRDF  LLRAGERAQ       0.4127       574.9             50.00     Sequence
DRB1_0101   73  GAPKLDPALLDLGVP  APKLDPALL       0.4124       576.8             50.00     Sequence
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DRB1_0101  495  ISTRITNEVAEVNRV  ITNEVAEVN         0.4115         582.3                 50.00     Sequence
DRB1_0101  169  DRRLAGVQYHPEVMH  LAGVQYHPE         0.4110         586.0                 50.00     Sequence
DRB1_0101  502  EVAEVNRVVLDITSK  EVAEVNRVV         0.4084         602.6                 50.00     Sequence
DRB1_0101   29  IARRVREARVFSEVI  VREARVFSE         0.4071         611.2                 50.00     Sequence
DRB1_0101  314  RAFEGAVRDVLDGKT  FEGAVRDVL         0.4066         614.2                 50.00     Sequence
DRB1_0101  379  KDEVRAVGRELGLPE  EVRAVGREL         0.4050         624.8                 50.00     Sequence
DRB1_0101  283  VTVDAAETFLEALSG  VDAAETFLE         0.4022         644.1                 50.00     Sequence
DRB1_0101    4  ADIDVPETPARPVLV  DVPETPARP         0.4014         649.9                 50.00     Sequence
DRB1_0101  168  FDRRLAGVQYHPEVM  LAGVQYHPE         0.4013         650.4                 50.00     Sequence
DRB1_0101  435  AAGLDNQIWQCPVVL  QIWQCPVVL         0.4012         651.6                 50.00     Sequence
DRB1_0101  266  ERAQVQRDFVAATGA  RDFVAATGA         0.3992         665.3                 50.00     Sequence
DRB1_0101  137  WMSHGDAVTAAPDGF  MSHGDAVTA         0.3968         683.1                 50.00     Sequence
DRB1_0101  413  EVTAKRLDTLRHADS  LDTLRHADS         0.3935         708.1                 50.00     Sequence
DRB1_0101   69  VYADGAPKLDPALLD  VYADGAPKL         0.3933         709.6                 50.00     Sequence
DRB1_0101  387  RELGLPEEIVARQPF  ELGLPEEIV         0.3927         713.7                 50.00     Sequence
DRB1_0101  423  RHADSIVREELTAAG  IVREELTAA         0.3914         724.1                 50.00     Sequence
DRB1_0101  157  SAGAPVAAFEAFDRR  GAPVAAFEA         0.3906         730.7                 50.00     Sequence
DRB1_0101  110  GTREYGRTELKVLGG  YGRTELKVL         0.3905         730.8                 50.00     Sequence
DRB1_0101  299  SAPEGKRKIIGRQFI  KRKIIGRQF         0.3895         738.9                 50.00     Sequence
DRB1_0101  223  GDGHAICGLSGGVDS  GHAICGLSG         0.3887         745.3                 50.00     Sequence
DRB1_0101  355  SHHNVGGLPDDLKFT  NVGGLPDDL         0.3879         751.9                 50.00     Sequence
DRB1_0101   70  YADGAPKLDPALLDL  APKLDPALL         0.3875         755.3                 50.00     Sequence
DRB1_0101  173  AGVQYHPEVMHTPHG  YHPEVMHTP         0.3868         760.8                 50.00     Sequence
DRB1_0101  382  VRAVGRELGLPEEIV  VGRELGLPE         0.3857         770.2                 50.00     Sequence
DRB1_0101  429  VREELTAAGLDNQIW  REELTAAGL         0.3844         781.4                 50.00     Sequence
DRB1_0101  175  VQYHPEVMHTPHGQQ  YHPEVMHTP         0.3803         816.2                 50.00     Sequence
DRB1_0101   30  ARRVREARVFSEVIP  VREARVFSE         0.3803         816.7                 50.00     Sequence
DRB1_0101  358  NVGGLPDDLKFTLVE  PDDLKFTLV         0.3782         835.2                 50.00     Sequence
DRB1_0101  339  PDVVESGGGSGTANI  VESGGGSGT         0.3775         841.5                 50.00     Sequence
DRB1_0101   44  PHTASIEEIRARQPV  IEEIRARQP         0.3773         843.6                 50.00     Sequence
DRB1_0101   32  RVREARVFSEVIPHT  EARVFSEVI         0.3752         862.7                 50.00     Sequence
DRB1_0101  171  RLAGVQYHPEVMHTP  LAGVQYHPE         0.3743         870.8                 50.00     Sequence
DRB1_0101  506  VNRVVLDITSKPPAT  VLDITSKPP         0.3740         874.5                 50.00     Sequence
DRB1_0101  359  VGGLPDDLKFTLVEP  PDDLKFTLV         0.3733         881.1                 50.00     Sequence
DRB1_0101  411  VGEVTAKRLDTLRHA  VGEVTAKRL         0.3696         916.2                 50.00     Sequence
DRB1_0101  357  HNVGGLPDDLKFTLV  PDDLKFTLV         0.3681         931.9                 50.00     Sequence
DRB1_0101  172  LAGVQYHPEVMHTPH  YHPEVMHTP         0.3656         957.5                 50.00     Sequence
DRB1_0101  295  LSGVSAPEGKRKIIG  LSGVSAPEG         0.3655         958.6                 50.00     Sequence
DRB1_0101  315  AFEGAVRDVLDGKTA  FEGAVRDVL         0.3617         998.7                 50.00     Sequence
DRB1_0101  176  QYHPEVMHTPHGQQV  YHPEVMHTP         0.3597        1020.5                 50.00     Sequence
DRB1_0101  138  MSHGDAVTAAPDGFD  MSHGDAVTA         0.3594        1023.8                 50.00     Sequence
DRB1_0101  131  PEVQPVWMSHGDAVT  VWMSHGDAV         0.3590        1027.8                 50.00     Sequence
DRB1_0101  332  LVQGTLYPDVVESGG  VQGTLYPDV         0.3586        1032.8                 50.00     Sequence
DRB1_0101  450  LADVRSVGVQGDGRT  VRSVGVQGD         0.3584        1034.5                 50.00     Sequence
DRB1_0101  127  HSDLPEVQPVWMSHG  LPEVQPVWM         0.3580        1039.6                 50.00     Sequence
DRB1_0101  126  LHSDLPEVQPVWMSH  LPEVQPVWM         0.3579        1040.3                 50.00     Sequence
DRB1_0101  457  GVQGDGRTYGHPIVL  DGRTYGHPI         0.3560        1061.8                 50.00     Sequence
DRB1_0101   31  RRVREARVFSEVIPH  VREARVFSE         0.3556        1066.2                 50.00     Sequence
DRB1_0101  261  LLRAGERAQVQRDFV  LLRAGERAQ         0.3541        1083.7                 50.00     Sequence
DRB1_0101  125  KLHSDLPEVQPVWMS  SDLPEVQPV         0.3535        1091.6                 50.00     Sequence
DRB1_0101  103  GGIVAHTGTREYGRT  IVAHTGTRE         0.3513        1117.9                 50.00     Sequence
DRB1_0101  340  DVVESGGGSGTANIK  VESGGGSGT         0.3510        1120.6                 50.00     Sequence
DRB1_0101  109  TGTREYGRTELKVLG  YGRTELKVL         0.3504        1127.8                 50.00     Sequence
DRB1_0101  341  VVESGGGSGTANIKS  VESGGGSGT         0.3391        1275.7                 50.00     Sequence
DRB1_0101  348  SGTANIKSHHNVGGL  ANIKSHHNV         0.3365        1311.9                 50.00     Sequence
DRB1_0101  316  FEGAVRDVLDGKTAE  FEGAVRDVL         0.3359        1319.8                 50.00     Sequence
DRB1_0101  391  LPEEIVARQPFPGPG  IVARQPFPG         0.3353        1329.0                 50.00     Sequence
DRB1_0101  337  LYPDVVESGGGSGTA  DVVESGGGS         0.3335        1355.2                 50.00     Sequence
DRB1_0101   41  EVIPHTASIEEIRAR  PHTASIEEI         0.3312        1389.1                 50.00     Sequence
DRB1_0101  388  ELGLPEEIVARQPFP  ELGLPEEIV         0.3306        1397.3                 50.00     Sequence
DRB1_0101  317  EGAVRDVLDGKTAEF  RDVLDGKTA         0.3302        1403.6                 50.00     Sequence
DRB1_0101  356  HHNVGGLPDDLKFTL  NVGGLPDDL         0.3297        1412.4                 50.00     Sequence
DRB1_0101  381  EVRAVGRELGLPEEI  EVRAVGREL         0.3286        1428.6                 50.00     Sequence
DRB1_0101  128  SDLPEVQPVWMSHGD  PEVQPVWMS         0.3284        1431.0                 50.00     Sequence
DRB1_0101  380  DEVRAVGRELGLPEE  EVRAVGREL         0.3282        1435.4                 50.00     Sequence
DRB1_0101  347  GSGTANIKSHHNVGG  TANIKSHHN         0.3261        1467.1                 50.00     Sequence
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DRB1_0101  430  REELTAAGLDNQIWQ  REELTAAGL         0.3260         1468.9                 50.00      Sequence
DRB1_0101  503  VAEVNRVVLDITSKP  EVNRVVLDI         0.3236         1508.3                 50.00      Sequence
DRB1_0101   62  LSGGPASVYADGAPK  LSGGPASVY         0.3236         1508.6                 50.00      Sequence
DRB1_0101  158  AGAPVAAFEAFDRRL  VAAFEAFDR         0.3217         1540.0                 50.00      Sequence
DRB1_0101  338  YPDVVESGGGSGTAN  VESGGGSGT         0.3216         1540.8                 50.00      Sequence
DRB1_0101  354  KSHHNVGGLPDDLKF  NVGGLPDDL         0.3216         1541.2                 50.00      Sequence
DRB1_0101  130  LPEVQPVWMSHGDAV  VWMSHGDAV         0.3207         1556.8                 50.00      Sequence
DRB1_0101   42  VIPHTASIEEIRARQ  PHTASIEEI         0.3198         1570.5                 50.00      Sequence
DRB1_0101  120  KVLGGKLHSDLPEVQ  LGGKLHSDL         0.3195         1576.5                 50.00      Sequence
DRB1_0101  389  LGLPEEIVARQPFPG  IVARQPFPG         0.3193         1580.0                 50.00      Sequence
DRB1_0101   43  IPHTASIEEIRARQP  IEEIRARQP         0.3154         1647.3                 50.00      Sequence
DRB1_0101  124  GKLHSDLPEVQPVWM  SDLPEVQPV         0.3094         1759.1                 50.00      Sequence
DRB1_0101  123  GGKLHSDLPEVQPVW  LHSDLPEVQ         0.3052         1840.2                 50.00      Sequence
DRB1_0101  349  GTANIKSHHNVGGLP  IKSHHNVGG         0.3049         1847.0                 50.00      Sequence
DRB1_0101  265  GERAQVQRDFVAATG  AQVQRDFVA         0.3047         1849.3                 50.00      Sequence
DRB1_0101  390  GLPEEIVARQPFPGP  IVARQPFPG         0.3045         1854.5                 50.00      Sequence
DRB1_0101  298  VSAPEGKRKIIGRQF  KRKIIGRQF         0.3018         1909.0                 50.00      Sequence
DRB1_0101  108  HTGTREYGRTELKVL  YGRTELKVL         0.3017         1911.4                 50.00      Sequence
DRB1_0101  342  VESGGGSGTANIKSH  VESGGGSGT         0.3007         1931.7                 50.00      Sequence
DRB1_0101  353  IKSHHNVGGLPDDLK  HHNVGGLPD         0.3000         1946.8                 50.00      Sequence
DRB1_0101  104  GIVAHTGTREYGRTE  IVAHTGTRE         0.2997         1952.5                 50.00      Sequence
DRB1_0101  144  VTAAPDGFDVVASSA  PDGFDVVAS         0.2995         1956.5                 50.00      Sequence
DRB1_0101  434  TAAGLDNQIWQCPVV  DNQIWQCPV         0.2994         1960.1                 50.00      Sequence
DRB1_0101   40  SEVIPHTASIEEIRA  PHTASIEEI         0.2989         1970.8                 50.00      Sequence
DRB1_0101  505  EVNRVVLDITSKPPA  VLDITSKPP         0.2968         2015.4                 50.00      Sequence
DRB1_0101  336  TLYPDVVESGGGSGT  VESGGGSGT         0.2935         2087.7                 50.00      Sequence
DRB1_0101  475  SSEDAMTADWTRVPY  EDAMTADWT         0.2922         2118.6                 50.00      Sequence
DRB1_0101  412  GEVTAKRLDTLRHAD  VTAKRLDTL         0.2914         2137.1                 50.00      Sequence
DRB1_0101  129  DLPEVQPVWMSHGDA  PEVQPVWMS         0.2910         2145.1                 50.00      Sequence
DRB1_0101  262  LRAGERAQVQRDFVA  GERAQVQRD         0.2909         2147.3                 50.00      Sequence
DRB1_0101  504  AEVNRVVLDITSKPP  EVNRVVLDI         0.2897         2177.0                 50.00      Sequence
DRB1_0101  350  TANIKSHHNVGGLPD  IKSHHNVGG         0.2888         2197.0                 50.00      Sequence
DRB1_0101  264  AGERAQVQRDFVAAT  AQVQRDFVA         0.2882         2211.7                 50.00      Sequence
DRB1_0101  333  VQGTLYPDVVESGGG  VQGTLYPDV         0.2858         2268.9                 50.00      Sequence
DRB1_0101  453  VRSVGVQGDGRTYGH  VGVQGDGRT         0.2843         2306.1                 50.00      Sequence
DRB1_0101  122  LGGKLHSDLPEVQPV  KLHSDLPEV         0.2826         2349.9                 50.00      Sequence
DRB1_0101  477  EDAMTADWTRVPYEV  MTADWTRVP         0.2793         2435.7                 50.00      Sequence
DRB1_0101  431  EELTAAGLDNQIWQC  TAAGLDNQI         0.2788         2448.5                 50.00      Sequence
DRB1_0101  476  SEDAMTADWTRVPYE  AMTADWTRV         0.2779         2471.7                 50.00      Sequence
DRB1_0101  451  ADVRSVGVQGDGRTY  VRSVGVQGD         0.2765         2510.7                 50.00      Sequence
DRB1_0101  143  AVTAAPDGFDVVASS  TAAPDGFDV         0.2762         2519.2                 50.00      Sequence
DRB1_0101  105  IVAHTGTREYGRTEL  IVAHTGTRE         0.2760         2524.2                 50.00      Sequence
DRB1_0101  346  GGSGTANIKSHHNVG  TANIKSHHN         0.2756         2534.7                 50.00      Sequence
DRB1_0101  452  DVRSVGVQGDGRTYG  VGVQGDGRT         0.2746         2562.6                 50.00      Sequence
DRB1_0101    3  PADIDVPETPARPVL  DVPETPARP         0.2742         2574.1                 50.00      Sequence
DRB1_0101  352  NIKSHHNVGGLPDDL  SHHNVGGLP         0.2733         2597.8                 50.00      Sequence
DRB1_0101  121  VLGGKLHSDLPEVQP  LGGKLHSDL         0.2718         2639.8                 50.00      Sequence
DRB1_0101  456  VGVQGDGRTYGHPIV  DGRTYGHPI         0.2703         2684.6                 50.00      Sequence
DRB1_0101  432  ELTAAGLDNQIWQCP  AAGLDNQIW         0.2701         2690.3                 50.00      Sequence
DRB1_0101  142  DAVTAAPDGFDVVAS  TAAPDGFDV         0.2691         2719.2                 50.00      Sequence
DRB1_0101  263  RAGERAQVQRDFVAA  AQVQRDFVA         0.2655         2827.5                 50.00      Sequence
DRB1_0101  454  RSVGVQGDGRTYGHP  VGVQGDGRT         0.2621         2933.0                 50.00      Sequence
DRB1_0101  433  LTAAGLDNQIWQCPV  AAGLDNQIW         0.2597         3010.9                 50.00      Sequence
DRB1_0101  351  ANIKSHHNVGGLPDD  IKSHHNVGG         0.2532         3230.2                 50.00      Sequence
DRB1_0101  335  GTLYPDVVESGGGSG  DVVESGGGS         0.2515         3290.2                 50.00      Sequence
DRB1_0101  344  SGGGSGTANIKSHHN  GSGTANIKS         0.2498         3350.4                 50.00      Sequence
DRB1_0101  345  GGGSGTANIKSHHNV  TANIKSHHN         0.2493         3370.2                 50.00      Sequence
DRB1_0101  334  QGTLYPDVVESGGGS  DVVESGGGS         0.2460         3491.6                 50.00      Sequence
DRB1_0101  455  SVGVQGDGRTYGHPI  DGRTYGHPI         0.2428         3615.1                 50.00      Sequence
DRB1_0101  139  SHGDAVTAAPDGFDV  DAVTAAPDG         0.2336         3995.0                 50.00      Sequence
DRB1_0101  343  ESGGGSGTANIKSHH  GSGTANIKS         0.2301         4148.1                 50.00      Sequence
DRB1_0101  141  GDAVTAAPDGFDVVA  TAAPDGFDV         0.2291         4191.9                 50.00      Sequence
DRB1_0101  140  HGDAVTAAPDGFDVV  AVTAAPDGF         0.2276         4263.0                 50.00      Sequence
DRB1_0101  296  SGVSAPEGKRKIIGR  VSAPEGKRK         0.2255         4357.2                 50.00      Sequence
DRB1_0101  106  VAHTGTREYGRTELK  GTREYGRTE         0.2253         4368.0                 50.00      Sequence
DRB1_0101    2  QPADIDVPETPARPV  DVPETPARP         0.2159         4838.0                 50.00      Sequence
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   DRB1_0101  107  AHTGTREYGRTELKV  GTREYGRTE        0.2137       4954.0                50.00     Sequence
   DRB1_0101  297  GVSAPEGKRKIIGRQ  VSAPEGKRK        0.2118       5052.6                50.00     Sequence
   DRB1_0101    0  VVQPADIDVPETPAR  VVQPADIDV        0.1992       5793.6                50.00     Sequence
   DRB1_0101    1  VQPADIDVPETPARP  DIDVPETPA        0.1735       7653.1                50.00     Sequence
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Allele: DRB1_0101. Number of high binders 123. Number of weak binders 231. Number of peptides 511

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0301  374  LRLLFKDEVRAVGRE  LRLLFKDEV        0.7710         11.9         SB     0.20     Sequence
   DRB1_0301  373  PLRLLFKDEVRAVGR  LRLLFKDEV        0.7628         13.0         SB     0.20     Sequence
   DRB1_0301  372  EPLRLLFKDEVRAVG  LRLLFKDEV        0.7359         17.4         SB     0.40     Sequence
   DRB1_0301  371  VEPLRLLFKDEVRAV  LRLLFKDEV        0.7080         23.6         SB     0.80     Sequence
   DRB1_0301  446  PVVLLADVRSVGVQG  VVLLADVRS        0.7053         24.2         SB     0.80     Sequence
   DRB1_0301  445  CPVVLLADVRSVGVQ  PVVLLADVR        0.6850         30.2         SB     0.80     Sequence
   DRB1_0301  252  LTCVFVDHGLLRAGE  VFVDHGLLR        0.6571         40.9         SB     2.00     Sequence
   DRB1_0301  375  RLLFKDEVRAVGREL  RLLFKDEVR        0.6521         43.1         SB     2.00     Sequence
   DRB1_0301  444  QCPVVLLADVRSVGV  PVVLLADVR        0.6498         44.2         SB     2.00     Sequence
   DRB1_0301   14  RPVLVVDFGAQYAQL  RPVLVVDFG        0.6416         48.3         SB     2.00     Sequence
   DRB1_0301  251  RLTCVFVDHGLLRAG  LTCVFVDHG        0.6348         52.0         WB     2.00     Sequence
   DRB1_0301  447  VVLLADVRSVGVQGD  VVLLADVRS        0.6288         55.5         WB     2.00     Sequence
   DRB1_0301   13  ARPVLVVDFGAQYAQ  RPVLVVDFG        0.6196         61.3         WB     2.00     Sequence
   DRB1_0301  370  LVEPLRLLFKDEVRA  LRLLFKDEV        0.6178         62.5         WB     2.00     Sequence
   DRB1_0301  250  DRLTCVFVDHGLLRA  LTCVFVDHG        0.6021         74.1         WB     4.00     Sequence
   DRB1_0301  443  WQCPVVLLADVRSVG  PVVLLADVR        0.5917         82.9         WB     4.00     Sequence
   DRB1_0301   12  PARPVLVVDFGAQYA  RPVLVVDFG        0.5835         90.6         WB     4.00     Sequence
   DRB1_0301  506  VNRVVLDITSKPPAT  VNRVVLDIT        0.5767         97.5         WB     4.00     Sequence
   DRB1_0301  249  GDRLTCVFVDHGLLR  LTCVFVDHG        0.5528        126.2         WB     4.00     Sequence
   DRB1_0301  422  LRHADSIVREELTAA  LRHADSIVR        0.5465        135.2         WB     8.00     Sequence
   DRB1_0301  419  LDTLRHADSIVREEL  LRHADSIVR        0.5440        138.9         WB     8.00     Sequence
   DRB1_0301   15  PVLVVDFGAQYAQLI  VLVVDFGAQ        0.5435        139.7         WB     8.00     Sequence
   DRB1_0301  505  EVNRVVLDITSKPPA  VNRVVLDIT        0.5427        140.8         WB     8.00     Sequence
   DRB1_0301  508  RVVLDITSKPPATIE  VVLDITSKP        0.5427        140.9         WB     8.00     Sequence
   DRB1_0301  376  LLFKDEVRAVGRELG  LLFKDEVRA        0.5393        146.1         WB     8.00     Sequence
   DRB1_0301   11  TPARPVLVVDFGAQY  RPVLVVDFG        0.5385        147.5         WB     8.00     Sequence
   DRB1_0301  421  TLRHADSIVREELTA  LRHADSIVR        0.5370        149.8         WB     8.00     Sequence
   DRB1_0301  190  VLSRFLHDFAGLGAQ  LSRFLHDFA        0.5344        154.1         WB     8.00     Sequence
   DRB1_0301  507  NRVVLDITSKPPATI  VVLDITSKP        0.5298        161.9         WB     8.00     Sequence
   DRB1_0301  191  LSRFLHDFAGLGAQW  LSRFLHDFA        0.5286        164.2         WB     8.00     Sequence
   DRB1_0301  420  DTLRHADSIVREELT  LRHADSIVR        0.5264        168.1         WB     8.00     Sequence
   DRB1_0301  408  IRIVGEVTAKRLDTL  IVGEVTAKR        0.5249        170.8         WB     8.00     Sequence
   DRB1_0301  509  VVLDITSKPPATIEW  VVLDITSKP        0.5185        183.0         WB     8.00     Sequence
   DRB1_0301  418  RLDTLRHADSIVREE  LRHADSIVR        0.5128        194.6         WB     8.00     Sequence
   DRB1_0301  259  HGLLRAGERAQVQRD  HGLLRAGER        0.5009        221.5         WB     8.00     Sequence
   DRB1_0301  366  LKFTLVEPLRLLFKD  LKFTLVEPL        0.4992        225.4         WB     8.00     Sequence
   DRB1_0301  253  TCVFVDHGLLRAGER  VFVDHGLLR        0.4984        227.4         WB     8.00     Sequence
   DRB1_0301  448  VLLADVRSVGVQGDG  VLLADVRSV        0.4962        232.9         WB     8.00     Sequence
   DRB1_0301  254  CVFVDHGLLRAGERA  VFVDHGLLR        0.4962        233.1         WB     8.00     Sequence
   DRB1_0301  189  QVLSRFLHDFAGLGA  LSRFLHDFA        0.4905        247.9         WB     8.00     Sequence
   DRB1_0301   58  VALVLSGGPASVYAD  LVLSGGPAS        0.4903        248.4         WB     8.00     Sequence
   DRB1_0301   16  VLVVDFGAQYAQLIA  VLVVDFGAQ        0.4899        249.4         WB     8.00     Sequence
   DRB1_0301  255  VFVDHGLLRAGERAQ  VFVDHGLLR        0.4894        250.9         WB     8.00     Sequence
   DRB1_0301  407  GIRIVGEVTAKRLDT  IVGEVTAKR        0.4891        251.5         WB     8.00     Sequence
   DRB1_0301  280  ANLVTVDAAETFLEA  LVTVDAAET        0.4881        254.3         WB     8.00     Sequence
   DRB1_0301  504  AEVNRVVLDITSKPP  VNRVVLDIT        0.4848        263.7         WB     8.00     Sequence
   DRB1_0301  365  DLKFTLVEPLRLLFK  LKFTLVEPL        0.4841        265.6         WB     8.00     Sequence
   DRB1_0301   25  YAQLIARRVREARVF  LIARRVREA        0.4835        267.2         WB     8.00     Sequence
   DRB1_0301  244  VQRAIGDRLTCVFVD  VQRAIGDRL        0.4820        271.6         WB     8.00     Sequence
   DRB1_0301  258  DHGLLRAGERAQVQR  HGLLRAGER        0.4818        272.4         WB     8.00     Sequence
   DRB1_0301  243  LVQRAIGDRLTCVFV  VQRAIGDRL        0.4771        286.5         WB    16.00     Sequence
   DRB1_0301   24  QYAQLIARRVREARV  YAQLIARRV        0.4707        306.9         WB    16.00     Sequence
   DRB1_0301   57  PVALVLSGGPASVYA  LVLSGGPAS        0.4695        310.9         WB    16.00     Sequence
   DRB1_0301  409  RIVGEVTAKRLDTLR  VGEVTAKRL        0.4684        314.7         WB    16.00     Sequence
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DRB1_0301  123  GGKLHSDLPEVQPVW  GGKLHSDLP        0.4660         322.9          WB    16.00      Sequence
DRB1_0301  417  KRLDTLRHADSIVRE  LRHADSIVR        0.4651         326.4          WB    16.00      Sequence
DRB1_0301  503  VAEVNRVVLDITSKP  VNRVVLDIT        0.4645         328.3          WB    16.00      Sequence
DRB1_0301  188  QQVLSRFLHDFAGLG  LSRFLHDFA        0.4632         333.1          WB    16.00      Sequence
DRB1_0301  510  VLDITSKPPATIEWE  VLDITSKPP        0.4621         337.1          WB    16.00      Sequence
DRB1_0301  163  AAFEAFDRRLAGVQY  AAFEAFDRR        0.4569         356.3          WB    16.00      Sequence
DRB1_0301  122  LGGKLHSDLPEVQPV  GGKLHSDLP        0.4562         359.2          WB    16.00      Sequence
DRB1_0301  281  NLVTVDAAETFLEAL  LVTVDAAET        0.4548         364.8          WB    16.00      Sequence
DRB1_0301  369  TLVEPLRLLFKDEVR  LRLLFKDEV        0.4523         374.5          WB    16.00      Sequence
DRB1_0301  279  GANLVTVDAAETFLE  LVTVDAAET        0.4493         387.1          WB    16.00      Sequence
DRB1_0301  162  VAAFEAFDRRLAGVQ  AAFEAFDRR        0.4490         388.5          WB    16.00      Sequence
DRB1_0301   26  AQLIARRVREARVFS  LIARRVREA        0.4481         392.2          WB    16.00      Sequence
DRB1_0301  310  RQFIRAFEGAVRDVL  IRAFEGAVR        0.4464         399.3          WB    16.00      Sequence
DRB1_0301  242  ALVQRAIGDRLTCVF  VQRAIGDRL        0.4451         405.1          WB    16.00      Sequence
DRB1_0301  282  LVTVDAAETFLEALS  LVTVDAAET        0.4445         407.6          WB    16.00      Sequence
DRB1_0301  257  VDHGLLRAGERAQVQ  HGLLRAGER        0.4436         411.8          WB    16.00      Sequence
DRB1_0301  367  KFTLVEPLRLLFKDE  FTLVEPLRL        0.4420         418.9          WB    16.00      Sequence
DRB1_0301  410  IVGEVTAKRLDTLRH  IVGEVTAKR        0.4405         425.8          WB    16.00      Sequence
DRB1_0301   23  AQYAQLIARRVREAR  YAQLIARRV        0.4362         446.0          WB    16.00      Sequence
DRB1_0301  364  DDLKFTLVEPLRLLF  LKFTLVEPL        0.4356         449.0          WB    16.00      Sequence
DRB1_0301  368  FTLVEPLRLLFKDEV  FTLVEPLRL        0.4323         465.1          WB    16.00      Sequence
DRB1_0301  406  LGIRIVGEVTAKRLD  IVGEVTAKR        0.4310         471.7          WB    16.00      Sequence
DRB1_0301  416  AKRLDTLRHADSIVR  LRHADSIVR        0.4305         474.4          WB    16.00      Sequence
DRB1_0301   17  LVVDFGAQYAQLIAR  VVDFGAQYA        0.4302         475.9          WB    16.00      Sequence
DRB1_0301  320  VRDVLDGKTAEFLVQ  RDVLDGKTA        0.4264         495.6          WB    16.00      Sequence
DRB1_0301  311  QFIRAFEGAVRDVLD  IRAFEGAVR        0.4251         502.8                16.00      Sequence
DRB1_0301  121  VLGGKLHSDLPEVQP  GGKLHSDLP        0.4238         510.0                16.00      Sequence
DRB1_0301  470  VLRPVSSEDAMTADW  PVSSEDAMT        0.4202         530.1                16.00      Sequence
DRB1_0301  312  FIRAFEGAVRDVLDG  IRAFEGAVR        0.4194         534.8                16.00      Sequence
DRB1_0301  319  AVRDVLDGKTAEFLV  RDVLDGKTA        0.4194         535.1                16.00      Sequence
DRB1_0301   56  QPVALVLSGGPASVY  LVLSGGPAS        0.4179         543.6                16.00      Sequence
DRB1_0301   28  LIARRVREARVFSEV  LIARRVREA        0.4171         548.3                16.00      Sequence
DRB1_0301  161  PVAAFEAFDRRLAGV  AAFEAFDRR        0.4155         558.0                16.00      Sequence
DRB1_0301  256  FVDHGLLRAGERAQV  HGLLRAGER        0.4146         563.3                16.00      Sequence
DRB1_0301   37  RVFSEVIPHTASIEE  FSEVIPHTA        0.4132         572.3                16.00      Sequence
DRB1_0301  471  LRPVSSEDAMTADWT  RPVSSEDAM        0.4117         581.4                16.00      Sequence
DRB1_0301   27  QLIARRVREARVFSE  LIARRVREA        0.4105         588.8                16.00      Sequence
DRB1_0301  120  KVLGGKLHSDLPEVQ  GGKLHSDLP        0.4092         597.3                16.00      Sequence
DRB1_0301  304  KRKIIGRQFIRAFEG  RKIIGRQFI        0.4050         625.0                16.00      Sequence
DRB1_0301  487  VPYEVLERISTRITN  VPYEVLERI        0.3998         661.5                16.00      Sequence
DRB1_0301  411  VGEVTAKRLDTLRHA  VGEVTAKRL        0.3990         667.1                16.00      Sequence
DRB1_0301  309  GRQFIRAFEGAVRDV  FIRAFEGAV        0.3981         673.3                16.00      Sequence
DRB1_0301  305  RKIIGRQFIRAFEGA  RKIIGRQFI        0.3962         687.3                32.00      Sequence
DRB1_0301  278  TGANLVTVDAAETFL  ANLVTVDAA        0.3941         703.5                32.00      Sequence
DRB1_0301  303  GKRKIIGRQFIRAFE  RKIIGRQFI        0.3940         704.1                32.00      Sequence
DRB1_0301  442  IWQCPVVLLADVRSV  PVVLLADVR        0.3933         709.1                32.00      Sequence
DRB1_0301  241  AALVQRAIGDRLTCV  VQRAIGDRL        0.3918         721.3                32.00      Sequence
DRB1_0301  306  KIIGRQFIRAFEGAV  IIGRQFIRA        0.3909         727.9                32.00      Sequence
DRB1_0301   39  FSEVIPHTASIEEIR  FSEVIPHTA        0.3880         751.0                32.00      Sequence
DRB1_0301   36  ARVFSEVIPHTASIE  FSEVIPHTA        0.3877         754.0                32.00      Sequence
DRB1_0301  469  IVLRPVSSEDAMTAD  PVSSEDAMT        0.3875         755.4                32.00      Sequence
DRB1_0301  307  IIGRQFIRAFEGAVR  IIGRQFIRA        0.3874         756.5                32.00      Sequence
DRB1_0301  449  LLADVRSVGVQGDGR  LLADVRSVG        0.3860         767.2                32.00      Sequence
DRB1_0301  318  GAVRDVLDGKTAEFL  RDVLDGKTA        0.3843         781.7                32.00      Sequence
DRB1_0301   38  VFSEVIPHTASIEEI  FSEVIPHTA        0.3826         796.6                32.00      Sequence
DRB1_0301  119  LKVLGGKLHSDLPEV  GGKLHSDLP        0.3824         798.1                32.00      Sequence
DRB1_0301  405  GLGIRIVGEVTAKRL  IRIVGEVTA        0.3809         810.8                32.00      Sequence
DRB1_0301  210  IANALIEQVRTQIGD  IANALIEQV        0.3802         817.3                32.00      Sequence
DRB1_0301   22  GAQYAQLIARRVREA  YAQLIARRV        0.3754         861.0                32.00      Sequence
DRB1_0301  187  GQQVLSRFLHDFAGL  LSRFLHDFA        0.3747         867.1                32.00      Sequence
DRB1_0301  455  SVGVQGDGRTYGHPI  SVGVQGDGR        0.3742         871.8                32.00      Sequence
DRB1_0301  425  ADSIVREELTAAGLD  ADSIVREEL        0.3721         892.4                32.00      Sequence
DRB1_0301   59  ALVLSGGPASVYADG  ALVLSGGPA        0.3714         899.2                32.00      Sequence
DRB1_0301   66  PASVYADGAPKLDPA  PASVYADGA        0.3708         904.9                32.00      Sequence
DRB1_0301  472  RPVSSEDAMTADWTR  RPVSSEDAM        0.3698         914.9                32.00      Sequence
DRB1_0301  302  EGKRKIIGRQFIRAF  RKIIGRQFI        0.3676         936.5                32.00      Sequence
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DRB1_0301  486  RVPYEVLERISTRIT  VPYEVLERI      0.3668      945.3         32.00    Sequence
DRB1_0301  502  EVAEVNRVVLDITSK  VAEVNRVVL      0.3666      947.1         32.00    Sequence
DRB1_0301  267  RAQVQRDFVAATGAN  RAQVQRDFV      0.3658      954.9         32.00    Sequence
DRB1_0301  363  PDDLKFTLVEPLRLL  LKFTLVEPL      0.3649      965.0         32.00    Sequence
DRB1_0301  488  PYEVLERISTRITNE  EVLERISTR      0.3632      982.5         32.00    Sequence
DRB1_0301  490  EVLERISTRITNEVA  VLERISTRI      0.3622      993.3         32.00    Sequence
DRB1_0301   43  IPHTASIEEIRARQP  IPHTASIEE      0.3591     1027.3         32.00    Sequence
DRB1_0301  377  LFKDEVRAVGRELGL  LFKDEVRAV      0.3572     1048.6         32.00    Sequence
DRB1_0301  211  ANALIEQVRTQIGDG  ANALIEQVR      0.3561     1060.6         32.00    Sequence
DRB1_0301  160  APVAAFEAFDRRLAG  AAFEAFDRR      0.3539     1086.5         32.00    Sequence
DRB1_0301  468  PIVLRPVSSEDAMTA  LRPVSSEDA      0.3537     1089.1         32.00    Sequence
DRB1_0301   77  LDPALLDLGVPVLGI  ALLDLGVPV      0.3512     1118.2         32.00    Sequence
DRB1_0301  209  NIANALIEQVRTQIG  ANALIEQVR      0.3509     1121.7         32.00    Sequence
DRB1_0301  489  YEVLERISTRITNEV  EVLERISTR      0.3508     1123.5         32.00    Sequence
DRB1_0301  454  RSVGVQGDGRTYGHP  SVGVQGDGR      0.3507     1124.5         32.00    Sequence
DRB1_0301  491  VLERISTRITNEVAE  VLERISTRI      0.3477     1162.2         32.00    Sequence
DRB1_0301  334  QGTLYPDVVESGGGS  QGTLYPDVV      0.3470     1170.5         32.00    Sequence
DRB1_0301  333  VQGTLYPDVVESGGG  QGTLYPDVV      0.3460     1183.8         32.00    Sequence
DRB1_0301  308  IGRQFIRAFEGAVRD  FIRAFEGAV      0.3455     1190.1         32.00    Sequence
DRB1_0301  424  HADSIVREELTAAGL  SIVREELTA      0.3447     1200.5         32.00    Sequence
DRB1_0301  266  ERAQVQRDFVAATGA  RAQVQRDFV      0.3435     1216.0         32.00    Sequence
DRB1_0301  124  GKLHSDLPEVQPVWM  LHSDLPEVQ      0.3421     1233.9         32.00    Sequence
DRB1_0301   55  RQPVALVLSGGPASV  VALVLSGGP      0.3419     1237.4         32.00    Sequence
DRB1_0301  260  GLLRAGERAQVQRDF  GLLRAGERA      0.3392     1273.6         32.00    Sequence
DRB1_0301  272  RDFVAATGANLVTVD  RDFVAATGA      0.3391     1275.3         32.00    Sequence
DRB1_0301   29  IARRVREARVFSEVI  IARRVREAR      0.3379     1291.3         32.00    Sequence
DRB1_0301   65  GPASVYADGAPKLDP  PASVYADGA      0.3368     1307.9         32.00    Sequence
DRB1_0301  270  VQRDFVAATGANLVT  RDFVAATGA      0.3363     1313.9         32.00    Sequence
DRB1_0301   35  EARVFSEVIPHTASI  FSEVIPHTA      0.3362     1315.4         32.00    Sequence
DRB1_0301  164  AFEAFDRRLAGVQYH  FEAFDRRLA      0.3356     1324.7         32.00    Sequence
DRB1_0301   10  ETPARPVLVVDFGAQ  RPVLVVDFG      0.3353     1328.8         32.00    Sequence
DRB1_0301   42  VIPHTASIEEIRARQ  IPHTASIEE      0.3341     1346.2         32.00    Sequence
DRB1_0301  321  RDVLDGKTAEFLVQG  RDVLDGKTA      0.3341     1346.7         32.00    Sequence
DRB1_0301  125  KLHSDLPEVQPVWMS  KLHSDLPEV      0.3322     1373.7         32.00    Sequence
DRB1_0301  423  RHADSIVREELTAAG  SIVREELTA      0.3316     1382.2         32.00    Sequence
DRB1_0301  413  EVTAKRLDTLRHADS  VTAKRLDTL      0.3314     1385.4         32.00    Sequence
DRB1_0301  118  ELKVLGGKLHSDLPE  ELKVLGGKL      0.3305     1400.1         32.00    Sequence
DRB1_0301  453  VRSVGVQGDGRTYGH  SVGVQGDGR      0.3297     1411.4         32.00    Sequence
DRB1_0301  426  DSIVREELTAAGLDN  SIVREELTA      0.3282     1434.8         32.00    Sequence
DRB1_0301  277  ATGANLVTVDAAETF  ANLVTVDAA      0.3279     1439.4         32.00    Sequence
DRB1_0301  313  IRAFEGAVRDVLDGK  IRAFEGAVR      0.3273     1449.1         32.00    Sequence
DRB1_0301  485  TRVPYEVLERISTRI  VPYEVLERI      0.3266     1460.0         32.00    Sequence
DRB1_0301  331  FLVQGTLYPDVVESG  QGTLYPDVV      0.3264     1463.3         32.00    Sequence
DRB1_0301  358  NVGGLPDDLKFTLVE  VGGLPDDLK      0.3253     1480.5         32.00    Sequence
DRB1_0301   60  LVLSGGPASVYADGA  LVLSGGPAS      0.3246     1491.0         32.00    Sequence
DRB1_0301  248  IGDRLTCVFVDHGLL  LTCVFVDHG      0.3246     1492.4         32.00    Sequence
DRB1_0301  414  VTAKRLDTLRHADSI  VTAKRLDTL      0.3243     1496.7         32.00    Sequence
DRB1_0301  501  NEVAEVNRVVLDITS  VAEVNRVVL      0.3238     1504.3         32.00    Sequence
DRB1_0301  269  QVQRDFVAATGANLV  RDFVAATGA      0.3216     1540.2         32.00    Sequence
DRB1_0301   21  FGAQYAQLIARRVRE  YAQLIARRV      0.3196     1574.6         32.00    Sequence
DRB1_0301  265  GERAQVQRDFVAATG  RAQVQRDFV      0.3188     1588.8         32.00    Sequence
DRB1_0301  271  QRDFVAATGANLVTV  RDFVAATGA      0.3178     1605.3         32.00    Sequence
DRB1_0301  495  ISTRITNEVAEVNRV  STRITNEVA      0.3154     1647.3         32.00    Sequence
DRB1_0301  332  LVQGTLYPDVVESGG  QGTLYPDVV      0.3142     1669.7         32.00    Sequence
DRB1_0301  208  ANIANALIEQVRTQI  ANALIEQVR      0.3139     1675.5         32.00    Sequence
DRB1_0301   76  KLDPALLDLGVPVLG  ALLDLGVPV      0.3129     1692.7         32.00    Sequence
DRB1_0301  317  EGAVRDVLDGKTAEF  RDVLDGKTA      0.3099     1748.3         32.00    Sequence
DRB1_0301  230  GLSGGVDSAVAAALV  GLSGGVDSA      0.3099     1748.8         32.00    Sequence
DRB1_0301   68  SVYADGAPKLDPALL  SVYADGAPK      0.3083     1778.6         32.00    Sequence
DRB1_0301  427  SIVREELTAAGLDNQ  SIVREELTA      0.3081     1782.6         32.00    Sequence
DRB1_0301  268  AQVQRDFVAATGANL  VQRDFVAAT      0.3081     1783.4         32.00    Sequence
DRB1_0301  359  VGGLPDDLKFTLVEP  VGGLPDDLK      0.3067     1810.1         32.00    Sequence
DRB1_0301  186  HGQQVLSRFLHDFAG  LSRFLHDFA      0.3065     1813.5         32.00    Sequence
DRB1_0301   67  ASVYADGAPKLDPAL  SVYADGAPK      0.3052     1840.1         32.00    Sequence
DRB1_0301  404  PGLGIRIVGEVTAKR  IRIVGEVTA      0.3046     1852.1         32.00    Sequence
DRB1_0301   18  VVDFGAQYAQLIARR  VVDFGAQYA      0.3046     1852.9         32.00    Sequence
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DRB1_0301	357	HNVGGLPDDLKFTLV	VGGLPDDLK	0.3045	1853.8	32.00	Sequence
DRB1_0301	362	LPDDLKFTLVEPLRL	LKFTLVEPL	0.3043	1857.8	32.00	Sequence
DRB1_0301	301	PEGKRKIIGRQFIRA	KIIGRQFIR	0.3035	1874.4	32.00	Sequence
DRB1_0301	78	DPALLDLGVPVLGIC	ALLDLGVPV	0.3021	1903.7	32.00	Sequence
DRB1_0301	452	DVRSVGVQGDGRTYG	SVGVQGDGR	0.2996	1954.3	50.00	Sequence
DRB1_0301	86	VPVLGICYGFQAMAQ	VPVLGICYG	0.2992	1963.7	50.00	Sequence
DRB1_0301	240	AAALVQRAIGDRLTC	VQRAIGDRL	0.2986	1975.8	50.00	Sequence
DRB1_0301	34	REARVFSEVIPHTAS	RVFSEVIPH	0.2979	1991.9	50.00	Sequence
DRB1_0301	75	PKLDPALLDLGVPVL	LDPALLDLG	0.2975	2000.9	50.00	Sequence
DRB1_0301	229	CGLSGGVDSAVAAAL	GLSGGVDSA	0.2968	2014.8	50.00	Sequence
DRB1_0301	467	HPIVLRPVSSEDAMT	VLRPVSSED	0.2962	2027.6	50.00	Sequence
DRB1_0301	185	PHGQQVLSRFLHDFA	LSRFLHDFA	0.2948	2058.3	50.00	Sequence
DRB1_0301	415	TAKRLDTLRHADSIV	KRLDTLRHA	0.2944	2068.3	50.00	Sequence
DRB1_0301	493	ERISTRITNEVAEVN	STRITNEVA	0.2944	2068.6	50.00	Sequence
DRB1_0301	231	LSGGVDSAVAAALVQ	SGGVDSAVA	0.2939	2079.7	50.00	Sequence
DRB1_0301	494	RISTRITNEVAEVNR	STRITNEVA	0.2931	2098.2	50.00	Sequence
DRB1_0301	473	PVSSEDAMTADWTRV	VSSEDAMTA	0.2913	2139.1	50.00	Sequence
DRB1_0301	117	TELKVLGGKLHSDLP	ELKVLGGKL	0.2910	2145.8	50.00	Sequence
DRB1_0301	64	GGPASVYADGAPKLD	PASVYADGA	0.2902	2163.9	50.00	Sequence
DRB1_0301	492	LERISTRITNEVAEV	LERISTRIT	0.2901	2166.9	50.00	Sequence
DRB1_0301	239	VAAALVQRAIGDRLT	VAAALVQRA	0.2867	2246.7	50.00	Sequence
DRB1_0301	264	AGERAQVQRDFVAAT	RAQVQRDFV	0.2859	2267.1	50.00	Sequence
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DRB1_0301	412	GEVTAKRLDTLRHAD	VTAKRLDTL	0.2844	2304.6	50.00	Sequence
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DRB1_0301	500	TNEVAEVNRVVLDIT	VAEVNRVVL	0.2829	2342.3	50.00	Sequence
DRB1_0301	135	PVWMSHGDAVTAAPD	VWMSHGDAV	0.2825	2352.8	50.00	Sequence
DRB1_0301	41	EVIPHTASIEEIRAR	IPHTASIEE	0.2822	2361.0	50.00	Sequence
DRB1_0301	477	EDAMTADWTRVPYEV	DAMTADWTR	0.2808	2395.1	50.00	Sequence
DRB1_0301	79	PALLDLGVPVLGICY	ALLDLGVPV	0.2768	2503.1	50.00	Sequence
DRB1_0301	30	ARRVREARVFSEVIP	ARRVREARV	0.2756	2535.1	50.00	Sequence
DRB1_0301	441	QIWQCPVVLLADVRS	PVVLLADVR	0.2747	2559.5	50.00	Sequence
DRB1_0301	228	ICGLSGGVDSAVAAA	ICGLSGGVD	0.2746	2561.6	50.00	Sequence
DRB1_0301	379	KDEVRAVGRELGLPE	KDEVRAVGR	0.2743	2570.9	50.00	Sequence
DRB1_0301	474	VSSEDAMTADWTRVP	VSSEDAMTA	0.2739	2580.7	50.00	Sequence
DRB1_0301	85	GVPVLGICYGFQAMA	VPVLGICYG	0.2723	2626.5	50.00	Sequence
DRB1_0301	238	AVAAALVQRAIGDRL	VAAALVQRA	0.2708	2669.8	50.00	Sequence
DRB1_0301	192	SRFLHDFAGLGAQWT	FLHDFAGLG	0.2677	2761.9	50.00	Sequence
DRB1_0301	316	FEGAVRDVLDGKTAE	FEGAVRDVL	0.2673	2772.5	50.00	Sequence
DRB1_0301	133	VQPVWMSHGDAVTAA	VWMSHGDAV	0.2672	2777.1	50.00	Sequence
DRB1_0301	245	QRAIGDRLTCVFVDH	QRAIGDRLT	0.2668	2789.0	50.00	Sequence
DRB1_0301	484	WTRVPYEVLERISTR	VPYEVLERI	0.2659	2815.6	50.00	Sequence
DRB1_0301	356	HHNVGGLPDDLKFTL	VGGLPDDLK	0.2644	2861.9	50.00	Sequence
DRB1_0301	136	VWMSHGDAVTAAPDG	VWMSHGDAV	0.2637	2883.6	50.00	Sequence
DRB1_0301	232	SGGVDSAVAAALVQR	SGGVDSAVA	0.2630	2906.5	50.00	Sequence
DRB1_0301	246	RAIGDRLTCVFVDHG	RAIGDRLTC	0.2623	2926.4	50.00	Sequence
DRB1_0301	134	QPVWMSHGDAVTAAP	VWMSHGDAV	0.2622	2929.0	50.00	Sequence
DRB1_0301	20	DFGAQYAQLIARRVR	QYAQLIARR	0.2622	2930.1	50.00	Sequence
DRB1_0301	476	SEDAMTADWTRVPYE	DAMTADWTR	0.2620	2937.2	50.00	Sequence
DRB1_0301	74	APKLDPALLDLGVPV	APKLDPALL	0.2619	2939.4	50.00	Sequence
DRB1_0301	33	VREARVFSEVIPHTA	RVFSEVIPH	0.2617	2946.8	50.00	Sequence
DRB1_0301	261	LLRAGERAQVQRDFV	LLRAGERAQ	0.2614	2955.2	50.00	Sequence
DRB1_0301	378	FKDEVRAVGRELGLP	KDEVRAVGR	0.2597	3009.3	50.00	Sequence
DRB1_0301	159	GAPVAAFEAFDRRLA	AAFEAFDRR	0.2581	3064.0	50.00	Sequence
DRB1_0301	273	DFVAATGANLVTVDA	VAATGANLV	0.2573	3090.2	50.00	Sequence
DRB1_0301	478	DAMTADWTRVPYEVL	DAMTADWTR	0.2556	3147.8	50.00	Sequence
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DRB1_0301	45	HTASIEEIRARQPVA	HTASIEEIR	0.2524	3257.1	50.00	Sequence
DRB1_0301	40	SEVIPHTASIEEIRA	IPHTASIEE	0.2521	3267.3	50.00	Sequence
DRB1_0301	80	ALLDLGVPVLGICYG	ALLDLGVPV	0.2520	3270.5	50.00	Sequence
DRB1_0301	247	AIGDRLTCVFVDHGL	LTCVFVDHG	0.2517	3282.4	50.00	Sequence
DRB1_0301	63	SGGPASVYADGAPKL	PASVYADGA	0.2513	3296.7	50.00	Sequence
DRB1_0301	274	FVAATGANLVTVDAA	VAATGANLV	0.2506	3323.5	50.00	Sequence
DRB1_0301	116	RTELKVLGGKLHSDL	LKVLGGKLH	0.2490	3378.7	50.00	Sequence
DRB1_0301	387	RELGLPEEIVARQPF	RELGLPEEI	0.2489	3385.5	50.00	Sequence
DRB1_0301	49	IEEIRARQPVALVLS	IEEIRARQP	0.2477	3427.5	50.00	Sequence

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DRB1_0301  451  ADVRSVGVQGDGRTY  SVGVQGDGR         0.2453        3519.1                  50.00     Sequence
DRB1_0301   46  TASIEEIRARQPVAL  IEEIRARQP         0.2451        3525.8                  50.00     Sequence
DRB1_0301    0  VVQPADIDVPETPAR  VQPADIDVP         0.2451        3526.7                  50.00     Sequence
DRB1_0301   72  DGAPKLDPALLDLGV  GAPKLDPAL         0.2451        3526.9                  50.00     Sequence
DRB1_0301  193  RFLHDFAGLGAQWTP  FLHDFAGLG         0.2431        3604.1                  50.00     Sequence
DRB1_0301  237  SAVAAALVQRAIGDR  VAAALVQRA         0.2418        3653.2                  50.00     Sequence
DRB1_0301  498  RITNEVAEVNRVVLD  RITNEVAEV         0.2417        3655.9                  50.00     Sequence
DRB1_0301  386  GRELGLPEEIVARQP  RELGLPEEI         0.2412        3676.0                  50.00     Sequence
DRB1_0301   47  ASIEEIRARQPVALV  IEEIRARQP         0.2410        3687.0                  50.00     Sequence
DRB1_0301  330  EFLVQGTLYPDVVES  FLVQGTLYP         0.2407        3696.3                  50.00     Sequence
DRB1_0301   69  VYADGAPKLDPALLD  VYADGAPKL         0.2393        3755.1                  50.00     Sequence
DRB1_0301  275  VAATGANLVTVDAAE  VAATGANLV         0.2380        3806.2                  50.00     Sequence
DRB1_0301  227  AICGLSGGVDSAVAA  CGLSGGVDS         0.2378        3813.9                  50.00     Sequence
DRB1_0301  360  GGLPDDLKFTLVEPL  PDDLKFTLV         0.2374        3833.3                  50.00     Sequence
DRB1_0301    3  PADIDVPETPARPVL  IDVPETPAR         0.2373        3835.2                  50.00     Sequence
DRB1_0301   32  RVREARVFSEVIPHT  RVFSEVIPH         0.2360        3890.1                  50.00     Sequence
DRB1_0301   84  LGVPVLGICYGFQAM  VPVLGICYG         0.2352        3922.7                  50.00     Sequence
DRB1_0301  361  GLPDDLKFTLVEPLR  LPDDLKFTL         0.2352        3923.4                  50.00     Sequence
DRB1_0301   48  SIEEIRARQPVALVL  IEEIRARQP         0.2347        3944.1                  50.00     Sequence
DRB1_0301  497  TRITNEVAEVNRVVL  TRITNEVAE         0.2347        3945.1                  50.00     Sequence
DRB1_0301   31  RRVREARVFSEVIPH  RRVREARVF         0.2344        3957.5                  50.00     Sequence
DRB1_0301  475  SSEDAMTADWTRVPY  DAMTADWTR         0.2343        3962.6                  50.00     Sequence
DRB1_0301    9  PETPARPVLVVDFGA  RPVLVVDFG         0.2334        4003.6                  50.00     Sequence
DRB1_0301  236  DSAVAAALVQRAIGD  VAAALVQRA         0.2328        4026.5                  50.00     Sequence
DRB1_0301  430  REELTAAGLDNQIWQ  REELTAAGL         0.2323        4050.1                  50.00     Sequence
DRB1_0301  212  NALIEQVRTQIGDGH  LIEQVRTQI         0.2318        4069.2                  50.00     Sequence
DRB1_0301   44  PHTASIEEIRARQPV  HTASIEEIR         0.2315        4083.9                  50.00     Sequence
DRB1_0301  132  EVQPVWMSHGDAVTA  VWMSHGDAV         0.2311        4100.3                  50.00     Sequence
DRB1_0301  235  VDSAVAAALVQRAIG  VDSAVAAAL         0.2302        4143.5                  50.00     Sequence
DRB1_0301  450  LADVRSVGVQGDGRT  LADVRSVGV         0.2292        4188.3                  50.00     Sequence
DRB1_0301  499  ITNEVAEVNRVVLDI  VAEVNRVVL         0.2290        4197.0                  50.00     Sequence
DRB1_0301   54  ARQPVALVLSGGPAS  LVLSGGPAS         0.2288        4203.5                  50.00     Sequence
DRB1_0301  233  GGVDSAVAAALVQRA  GGVDSAVAA         0.2281        4240.0                  50.00     Sequence
DRB1_0301    1  VQPADIDVPETPARP  VQPADIDVP         0.2280        4241.4                  50.00     Sequence
DRB1_0301  428  IVREELTAAGLDNQI  IVREELTAA         0.2272        4277.0                  50.00     Sequence
DRB1_0301  388  ELGLPEEIVARQPFP  LPEEIVARQ         0.2262        4327.5                  50.00     Sequence
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DRB1_0301  403  GPGLGIRIVGEVTAK  IRIVGEVTA         0.2230        4478.6                  50.00     Sequence
DRB1_0301  166  EAFDRRLAGVQYHPE  EAFDRRLAG         0.2229        4484.8                  50.00     Sequence
DRB1_0301  290  TFLEALSGVSAPEGK  FLEALSGVS         0.2224        4508.1                  50.00     Sequence
DRB1_0301  464  TYGHPIVLRPVSSED  YGHPIVLRP         0.2221        4522.0                  50.00     Sequence
DRB1_0301  465  YGHPIVLRPVSSEDA  YGHPIVLRP         0.2217        4541.9                  50.00     Sequence
DRB1_0301    5  DIDVPETPARPVLVV  IDVPETPAR         0.2216        4544.8                  50.00     Sequence
DRB1_0301    4  ADIDVPETPARPVLV  IDVPETPAR         0.2196        4645.5                  50.00     Sequence
DRB1_0301  291  FLEALSGVSAPEGKR  FLEALSGVS         0.2189        4680.0                  50.00     Sequence
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DRB1_0301  102  LGGIVAHTGTREYGR  LGGIVAHTG         0.2158        4839.0                  50.00     Sequence
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DRB1_0301   71  ADGAPKLDPALLDLG  APKLDPALL         0.2138        4945.5                  50.00     Sequence
DRB1_0301  466  GHPIVLRPVSSEDAM  PIVLRPVSS         0.2137        4953.0                  50.00     Sequence
DRB1_0301  207  PANIANALIEQVRTQ  IANALIEQV         0.2132        4978.2                  50.00     Sequence
DRB1_0301  126  LHSDLPEVQPVWMSH  LHSDLPEVQ         0.2125        5019.2                  50.00     Sequence
DRB1_0301    2  QPADIDVPETPARPV  IDVPETPAR         0.2124        5022.4                  50.00     Sequence
DRB1_0301  335  GTLYPDVVESGGGSG  TLYPDVVES         0.2106        5120.6                  50.00     Sequence
DRB1_0301  289  ETFLEALSGVSAPEG  FLEALSGVS         0.2095        5180.3                  50.00     Sequence
DRB1_0301  336  TLYPDVVESGGGSGT  TLYPDVVES         0.2082        5255.8                  50.00     Sequence
DRB1_0301  432  ELTAAGLDNQIWQCP  LTAAGLDNQ         0.2057        5401.6                  50.00     Sequence
DRB1_0301   83  DLGVPVLGICYGFQA  VPVLGICYG         0.2056        5403.9                  50.00     Sequence
DRB1_0301    6  IDVPETPARPVLVVD  IDVPETPAR         0.2055        5411.0                  50.00     Sequence
DRB1_0301  438  LDNQIWQCPVVLLAD  NQIWQCPVV         0.2054        5416.7                  50.00     Sequence
DRB1_0301  381  EVRAVGRELGLPEEI  VRAVGRELG         0.2053        5424.4                  50.00     Sequence
DRB1_0301  263  RAGERAQVQRDFVAA  RAQVQRDFV         0.2051        5435.5                  50.00     Sequence
DRB1_0301  234  GVDSAVAAALVQRAI  VDSAVAAAL         0.2048        5455.1                  50.00     Sequence
DRB1_0301  483  DWTRVPYEVLERIST  VPYEVLERI         0.2046        5464.7                  50.00     Sequence
DRB1_0301  300  APEGKRKIIGRQFIR  KIIGRQFIR         0.2041        5495.6                  50.00     Sequence
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DRB1_0301  463  RTYGHPIVLRPVSSE  YGHPIVLRP       0.2040       5502.3                50.00     Sequence
DRB1_0301  172  LAGVQYHPEVMHTPH  VQYHPEVMH       0.2039       5507.4                50.00     Sequence
DRB1_0301  401  FPGPGLGIRIVGEVT  FPGPGLGIR       0.2036       5524.0                50.00     Sequence
DRB1_0301  104  GIVAHTGTREYGRTE  GIVAHTGTR       0.2034       5535.2                50.00     Sequence
DRB1_0301  115  GRTELKVLGGKLHSD  RTELKVLGG       0.2034       5537.7                50.00     Sequence
DRB1_0301  276  AATGANLVTVDAAET  ANLVTVDAA       0.2022       5606.1                50.00     Sequence
DRB1_0301  389  LGLPEEIVARQPFPG  LPEEIVARQ       0.2008       5695.3                50.00     Sequence
DRB1_0301  355  SHHNVGGLPDDLKFT  NVGGLPDDL       0.2005       5709.8                50.00     Sequence
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DRB1_0301  402  PGPGLGIRIVGEVTA  IRIVGEVTA       0.1970       5931.8                50.00     Sequence
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DRB1_0301   87  PVLGICYGFQAMAQA  GICYGFQAM       0.1934       6167.8                50.00     Sequence
DRB1_0301  440  NQIWQCPVVLLADVR  PVVLLADVR       0.1933       6173.6                50.00     Sequence
DRB1_0301  101  ALGGIVAHTGTREYG  LGGIVAHTG       0.1924       6236.5                50.00     Sequence
DRB1_0301  103  GGIVAHTGTREYGRT  GIVAHTGTR       0.1921       6257.4                50.00     Sequence
DRB1_0301  167  AFDRRLAGVQYHPEV  RRLAGVQYH       0.1901       6394.5                50.00     Sequence
DRB1_0301  390  GLPEEIVARQPFPGP  GLPEEIVAR       0.1901       6395.5                50.00     Sequence
DRB1_0301  194  FLHDFAGLGAQWTPA  FLHDFAGLG       0.1894       6440.4                50.00     Sequence
DRB1_0301  288  AETFLEALSGVSAPE  FLEALSGVS       0.1891       6465.9                50.00     Sequence
DRB1_0301   19  VDFGAQYAQLIARRV  QYAQLIARR       0.1887       6489.7                50.00     Sequence
DRB1_0301  169  DRRLAGVQYHPEVMH  DRRLAGVQY       0.1882       6524.1                50.00     Sequence
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DRB1_0301  283  VTVDAAETFLEALSG  VTVDAAETF       0.1879       6544.2                50.00     Sequence
DRB1_0301  131  PEVQPVWMSHGDAVT  VWMSHGDAV       0.1877       6561.6                50.00     Sequence
DRB1_0301  460  GDGRTYGHPIVLRPV  DGRTYGHPI       0.1874       6585.2                50.00     Sequence
DRB1_0301  329  AEFLVQGTLYPDVVE  FLVQGTLYP       0.1872       6596.4                50.00     Sequence
DRB1_0301   89  LGICYGFQAMAQALG  ICYGFQAMA       0.1861       6672.9                50.00     Sequence
DRB1_0301  437  GLDNQIWQCPVVLLA  NQIWQCPVV       0.1852       6743.9                50.00     Sequence
DRB1_0301   88  VLGICYGFQAMAQAL  ICYGFQAMA       0.1847       6778.0                50.00     Sequence
DRB1_0301  434  TAAGLDNQIWQCPVV  TAAGLDNQI       0.1839       6833.7                50.00     Sequence
DRB1_0301  382  VRAVGRELGLPEEIV  VRAVGRELG       0.1834       6871.8                50.00     Sequence
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DRB1_0301   81  LLDLGVPVLGICYGF  LLDLGVPVL       0.1808       7067.5                50.00     Sequence
DRB1_0301  171  RLAGVQYHPEVMHTP  LAGVQYHPE       0.1805       7088.9                50.00     Sequence
DRB1_0301  170  RRLAGVQYHPEVMHT  LAGVQYHPE       0.1805       7090.4                50.00     Sequence
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DRB1_0301  100  QALGGIVAHTGTREY  LGGIVAHTG       0.1784       7259.0                50.00     Sequence
DRB1_0301  456  VGVQGDGRTYGHPIV  VGVQGDGRT       0.1781       7277.5                50.00     Sequence
DRB1_0301  400  PFPGPGLGIRIVGEV  FPGPGLGIR       0.1781       7279.4                50.00     Sequence
DRB1_0301  461  DGRTYGHPIVLRPVS  DGRTYGHPI       0.1772       7348.0                50.00     Sequence
DRB1_0301  105  IVAHTGTREYGRTEL  IVAHTGTRE       0.1767       7394.3                50.00     Sequence
DRB1_0301  436  AGLDNQIWQCPVVLL  LDNQIWQCP       0.1765       7408.3                50.00     Sequence
DRB1_0301  479  AMTADWTRVPYEVLE  AMTADWTRV       0.1763       7420.4                50.00     Sequence
DRB1_0301  384  AVGRELGLPEEIVAR  RELGLPEEI       0.1757       7471.7                50.00     Sequence
DRB1_0301   82  LDLGVPVLGICYGFQ  VPVLGICYG       0.1754       7497.2                50.00     Sequence
DRB1_0301  150  GFDVVASSAGAPVAA  GFDVVASSA       0.1748       7543.6                50.00     Sequence
DRB1_0301   50  EEIRARQPVALVLSG  IRARQPVAL       0.1740       7607.3                50.00     Sequence
DRB1_0301   51  EIRARQPVALVLSGG  IRARQPVAL       0.1734       7657.9                50.00     Sequence
DRB1_0301  314  RAFEGAVRDVLDGKT  FEGAVRDVL       0.1708       7879.5                50.00     Sequence
DRB1_0301  173  AGVQYHPEVMHTPHG  VQYHPEVMH       0.1694       7998.8                50.00     Sequence
DRB1_0301    8  VPETPARPVLVVDFG  RPVLVVDFG       0.1692       8015.5                50.00     Sequence
DRB1_0301  174  GVQYHPEVMHTPHGQ  VQYHPEVMH       0.1691       8024.9                50.00     Sequence
DRB1_0301  138  MSHGDAVTAAPDGFD  MSHGDAVTA       0.1683       8091.7                50.00     Sequence
DRB1_0301  114  YGRTELKVLGGKLHS  GRTELKVLG       0.1674       8176.0                50.00     Sequence
DRB1_0301   90  GICYGFQAMAQALGG  ICYGFQAMA       0.1670       8209.2                50.00     Sequence
DRB1_0301  458  VQGDGRTYGHPIVLR  VQGDGRTYG       0.1664       8258.1                50.00     Sequence
DRB1_0301  149  DGFDVVASSAGAPVA  GFDVVASSA       0.1664       8265.4                50.00     Sequence
DRB1_0301  322  DVLDGKTAEFLVQGT  DVLDGKTAE       0.1657       8327.5                50.00     Sequence
DRB1_0301  292  LEALSGVSAPEGKRK  LEALSGVSA       0.1625       8618.5                50.00     Sequence
DRB1_0301  151  FDVVASSAGAPVAAF  FDVVASSAG       0.1615       8710.4                50.00     Sequence
DRB1_0301  459  QGDGRTYGHPIVLRP  DGRTYGHPI       0.1610       8759.5                50.00     Sequence
DRB1_0301  287  AAETFLEALSGVSAP  FLEALSGVS       0.1601       8842.1                50.00     Sequence
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DRB1_0301	225	GHAICGLSGGVDSAV	ICGLSGGVD	0.1579	9060.0	50.00	Sequence
DRB1_0301	168	FDRRLAGVQYHPEVM	DRRLAGVQY	0.1575	9094.1	50.00	Sequence
DRB1_0301	206	TPANIANALIEQVRT	IANALIEQV	0.1570	9147.3	50.00	Sequence
DRB1_0301	148	PDGFDVVASSAGAPV	DGFDVVASS	0.1545	9395.7	50.00	Sequence
DRB1_0301	183	HTPHGQQVLSRFLHD	PHGQQVLSR	0.1540	9446.0	50.00	Sequence
DRB1_0301	435	AAGLDNQIWQCPVVL	LDNQIWQCP	0.1540	9446.6	50.00	Sequence
DRB1_0301	327	KTAEFLVQGTLYPDV	TAEFLVQGT	0.1526	9594.2	50.00	Sequence
DRB1_0301	158	AGAPVAAFEAFDRRL	AAFEAFDRR	0.1525	9604.5	50.00	Sequence
DRB1_0301	457	GVQGDGRTYGHPIVL	VQGDGRTYG	0.1523	9620.6	50.00	Sequence
DRB1_0301	112	REYGRTELKVLGGKL	REYGRTELK	0.1522	9635.6	50.00	Sequence
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DRB1_0301	130	LPEVQPVWMSHGDAV	VWMSHGDAV	0.1516	9691.7	50.00	Sequence
DRB1_0301	482	ADWTRVPYEVLERIS	VPYEVLERI	0.1516	9694.1	50.00	Sequence
DRB1_0301	113	EYGRTELKVLGGKLH	EYGRTELKV	0.1510	9754.8	50.00	Sequence
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DRB1_0301	398	RQPFPGPGLGIRIVG	FPGPGLGIR	0.1236	13127.6	50.00	Sequence
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DRB1_0301	326	GKTAEFLVQGTLYPD	TAEFLVQGT	0.1170	14104.3	50.00	Sequence
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DRB1_0301	181	VMHTPHGQQVLSRFL	PHGQQVLSR	0.1136	14627.1	50.00	Sequence
DRB1_0301	180	EVMHTPHGQQVLSRF	VMHTPHGQQ	0.1124	14811.2	50.00	Sequence
DRB1_0301	221	QIGDGHAICGLSGGV	DGHAICGLS	0.1121	14865.4	50.00	Sequence
DRB1_0301	293	EALSGVSAPEGKRKI	LSGVSAPEG	0.1111	15026.7	50.00	Sequence
DRB1_0301	205	WTPANIANALIEQVR	IANALIEQV	0.1096	15274.2	50.00	Sequence
DRB1_0301	139	SHGDAVTAAPDGFDV	SHGDAVTAA	0.1091	15352.9	50.00	Sequence
DRB1_0301	179	PEVMHTPHGQQVLSR	VMHTPHGQQ	0.1087	15424.7	50.00	Sequence
DRB1_0301	178	HPEVMHTPHGQQVLS	VMHTPHGQQ	0.1083	15482.5	50.00	Sequence
DRB1_0301	143	AVTAAPDGFDVVASS	AVTAAPDGF	0.1076	15605.6	50.00	Sequence
DRB1_0301	62	LSGGPASVYADGAPK	PASVYADGA	0.1062	15840.7	50.00	Sequence

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   DRB1_0301  350  TANIKSHHNVGGLPD  TANIKSHHN        0.1058      15918.7               50.00     Sequence
   DRB1_0301   97  AMAQALGGIVAHTGT  MAQALGGIV        0.1053      16003.9               50.00     Sequence
   DRB1_0301  140  HGDAVTAAPDGFDVV  GDAVTAAPD        0.1050      16061.5               50.00     Sequence
   DRB1_0301  145  TAAPDGFDVVASSAG  DGFDVVASS        0.1031      16380.0               50.00     Sequence
   DRB1_0301  345  GGGSGTANIKSHHNV  GGSGTANIK        0.1031      16386.7               50.00     Sequence
   DRB1_0301  299  SAPEGKRKIIGRQFI  RKIIGRQFI        0.1001      16933.2               50.00     Sequence
   DRB1_0301  195  LHDFAGLGAQWTPAN  LHDFAGLGA        0.0994      17050.5               50.00     Sequence
   DRB1_0301  285  VDAAETFLEALSGVS  AAETFLEAL        0.0980      17317.9               50.00     Sequence
   DRB1_0301  222  IGDGHAICGLSGGVD  DGHAICGLS        0.0979      17331.7               50.00     Sequence
   DRB1_0301  349  GTANIKSHHNVGGLP  TANIKSHHN        0.0974      17427.3               50.00     Sequence
   DRB1_0301  348  SGTANIKSHHNVGGL  TANIKSHHN        0.0959      17706.1               50.00     Sequence
   DRB1_0301  325  DGKTAEFLVQGTLYP  TAEFLVQGT        0.0947      17952.0               50.00     Sequence
   DRB1_0301  347  GSGTANIKSHHNVGG  GSGTANIKS        0.0946      17967.6               50.00     Sequence
   DRB1_0301  177  YHPEVMHTPHGQQVL  VMHTPHGQQ        0.0938      18130.1               50.00     Sequence
   DRB1_0301  142  DAVTAAPDGFDVVAS  AVTAAPDGF        0.0916      18562.2               50.00     Sequence
   DRB1_0301  392  PEEIVARQPFPGPGL  PEEIVARQP        0.0913      18609.2               50.00     Sequence
   DRB1_0301  108  HTGTREYGRTELKVL  HTGTREYGR        0.0909      18707.4               50.00     Sequence
   DRB1_0301  297  GVSAPEGKRKIIGRQ  GVSAPEGKR        0.0892      19039.2               50.00     Sequence
   DRB1_0301  144  VTAAPDGFDVVASSA  DGFDVVASS        0.0883      19223.4               50.00     Sequence
   DRB1_0301  353  IKSHHNVGGLPDDLK  VGGLPDDLK        0.0868      19546.0               50.00     Sequence
   DRB1_0301   96  QAMAQALGGIVAHTG  AQALGGIVA        0.0865      19606.1               50.00     Sequence
   DRB1_0301  298  VSAPEGKRKIIGRQF  VSAPEGKRK        0.0863      19649.0               50.00     Sequence
   DRB1_0301  344  SGGGSGTANIKSHHN  GSGTANIKS        0.0853      19876.5               50.00     Sequence
   DRB1_0301   92  CYGFQAMAQALGGIV  CYGFQAMAQ        0.0831      20343.9               50.00     Sequence
   DRB1_0301  203  AQWTPANIANALIEQ  AQWTPANIA        0.0828      20416.7               50.00     Sequence
   DRB1_0301  157  SAGAPVAAFEAFDRR  AAFEAFDRR        0.0816      20671.8               50.00     Sequence
   DRB1_0301  129  DLPEVQPVWMSHGDA  LPEVQPVWM        0.0796      21123.8               50.00     Sequence
   DRB1_0301   94  GFQAMAQALGGIVAH  GFQAMAQAL        0.0785      21380.0               50.00     Sequence
   DRB1_0301  176  QYHPEVMHTPHGQQV  VMHTPHGQQ        0.0772      21692.4               50.00     Sequence
   DRB1_0301  107  AHTGTREYGRTELKV  HTGTREYGR        0.0771      21707.2               50.00     Sequence
   DRB1_0301  202  GAQWTPANIANALIE  AQWTPANIA        0.0771      21717.6               50.00     Sequence
   DRB1_0301   95  FQAMAQALGGIVAHT  MAQALGGIV        0.0769      21756.1               50.00     Sequence
   DRB1_0301   53  RARQPVALVLSGGPA  VALVLSGGP        0.0753      22140.6               50.00     Sequence
   DRB1_0301  397  ARQPFPGPGLGIRIV  PGPGLGIRI        0.0747      22290.6               50.00     Sequence
   DRB1_0301  128  SDLPEVQPVWMSHGD  SDLPEVQPV        0.0744      22364.0               50.00     Sequence
   DRB1_0301  351  ANIKSHHNVGGLPDD  ANIKSHHNV        0.0739      22477.1               50.00     Sequence
   DRB1_0301  324  LDGKTAEFLVQGTLY  LDGKTAEFL        0.0724      22832.0               50.00     Sequence
   DRB1_0301  204  QWTPANIANALIEQV  TPANIANAL        0.0720      22948.6               50.00     Sequence
   DRB1_0301  127  HSDLPEVQPVWMSHG  SDLPEVQPV        0.0712      23138.6               50.00     Sequence
   DRB1_0301  343  ESGGGSGTANIKSHH  GSGTANIKS        0.0712      23147.4               50.00     Sequence
   DRB1_0301   93  YGFQAMAQALGGIVA  GFQAMAQAL        0.0701      23428.1               50.00     Sequence
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   DRB1_0301  201  LGAQWTPANIANALI  AQWTPANIA        0.0679      23984.4               50.00     Sequence
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   DRB1_0301  338  YPDVVESGGGSGTAN  YPDVVESGG        0.0627      25362.4               50.00     Sequence
   DRB1_0301  200  GLGAQWTPANIANAL  AQWTPANIA        0.0609      25870.7               50.00     Sequence
   DRB1_0301  197  DFAGLGAQWTPANIA  FAGLGAQWT        0.0591      26383.4               50.00     Sequence
   DRB1_0301  198  FAGLGAQWTPANIAN  FAGLGAQWT        0.0548      27631.3               50.00     Sequence
   DRB1_0301  340  DVVESGGGSGTANIK  VVESGGGSG        0.0540      27872.4               50.00     Sequence
   DRB1_0301  342  VESGGGSGTANIKSH  VESGGGSGT        0.0531      28134.1               50.00     Sequence
   DRB1_0301  339  PDVVESGGGSGTANI  VVESGGGSG        0.0511      28766.4               50.00     Sequence
   DRB1_0301  393  EEIVARQPFPGPGLG  EEIVARQPF        0.0509      28822.5               50.00     Sequence
   DRB1_0301  341  VVESGGGSGTANIKS  VVESGGGSG        0.0501      29061.7               50.00     Sequence
   DRB1_0301  156  SSAGAPVAAFEAFDR  SSAGAPVAA        0.0463      30289.0               50.00     Sequence
   DRB1_0301  199  AGLGAQWTPANIANA  GLGAQWTPA        0.0453      30633.8               50.00     Sequence
   DRB1_0301  396  VARQPFPGPGLGIRI  FPGPGLGIR        0.0423      31653.4               50.00     Sequence
   DRB1_0301  155  ASSAGAPVAAFEAFD  ASSAGAPVA        0.0409      32125.7               50.00     Sequence
   DRB1_0301  394  EIVARQPFPGPGLGI  EIVARQPFP        0.0298      36211.9               50.00     Sequence
   DRB1_0301  395  IVARQPFPGPGLGIR  IVARQPFPG        0.0296      36306.5               50.00     Sequence
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Allele: DRB1_0301. Number of high binders 10. Number of weak binders 69. Number of peptides 511

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0401  407  GIRIVGEVTAKRLDT  IRIVGEVTA        0.7046         24.4         SB     2.00     Sequence
   DRB1_0401  408  IRIVGEVTAKRLDTL  IRIVGEVTA        0.7003         25.6         SB     2.00     Sequence
   DRB1_0401  406  LGIRIVGEVTAKRLD  IRIVGEVTA        0.6777         32.7         SB     4.00     Sequence
   DRB1_0401  421  TLRHADSIVREELTA  LRHADSIVR        0.6630         38.3         SB     4.00     Sequence
   DRB1_0401  422  LRHADSIVREELTAA  LRHADSIVR        0.6456         46.3         SB     4.00     Sequence
   DRB1_0401  405  GLGIRIVGEVTAKRL  IRIVGEVTA        0.6448         46.7         SB     4.00     Sequence
   DRB1_0401  506  VNRVVLDITSKPPAT  RVVLDITSK        0.6269         56.6         WB     8.00     Sequence
   DRB1_0401  507  NRVVLDITSKPPATI  RVVLDITSK        0.6230         59.1         WB     8.00     Sequence
   DRB1_0401  420  DTLRHADSIVREELT  LRHADSIVR        0.6204         60.7         WB     8.00     Sequence
   DRB1_0401  505  EVNRVVLDITSKPPA  RVVLDITSK        0.6167         63.3         WB     8.00     Sequence
   DRB1_0401  419  LDTLRHADSIVREEL  LRHADSIVR        0.5920         82.7         WB     8.00     Sequence
   DRB1_0401  404  PGLGIRIVGEVTAKR  IRIVGEVTA        0.5690        106.0         WB    16.00     Sequence
   DRB1_0401  504  AEVNRVVLDITSKPP  RVVLDITSK        0.5601        116.7         WB    16.00     Sequence
   DRB1_0401   90  GICYGFQAMAQALGG  YGFQAMAQA        0.5531        125.8         WB    16.00     Sequence
   DRB1_0401  135  PVWMSHGDAVTAAPD  WMSHGDAVT        0.5487        132.0         WB    16.00     Sequence
   DRB1_0401   93  YGFQAMAQALGGIVA  FQAMAQALG        0.5479        133.2         WB    16.00     Sequence
   DRB1_0401  375  RLLFKDEVRAVGREL  LLFKDEVRA        0.5463        135.4         WB    16.00     Sequence
   DRB1_0401  193  RFLHDFAGLGAQWTP  RFLHDFAGL        0.5454        136.9         WB    16.00     Sequence
   DRB1_0401   92  CYGFQAMAQALGGIV  YGFQAMAQA        0.5440        138.9         WB    16.00     Sequence
   DRB1_0401  374  LRLLFKDEVRAVGRE  LLFKDEVRA        0.5435        139.7         WB    16.00     Sequence
   DRB1_0401   91  ICYGFQAMAQALGGI  YGFQAMAQA        0.5426        141.0         WB    16.00     Sequence
   DRB1_0401  373  PLRLLFKDEVRAVGR  LLFKDEVRA        0.5414        142.8         WB    16.00     Sequence
   DRB1_0401  307  IIGRQFIRAFEGAVR  RQFIRAFEG        0.5413        143.0         WB    16.00     Sequence
   DRB1_0401   89  LGICYGFQAMAQALG  CYGFQAMAQ        0.5413        143.0         WB    16.00     Sequence
   DRB1_0401  409  RIVGEVTAKRLDTLR  RIVGEVTAK        0.5383        147.7         WB    16.00     Sequence
   DRB1_0401  192  SRFLHDFAGLGAQWT  RFLHDFAGL        0.5379        148.3         WB    16.00     Sequence
   DRB1_0401  508  RVVLDITSKPPATIE  RVVLDITSK        0.5332        156.2         WB    16.00     Sequence
   DRB1_0401  137  WMSHGDAVTAAPDGF  MSHGDAVTA        0.5332        156.2         WB    16.00     Sequence
   DRB1_0401  134  QPVWMSHGDAVTAAP  WMSHGDAVT        0.5238        172.9         WB    16.00     Sequence
   DRB1_0401  418  RLDTLRHADSIVREE  LRHADSIVR        0.5228        174.8         WB    16.00     Sequence
   DRB1_0401  136  VWMSHGDAVTAAPDG  MSHGDAVTA        0.5222        175.9         WB    16.00     Sequence
   DRB1_0401   36  ARVFSEVIPHTASIE  RVFSEVIPH        0.5219        176.4         WB    16.00     Sequence
   DRB1_0401  191  LSRFLHDFAGLGAQW  RFLHDFAGL        0.5185        183.1         WB    16.00     Sequence
   DRB1_0401  269  QVQRDFVAATGANLV  QVQRDFVAA        0.5124        195.5         WB    16.00     Sequence
   DRB1_0401  309  GRQFIRAFEGAVRDV  QFIRAFEGA        0.5118        196.7         WB    16.00     Sequence
   DRB1_0401  310  RQFIRAFEGAVRDVL  QFIRAFEGA        0.5109        198.8         WB    16.00     Sequence
   DRB1_0401  416  AKRLDTLRHADSIVR  KRLDTLRHA        0.5075        206.1         WB    16.00     Sequence
   DRB1_0401  417  KRLDTLRHADSIVRE  LRHADSIVR        0.5067        207.9         WB    16.00     Sequence
   DRB1_0401  372  EPLRLLFKDEVRAVG  LLFKDEVRA        0.5053        211.2         WB    16.00     Sequence
   DRB1_0401  308  IGRQFIRAFEGAVRD  QFIRAFEGA        0.5042        213.8         WB    16.00     Sequence
   DRB1_0401  306  KIIGRQFIRAFEGAV  QFIRAFEGA        0.5024        217.8         WB    16.00     Sequence
   DRB1_0401  195  LHDFAGLGAQWTPAN  FAGLGAQWT        0.5016        219.8         WB    16.00     Sequence
   DRB1_0401   31  RRVREARVFSEVIPH  RVREARVFS        0.5014        220.2         WB    16.00     Sequence
   DRB1_0401   35  EARVFSEVIPHTASI  RVFSEVIPH        0.4995        224.8         WB    16.00     Sequence
   DRB1_0401  268  AQVQRDFVAATGANL  QVQRDFVAA        0.4992        225.5         WB    16.00     Sequence
   DRB1_0401  446  PVVLLADVRSVGVQG  VVLLADVRS        0.4965        232.3         WB    16.00     Sequence
   DRB1_0401  365  DLKFTLVEPLRLLFK  FTLVEPLRL        0.4959        233.8         WB    16.00     Sequence
   DRB1_0401  489  YEVLERISTRITNEV  LERISTRIT        0.4863        259.4         WB    32.00     Sequence
   DRB1_0401  194  FLHDFAGLGAQWTPA  LHDFAGLGA        0.4859        260.4         WB    32.00     Sequence
   DRB1_0401  364  DDLKFTLVEPLRLLF  FTLVEPLRL        0.4852        262.4         WB    32.00     Sequence
   DRB1_0401  190  VLSRFLHDFAGLGAQ  RFLHDFAGL        0.4840        266.0         WB    32.00     Sequence
   DRB1_0401   88  VLGICYGFQAMAQAL  LGICYGFQA        0.4816        272.9         WB    32.00     Sequence
   DRB1_0401  267  RAQVQRDFVAATGAN  QVQRDFVAA        0.4803        276.6         WB    32.00     Sequence
   DRB1_0401  289  ETFLEALSGVSAPEG  LEALSGVSA        0.4753        292.0         WB    32.00     Sequence
   DRB1_0401   34  REARVFSEVIPHTAS  RVFSEVIPH        0.4744        295.0         WB    32.00     Sequence
   DRB1_0401  445  CPVVLLADVRSVGVQ  VVLLADVRS        0.4739        296.6         WB    32.00     Sequence
   DRB1_0401  443  WQCPVVLLADVRSVG  VVLLADVRS        0.4734        298.1         WB    32.00     Sequence
   DRB1_0401  491  VLERISTRITNEVAE  LERISTRIT        0.4734        298.3         WB    32.00     Sequence
   DRB1_0401   30  ARRVREARVFSEVIP  RVREARVFS        0.4725        301.2         WB    32.00     Sequence
   DRB1_0401  490  EVLERISTRITNEVA  LERISTRIT        0.4700        309.4         WB    32.00     Sequence
   DRB1_0401  488  PYEVLERISTRITNE  LERISTRIT        0.4683        315.1         WB    32.00     Sequence
   DRB1_0401  413  EVTAKRLDTLRHADS  AKRLDTLRH        0.4672        318.8         WB    32.00     Sequence
   DRB1_0401  444  QCPVVLLADVRSVGV  VVLLADVRS        0.4659        323.5         WB    32.00     Sequence
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DRB1_0401  503  VAEVNRVVLDITSKP  RVVLDITSK       0.4654       325.3       WB   32.00      Sequence
DRB1_0401   94  GFQAMAQALGGIVAH  FQAMAQALG       0.4648       327.3       WB   32.00      Sequence
DRB1_0401  426  DSIVREELTAAGLDN  SIVREELTA       0.4645       328.3       WB   32.00      Sequence
DRB1_0401  403  GPGLGIRIVGEVTAK  IRIVGEVTA       0.4621       337.1       WB   32.00      Sequence
DRB1_0401  133  VQPVWMSHGDAVTAA  WMSHGDAVT       0.4620       337.5       WB   32.00      Sequence
DRB1_0401   32  RVREARVFSEVIPHT  RVREARVFS       0.4602       343.9       WB   32.00      Sequence
DRB1_0401  447  VVLLADVRSVGVQGD  VVLLADVRS       0.4599       345.0       WB   32.00      Sequence
DRB1_0401  305  RKIIGRQFIRAFEGA  QFIRAFEGA       0.4593       347.3       WB   32.00      Sequence
DRB1_0401   29  IARRVREARVFSEVI  RVREARVFS       0.4586       350.0       WB   32.00      Sequence
DRB1_0401  290  TFLEALSGVSAPEGK  LEALSGVSA       0.4577       353.3       WB   32.00      Sequence
DRB1_0401  363  PDDLKFTLVEPLRLL  FTLVEPLRL       0.4547       364.9       WB   32.00      Sequence
DRB1_0401   37  RVFSEVIPHTASIEE  RVFSEVIPH       0.4540       367.8       WB   32.00      Sequence
DRB1_0401  468  PIVLRPVSSEDAMTA  PIVLRPVSS       0.4532       370.9       WB   32.00      Sequence
DRB1_0401  463  RTYGHPIVLRPVSSE  PIVLRPVSS       0.4524       374.4       WB   32.00      Sequence
DRB1_0401  288  AETFLEALSGVSAPE  TFLEALSGV       0.4511       379.6       WB   32.00      Sequence
DRB1_0401  410  IVGEVTAKRLDTLRH  IVGEVTAKR       0.4494       386.8       WB   32.00      Sequence
DRB1_0401  427  SIVREELTAAGLDNQ  SIVREELTA       0.4475       394.6       WB   32.00      Sequence
DRB1_0401  328  TAEFLVQGTLYPDVV  FLVQGTLYP       0.4464       399.4       WB   32.00      Sequence
DRB1_0401  311  QFIRAFEGAVRDVLD  QFIRAFEGA       0.4462       400.1       WB   32.00      Sequence
DRB1_0401   20  DFGAQYAQLIARRVR  AQYAQLIAR       0.4440       409.7       WB   32.00      Sequence
DRB1_0401  330  EFLVQGTLYPDVVES  FLVQGTLYP       0.4440       409.9       WB   32.00      Sequence
DRB1_0401  415  TAKRLDTLRHADSIV  AKRLDTLRH       0.4428       415.4       WB   32.00      Sequence
DRB1_0401  189  QVLSRFLHDFAGLGA  RFLHDFAGL       0.4414       421.6       WB   32.00      Sequence
DRB1_0401  412  GEVTAKRLDTLRHAD  AKRLDTLRH       0.4413       421.9       WB   32.00      Sequence
DRB1_0401  425  ADSIVREELTAAGLD  IVREELTAA       0.4409       424.1       WB   32.00      Sequence
DRB1_0401  371  VEPLRLLFKDEVRAV  LLFKDEVRA       0.4395       430.2       WB   32.00      Sequence
DRB1_0401  329  AEFLVQGTLYPDVVE  FLVQGTLYP       0.4384       435.5       WB   32.00      Sequence
DRB1_0401   87  PVLGICYGFQAMAQA  LGICYGFQA       0.4379       437.7       WB   32.00      Sequence
DRB1_0401  414  VTAKRLDTLRHADSI  AKRLDTLRH       0.4372       441.4       WB   32.00      Sequence
DRB1_0401  266  ERAQVQRDFVAATGA  QVQRDFVAA       0.4367       443.6       WB   32.00      Sequence
DRB1_0401  270  VQRDFVAATGANLVT  DFVAATGAN       0.4336       458.9       WB   32.00      Sequence
DRB1_0401  467  HPIVLRPVSSEDAMT  PIVLRPVSS       0.4330       461.8       WB   32.00      Sequence
DRB1_0401  462  GRTYGHPIVLRPVSS  TYGHPIVLR       0.4324       464.7       WB   32.00      Sequence
DRB1_0401  464  TYGHPIVLRPVSSED  PIVLRPVSS       0.4323       465.1       WB   32.00      Sequence
DRB1_0401  327  KTAEFLVQGTLYPDV  FLVQGTLYP       0.4316       468.7       WB   32.00      Sequence
DRB1_0401   21  FGAQYAQLIARRVRE  AQYAQLIAR       0.4308       473.0       WB   32.00      Sequence
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DRB1_0401   28  LIARRVREARVFSEV  RRVREARVF       0.4263       496.6       WB   32.00      Sequence
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DRB1_0401  442  IWQCPVVLLADVRSV  VVLLADVRS       0.4212       524.5            32.00      Sequence
DRB1_0401  287  AAETFLEALSGVSAP  ETFLEALSG       0.4205       528.4            32.00      Sequence
DRB1_0401  271  QRDFVAATGANLVTV  DFVAATGAN       0.4200       531.6            32.00      Sequence
DRB1_0401  487  VPYEVLERISTRITN  LERISTRIT       0.4193       535.4            32.00      Sequence
DRB1_0401  492  LERISTRITNEVAEV  LERISTRIT       0.4191       536.7            32.00      Sequence
DRB1_0401   95  FQAMAQALGGIVAHT  FQAMAQALG       0.4129       574.1            32.00      Sequence
DRB1_0401   33  VREARVFSEVIPHTA  RVFSEVIPH       0.4127       575.1            32.00      Sequence
DRB1_0401  138  MSHGDAVTAAPDGFD  MSHGDAVTA       0.4111       584.9            32.00      Sequence
DRB1_0401  424  HADSIVREELTAAGL  SIVREELTA       0.4108       586.8            32.00      Sequence
DRB1_0401  423  RHADSIVREELTAAG  SIVREELTA       0.4096       594.4            32.00      Sequence
DRB1_0401  291  FLEALSGVSAPEGKR  LEALSGVSA       0.4090       598.4            32.00      Sequence
DRB1_0401   22  GAQYAQLIARRVREA  AQYAQLIAR       0.4081       604.1            32.00      Sequence
DRB1_0401   13  ARPVLVVDFGAQYAQ  VLVVDFGAQ       0.4067       613.3            32.00      Sequence
DRB1_0401  196  HDFAGLGAQWTPANI  FAGLGAQWT       0.4060       618.2            32.00      Sequence
DRB1_0401  441  QIWQCPVVLLADVRS  VVLLADVRS       0.4058       619.4            32.00      Sequence
DRB1_0401   19  VDFGAQYAQLIARRV  AQYAQLIAR       0.4053       623.2            32.00      Sequence
DRB1_0401  362  LPDDLKFTLVEPLRL  FTLVEPLRL       0.4042       630.1            32.00      Sequence
DRB1_0401  132  EVQPVWMSHGDAVTA  WMSHGDAVT       0.4041       630.8            32.00      Sequence
DRB1_0401  465  YGHPIVLRPVSSEDA  PIVLRPVSS       0.4021       645.0            32.00      Sequence
DRB1_0401  185  PHGQQVLSRFLHDFA  PHGQQVLSR       0.3992       665.8            32.00      Sequence
DRB1_0401  198  FAGLGAQWTPANIAN  FAGLGAQWT       0.3991       665.9            32.00      Sequence
DRB1_0401  411  VGEVTAKRLDTLRHA  AKRLDTLRH       0.3986       669.6            32.00      Sequence
DRB1_0401  175  VQYHPEVMHTPHGQQ  VQYHPEVMH       0.3984       671.6            32.00      Sequence
DRB1_0401  326  GKTAEFLVQGTLYPD  FLVQGTLYP       0.3978       675.9            32.00      Sequence
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DRB1_0401	331	FLVQGTLYPDVVESG	FLVQGTLYP	0.3930	711.9	32.00	Sequence
DRB1_0401	292	LEALSGVSAPEGKRK	LEALSGVSA	0.3927	714.0	32.00	Sequence
DRB1_0401	174	GVQYHPEVMHTPHGQ	VQYHPEVMH	0.3914	723.7	32.00	Sequence
DRB1_0401	200	GLGAQWTPANIANAL	LGAQWTPAN	0.3897	737.7	32.00	Sequence
DRB1_0401	188	QQVLSRFLHDFAGLG	RFLHDFAGL	0.3869	760.0	50.00	Sequence
DRB1_0401	486	RVPYEVLERISTRIT	YEVLERIST	0.3864	764.7	50.00	Sequence
DRB1_0401	27	QLIARRVREARVFSE	RRVREARVF	0.3842	782.5	50.00	Sequence
DRB1_0401	12	PARPVLVVDFGAQYA	PVLVVDFGA	0.3833	790.0	50.00	Sequence
DRB1_0401	199	AGLGAQWTPANIANA	LGAQWTPAN	0.3829	793.8	50.00	Sequence
DRB1_0401	370	LVEPLRLLFKDEVRA	RLLFKDEVR	0.3794	824.4	50.00	Sequence
DRB1_0401	367	KFTLVEPLRLLFKDE	FTLVEPLRL	0.3761	854.6	50.00	Sequence
DRB1_0401	286	DAAETFLEALSGVSA	ETFLEALSG	0.3748	866.4	50.00	Sequence
DRB1_0401	304	KRKIIGRQFIRAFEG	IIGRQFIRA	0.3727	886.6	50.00	Sequence
DRB1_0401	197	DFAGLGAQWTPANIA	FAGLGAQWT	0.3727	886.7	50.00	Sequence
DRB1_0401	173	AGVQYHPEVMHTPHG	VQYHPEVMH	0.3714	899.5	50.00	Sequence
DRB1_0401	279	GANLVTVDAAETFLE	LVTVDAAET	0.3700	912.5	50.00	Sequence
DRB1_0401	272	RDFVAATGANLVTVD	DFVAATGAN	0.3700	912.8	50.00	Sequence
DRB1_0401	79	PALLDLGVPVLGICY	ALLDLGVPV	0.3697	915.3	50.00	Sequence
DRB1_0401	251	RLTCVFVDHGLLRAG	RLTCVFVDH	0.3689	923.9	50.00	Sequence
DRB1_0401	440	NQIWQCPVVLLADVR	QIWQCPVVL	0.3681	931.9	50.00	Sequence
DRB1_0401	502	EVAEVNRVVLDITSK	RVVLDITSK	0.3666	946.7	50.00	Sequence
DRB1_0401	16	VLVVDFGAQYAQLIA	VLVVDFGAQ	0.3664	948.9	50.00	Sequence
DRB1_0401	250	DRLTCVFVDHGLLRA	RLTCVFVDH	0.3653	960.2	50.00	Sequence
DRB1_0401	23	AQYAQLIARRVREAR	AQYAQLIAR	0.3590	1028.4	50.00	Sequence
DRB1_0401	325	DGKTAEFLVQGTLYP	FLVQGTLYP	0.3574	1045.6	50.00	Sequence
DRB1_0401	184	TPHGQQVLSRFLHDF	PHGQQVLSR	0.3559	1062.7	50.00	Sequence
DRB1_0401	112	REYGRTELKVLGGKL	REYGRTELK	0.3551	1072.2	50.00	Sequence
DRB1_0401	265	GERAQVQRDFVAATG	QVQRDFVAA	0.3535	1091.1	50.00	Sequence
DRB1_0401	402	PGPGLGIRIVGEVTA	IRIVGEVTA	0.3508	1123.6	50.00	Sequence
DRB1_0401	18	VVDFGAQYAQLIARR	FGAQYAQLI	0.3504	1128.2	50.00	Sequence
DRB1_0401	171	RLAGVQYHPEVMHTP	VQYHPEVMH	0.3503	1129.9	50.00	Sequence
DRB1_0401	249	GDRLTCVFVDHGLLR	RLTCVFVDH	0.3497	1136.6	50.00	Sequence
DRB1_0401	78	DPALLDLGVPVLGIC	ALLDLGVPV	0.3496	1138.0	50.00	Sequence
DRB1_0401	86	VPVLGICYGFQAMAQ	LGICYGFQA	0.3460	1183.4	50.00	Sequence
DRB1_0401	111	TREYGRTELKVLGGK	REYGRTELK	0.3422	1232.8	50.00	Sequence
DRB1_0401	183	HTPHGQQVLSRFLHD	PHGQQVLSR	0.3399	1264.5	50.00	Sequence
DRB1_0401	278	TGANLVTVDAAETFL	LVTVDAAET	0.3387	1280.5	50.00	Sequence
DRB1_0401	471	LRPVSSEDAMTADWT	VSSEDAMTA	0.3386	1282.7	50.00	Sequence
DRB1_0401	201	LGAQWTPANIANALI	LGAQWTPAN	0.3373	1299.8	50.00	Sequence
DRB1_0401	131	PEVQPVWMSHGDAVT	PEVQPVWMS	0.3371	1303.2	50.00	Sequence
DRB1_0401	461	DGRTYGHPIVLRPVS	TYGHPIVLR	0.3356	1324.0	50.00	Sequence
DRB1_0401	125	KLHSDLPEVQPVWMS	KLHSDLPEV	0.3347	1337.4	50.00	Sequence
DRB1_0401	59	ALVLSGGPASVYADG	LVLSGGPAS	0.3346	1338.9	50.00	Sequence
DRB1_0401	172	LAGVQYHPEVMHTPH	VQYHPEVMH	0.3344	1341.2	50.00	Sequence
DRB1_0401	26	AQLIARRVREARVFS	RRVREARVF	0.3342	1345.0	50.00	Sequence
DRB1_0401	273	DFVAATGANLVTVDA	DFVAATGAN	0.3337	1351.9	50.00	Sequence
DRB1_0401	55	RQPVALVLSGGPASV	RQPVALVLS	0.3336	1353.1	50.00	Sequence
DRB1_0401	439	DNQIWQCPVVLLADV	QIWQCPVVL	0.3331	1361.2	50.00	Sequence
DRB1_0401	277	ATGANLVTVDAAETF	ATGANLVTV	0.3326	1367.8	50.00	Sequence
DRB1_0401	170	RRLAGVQYHPEVMHT	VQYHPEVMH	0.3317	1381.4	50.00	Sequence
DRB1_0401	187	GQQVLSRFLHDFAGL	RFLHDFAGL	0.3317	1381.5	50.00	Sequence
DRB1_0401	58	VALVLSGGPASVYAD	LVLSGGPAS	0.3283	1433.0	50.00	Sequence
DRB1_0401	110	GTREYGRTELKVLGG	REYGRTELK	0.3283	1433.5	50.00	Sequence
DRB1_0401	77	LDPALLDLGVPVLGI	ALLDLGVPV	0.3283	1433.9	50.00	Sequence
DRB1_0401	472	RPVSSEDAMTADWTR	VSSEDAMTA	0.3271	1452.1	50.00	Sequence
DRB1_0401	448	VLLADVRSVGVQGDG	VLLADVRSV	0.3270	1452.7	50.00	Sequence
DRB1_0401	17	LVVDFGAQYAQLIAR	LVVDFGAQY	0.3247	1490.3	50.00	Sequence
DRB1_0401	57	PVALVLSGGPASVYA	LVLSGGPAS	0.3243	1496.2	50.00	Sequence
DRB1_0401	124	GKLHSDLPEVQPVWM	KLHSDLPEV	0.3238	1504.1	50.00	Sequence
DRB1_0401	75	PKLDPALLDLGVPVL	PKLDPALLD	0.3237	1506.3	50.00	Sequence
DRB1_0401	148	PDGFDVVASSAGAPV	GFDVVASSA	0.3235	1509.4	50.00	Sequence
DRB1_0401	280	ANLVTVDAAETFLEA	LVTVDAAET	0.3217	1539.5	50.00	Sequence
DRB1_0401	493	ERISTRITNEVAEVN	ERISTRITN	0.3201	1565.9	50.00	Sequence
DRB1_0401	474	VSSEDAMTADWTRVP	VSSEDAMTA	0.3171	1618.1	50.00	Sequence
DRB1_0401	368	FTLVEPLRLLFKDEV	FTLVEPLRL	0.3165	1628.4	50.00	Sequence
DRB1_0401	248	IGDRLTCVFVDHGLL	RLTCVFVDH	0.3157	1642.2	50.00	Sequence

DRB1_0401	478	DAMTADWTRVPYEVL	DAMTADWTR	0.3132	1688.3	50.00	Sequence
DRB1_0401	303	GKRKIIGRQFIRAFE	KIIGRQFIR	0.3131	1689.4	50.00	Sequence
DRB1_0401	276	AATGANLVTVDAAET	ATGANLVTV	0.3127	1695.8	50.00	Sequence
DRB1_0401	120	KVLGGKLHSDLPEVQ	KVLGGKLHS	0.3126	1698.2	50.00	Sequence
DRB1_0401	11	TPARPVLVVDFGAQY	PVLVVDFGA	0.3120	1709.1	50.00	Sequence
DRB1_0401	252	LTCVFVDHGLLRAGE	VFVDHGLLR	0.3111	1725.7	50.00	Sequence
DRB1_0401	147	APDGFDVVASSAGAP	GFDVVASSA	0.3108	1731.8	50.00	Sequence
DRB1_0401	119	LKVLGGKLHSDLPEV	LKVLGGKLH	0.3107	1734.6	50.00	Sequence
DRB1_0401	56	QPVALVLSGGPASVY	ALVLSGGPA	0.3087	1772.3	50.00	Sequence
DRB1_0401	149	DGFDVVASSAGAPVA	GFDVVASSA	0.3082	1781.9	50.00	Sequence
DRB1_0401	383	RAVGRELGLPEEIVA	RAVGRELGL	0.3081	1783.2	50.00	Sequence
DRB1_0401	96	QAMAQALGGIVAHTG	QAMAQALGG	0.3081	1783.9	50.00	Sequence
DRB1_0401	182	MHTPHGQQVLSRFLH	PHGQQVLSR	0.3065	1814.2	50.00	Sequence
DRB1_0401	109	TGTREYGRTELKVLG	REYGRTELK	0.3055	1833.7	50.00	Sequence
DRB1_0401	438	LDNQIWQCPVVLLAD	QIWQCPVVL	0.3048	1847.7	50.00	Sequence
DRB1_0401	52	IRARQPVALVLSGGP	IRARQPVAL	0.3041	1862.0	50.00	Sequence
DRB1_0401	54	ARQPVALVLSGGPAS	RQPVALVLS	0.3038	1867.3	50.00	Sequence
DRB1_0401	281	NLVTVDAAETFLEAL	LVTVDAAET	0.3037	1869.3	50.00	Sequence
DRB1_0401	460	GDGRTYGHPIVLRPV	TYGHPIVLR	0.3036	1872.5	50.00	Sequence
DRB1_0401	470	VLRPVSSEDAMTADW	VSSEDAMTA	0.3030	1883.9	50.00	Sequence
DRB1_0401	469	IVLRPVSSEDAMTAD	LRPVSSEDA	0.3022	1900.7	50.00	Sequence
DRB1_0401	347	GSGTANIKSHHNVGG	GSGTANIKS	0.3015	1914.9	50.00	Sequence
DRB1_0401	387	RELGLPEEIVARQPF	LGLPEEIVA	0.2995	1958.2	50.00	Sequence
DRB1_0401	49	IEEIRARQPVALVLS	IRARQPVAL	0.2994	1959.1	50.00	Sequence
DRB1_0401	230	GLSGGVDSAVAAALV	GGVDSAVAA	0.2990	1968.5	50.00	Sequence
DRB1_0401	231	LSGGVDSAVAAALVQ	GGVDSAVAA	0.2985	1977.5	50.00	Sequence
DRB1_0401	169	DRRLAGVQYHPEVMH	RLAGVQYHP	0.2984	1980.2	50.00	Sequence
DRB1_0401	50	EEIRARQPVALVLSG	IRARQPVAL	0.2980	1989.7	50.00	Sequence
DRB1_0401	428	IVREELTAAGLDNQI	IVREELTAA	0.2978	1992.9	50.00	Sequence
DRB1_0401	123	GGKLHSDLPEVQPVW	LHSDLPEVQ	0.2960	2032.2	50.00	Sequence
DRB1_0401	51	EIRARQPVALVLSGG	IRARQPVAL	0.2958	2037.4	50.00	Sequence
DRB1_0401	66	PASVYADGAPKLDPA	SVYADGAPK	0.2955	2043.9	50.00	Sequence
DRB1_0401	346	GGSGTANIKSHHNVG	GSGTANIKS	0.2955	2044.6	50.00	Sequence
DRB1_0401	473	PVSSEDAMTADWTRV	VSSEDAMTA	0.2948	2060.1	50.00	Sequence
DRB1_0401	130	LPEVQPVWMSHGDAV	PEVQPVWMS	0.2942	2072.1	50.00	Sequence
DRB1_0401	246	RAIGDRLTCVFVDHG	RAIGDRLTC	0.2929	2101.0	50.00	Sequence
DRB1_0401	255	VFVDHGLLRAGERAQ	VFVDHGLLR	0.2918	2128.2	50.00	Sequence
DRB1_0401	345	GGGSGTANIKSHHNV	GSGTANIKS	0.2914	2136.0	50.00	Sequence
DRB1_0401	477	EDAMTADWTRVPYEV	DAMTADWTR	0.2912	2140.6	50.00	Sequence
DRB1_0401	432	ELTAAGLDNQIWQCP	ELTAAGLDN	0.2899	2170.3	50.00	Sequence
DRB1_0401	67	ASVYADGAPKLDPAL	SVYADGAPK	0.2899	2171.2	50.00	Sequence
DRB1_0401	386	GRELGLPEEIVARQP	LGLPEEIVA	0.2888	2196.5	50.00	Sequence
DRB1_0401	264	AGERAQVQRDFVAAT	AQVQRDFVA	0.2872	2236.7	50.00	Sequence
DRB1_0401	212	NALIEQVRTQIGDGH	NALIEQVRT	0.2868	2244.8	50.00	Sequence
DRB1_0401	509	VVLDITSKPPATIEW	VVLDITSKP	0.2849	2291.5	50.00	Sequence
DRB1_0401	53	RARQPVALVLSGGPA	RQPVALVLS	0.2848	2294.2	50.00	Sequence
DRB1_0401	369	TLVEPLRLLFKDEVR	RLLFKDEVR	0.2846	2300.7	50.00	Sequence
DRB1_0401	429	VREELTAAGLDNQIW	VREELTAAG	0.2840	2314.5	50.00	Sequence
DRB1_0401	80	ALLDLGVPVLGICYG	ALLDLGVPV	0.2833	2333.1	50.00	Sequence
DRB1_0401	485	TRVPYEVLERISTRI	YEVLERIST	0.2825	2353.0	50.00	Sequence
DRB1_0401	247	AIGDRLTCVFVDHGL	RLTCVFVDH	0.2821	2362.9	50.00	Sequence
DRB1_0401	335	GTLYPDVVESGGGSG	TLYPDVVES	0.2809	2392.6	50.00	Sequence
DRB1_0401	25	YAQLIARRVREARVF	RRVREARVF	0.2809	2393.8	50.00	Sequence
DRB1_0401	24	QYAQLIARRVREARV	QYAQLIARR	0.2809	2394.2	50.00	Sequence
DRB1_0401	118	ELKVLGGKLHSDLPE	KVLGGKLHS	0.2800	2416.4	50.00	Sequence
DRB1_0401	344	SGGGSGTANIKSHHN	GSGTANIKS	0.2799	2419.9	50.00	Sequence
DRB1_0401	38	VFSEVIPHTASIEEI	VFSEVIPHT	0.2796	2426.4	50.00	Sequence
DRB1_0401	48	SIEEIRARQPVALVL	IRARQPVAL	0.2792	2436.8	50.00	Sequence
DRB1_0401	65	GPASVYADGAPKLDP	SVYADGAPK	0.2769	2498.8	50.00	Sequence
DRB1_0401	211	ANALIEQVRTQIGDG	NALIEQVRT	0.2768	2501.2	50.00	Sequence
DRB1_0401	334	QGTLYPDVVESGGGS	TLYPDVVES	0.2758	2528.0	50.00	Sequence
DRB1_0401	74	APKLDPALLDLGVPV	PKLDPALLD	0.2747	2559.1	50.00	Sequence
DRB1_0401	122	LGGKLHSDLPEVQPV	KLHSDLPEV	0.2738	2584.9	50.00	Sequence
DRB1_0401	476	SEDAMTADWTRVPYE	DAMTADWTR	0.2736	2589.9	50.00	Sequence
DRB1_0401	312	FIRAFEGAVRDVLDG	IRAFEGAVR	0.2730	2607.4	50.00	Sequence
DRB1_0401	484	WTRVPYEVLERISTR	YEVLERIST	0.2728	2613.0	50.00	Sequence

DRB1_0401	385	VGRELGLPEEIVARQ	LGLPEEIVA	0.2724	2623.6	50.00	Sequence
DRB1_0401	146	AAPDGFDVVASSAGA	GFDVVASSA	0.2724	2624.6	50.00	Sequence
DRB1_0401	76	KLDPALLDLGVPVLG	ALLDLGVPV	0.2723	2626.5	50.00	Sequence
DRB1_0401	494	RISTRITNEVAEVNR	TRITNEVAE	0.2722	2628.7	50.00	Sequence
DRB1_0401	431	EELTAAGLDNQIWQC	ELTAAGLDN	0.2721	2632.6	50.00	Sequence
DRB1_0401	437	GLDNQIWQCPVVLLA	NQIWQCPVV	0.2716	2647.9	50.00	Sequence
DRB1_0401	108	HTGTREYGRTELKVL	REYGRTELK	0.2713	2655.3	50.00	Sequence
DRB1_0401	129	DLPEVQPVWMSHGDA	PEVQPVWMS	0.2712	2658.5	50.00	Sequence
DRB1_0401	150	GFDVVASSAGAPVAA	FDVVASSAG	0.2709	2667.0	50.00	Sequence
DRB1_0401	99	AQALGGIVAHTGTRE	QALGGIVAH	0.2707	2674.1	50.00	Sequence
DRB1_0401	382	VRAVGRELGLPEEIV	RAVGRELGL	0.2696	2703.9	50.00	Sequence
DRB1_0401	254	CVFVDHGLLRAGERA	VFVDHGLLR	0.2689	2725.3	50.00	Sequence
DRB1_0401	274	FVAATGANLVTVDAA	FVAATGANL	0.2683	2742.4	50.00	Sequence
DRB1_0401	126	LHSDLPEVQPVWMSH	LHSDLPEVQ	0.2680	2753.1	50.00	Sequence
DRB1_0401	176	QYHPEVMHTPHGQQV	QYHPEVMHT	0.2674	2768.9	50.00	Sequence
DRB1_0401	232	SGGVDSAVAAALVQR	GGVDSAVAA	0.2648	2849.5	50.00	Sequence
DRB1_0401	263	RAGERAQVQRDFVAA	RAGERAQVQ	0.2645	2858.0	50.00	Sequence
DRB1_0401	245	QRAIGDRLTCVFVDH	RAIGDRLTC	0.2640	2874.9	50.00	Sequence
DRB1_0401	97	AMAQALGGIVAHTGT	QALGGIVAH	0.2639	2876.7	50.00	Sequence
DRB1_0401	449	LLADVRSVGVQGDGR	LADVRSVGV	0.2637	2881.9	50.00	Sequence
DRB1_0401	302	EGKRKIIGRQFIRAF	KIIGRQFIR	0.2630	2903.5	50.00	Sequence
DRB1_0401	496	STRITNEVAEVNRVV	TRITNEVAE	0.2628	2910.9	50.00	Sequence
DRB1_0401	285	VDAAETFLEALSGVS	ETFLEALSG	0.2597	3011.2	50.00	Sequence
DRB1_0401	384	AVGRELGLPEEIVAR	RELGLPEEI	0.2594	3019.0	50.00	Sequence
DRB1_0401	46	TASIEEIRARQPVAL	IRARQPVAL	0.2593	3022.9	50.00	Sequence
DRB1_0401	117	TELKVLGGKLHSDLP	LKVLGGKLH	0.2590	3032.2	50.00	Sequence
DRB1_0401	313	IRAFEGAVRDVLDGK	IRAFEGAVR	0.2585	3048.4	50.00	Sequence
DRB1_0401	430	REELTAAGLDNQIWQ	ELTAAGLDN	0.2578	3071.8	50.00	Sequence
DRB1_0401	333	VQGTLYPDVVESGGG	TLYPDVVES	0.2578	3074.2	50.00	Sequence
DRB1_0401	202	GAQWTPANIANALIE	WTPANIANA	0.2576	3078.9	50.00	Sequence
DRB1_0401	168	FDRRLAGVQYHPEVM	RLAGVQYHP	0.2574	3085.2	50.00	Sequence
DRB1_0401	229	CGLSGGVDSAVAAAL	GGVDSAVAA	0.2566	3112.3	50.00	Sequence
DRB1_0401	100	QALGGIVAHTGTREY	QALGGIVAH	0.2561	3129.3	50.00	Sequence
DRB1_0401	121	VLGGKLHSDLPEVQP	VLGGKLHSD	0.2551	3164.8	50.00	Sequence
DRB1_0401	210	IANALIEQVRTQIGD	NALIEQVRT	0.2549	3169.4	50.00	Sequence
DRB1_0401	253	TCVFVDHGLLRAGER	VFVDHGLLR	0.2547	3177.0	50.00	Sequence
DRB1_0401	60	LVLSGGPASVYADGA	LVLSGGPAS	0.2547	3177.4	50.00	Sequence
DRB1_0401	47	ASIEEIRARQPVALV	IRARQPVAL	0.2538	3209.2	50.00	Sequence
DRB1_0401	203	AQWTPANIANALIEQ	WTPANIANA	0.2538	3210.6	50.00	Sequence
DRB1_0401	275	VAATGANLVTVDAAE	ATGANLVTV	0.2532	3230.5	50.00	Sequence
DRB1_0401	204	QWTPANIANALIEQV	WTPANIANA	0.2531	3233.2	50.00	Sequence
DRB1_0401	497	TRITNEVAEVNRVVL	TRITNEVAE	0.2529	3239.0	50.00	Sequence
DRB1_0401	483	DWTRVPYEVLERIST	YEVLERIST	0.2524	3258.1	50.00	Sequence
DRB1_0401	495	ISTRITNEVAEVNRV	TRITNEVAE	0.2514	3294.8	50.00	Sequence
DRB1_0401	361	GLPDDLKFTLVEPLR	KFTLVEPLR	0.2505	3324.5	50.00	Sequence
DRB1_0401	98	MAQALGGIVAHTGTR	QALGGIVAH	0.2505	3325.2	50.00	Sequence
DRB1_0401	479	AMTADWTRVPYEVLE	MTADWTRVP	0.2501	3339.2	50.00	Sequence
DRB1_0401	475	SSEDAMTADWTRVPY	DAMTADWTR	0.2501	3341.2	50.00	Sequence
DRB1_0401	388	ELGLPEEIVARQPFP	LGLPEEIVA	0.2488	3388.6	50.00	Sequence
DRB1_0401	116	RTELKVLGGKLHSDL	LKVLGGKLH	0.2483	3407.1	50.00	Sequence
DRB1_0401	186	HGQQVLSRFLHDFAG	QVLSRFLHD	0.2454	3514.7	50.00	Sequence
DRB1_0401	209	NIANALIEQVRTQIG	NALIEQVRT	0.2452	3522.5	50.00	Sequence
DRB1_0401	459	QGDGRTYGHPIVLRP	TYGHPIVLR	0.2445	3549.9	50.00	Sequence
DRB1_0401	224	DGHAICGLSGGVDSA	GHAICGLSG	0.2439	3570.3	50.00	Sequence
DRB1_0401	258	DHGLLRAGERAQVQR	LLRAGERAQ	0.2413	3672.2	50.00	Sequence
DRB1_0401	259	HGLLRAGERAQVQRD	LLRAGERAQ	0.2410	3686.4	50.00	Sequence
DRB1_0401	450	LADVRSVGVQGDGRT	LADVRSVGV	0.2406	3702.6	50.00	Sequence
DRB1_0401	332	LVQGTLYPDVVESGG	TLYPDVVES	0.2403	3713.8	50.00	Sequence
DRB1_0401	225	GHAICGLSGGVDSAV	GHAICGLSG	0.2399	3729.3	50.00	Sequence
DRB1_0401	282	LVTVDAAETFLEALS	LVTVDAAET	0.2398	3733.3	50.00	Sequence
DRB1_0401	260	GLLRAGERAQVQRDF	LLRAGERAQ	0.2394	3749.9	50.00	Sequence
DRB1_0401	167	AFDRRLAGVQYHPEV	RLAGVQYHP	0.2390	3767.5	50.00	Sequence
DRB1_0401	242	ALVQRAIGDRLTCVF	ALVQRAIGD	0.2381	3804.4	50.00	Sequence
DRB1_0401	343	ESGGGSGTANIKSHH	GSGTANIKS	0.2380	3809.2	50.00	Sequence
DRB1_0401	85	GVPVLGICYGFQAMA	LGICYGFQA	0.2379	3811.5	50.00	Sequence
DRB1_0401	127	HSDLPEVQPVWMSHG	PEVQPVWMS	0.2375	3828.9	50.00	Sequence

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DRB1_0401  113  EYGRTELKVLGGKLH  EYGRTELKV         0.2371        3846.5                  50.00     Sequence
DRB1_0401   68  SVYADGAPKLDPALL  SVYADGAPK         0.2365        3869.0                  50.00     Sequence
DRB1_0401  213  ALIEQVRTQIGDGHA  IEQVRTQIG         0.2363        3880.0                  50.00     Sequence
DRB1_0401  181  VMHTPHGQQVLSRFL  PHGQQVLSR         0.2361        3885.9                  50.00     Sequence
DRB1_0401   64  GGPASVYADGAPKLD  SVYADGAPK         0.2343        3961.0                  50.00     Sequence
DRB1_0401   62  LSGGPASVYADGAPK  LSGGPASVY         0.2338        3986.2                  50.00     Sequence
DRB1_0401  381  EVRAVGRELGLPEEI  RAVGRELGL         0.2329        4023.1                  50.00     Sequence
DRB1_0401  151  FDVVASSAGAPVAAF  FDVVASSAG         0.2326        4037.8                  50.00     Sequence
DRB1_0401  128  SDLPEVQPVWMSHGD  PEVQPVWMS         0.2308        4114.3                  50.00     Sequence
DRB1_0401  241  AALVQRAIGDRLTCV  ALVQRAIGD         0.2283        4229.5                  50.00     Sequence
DRB1_0401  223  GDGHAICGLSGGVDS  GHAICGLSG         0.2268        4296.5                  50.00     Sequence
DRB1_0401  107  AHTGTREYGRTELKV  REYGRTELK         0.2267        4302.4                  50.00     Sequence
DRB1_0401  214  LIEQVRTQIGDGHAI  IEQVRTQIG         0.2265        4311.7                  50.00     Sequence
DRB1_0401  336  TLYPDVVESGGGSGT  TLYPDVVES         0.2262        4327.8                  50.00     Sequence
DRB1_0401  433  LTAAGLDNQIWQCPV  LTAAGLDNQ         0.2261        4328.6                  50.00     Sequence
DRB1_0401  480  MTADWTRVPYEVLER  MTADWTRVP         0.2260        4332.8                  50.00     Sequence
DRB1_0401  145  TAAPDGFDVVASSAG  PDGFDVVAS         0.2233        4461.6                  50.00     Sequence
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DRB1_0401  215  IEQVRTQIGDGHAIC  IEQVRTQIG         0.2210        4576.7                  50.00     Sequence
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DRB1_0401  434  TAAGLDNQIWQCPVV  NQIWQCPVV         0.2168        4788.1                  50.00     Sequence
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DRB1_0401  205  WTPANIANALIEQVR  WTPANIANA         0.1992        5794.7                  50.00     Sequence
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DRB1_0401  342  VESGGGSGTANIKSH  GSGTANIKS         0.1974        5909.5                  50.00     Sequence
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DRB1_0401  401  FPGPGLGIRIVGEVT  GLGIRIVGE         0.1966        5957.9                  50.00     Sequence
DRB1_0401  165  FEAFDRRLAGVQYHP  RLAGVQYHP         0.1964        5969.7                  50.00     Sequence
DRB1_0401  179  PEVMHTPHGQQVLSR  PHGQQVLSR         0.1957        6015.2                  50.00     Sequence
DRB1_0401  293  EALSGVSAPEGKRKI  LSGVSAPEG         0.1956        6023.5                  50.00     Sequence
DRB1_0401  481  TADWTRVPYEVLERI  WTRVPYEVL         0.1949        6072.1                  50.00     Sequence
DRB1_0401  177  YHPEVMHTPHGQQVL  YHPEVMHTP         0.1939        6135.6                  50.00     Sequence
DRB1_0401  227  AICGLSGGVDSAVAA  SGGVDSAVA         0.1919        6272.2                  50.00     Sequence
DRB1_0401   42  VIPHTASIEEIRARQ  TASIEEIRA         0.1917        6284.7                  50.00     Sequence
DRB1_0401  390  GLPEEIVARQPFPGP  GLPEEIVAR         0.1905        6365.0                  50.00     Sequence
DRB1_0401  180  EVMHTPHGQQVLSRF  PHGQQVLSR         0.1904        6371.8                  50.00     Sequence
DRB1_0401  360  GGLPDDLKFTLVEPL  DLKFTLVEP         0.1901        6396.2                  50.00     Sequence
DRB1_0401   41  EVIPHTASIEEIRAR  TASIEEIRA         0.1895        6435.8                  50.00     Sequence
DRB1_0401   82  LDLGVPVLGICYGFQ  LDLGVPVLG         0.1893        6451.5                  50.00     Sequence
DRB1_0401   39  FSEVIPHTASIEEIR  FSEVIPHTA         0.1888        6484.9                  50.00     Sequence
DRB1_0401  152  DVVASSAGAPVAAFE  DVVASSAGA         0.1884        6514.3                  50.00     Sequence
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DRB1_0401  318  GAVRDVLDGKTAEFL  RDVLDGKTA        0.1881      6535.5                 50.00     Sequence
DRB1_0401  314  RAFEGAVRDVLDGKT  RAFEGAVRD        0.1876      6569.9                 50.00     Sequence
DRB1_0401  482  ADWTRVPYEVLERIS  WTRVPYEVL        0.1873      6590.8                 50.00     Sequence
DRB1_0401  510  VLDITSKPPATIEWE  VLDITSKPP        0.1872      6593.6                 50.00     Sequence
DRB1_0401  354  KSHHNVGGLPDDLKF  HHNVGGLPD        0.1870      6613.6                 50.00     Sequence
DRB1_0401  435  AAGLDNQIWQCPVVL  NQIWQCPVV        0.1854      6729.0                 50.00     Sequence
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DRB1_0401  320  VRDVLDGKTAEFLVQ  RDVLDGKTA        0.1814      7020.3                 50.00     Sequence
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DRB1_0401  319  AVRDVLDGKTAEFLV  RDVLDGKTA        0.1789      7213.1                 50.00     Sequence
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DRB1_0401  208  ANIANALIEQVRTQI  NALIEQVRT        0.1789      7220.2                 50.00     Sequence
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DRB1_0401  351  ANIKSHHNVGGLPDD  IKSHHNVGG        0.1692      8011.0                 50.00     Sequence
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DRB1_0401  359  VGGLPDDLKFTLVEP  VGGLPDDLK        0.1688      8051.8                 50.00     Sequence
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DRB1_0401  218  VRTQIGDGHAICGLS  VRTQIGDGH        0.1624      8625.2                 50.00     Sequence
DRB1_0401  207  PANIANALIEQVRTQ  NALIEQVRT        0.1623      8634.6                 50.00     Sequence
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DRB1_0401   69  VYADGAPKLDPALLD  VYADGAPKL        0.1614      8723.0                 50.00     Sequence
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DRB1_0401   84  LGVPVLGICYGFQAM  LGICYGFQA        0.1605      8806.9                 50.00     Sequence
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DRB1_0401  341  VVESGGGSGTANIKS  GSGTANIKS        0.1550      9341.2                 50.00     Sequence
DRB1_0401  104  GIVAHTGTREYGRTE  IVAHTGTRE        0.1530      9545.9                 50.00     Sequence
DRB1_0401  105  IVAHTGTREYGRTEL  IVAHTGTRE        0.1516      9699.2                 50.00     Sequence
DRB1_0401  162  VAAFEAFDRRLAGVQ  VAAFEAFDR        0.1512      9739.9                 50.00     Sequence
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DRB1_0401  164  AFEAFDRRLAGVQYH  FEAFDRRLA        0.1501      9857.3                 50.00     Sequence
DRB1_0401  400  PFPGPGLGIRIVGEV  GLGIRIVGE        0.1498      9890.8                 50.00     Sequence
DRB1_0401  453  VRSVGVQGDGRTYGH  VGVQGDGRT        0.1489      9986.6                 50.00     Sequence
DRB1_0401  238  AVAAALVQRAIGDRL  ALVQRAIGD        0.1461     10289.0                 50.00     Sequence
DRB1_0401  323  VLDGKTAEFLVQGTL  VLDGKTAEF        0.1461     10291.1                 50.00     Sequence
DRB1_0401  178  HPEVMHTPHGQQVLS  PEVMHTPHG        0.1451     10404.5                 50.00     Sequence
DRB1_0401  283  VTVDAAETFLEALSG  VTVDAAETF        0.1424     10709.5                 50.00     Sequence
DRB1_0401  295  LSGVSAPEGKRKIIG  LSGVSAPEG        0.1418     10779.9                 50.00     Sequence
DRB1_0401  237  SAVAAALVQRAIGDR  SAVAAALVQ        0.1417     10796.8                 50.00     Sequence
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   DRB1_0401  153  VVASSAGAPVAAFEA  VVASSAGAP        0.1357      11518.0                 50.00     Sequence
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   DRB1_0401  156  SSAGAPVAAFEAFDR  SSAGAPVAA        0.1327      11890.6                 50.00     Sequence
   DRB1_0401  159  GAPVAAFEAFDRRLA  VAAFEAFDR        0.1325      11918.1                 50.00     Sequence
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   DRB1_0401  457  GVQGDGRTYGHPIVL  RTYGHPIVL        0.1159      14267.0                 50.00     Sequence
   DRB1_0401  157  SAGAPVAAFEAFDRR  SAGAPVAAF        0.1126      14789.6                 50.00     Sequence
   DRB1_0401  315  AFEGAVRDVLDGKTA  GAVRDVLDG        0.1114      14981.0                 50.00     Sequence
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   DRB1_0401    3  PADIDVPETPARPVL  IDVPETPAR        0.0827      20433.9                 50.00     Sequence
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   DRB1_0401    2  QPADIDVPETPARPV  IDVPETPAR        0.0782      21445.3                 50.00     Sequence
   DRB1_0401    4  ADIDVPETPARPVLV  DVPETPARP        0.0773      21669.7                 50.00     Sequence
   DRB1_0401    6  IDVPETPARPVLVVD  DVPETPARP        0.0767      21806.1                 50.00     Sequence
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   DRB1_0401    7  DVPETPARPVLVVDF  DVPETPARP        0.0619      25605.0                 50.00     Sequence
   DRB1_0401  297  GVSAPEGKRKIIGRQ  EGKRKIIGR        0.0596      26235.7                 50.00     Sequence
   DRB1_0401  296  SGVSAPEGKRKIIGR  GVSAPEGKR        0.0569      27016.1                 50.00     Sequence
   DRB1_0401    8  VPETPARPVLVVDFG  ETPARPVLV        0.0558      27345.7                 50.00     Sequence
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Allele: DRB1_0401. Number of high binders 6. Number of weak binders 98. Number of peptides 511

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0404  445  CPVVLLADVRSVGVQ  PVVLLADVR        0.6533         42.6          SB     8.00     Sequence
   DRB1_0404  446  PVVLLADVRSVGVQG  VLLADVRSV        0.6472         45.5          SB     8.00     Sequence
   DRB1_0404   90  GICYGFQAMAQALGG  GICYGFQAM        0.6426         47.8          SB     8.00     Sequence
   DRB1_0404  444  QCPVVLLADVRSVGV  PVVLLADVR        0.6401         49.1          SB     8.00     Sequence
   DRB1_0404   89  LGICYGFQAMAQALG  GICYGFQAM        0.6231         59.0          WB     8.00     Sequence
   DRB1_0404  443  WQCPVVLLADVRSVG  PVVLLADVR        0.6152         64.3          WB     8.00     Sequence
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DRB1_0404  309  GRQFIRAFEGAVRDV  FIRAFEGAV        0.6080         69.5          WB    16.00      Sequence
DRB1_0404  505  EVNRVVLDITSKPPA  RVVLDITSK        0.6067         70.5          WB    16.00      Sequence
DRB1_0404  506  VNRVVLDITSKPPAT  RVVLDITSK        0.6011         74.9          WB    16.00      Sequence
DRB1_0404  310  RQFIRAFEGAVRDVL  FIRAFEGAV        0.6010         75.0          WB    16.00      Sequence
DRB1_0404  507  NRVVLDITSKPPATI  RVVLDITSK        0.5998         75.9          WB    16.00      Sequence
DRB1_0404  365  DLKFTLVEPLRLLFK  LKFTLVEPL        0.5997         76.0          WB    16.00      Sequence
DRB1_0404  366  LKFTLVEPLRLLFKD  LKFTLVEPL        0.5940         80.8          WB    16.00      Sequence
DRB1_0404  308  IGRQFIRAFEGAVRD  FIRAFEGAV        0.5889         85.4          WB    16.00      Sequence
DRB1_0404   86  VPVLGICYGFQAMAQ  PVLGICYGF        0.5880         86.3          WB    16.00      Sequence
DRB1_0404  364  DDLKFTLVEPLRLLF  LKFTLVEPL        0.5809         93.2          WB    16.00      Sequence
DRB1_0404  467  HPIVLRPVSSEDAMT  IVLRPVSSE        0.5801         94.0          WB    16.00      Sequence
DRB1_0404  466  GHPIVLRPVSSEDAM  IVLRPVSSE        0.5800         94.1          WB    16.00      Sequence
DRB1_0404   85  GVPVLGICYGFQAMA  PVLGICYGF        0.5790         95.2          WB    16.00      Sequence
DRB1_0404   87  PVLGICYGFQAMAQA  GICYGFQAM        0.5742        100.2          WB    16.00      Sequence
DRB1_0404   88  VLGICYGFQAMAQAL  GICYGFQAM        0.5669        108.4          WB    16.00      Sequence
DRB1_0404  468  PIVLRPVSSEDAMTA  IVLRPVSSE        0.5615        115.0          WB    16.00      Sequence
DRB1_0404  504  AEVNRVVLDITSKPP  RVVLDITSK        0.5582        119.2          WB    16.00      Sequence
DRB1_0404  307  IIGRQFIRAFEGAVR  FIRAFEGAV        0.5562        121.8          WB    16.00      Sequence
DRB1_0404  508  RVVLDITSKPPATIE  RVVLDITSK        0.5515        128.1          WB    16.00      Sequence
DRB1_0404  465  YGHPIVLRPVSSEDA  IVLRPVSSE        0.5510        128.8          WB    16.00      Sequence
DRB1_0404  442  IWQCPVVLLADVRSV  PVVLLADVR        0.5484        132.5          WB    16.00      Sequence
DRB1_0404  406  LGIRIVGEVTAKRLD  RIVGEVTAK        0.5473        134.0          WB    16.00      Sequence
DRB1_0404  363  PDDLKFTLVEPLRLL  LKFTLVEPL        0.5466        135.1          WB    16.00      Sequence
DRB1_0404  447  VVLLADVRSVGVQGD  VLLADVRSV        0.5414        142.9          WB    16.00      Sequence
DRB1_0404  311  QFIRAFEGAVRDVLD  FIRAFEGAV        0.5359        151.7          WB    16.00      Sequence
DRB1_0404  405  GLGIRIVGEVTAKRL  IRIVGEVTA        0.5315        159.0          WB    16.00      Sequence
DRB1_0404  407  GIRIVGEVTAKRLDT  RIVGEVTAK        0.5303        161.1          WB    16.00      Sequence
DRB1_0404   91  ICYGFQAMAQALGGI  GFQAMAQAL        0.5298        162.0          WB    16.00      Sequence
DRB1_0404   84  LGVPVLGICYGFQAM  PVLGICYGF        0.5265        167.9          WB    16.00      Sequence
DRB1_0404   93  YGFQAMAQALGGIVA  GFQAMAQAL        0.5245        171.5          WB    32.00      Sequence
DRB1_0404  279  GANLVTVDAAETFLE  NLVTVDAAE        0.5222        175.9          WB    32.00      Sequence
DRB1_0404   94  GFQAMAQALGGIVAH  GFQAMAQAL        0.5217        176.8          WB    32.00      Sequence
DRB1_0404  306  KIIGRQFIRAFEGAV  FIRAFEGAV        0.5204        179.3          WB    32.00      Sequence
DRB1_0404  280  ANLVTVDAAETFLEA  NLVTVDAAE        0.5196        181.0          WB    32.00      Sequence
DRB1_0404   92  CYGFQAMAQALGGIV  GFQAMAQAL        0.5170        186.1          WB    32.00      Sequence
DRB1_0404  289  ETFLEALSGVSAPEG  TFLEALSGV        0.5139        192.4          WB    32.00      Sequence
DRB1_0404  312  FIRAFEGAVRDVLDG  FIRAFEGAV        0.5137        192.9          WB    32.00      Sequence
DRB1_0404  288  AETFLEALSGVSAPE  TFLEALSGV        0.5135        193.2          WB    32.00      Sequence
DRB1_0404  441  QIWQCPVVLLADVRS  QIWQCPVVL        0.5087        203.5          WB    32.00      Sequence
DRB1_0404  278  TGANLVTVDAAETFL  NLVTVDAAE        0.5058        210.0          WB    32.00      Sequence
DRB1_0404  488  PYEVLERISTRITNE  EVLERISTR        0.5016        219.7          WB    32.00      Sequence
DRB1_0404  287  AAETFLEALSGVSAP  TFLEALSGV        0.4996        224.5          WB    32.00      Sequence
DRB1_0404   37  RVFSEVIPHTASIEE  RVFSEVIPH        0.4996        224.7          WB    32.00      Sequence
DRB1_0404  193  RFLHDFAGLGAQWTP  RFLHDFAGL        0.4991        225.7          WB    32.00      Sequence
DRB1_0404  408  IRIVGEVTAKRLDTL  RIVGEVTAK        0.4985        227.3          WB    32.00      Sequence
DRB1_0404  464  TYGHPIVLRPVSSED  IVLRPVSSE        0.4981        228.3          WB    32.00      Sequence
DRB1_0404  404  PGLGIRIVGEVTAKR  IRIVGEVTA        0.4970        231.1          WB    32.00      Sequence
DRB1_0404  367  KFTLVEPLRLLFKDE  TLVEPLRLL        0.4958        233.9          WB    32.00      Sequence
DRB1_0404  489  YEVLERISTRITNEV  EVLERISTR        0.4955        234.7          WB    32.00      Sequence
DRB1_0404  503  VAEVNRVVLDITSKP  RVVLDITSK        0.4941        238.4          WB    32.00      Sequence
DRB1_0404  192  SRFLHDFAGLGAQWT  RFLHDFAGL        0.4927        242.0          WB    32.00      Sequence
DRB1_0404  440  NQIWQCPVVLLADVR  QIWQCPVVL        0.4924        242.7          WB    32.00      Sequence
DRB1_0404  281  NLVTVDAAETFLEAL  NLVTVDAAE        0.4898        249.7          WB    32.00      Sequence
DRB1_0404   36  ARVFSEVIPHTASIE  RVFSEVIPH        0.4895        250.5          WB    32.00      Sequence
DRB1_0404  290  TFLEALSGVSAPEGK  TFLEALSGV        0.4849        263.2          WB    32.00      Sequence
DRB1_0404  487  VPYEVLERISTRITN  EVLERISTR        0.4847        263.7          WB    32.00      Sequence
DRB1_0404   95  FQAMAQALGGIVAHT  FQAMAQALG        0.4825        270.1          WB    32.00      Sequence
DRB1_0404  448  VLLADVRSVGVQGDG  VLLADVRSV        0.4790        280.8          WB    32.00      Sequence
DRB1_0404  439  DNQIWQCPVVLLADV  QIWQCPVVL        0.4712        305.4          WB    32.00      Sequence
DRB1_0404  438  LDNQIWQCPVVLLAD  QIWQCPVVL        0.4705        307.5          WB    32.00      Sequence
DRB1_0404   83  DLGVPVLGICYGFQA  PVLGICYGF        0.4673        318.7          WB    32.00      Sequence
DRB1_0404  211  ANALIEQVRTQIGDG  LIEQVRTQI        0.4672        319.0          WB    32.00      Sequence
DRB1_0404   14  RPVLVVDFGAQYAQL  VLVVDFGAQ        0.4671        319.1          WB    32.00      Sequence
DRB1_0404  212  NALIEQVRTQIGDGH  LIEQVRTQI        0.4656        324.5          WB    32.00      Sequence
DRB1_0404  272  RDFVAATGANLVTVD  FVAATGANL        0.4652        325.9          WB    32.00      Sequence
DRB1_0404  271  QRDFVAATGANLVTV  FVAATGANL        0.4636        331.5          WB    32.00      Sequence
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DRB1_0404  251  RLTCVFVDHGLLRAG  RLTCVFVDH        0.4616        338.9         WB    32.00       Sequence
DRB1_0404  362  LPDDLKFTLVEPLRL  LKFTLVEPL        0.4605        342.8         WB    32.00       Sequence
DRB1_0404   13  ARPVLVVDFGAQYAQ  VLVVDFGAQ        0.4577        353.4         WB    32.00       Sequence
DRB1_0404  486  RVPYEVLERISTRIT  EVLERISTR        0.4556        361.5         WB    32.00       Sequence
DRB1_0404  329  AEFLVQGTLYPDVVE  FLVQGTLYP        0.4554        362.3         WB    32.00       Sequence
DRB1_0404   35  EARVFSEVIPHTASI  RVFSEVIPH        0.4553        362.5         WB    32.00       Sequence
DRB1_0404  250  DRLTCVFVDHGLLRA  RLTCVFVDH        0.4542        367.1         WB    32.00       Sequence
DRB1_0404  189  QVLSRFLHDFAGLGA  RFLHDFAGL        0.4541        367.3         WB    32.00       Sequence
DRB1_0404  273  DFVAATGANLVTVDA  FVAATGANL        0.4533        370.7         WB    32.00       Sequence
DRB1_0404  191  LSRFLHDFAGLGAQW  RFLHDFAGL        0.4530        371.8         WB    32.00       Sequence
DRB1_0404  249  GDRLTCVFVDHGLLR  RLTCVFVDH        0.4526        373.4         WB    32.00       Sequence
DRB1_0404  328  TAEFLVQGTLYPDVV  FLVQGTLYP        0.4520        375.7         WB    32.00       Sequence
DRB1_0404   56  QPVALVLSGGPASVY  QPVALVLSG        0.4515        378.0         WB    32.00       Sequence
DRB1_0404  277  ATGANLVTVDAAETF  NLVTVDAAE        0.4512        379.1         WB    32.00       Sequence
DRB1_0404  469  IVLRPVSSEDAMTAD  IVLRPVSSE        0.4499        384.6         WB    32.00       Sequence
DRB1_0404  286  DAAETFLEALSGVSA  TFLEALSGV        0.4488        389.0         WB    32.00       Sequence
DRB1_0404   15  PVLVVDFGAQYAQLI  VLVVDFGAQ        0.4485        390.4         WB    32.00       Sequence
DRB1_0404  190  VLSRFLHDFAGLGAQ  RFLHDFAGL        0.4465        398.9         WB    32.00       Sequence
DRB1_0404  368  FTLVEPLRLLFKDEV  TLVEPLRLL        0.4448        406.2         WB    32.00       Sequence
DRB1_0404   55  RQPVALVLSGGPASV  QPVALVLSG        0.4444        408.1         WB    32.00       Sequence
DRB1_0404  437  GLDNQIWQCPVVLLA  QIWQCPVVL        0.4435        412.2         WB    32.00       Sequence
DRB1_0404  403  GPGLGIRIVGEVTAK  IRIVGEVTA        0.4435        412.3         WB    32.00       Sequence
DRB1_0404  225  GHAICGLSGGVDSAV  AICGLSGGV        0.4434        412.6         WB    32.00       Sequence
DRB1_0404  224  DGHAICGLSGGVDSA  AICGLSGGV        0.4394        431.0         WB    32.00       Sequence
DRB1_0404   38  VFSEVIPHTASIEEI  EVIPHTASI        0.4388        433.6         WB    32.00       Sequence
DRB1_0404   39  FSEVIPHTASIEEIR  EVIPHTASI        0.4377        438.9         WB    32.00       Sequence
DRB1_0404   34  REARVFSEVIPHTAS  RVFSEVIPH        0.4365        444.7         WB    32.00       Sequence
DRB1_0404  269  QVQRDFVAATGANLV  FVAATGANL        0.4363        445.3         WB    32.00       Sequence
DRB1_0404  369  TLVEPLRLLFKDEVR  TLVEPLRLL        0.4360        446.8         WB    32.00       Sequence
DRB1_0404   82  LDLGVPVLGICYGFQ  PVLGICYGF        0.4354        449.8         WB    32.00       Sequence
DRB1_0404  270  VQRDFVAATGANLVT  FVAATGANL        0.4350        451.9         WB    32.00       Sequence
DRB1_0404  330  EFLVQGTLYPDVVES  FLVQGTLYP        0.4337        458.4         WB    32.00       Sequence
DRB1_0404  490  EVLERISTRITNEVA  EVLERISTR        0.4333        460.0         WB    32.00       Sequence
DRB1_0404  188  QQVLSRFLHDFAGLG  RFLHDFAGL        0.4325        464.3         WB    32.00       Sequence
DRB1_0404  291  FLEALSGVSAPEGKR  EALSGVSAP        0.4323        465.4         WB    32.00       Sequence
DRB1_0404   96  QAMAQALGGIVAHTG  QALGGIVAH        0.4319        467.1         WB    32.00       Sequence
DRB1_0404   16  VLVVDFGAQYAQLIA  VLVVDFGAQ        0.4314        470.0         WB    32.00       Sequence
DRB1_0404   97  AMAQALGGIVAHTGT  QALGGIVAH        0.4310        471.9         WB    32.00       Sequence
DRB1_0404  210  IANALIEQVRTQIGD  LIEQVRTQI        0.4284        485.2         WB    32.00       Sequence
DRB1_0404  502  EVAEVNRVVLDITSK  RVVLDITSK        0.4276        489.3         WB    32.00       Sequence
DRB1_0404  213  ALIEQVRTQIGDGHA  LIEQVRTQI        0.4262        496.6         WB    32.00       Sequence
DRB1_0404  463  RTYGHPIVLRPVSSE  IVLRPVSSE        0.4256        500.3               32.00       Sequence
DRB1_0404   80  ALLDLGVPVLGICYG  ALLDLGVPV        0.4238        509.9               32.00       Sequence
DRB1_0404   40  SEVIPHTASIEEIRA  EVIPHTASI        0.4233        512.7               32.00       Sequence
DRB1_0404   57  PVALVLSGGPASVYA  LVLSGGPAS        0.4223        518.3               32.00       Sequence
DRB1_0404  327  KTAEFLVQGTLYPDV  FLVQGTLYP        0.4196        533.8               32.00       Sequence
DRB1_0404   54  ARQPVALVLSGGPAS  QPVALVLSG        0.4192        536.2               32.00       Sequence
DRB1_0404   12  PARPVLVVDFGAQYA  VLVVDFGAQ        0.4191        536.3               32.00       Sequence
DRB1_0404   81  LLDLGVPVLGICYGF  PVLGICYGF        0.4173        547.1               32.00       Sequence
DRB1_0404   79  PALLDLGVPVLGICY  ALLDLGVPV        0.4172        547.6               32.00       Sequence
DRB1_0404  248  IGDRLTCVFVDHGLL  RLTCVFVDH        0.4150        560.6               32.00       Sequence
DRB1_0404  485  TRVPYEVLERISTRI  EVLERISTR        0.4150        560.8               32.00       Sequence
DRB1_0404  274  FVAATGANLVTVDAA  FVAATGANL        0.4149        561.8               32.00       Sequence
DRB1_0404  305  RKIIGRQFIRAFEGA  IGRQFIRAF        0.4144        564.4               32.00       Sequence
DRB1_0404  268  AQVQRDFVAATGANL  FVAATGANL        0.4136        569.5               32.00       Sequence
DRB1_0404  226  HAICGLSGGVDSAVA  AICGLSGGV        0.4128        574.2               32.00       Sequence
DRB1_0404   53  RARQPVALVLSGGPA  QPVALVLSG        0.4108        586.9               32.00       Sequence
DRB1_0404   78  DPALLDLGVPVLGIC  ALLDLGVPV        0.4085        601.9               32.00       Sequence
DRB1_0404   58  VALVLSGGPASVYAD  LVLSGGPAS        0.4052        623.6               50.00       Sequence
DRB1_0404  214  LIEQVRTQIGDGHAI  LIEQVRTQI        0.4019        646.6               50.00       Sequence
DRB1_0404   33  VREARVFSEVIPHTA  RVFSEVIPH        0.4003        657.8               50.00       Sequence
DRB1_0404   98  MAQALGGIVAHTGTR  QALGGIVAH        0.3982        673.0               50.00       Sequence
DRB1_0404  197  DFAGLGAQWTPANIA  GLGAQWTPA        0.3981        673.6               50.00       Sequence
DRB1_0404  223  GDGHAICGLSGGVDS  AICGLSGGV        0.3979        674.7               50.00       Sequence
DRB1_0404  198  FAGLGAQWTPANIAN  GLGAQWTPA        0.3961        688.0               50.00       Sequence
DRB1_0404   52  IRARQPVALVLSGGP  QPVALVLSG        0.3956        691.6               50.00       Sequence
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DRB1_0404  292  LEALSGVSAPEGKRK  EALSGVSAP        0.3908        729.0                   50.00     Sequence
DRB1_0404   41  EVIPHTASIEEIRAR  EVIPHTASI        0.3902        733.9                   50.00     Sequence
DRB1_0404  484  WTRVPYEVLERISTR  EVLERISTR        0.3901        734.2                   50.00     Sequence
DRB1_0404  418  RLDTLRHADSIVREE  TLRHADSIV        0.3885        747.2                   50.00     Sequence
DRB1_0404   77  LDPALLDLGVPVLGI  ALLDLGVPV        0.3881        750.5                   50.00     Sequence
DRB1_0404  409  RIVGEVTAKRLDTLR  RIVGEVTAK        0.3870        759.2                   50.00     Sequence
DRB1_0404  419  LDTLRHADSIVREEL  TLRHADSIV        0.3870        759.7                   50.00     Sequence
DRB1_0404  285  VDAAETFLEALSGVS  TFLEALSGV        0.3864        764.2                   50.00     Sequence
DRB1_0404  370  LVEPLRLLFKDEVRA  LVEPLRLLF        0.3848        777.5                   50.00     Sequence
DRB1_0404  209  NIANALIEQVRTQIG  LIEQVRTQI        0.3840        784.4                   50.00     Sequence
DRB1_0404  436  AGLDNQIWQCPVVLL  NQIWQCPVV        0.3836        788.2                   50.00     Sequence
DRB1_0404   51  EIRARQPVALVLSGG  QPVALVLSG        0.3830        793.4                   50.00     Sequence
DRB1_0404  276  AATGANLVTVDAAET  NLVTVDAAE        0.3818        803.1                   50.00     Sequence
DRB1_0404  187  GQQVLSRFLHDFAGL  QVLSRFLHD        0.3818        803.7                   50.00     Sequence
DRB1_0404  196  HDFAGLGAQWTPANI  FAGLGAQWT        0.3815        806.0                   50.00     Sequence
DRB1_0404   11  TPARPVLVVDFGAQY  VLVVDFGAQ        0.3779        837.9                   50.00     Sequence
DRB1_0404   59  ALVLSGGPASVYADG  LVLSGGPAS        0.3765        850.7                   50.00     Sequence
DRB1_0404  420  DTLRHADSIVREELT  TLRHADSIV        0.3765        850.9                   50.00     Sequence
DRB1_0404  331  FLVQGTLYPDVVESG  FLVQGTLYP        0.3753        861.9                   50.00     Sequence
DRB1_0404  417  KRLDTLRHADSIVRE  TLRHADSIV        0.3737        877.2                   50.00     Sequence
DRB1_0404   32  RVREARVFSEVIPHT  RVFSEVIPH        0.3719        894.7                   50.00     Sequence
DRB1_0404  326  GKTAEFLVQGTLYPD  FLVQGTLYP        0.3708        905.1                   50.00     Sequence
DRB1_0404  372  EPLRLLFKDEVRAVG  LRLLFKDEV        0.3688        924.6                   50.00     Sequence
DRB1_0404  373  PLRLLFKDEVRAVGR  LRLLFKDEV        0.3679        934.1                   50.00     Sequence
DRB1_0404  194  FLHDFAGLGAQWTPA  FLHDFAGLG        0.3677        935.3                   50.00     Sequence
DRB1_0404  304  KRKIIGRQFIRAFEG  IGRQFIRAF        0.3674        938.9                   50.00     Sequence
DRB1_0404  131  PEVQPVWMSHGDAVT  EVQPVWMSH        0.3666        946.8                   50.00     Sequence
DRB1_0404  371  VEPLRLLFKDEVRAV  LRLLFKDEV        0.3659        954.1                   50.00     Sequence
DRB1_0404  247  AIGDRLTCVFVDHGL  RLTCVFVDH        0.3655        958.8                   50.00     Sequence
DRB1_0404  267  RAQVQRDFVAATGAN  QVQRDFVAA        0.3635        979.7                   50.00     Sequence
DRB1_0404  195  LHDFAGLGAQWTPAN  FAGLGAQWT        0.3633        981.9                   50.00     Sequence
DRB1_0404  132  EVQPVWMSHGDAVTA  EVQPVWMSH        0.3630        985.0                   50.00     Sequence
DRB1_0404  227  AICGLSGGVDSAVAA  AICGLSGGV        0.3572       1048.3                   50.00     Sequence
DRB1_0404  491  VLERISTRITNEVAE  ERISTRITN        0.3570       1051.0                   50.00     Sequence
DRB1_0404   20  DFGAQYAQLIARRVR  DFGAQYAQL        0.3546       1078.5                   50.00     Sequence
DRB1_0404   60  LVLSGGPASVYADGA  LVLSGGPAS        0.3540       1085.5                   50.00     Sequence
DRB1_0404   50  EEIRARQPVALVLSG  RARQPVALV        0.3539       1086.9                   50.00     Sequence
DRB1_0404  130  LPEVQPVWMSHGDAV  EVQPVWMSH        0.3528       1100.0                   50.00     Sequence
DRB1_0404  361  GLPDDLKFTLVEPLR  LKFTLVEPL        0.3527       1100.9                   50.00     Sequence
DRB1_0404  252  LTCVFVDHGLLRAGE  LTCVFVDHG        0.3520       1109.4                   50.00     Sequence
DRB1_0404   76  KLDPALLDLGVPVLG  ALLDLGVPV        0.3503       1130.1                   50.00     Sequence
DRB1_0404  421  TLRHADSIVREELTA  TLRHADSIV        0.3489       1146.4                   50.00     Sequence
DRB1_0404  117  TELKVLGGKLHSDLP  ELKVLGGKL        0.3487       1149.7                   50.00     Sequence
DRB1_0404   99  AQALGGIVAHTGTRE  QALGGIVAH        0.3485       1151.8                   50.00     Sequence
DRB1_0404  416  AKRLDTLRHADSIVR  TLRHADSIV        0.3447       1199.8                   50.00     Sequence
DRB1_0404  100  QALGGIVAHTGTREY  QALGGIVAH        0.3438       1212.2                   50.00     Sequence
DRB1_0404  435  AAGLDNQIWQCPVVL  NQIWQCPVV        0.3436       1214.1                   50.00     Sequence
DRB1_0404  118  ELKVLGGKLHSDLPE  ELKVLGGKL        0.3425       1229.4                   50.00     Sequence
DRB1_0404  116  RTELKVLGGKLHSDL  ELKVLGGKL        0.3423       1231.1                   50.00     Sequence
DRB1_0404  200  GLGAQWTPANIANAL  GLGAQWTPA        0.3416       1241.0                   50.00     Sequence
DRB1_0404  222  IGDGHAICGLSGGVD  AICGLSGGV        0.3411       1248.1                   50.00     Sequence
DRB1_0404  186  HGQQVLSRFLHDFAG  QVLSRFLHD        0.3408       1251.6                   50.00     Sequence
DRB1_0404   17  LVVDFGAQYAQLIAR  LVVDFGAQY        0.3381       1289.1                   50.00     Sequence
DRB1_0404  402  PGPGLGIRIVGEVTA  IRIVGEVTA        0.3380       1290.5                   50.00     Sequence
DRB1_0404  246  RAIGDRLTCVFVDHG  RLTCVFVDH        0.3366       1309.8                   50.00     Sequence
DRB1_0404   31  RRVREARVFSEVIPH  RVFSEVIPH        0.3345       1340.5                   50.00     Sequence
DRB1_0404  293  EALSGVSAPEGKRKI  EALSGVSAP        0.3337       1351.7                   50.00     Sequence
DRB1_0404  434  TAAGLDNQIWQCPVV  TAAGLDNQI        0.3322       1373.7                   50.00     Sequence
DRB1_0404  129  DLPEVQPVWMSHGDA  EVQPVWMSH        0.3320       1377.3                   50.00     Sequence
DRB1_0404   10  ETPARPVLVVDFGAQ  VLVVDFGAQ        0.3318       1380.5                   50.00     Sequence
DRB1_0404  159  GAPVAAFEAFDRRLA  APVAAFEAF        0.3282       1435.3                   50.00     Sequence
DRB1_0404  266  ERAQVQRDFVAATGA  QVQRDFVAA        0.3269       1454.6                   50.00     Sequence
DRB1_0404  115  GRTELKVLGGKLHSD  ELKVLGGKL        0.3264       1463.0                   50.00     Sequence
DRB1_0404  462  GRTYGHPIVLRPVSS  PIVLRPVSS        0.3258       1472.5                   50.00     Sequence
DRB1_0404  208  ANIANALIEQVRTQI  LIEQVRTQI        0.3255       1477.5                   50.00     Sequence
DRB1_0404  150  GFDVVASSAGAPVAA  FDVVASSAG        0.3238       1504.7                   50.00     Sequence
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DRB1_0404	415	TAKRLDTLRHADSIV	TLRHADSIV	0.3210	1551.5	50.00	Sequence
DRB1_0404	426	DSIVREELTAAGLDN	IVREELTAA	0.3206	1557.6	50.00	Sequence
DRB1_0404	427	SIVREELTAAGLDNQ	IVREELTAA	0.3204	1561.0	50.00	Sequence
DRB1_0404	199	AGLGAQWTPANIANA	GLGAQWTPA	0.3188	1587.7	50.00	Sequence
DRB1_0404	114	YGRTELKVLGGKLHS	ELKVLGGKL	0.3183	1596.5	50.00	Sequence
DRB1_0404	19	VDFGAQYAQLIARRV	DFGAQYAQL	0.3181	1599.6	50.00	Sequence
DRB1_0404	102	LGGIVAHTGTREYGR	GIVAHTGTR	0.3179	1604.4	50.00	Sequence
DRB1_0404	149	DGFDVVASSAGAPVA	FDVVASSAG	0.3166	1625.8	50.00	Sequence
DRB1_0404	413	EVTAKRLDTLRHADS	VTAKRLDTL	0.3163	1632.1	50.00	Sequence
DRB1_0404	160	APVAAFEAFDRRLAG	APVAAFEAF	0.3162	1633.7	50.00	Sequence
DRB1_0404	325	DGKTAEFLVQGTLYP	FLVQGTLYP	0.3143	1668.3	50.00	Sequence
DRB1_0404	303	GKRKIIGRQFIRAFE	RKIIGRQFI	0.3135	1681.9	50.00	Sequence
DRB1_0404	425	ADSIVREELTAAGLD	IVREELTAA	0.3128	1695.4	50.00	Sequence
DRB1_0404	158	AGAPVAAFEAFDRRL	APVAAFEAF	0.3117	1715.3	50.00	Sequence
DRB1_0404	21	FGAQYAQLIARRVRE	AQYAQLIAR	0.3115	1719.2	50.00	Sequence
DRB1_0404	101	ALGGIVAHTGTREYG	GIVAHTGTR	0.3113	1721.7	50.00	Sequence
DRB1_0404	148	PDGFDVVASSAGAPV	FDVVASSAG	0.3112	1723.7	50.00	Sequence
DRB1_0404	374	LRLLFKDEVRAVGRE	LRLLFKDEV	0.3106	1735.2	50.00	Sequence
DRB1_0404	18	VVDFGAQYAQLIARR	DFGAQYAQL	0.3098	1750.4	50.00	Sequence
DRB1_0404	412	GEVTAKRLDTLRHAD	VTAKRLDTL	0.3080	1785.2	50.00	Sequence
DRB1_0404	128	SDLPEVQPVWMSHGD	EVQPVWMSH	0.3074	1796.8	50.00	Sequence
DRB1_0404	49	IEEIRARQPVALVLS	EIRARQPVA	0.3074	1797.4	50.00	Sequence
DRB1_0404	103	GGIVAHTGTREYGRT	GIVAHTGTR	0.3063	1817.7	50.00	Sequence
DRB1_0404	151	FDVVASSAGAPVAAF	FDVVASSAG	0.3043	1858.0	50.00	Sequence
DRB1_0404	492	LERISTRITNEVAEV	ERISTRITN	0.3035	1873.4	50.00	Sequence
DRB1_0404	75	PKLDPALLDLGVPVL	ALLDLGVPV	0.3032	1881.3	50.00	Sequence
DRB1_0404	483	DWTRVPYEVLERIST	WTRVPYEVL	0.3030	1885.1	50.00	Sequence
DRB1_0404	284	TVDAAETFLEALSGV	TFLEALSGV	0.3011	1923.1	50.00	Sequence
DRB1_0404	204	QWTPANIANALIEQV	TPANIANAL	0.2982	1985.8	50.00	Sequence
DRB1_0404	203	AQWTPANIANALIEQ	TPANIANAL	0.2974	2002.4	50.00	Sequence
DRB1_0404	275	VAATGANLVTVDAAE	NLVTVDAAE	0.2974	2003.1	50.00	Sequence
DRB1_0404	414	VTAKRLDTLRHADSI	TAKRLDTLR	0.2972	2005.7	50.00	Sequence
DRB1_0404	428	IVREELTAAGLDNQI	IVREELTAA	0.2969	2013.9	50.00	Sequence
DRB1_0404	185	PHGQQVLSRFLHDFA	QVLSRFLHD	0.2966	2020.4	50.00	Sequence
DRB1_0404	253	TCVFVDHGLLRAGER	TCVFVDHGL	0.2957	2038.7	50.00	Sequence
DRB1_0404	22	GAQYAQLIARRVREA	AQYAQLIAR	0.2940	2077.1	50.00	Sequence
DRB1_0404	119	LKVLGGKLHSDLPEV	LKVLGGKLH	0.2935	2088.5	50.00	Sequence
DRB1_0404	432	ELTAAGLDNQIWQCP	TAAGLDNQI	0.2928	2104.4	50.00	Sequence
DRB1_0404	205	WTPANIANALIEQVR	TPANIANAL	0.2924	2112.6	50.00	Sequence
DRB1_0404	133	VQPVWMSHGDAVTAA	VWMSHGDAV	0.2908	2149.4	50.00	Sequence
DRB1_0404	282	LVTVDAAETFLEALS	LVTVDAAET	0.2903	2160.9	50.00	Sequence
DRB1_0404	23	AQYAQLIARRVREAR	QYAQLIARR	0.2900	2168.0	50.00	Sequence
DRB1_0404	147	APDGFDVVASSAGAP	GFDVVASSA	0.2897	2175.1	50.00	Sequence
DRB1_0404	302	EGKRKIIGRQFIRAF	RKIIGRQFI	0.2879	2217.9	50.00	Sequence
DRB1_0404	245	QRAIGDRLTCVFVDH	RLTCVFVDH	0.2870	2239.9	50.00	Sequence
DRB1_0404	501	NEVAEVNRVVLDITS	NRVVLDITS	0.2856	2274.5	50.00	Sequence
DRB1_0404	113	EYGRTELKVLGGKLH	ELKVLGGKL	0.2853	2283.3	50.00	Sequence
DRB1_0404	433	LTAAGLDNQIWQCPV	TAAGLDNQI	0.2834	2329.0	50.00	Sequence
DRB1_0404	157	SAGAPVAAFEAFDRR	APVAAFEAF	0.2826	2350.3	50.00	Sequence
DRB1_0404	265	GERAQVQRDFVAATG	QVQRDFVAA	0.2820	2366.0	50.00	Sequence
DRB1_0404	221	QIGDGHAICGLSGGV	AICGLSGGV	0.2817	2373.0	50.00	Sequence
DRB1_0404	393	EEIVARQPFPGPGLG	EEIVARQPF	0.2807	2397.6	50.00	Sequence
DRB1_0404	431	EELTAAGLDNQIWQC	TAAGLDNQI	0.2786	2454.4	50.00	Sequence
DRB1_0404	201	LGAQWTPANIANALI	LGAQWTPAN	0.2779	2471.3	50.00	Sequence
DRB1_0404	125	KLHSDLPEVQPVWMS	KLHSDLPEV	0.2775	2483.2	50.00	Sequence
DRB1_0404	127	HSDLPEVQPVWMSHG	EVQPVWMSH	0.2766	2508.4	50.00	Sequence
DRB1_0404	424	HADSIVREELTAAGL	IVREELTAA	0.2759	2526.9	50.00	Sequence
DRB1_0404	493	ERISTRITNEVAEVN	ERISTRITN	0.2732	2602.4	50.00	Sequence
DRB1_0404	202	GAQWTPANIANALIE	TPANIANAL	0.2729	2608.8	50.00	Sequence
DRB1_0404	104	GIVAHTGTREYGRTE	GIVAHTGTR	0.2721	2633.4	50.00	Sequence
DRB1_0404	394	EIVARQPFPGPGLGI	EIVARQPFP	0.2717	2645.1	50.00	Sequence
DRB1_0404	48	SIEEIRARQPVALVL	EIRARQPVA	0.2712	2657.9	50.00	Sequence
DRB1_0404	411	VGEVTAKRLDTLRHA	VTAKRLDTL	0.2698	2698.4	50.00	Sequence
DRB1_0404	392	PEEIVARQPFPGPGL	EEIVARQPF	0.2662	2807.0	50.00	Sequence
DRB1_0404	509	VVLDITSKPPATIEW	VVLDITSKP	0.2637	2883.5	50.00	Sequence
DRB1_0404	124	GKLHSDLPEVQPVWM	KLHSDLPEV	0.2629	2909.3	50.00	Sequence

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DRB1_0404  184  TPHGQQVLSRFLHDF  QVLSRFLHD         0.2612        2963.4                 50.00      Sequence
DRB1_0404   74  APKLDPALLDLGVPV  ALLDLGVPV         0.2596        3014.7                 50.00      Sequence
DRB1_0404  470  VLRPVSSEDAMTADW  RPVSSEDAM         0.2588        3040.4                 50.00      Sequence
DRB1_0404  120  KVLGGKLHSDLPEVQ  KVLGGKLHS         0.2569        3102.0                 50.00      Sequence
DRB1_0404  430  REELTAAGLDNQIWQ  TAAGLDNQI         0.2551        3164.1                 50.00      Sequence
DRB1_0404  123  GGKLHSDLPEVQPVW  KLHSDLPEV         0.2550        3166.6                 50.00      Sequence
DRB1_0404  360  GGLPDDLKFTLVEPL  LKFTLVEPL         0.2531        3234.1                 50.00      Sequence
DRB1_0404   73  GAPKLDPALLDLGVP  GAPKLDPAL         0.2521        3268.4                 50.00      Sequence
DRB1_0404  152  DVVASSAGAPVAAFE  DVVASSAGA         0.2516        3286.3                 50.00      Sequence
DRB1_0404  146  AAPDGFDVVASSAGA  GFDVVASSA         0.2512        3299.4                 50.00      Sequence
DRB1_0404  254  CVFVDHGLLRAGERA  CVFVDHGLL         0.2492        3371.7                 50.00      Sequence
DRB1_0404  206  TPANIANALIEQVRT  TPANIANAL         0.2461        3487.7                 50.00      Sequence
DRB1_0404  241  AALVQRAIGDRLTCV  AALVQRAIG         0.2443        3557.4                 50.00      Sequence
DRB1_0404  170  RRLAGVQYHPEVMHT  RRLAGVQYH         0.2440        3566.6                 50.00      Sequence
DRB1_0404  264  AGERAQVQRDFVAAT  QVQRDFVAA         0.2439        3573.5                 50.00      Sequence
DRB1_0404  176  QYHPEVMHTPHGQQV  PEVMHTPHG         0.2438        3574.7                 50.00      Sequence
DRB1_0404  395  IVARQPFPGPGLGIR  VARQPFPGP         0.2438        3576.7                 50.00      Sequence
DRB1_0404  422  LRHADSIVREELTAA  LRHADSIVR         0.2436        3585.1                 50.00      Sequence
DRB1_0404  375  RLLFKDEVRAVGREL  LLFKDEVRA         0.2433        3594.6                 50.00      Sequence
DRB1_0404  348  SGTANIKSHHNVGGL  NIKSHHNVG         0.2431        3601.4                 50.00      Sequence
DRB1_0404  349  GTANIKSHHNVGGLP  NIKSHHNVG         0.2426        3621.9                 50.00      Sequence
DRB1_0404  122  LGGKLHSDLPEVQPV  KLHSDLPEV         0.2424        3628.6                 50.00      Sequence
DRB1_0404  168  FDRRLAGVQYHPEVM  RRLAGVQYH         0.2409        3691.1                 50.00      Sequence
DRB1_0404  350  TANIKSHHNVGGLPD  NIKSHHNVG         0.2406        3703.6                 50.00      Sequence
DRB1_0404  134  QPVWMSHGDAVTAAP  VWMSHGDAV         0.2398        3734.3                 50.00      Sequence
DRB1_0404  135  PVWMSHGDAVTAAPD  VWMSHGDAV         0.2397        3735.9                 50.00      Sequence
DRB1_0404  391  LPEEIVARQPFPGPG  EIVARQPFP         0.2396        3743.0                 50.00      Sequence
DRB1_0404  175  VQYHPEVMHTPHGQQ  HPEVMHTPH         0.2391        3762.9                 50.00      Sequence
DRB1_0404  169  DRRLAGVQYHPEVMH  RRLAGVQYH         0.2375        3828.1                 50.00      Sequence
DRB1_0404  482  ADWTRVPYEVLERIS  WTRVPYEVL         0.2373        3837.8                 50.00      Sequence
DRB1_0404  173  AGVQYHPEVMHTPHG  VQYHPEVMH         0.2341        3973.1                 50.00      Sequence
DRB1_0404   47  ASIEEIRARQPVALV  EIRARQPVA         0.2338        3983.1                 50.00      Sequence
DRB1_0404  410  IVGEVTAKRLDTLRH  VTAKRLDTL         0.2324        4046.8                 50.00      Sequence
DRB1_0404  156  SSAGAPVAAFEAFDR  APVAAFEAF         0.2323        4051.5                 50.00      Sequence
DRB1_0404  167  AFDRRLAGVQYHPEV  RRLAGVQYH         0.2321        4059.4                 50.00      Sequence
DRB1_0404  238  AVAAALVQRAIGDRL  AALVQRAIG         0.2317        4077.2                 50.00      Sequence
DRB1_0404  301  PEGKRKIIGRQFIRA  RKIIGRQFI         0.2313        4094.7                 50.00      Sequence
DRB1_0404   24  QYAQLIARRVREARV  QYAQLIARR         0.2312        4098.4                 50.00      Sequence
DRB1_0404  240  AAALVQRAIGDRLTC  AALVQRAIG         0.2308        4114.9                 50.00      Sequence
DRB1_0404  243  LVQRAIGDRLTCVFV  RAIGDRLTC         0.2292        4188.6                 50.00      Sequence
DRB1_0404  351  ANIKSHHNVGGLPDD  NIKSHHNVG         0.2284        4223.0                 50.00      Sequence
DRB1_0404    9  PETPARPVLVVDFGA  RPVLVVDFG         0.2283        4229.3                 50.00      Sequence
DRB1_0404  429  VREELTAAGLDNQIW  TAAGLDNQI         0.2281        4237.0                 50.00      Sequence
DRB1_0404  352  NIKSHHNVGGLPDDL  NIKSHHNVG         0.2279        4247.3                 50.00      Sequence
DRB1_0404  172  LAGVQYHPEVMHTPH  VQYHPEVMH         0.2270        4288.6                 50.00      Sequence
DRB1_0404  244  VQRAIGDRLTCVFVD  RAIGDRLTC         0.2270        4289.0                 50.00      Sequence
DRB1_0404  177  YHPEVMHTPHGQQVL  PEVMHTPHG         0.2269        4294.5                 50.00      Sequence
DRB1_0404  207  PANIANALIEQVRTQ  IANALIEQV         0.2267        4300.3                 50.00      Sequence
DRB1_0404  183  HTPHGQQVLSRFLHD  QVLSRFLHD         0.2259        4340.6                 50.00      Sequence
DRB1_0404  136  VWMSHGDAVTAAPDG  VWMSHGDAV         0.2255        4357.6                 50.00      Sequence
DRB1_0404  112  REYGRTELKVLGGKL  YGRTELKVL         0.2251        4377.2                 50.00      Sequence
DRB1_0404   72  DGAPKLDPALLDLGV  GAPKLDPAL         0.2248        4392.9                 50.00      Sequence
DRB1_0404  239  VAAALVQRAIGDRLT  AALVQRAIG         0.2239        4434.5                 50.00      Sequence
DRB1_0404  283  VTVDAAETFLEALSG  VTVDAAETF         0.2238        4437.6                 50.00      Sequence
DRB1_0404  347  GSGTANIKSHHNVGG  SGTANIKSH         0.2237        4445.5                 50.00      Sequence
DRB1_0404  423  RHADSIVREELTAAG  IVREELTAA         0.2222        4517.9                 50.00      Sequence
DRB1_0404  481  TADWTRVPYEVLERI  WTRVPYEVL         0.2215        4553.6                 50.00      Sequence
DRB1_0404  174  GVQYHPEVMHTPHGQ  HPEVMHTPH         0.2201        4621.7                 50.00      Sequence
DRB1_0404  479  AMTADWTRVPYEVLE  AMTADWTRV         0.2195        4652.2                 50.00      Sequence
DRB1_0404  355  SHHNVGGLPDDLKFT  NVGGLPDDL         0.2193        4661.6                 50.00      Sequence
DRB1_0404   71  ADGAPKLDPALLDLG  GAPKLDPAL         0.2192        4664.8                 50.00      Sequence
DRB1_0404   30  ARRVREARVFSEVIP  EARVFSEVI         0.2178        4737.9                 50.00      Sequence
DRB1_0404  478  DAMTADWTRVPYEVL  AMTADWTRV         0.2171        4772.4                 50.00      Sequence
DRB1_0404  356  HHNVGGLPDDLKFTL  NVGGLPDDL         0.2167        4792.4                 50.00      Sequence
DRB1_0404  494  RISTRITNEVAEVNR  RISTRITNE         0.2165        4806.1                 50.00      Sequence
DRB1_0404  313  IRAFEGAVRDVLDGK  FEGAVRDVL         0.2163        4812.7                 50.00      Sequence
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DRB1_0404  396  VARQPFPGPGLGIRI  VARQPFPGP        0.2160        4829.1                 50.00     Sequence
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DRB1_0404  161  PVAAFEAFDRRLAGV  PVAAFEAFD        0.2144        4914.4                 50.00     Sequence
DRB1_0404  171  RLAGVQYHPEVMHTP  AGVQYHPEV        0.2143        4922.5                 50.00     Sequence
DRB1_0404  242  ALVQRAIGDRLTCVF  RAIGDRLTC        0.2139        4939.0                 50.00     Sequence
DRB1_0404  500  TNEVAEVNRVVLDIT  VAEVNRVVL        0.2138        4949.2                 50.00     Sequence
DRB1_0404  357  HNVGGLPDDLKFTLV  NVGGLPDDL        0.2133        4971.6                 50.00     Sequence
DRB1_0404  382  VRAVGRELGLPEEIV  RAVGRELGL        0.2113        5080.3                 50.00     Sequence
DRB1_0404  332  LVQGTLYPDVVESGG  LVQGTLYPD        0.2110        5098.8                 50.00     Sequence
DRB1_0404  383  RAVGRELGLPEEIVA  RAVGRELGL        0.2107        5114.6                 50.00     Sequence
DRB1_0404  381  EVRAVGRELGLPEEI  RAVGRELGL        0.2090        5208.3                 50.00     Sequence
DRB1_0404   29  IARRVREARVFSEVI  RVREARVFS        0.2081        5262.2                 50.00     Sequence
DRB1_0404  126  LHSDLPEVQPVWMSH  EVQPVWMSH        0.2079        5271.9                 50.00     Sequence
DRB1_0404  449  LLADVRSVGVQGDGR  DVRSVGVQG        0.2072        5314.0                 50.00     Sequence
DRB1_0404  178  HPEVMHTPHGQQVLS  HPEVMHTPH        0.2071        5317.3                 50.00     Sequence
DRB1_0404  237  SAVAAALVQRAIGDR  AVAAALVQR        0.2070        5324.0                 50.00     Sequence
DRB1_0404  354  KSHHNVGGLPDDLKF  NVGGLPDDL        0.2067        5339.7                 50.00     Sequence
DRB1_0404  390  GLPEEIVARQPFPGP  EIVARQPFP        0.2038        5510.1                 50.00     Sequence
DRB1_0404  220  TQIGDGHAICGLSGG  HAICGLSGG        0.2035        5528.3                 50.00     Sequence
DRB1_0404  510  VLDITSKPPATIEWE  DITSKPPAT        0.2027        5579.8                 50.00     Sequence
DRB1_0404  480  MTADWTRVPYEVLER  WTRVPYEVL        0.2024        5595.9                 50.00     Sequence
DRB1_0404   42  VIPHTASIEEIRARQ  VIPHTASIE        0.2009        5685.3                 50.00     Sequence
DRB1_0404  263  RAGERAQVQRDFVAA  QVQRDFVAA        0.2009        5687.5                 50.00     Sequence
DRB1_0404  165  FEAFDRRLAGVQYHP  RRLAGVQYH        0.2007        5697.7                 50.00     Sequence
DRB1_0404  164  AFEAFDRRLAGVQYH  AFEAFDRRL        0.1998        5757.9                 50.00     Sequence
DRB1_0404   70  YADGAPKLDPALLDL  GAPKLDPAL        0.1990        5803.6                 50.00     Sequence
DRB1_0404  228  ICGLSGGVDSAVAAA  GLSGGVDSA        0.1984        5844.1                 50.00     Sequence
DRB1_0404  166  EAFDRRLAGVQYHPE  RRLAGVQYH        0.1957        6016.5                 50.00     Sequence
DRB1_0404  236  DSAVAAALVQRAIGD  AVAAALVQR        0.1955        6027.3                 50.00     Sequence
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DRB1_0404  353  IKSHHNVGGLPDDLK  NVGGLPDDL        0.1946        6086.7                 50.00     Sequence
DRB1_0404  477  EDAMTADWTRVPYEV  AMTADWTRV        0.1934        6166.6                 50.00     Sequence
DRB1_0404  300  APEGKRKIIGRQFIR  RKIIGRQFI        0.1930        6192.9                 50.00     Sequence
DRB1_0404   28  LIARRVREARVFSEV  RVREARVFS        0.1926        6222.9                 50.00     Sequence
DRB1_0404  461  DGRTYGHPIVLRPVS  RTYGHPIVL        0.1926        6224.6                 50.00     Sequence
DRB1_0404  471  LRPVSSEDAMTADWT  RPVSSEDAM        0.1912        6314.0                 50.00     Sequence
DRB1_0404  385  VGRELGLPEEIVARQ  RELGLPEEI        0.1910        6328.0                 50.00     Sequence
DRB1_0404  380  DEVRAVGRELGLPEE  RAVGRELGL        0.1900        6399.2                 50.00     Sequence
DRB1_0404  162  VAAFEAFDRRLAGVQ  AFEAFDRRL        0.1894        6441.5                 50.00     Sequence
DRB1_0404  346  GGSGTANIKSHHNVG  SGTANIKSH        0.1872        6597.1                 50.00     Sequence
DRB1_0404   46  TASIEEIRARQPVAL  EIRARQPVA        0.1860        6679.6                 50.00     Sequence
DRB1_0404  450  LADVRSVGVQGDGRT  DVRSVGVQG        0.1858        6698.3                 50.00     Sequence
DRB1_0404  235  VDSAVAAALVQRAIG  AVAAALVQR        0.1854        6726.3                 50.00     Sequence
DRB1_0404  215  IEQVRTQIGDGHAIC  QVRTQIGDG        0.1849        6763.3                 50.00     Sequence
DRB1_0404  229  CGLSGGVDSAVAAAL  GLSGGVDSA        0.1848        6769.0                 50.00     Sequence
DRB1_0404  333  VQGTLYPDVVESGGG  TLYPDVVES        0.1842        6810.6                 50.00     Sequence
DRB1_0404  476  SEDAMTADWTRVPYE  AMTADWTRV        0.1841        6823.3                 50.00     Sequence
DRB1_0404  324  LDGKTAEFLVQGTLY  EFLVQGTLY        0.1833        6882.7                 50.00     Sequence
DRB1_0404  384  AVGRELGLPEEIVAR  RELGLPEEI        0.1830        6904.4                 50.00     Sequence
DRB1_0404  111  TREYGRTELKVLGGK  YGRTELKVL        0.1818        6995.5                 50.00     Sequence
DRB1_0404  401  FPGPGLGIRIVGEVT  LGIRIVGEV        0.1811        7048.7                 50.00     Sequence
DRB1_0404  261  LLRAGERAQVQRDFV  LLRAGERAQ        0.1802        7116.1                 50.00     Sequence
DRB1_0404    8  VPETPARPVLVVDFG  ARPVLVVDF        0.1798        7147.7                 50.00     Sequence
DRB1_0404  334  QGTLYPDVVESGGGS  TLYPDVVES        0.1787        7231.9                 50.00     Sequence
DRB1_0404   26  AQLIARRVREARVFS  LIARRVREA        0.1787        7233.0                 50.00     Sequence
DRB1_0404  358  NVGGLPDDLKFTLVE  NVGGLPDDL        0.1760        7449.4                 50.00     Sequence
DRB1_0404   27  QLIARRVREARVFSE  LIARRVREA        0.1758        7462.9                 50.00     Sequence
DRB1_0404  376  LLFKDEVRAVGRELG  LLFKDEVRA        0.1740        7606.1                 50.00     Sequence
DRB1_0404  389  LGLPEEIVARQPFPG  EIVARQPFP        0.1733        7664.7                 50.00     Sequence
DRB1_0404   69  VYADGAPKLDPALLD  GAPKLDPAL        0.1733        7668.2                 50.00     Sequence
DRB1_0404  314  RAFEGAVRDVLDGKT  FEGAVRDVL        0.1727        7715.7                 50.00     Sequence
DRB1_0404  335  GTLYPDVVESGGGSG  TLYPDVVES        0.1720        7777.6                 50.00     Sequence
DRB1_0404  499  ITNEVAEVNRVVLDI  VAEVNRVVL        0.1716        7808.2                 50.00     Sequence
DRB1_0404  387  RELGLPEEIVARQPF  LGLPEEIVA        0.1716        7810.3                 50.00     Sequence
DRB1_0404  315  AFEGAVRDVLDGKTA  FEGAVRDVL        0.1716        7810.6                 50.00     Sequence
DRB1_0404  179  PEVMHTPHGQQVLSR  PEVMHTPHG        0.1701        7939.0                 50.00     Sequence
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DRB1_0404  472  RPVSSEDAMTADWTR  RPVSSEDAM        0.1701       7941.2                    50.00     Sequence
DRB1_0404  217  QVRTQIGDGHAICGL  QVRTQIGDG        0.1697       7975.1                    50.00     Sequence
DRB1_0404  379  KDEVRAVGRELGLPE  EVRAVGREL        0.1688       8045.5                    50.00     Sequence
DRB1_0404  294  ALSGVSAPEGKRKII  ALSGVSAPE        0.1684       8084.6                    50.00     Sequence
DRB1_0404  386  GRELGLPEEIVARQP  LGLPEEIVA        0.1673       8180.3                    50.00     Sequence
DRB1_0404  230  GLSGGVDSAVAAALV  GLSGGVDSA        0.1671       8201.4                    50.00     Sequence
DRB1_0404  153  VVASSAGAPVAAFEA  VVASSAGAP        0.1663       8270.1                    50.00     Sequence
DRB1_0404   68  SVYADGAPKLDPALL  SVYADGAPK        0.1656       8332.4                    50.00     Sequence
DRB1_0404  216  EQVRTQIGDGHAICG  QVRTQIGDG        0.1646       8426.8                    50.00     Sequence
DRB1_0404  234  GVDSAVAAALVQRAI  AVAAALVQR        0.1636       8512.1                    50.00     Sequence
DRB1_0404  182  MHTPHGQQVLSRFLH  HGQQVLSRF        0.1622       8641.5                    50.00     Sequence
DRB1_0404  495  ISTRITNEVAEVNRV  RITNEVAEV        0.1616       8701.3                    50.00     Sequence
DRB1_0404  498  RITNEVAEVNRVVLD  RITNEVAEV        0.1616       8703.5                    50.00     Sequence
DRB1_0404  388  ELGLPEEIVARQPFP  LGLPEEIVA        0.1606       8797.8                    50.00     Sequence
DRB1_0404  451  ADVRSVGVQGDGRTY  DVRSVGVQG        0.1601       8841.4                    50.00     Sequence
DRB1_0404  497  TRITNEVAEVNRVVL  RITNEVAEV        0.1600       8855.9                    50.00     Sequence
DRB1_0404  163  AAFEAFDRRLAGVQY  AFEAFDRRL        0.1596       8891.0                    50.00     Sequence
DRB1_0404  452  DVRSVGVQGDGRTYG  DVRSVGVQG        0.1595       8901.9                    50.00     Sequence
DRB1_0404   25  YAQLIARRVREARVF  LIARRVREA        0.1594       8910.5                    50.00     Sequence
DRB1_0404  377  LFKDEVRAVGRELGL  LFKDEVRAV        0.1594       8915.7                    50.00     Sequence
DRB1_0404  336  TLYPDVVESGGGSGT  TLYPDVVES        0.1581       9033.2                    50.00     Sequence
DRB1_0404  460  GDGRTYGHPIVLRPV  RTYGHPIVL        0.1569       9157.9                    50.00     Sequence
DRB1_0404  316  FEGAVRDVLDGKTAE  FEGAVRDVL        0.1564       9208.7                    50.00     Sequence
DRB1_0404  475  SSEDAMTADWTRVPY  AMTADWTRV        0.1563       9218.7                    50.00     Sequence
DRB1_0404  110  GTREYGRTELKVLGG  YGRTELKVL        0.1554       9304.7                    50.00     Sequence
DRB1_0404  155  ASSAGAPVAAFEAFD  APVAAFEAF        0.1549       9357.0                    50.00     Sequence
DRB1_0404  496  STRITNEVAEVNRVV  TRITNEVAE        0.1541       9436.2                    50.00     Sequence
DRB1_0404  259  HGLLRAGERAQVQRD  LLRAGERAQ        0.1525       9597.6                    50.00     Sequence
DRB1_0404  233  GGVDSAVAAALVQRA  VDSAVAAAL        0.1513       9724.4                    50.00     Sequence
DRB1_0404  232  SGGVDSAVAAALVQR  VDSAVAAAL        0.1513       9731.5                    50.00     Sequence
DRB1_0404   61  VLSGGPASVYADGAP  VLSGGPASV        0.1507       9794.3                    50.00     Sequence
DRB1_0404  137  WMSHGDAVTAAPDGF  MSHGDAVTA        0.1499       9880.4                    50.00     Sequence
DRB1_0404  260  GLLRAGERAQVQRDF  LLRAGERAQ        0.1498       9885.6                    50.00     Sequence
DRB1_0404    0  VVQPADIDVPETPAR  VQPADIDVP        0.1494       9929.3                    50.00     Sequence
DRB1_0404  258  DHGLLRAGERAQVQR  LLRAGERAQ        0.1481      10074.0                    50.00     Sequence
DRB1_0404   45  HTASIEEIRARQPVA  EIRARQPVA        0.1465      10245.7                    50.00     Sequence
DRB1_0404   67  ASVYADGAPKLDPAL  SVYADGAPK        0.1455      10352.3                    50.00     Sequence
DRB1_0404  231  LSGGVDSAVAAALVQ  LSGGVDSAV        0.1455      10360.0                    50.00     Sequence
DRB1_0404  255  VFVDHGLLRAGERAQ  VFVDHGLLR        0.1453      10382.8                    50.00     Sequence
DRB1_0404  142  DAVTAAPDGFDVVAS  AVTAAPDGF        0.1431      10627.5                    50.00     Sequence
DRB1_0404  143  AVTAAPDGFDVVASS  AVTAAPDGF        0.1421      10741.6                    50.00     Sequence
DRB1_0404  299  SAPEGKRKIIGRQFI  RKIIGRQFI        0.1417      10797.7                    50.00     Sequence
DRB1_0404  474  VSSEDAMTADWTRVP  AMTADWTRV        0.1408      10902.0                    50.00     Sequence
DRB1_0404  345  GGGSGTANIKSHHNV  SGTANIKSH        0.1407      10913.7                    50.00     Sequence
DRB1_0404  378  FKDEVRAVGRELGLP  EVRAVGREL        0.1404      10945.2                    50.00     Sequence
DRB1_0404  219  RTQIGDGHAICGLSG  TQIGDGHAI        0.1396      11044.8                    50.00     Sequence
DRB1_0404  141  GDAVTAAPDGFDVVA  AVTAAPDGF        0.1384      11184.1                    50.00     Sequence
DRB1_0404  154  VASSAGAPVAAFEAF  VASSAGAPV        0.1366      11402.4                    50.00     Sequence
DRB1_0404  473  PVSSEDAMTADWTRV  AMTADWTRV        0.1356      11525.7                    50.00     Sequence
DRB1_0404  218  VRTQIGDGHAICGLS  VRTQIGDGH        0.1320      11984.7                    50.00     Sequence
DRB1_0404  138  MSHGDAVTAAPDGFD  MSHGDAVTA        0.1312      12084.5                    50.00     Sequence
DRB1_0404  140  HGDAVTAAPDGFDVV  AVTAAPDGF        0.1312      12085.2                    50.00     Sequence
DRB1_0404  400  PFPGPGLGIRIVGEV  LGIRIVGEV        0.1311      12109.3                    50.00     Sequence
DRB1_0404  144  VTAAPDGFDVVASSA  GFDVVASSA        0.1311      12109.7                    50.00     Sequence
DRB1_0404  181  VMHTPHGQQVLSRFL  HTPHGQQVL        0.1302      12220.5                    50.00     Sequence
DRB1_0404  262  LRAGERAQVQRDFVA  LRAGERAQV        0.1286      12432.8                    50.00     Sequence
DRB1_0404  180  EVMHTPHGQQVLSRF  HTPHGQQVL        0.1285      12447.2                    50.00     Sequence
DRB1_0404    1  VQPADIDVPETPARP  VQPADIDVP        0.1284      12465.7                    50.00     Sequence
DRB1_0404    7  DVPETPARPVLVVDF  ARPVLVVDF        0.1283      12473.0                    50.00     Sequence
DRB1_0404  459  QGDGRTYGHPIVLRP  RTYGHPIVL        0.1281      12500.1                    50.00     Sequence
DRB1_0404  397  ARQPFPGPGLGIRIV  RQPFPGPGL        0.1279      12530.6                    50.00     Sequence
DRB1_0404  257  VDHGLLRAGERAQVQ  LLRAGERAQ        0.1255      12857.0                    50.00     Sequence
DRB1_0404  344  SGGGSGTANIKSHHN  SGTANIKSH        0.1246      12982.4                    50.00     Sequence
DRB1_0404  105  IVAHTGTREYGRTEL  IVAHTGTRE        0.1234      13154.2                    50.00     Sequence
DRB1_0404  458  VQGDGRTYGHPIVLR  RTYGHPIVL        0.1229      13232.3                    50.00     Sequence
DRB1_0404   66  PASVYADGAPKLDPA  SVYADGAPK        0.1226      13269.7                    50.00     Sequence
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   DRB1_0404  256  FVDHGLLRAGERAQV  HGLLRAGER        0.1223      13314.5               50.00     Sequence
   DRB1_0404  318  GAVRDVLDGKTAEFL  AVRDVLDGK        0.1211      13483.1               50.00     Sequence
   DRB1_0404  139  SHGDAVTAAPDGFDV  AVTAAPDGF        0.1192      13771.9               50.00     Sequence
   DRB1_0404   65  GPASVYADGAPKLDP  SVYADGAPK        0.1183      13900.0               50.00     Sequence
   DRB1_0404  317  EGAVRDVLDGKTAEF  AVRDVLDGK        0.1170      14102.6               50.00     Sequence
   DRB1_0404  109  TGTREYGRTELKVLG  YGRTELKVL        0.1127      14777.7               50.00     Sequence
   DRB1_0404  323  VLDGKTAEFLVQGTL  AEFLVQGTL        0.1126      14794.2               50.00     Sequence
   DRB1_0404  343  ESGGGSGTANIKSHH  SGTANIKSH        0.1113      14989.2               50.00     Sequence
   DRB1_0404  398  RQPFPGPGLGIRIVG  RQPFPGPGL        0.1079      15549.8               50.00     Sequence
   DRB1_0404  319  AVRDVLDGKTAEFLV  AVRDVLDGK        0.1077      15586.7               50.00     Sequence
   DRB1_0404  337  LYPDVVESGGGSGTA  LYPDVVESG        0.1076      15603.6               50.00     Sequence
   DRB1_0404  457  GVQGDGRTYGHPIVL  RTYGHPIVL        0.1051      16042.4               50.00     Sequence
   DRB1_0404  359  VGGLPDDLKFTLVEP  DLKFTLVEP        0.1048      16082.3               50.00     Sequence
   DRB1_0404   64  GGPASVYADGAPKLD  SVYADGAPK        0.1045      16135.0               50.00     Sequence
   DRB1_0404    5  DIDVPETPARPVLVV  DVPETPARP        0.1034      16336.3               50.00     Sequence
   DRB1_0404    6  IDVPETPARPVLVVD  IDVPETPAR        0.1013      16716.6               50.00     Sequence
   DRB1_0404  321  RDVLDGKTAEFLVQG  DVLDGKTAE        0.1002      16913.4               50.00     Sequence
   DRB1_0404  453  VRSVGVQGDGRTYGH  VGVQGDGRT        0.1001      16922.8               50.00     Sequence
   DRB1_0404  320  VRDVLDGKTAEFLVQ  DVLDGKTAE        0.0994      17065.3               50.00     Sequence
   DRB1_0404   44  PHTASIEEIRARQPV  HTASIEEIR        0.0983      17268.3               50.00     Sequence
   DRB1_0404    4  ADIDVPETPARPVLV  DIDVPETPA        0.0968      17552.4               50.00     Sequence
   DRB1_0404  341  VVESGGGSGTANIKS  VVESGGGSG        0.0966      17581.6               50.00     Sequence
   DRB1_0404  108  HTGTREYGRTELKVL  YGRTELKVL        0.0953      17839.4               50.00     Sequence
   DRB1_0404  399  QPFPGPGLGIRIVGE  PFPGPGLGI        0.0943      18025.8               50.00     Sequence
   DRB1_0404   43  IPHTASIEEIRARQP  HTASIEEIR        0.0932      18232.6               50.00     Sequence
   DRB1_0404  340  DVVESGGGSGTANIK  VVESGGGSG        0.0932      18241.2               50.00     Sequence
   DRB1_0404  455  SVGVQGDGRTYGHPI  VGVQGDGRT        0.0930      18280.4               50.00     Sequence
   DRB1_0404   63  SGGPASVYADGAPKL  SVYADGAPK        0.0917      18531.5               50.00     Sequence
   DRB1_0404  342  VESGGGSGTANIKSH  SGTANIKSH        0.0903      18822.7               50.00     Sequence
   DRB1_0404  454  RSVGVQGDGRTYGHP  VGVQGDGRT        0.0898      18929.1               50.00     Sequence
   DRB1_0404  456  VGVQGDGRTYGHPIV  GVQGDGRTY        0.0886      19181.0               50.00     Sequence
   DRB1_0404  339  PDVVESGGGSGTANI  VVESGGGSG        0.0874      19422.0               50.00     Sequence
   DRB1_0404   62  LSGGPASVYADGAPK  PASVYADGA        0.0864      19625.0               50.00     Sequence
   DRB1_0404  295  LSGVSAPEGKRKIIG  LSGVSAPEG        0.0837      20209.2               50.00     Sequence
   DRB1_0404    2  QPADIDVPETPARPV  QPADIDVPE        0.0810      20809.2               50.00     Sequence
   DRB1_0404  338  YPDVVESGGGSGTAN  VVESGGGSG        0.0803      20965.8               50.00     Sequence
   DRB1_0404  322  DVLDGKTAEFLVQGT  DVLDGKTAE        0.0797      21098.7               50.00     Sequence
   DRB1_0404  298  VSAPEGKRKIIGRQF  KRKIIGRQF        0.0740      22444.0               50.00     Sequence
   DRB1_0404    3  PADIDVPETPARPVL  DIDVPETPA        0.0730      22693.3               50.00     Sequence
   DRB1_0404  106  VAHTGTREYGRTELK  VAHTGTREY        0.0680      23961.0               50.00     Sequence
   DRB1_0404  107  AHTGTREYGRTELKV  TREYGRTEL        0.0640      25007.3               50.00     Sequence
   DRB1_0404  296  SGVSAPEGKRKIIGR  SGVSAPEGK        0.0489      29453.0               50.00     Sequence
   DRB1_0404  297  GVSAPEGKRKIIGRQ  SAPEGKRKI        0.0410      32094.1               50.00     Sequence
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Allele: DRB1_0404. Number of high binders 4. Number of weak binders 109. Number of peptides 511

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0405  447  VVLLADVRSVGVQGD  LLADVRSVG        0.6512         43.6         SB     8.00     Sequence
   DRB1_0405  448  VLLADVRSVGVQGDG  VLLADVRSV        0.6402         49.0         SB     8.00     Sequence
   DRB1_0405  446  PVVLLADVRSVGVQG  VLLADVRSV        0.6269         56.6         WB    16.00     Sequence
   DRB1_0405  329  AEFLVQGTLYPDVVE  FLVQGTLYP        0.6252         57.7         WB    16.00     Sequence
   DRB1_0405  445  CPVVLLADVRSVGVQ  VVLLADVRS        0.6223         59.6         WB    16.00     Sequence
   DRB1_0405   20  DFGAQYAQLIARRVR  AQYAQLIAR        0.6153         64.2         WB    16.00     Sequence
   DRB1_0405  404  PGLGIRIVGEVTAKR  GIRIVGEVT        0.6133         65.6         WB    16.00     Sequence
   DRB1_0405  193  RFLHDFAGLGAQWTP  HDFAGLGAQ        0.6099         68.1         WB    16.00     Sequence
   DRB1_0405  467  HPIVLRPVSSEDAMT  IVLRPVSSE        0.6091         68.6         WB    16.00     Sequence
   DRB1_0405  405  GLGIRIVGEVTAKRL  GIRIVGEVT        0.6089         68.8         WB    16.00     Sequence
   DRB1_0405  192  SRFLHDFAGLGAQWT  FLHDFAGLG        0.6084         69.2         WB    16.00     Sequence
   DRB1_0405   19  VDFGAQYAQLIARRV  AQYAQLIAR        0.6071         70.2         WB    16.00     Sequence
   DRB1_0405  444  QCPVVLLADVRSVGV  VVLLADVRS        0.6050         71.8         WB    16.00     Sequence
   DRB1_0405  468  PIVLRPVSSEDAMTA  IVLRPVSSE        0.6037         72.8         WB    16.00     Sequence
   DRB1_0405  330  EFLVQGTLYPDVVES  FLVQGTLYP        0.6019         74.2         WB    16.00     Sequence
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DRB1_0405  196  HDFAGLGAQWTPANI  HDFAGLGAQ        0.6000         75.8          WB    16.00      Sequence
DRB1_0405  331  FLVQGTLYPDVVESG  FLVQGTLYP        0.5954         79.6          WB    16.00      Sequence
DRB1_0405   21  FGAQYAQLIARRVRE  AQYAQLIAR        0.5954         79.6          WB    16.00      Sequence
DRB1_0405  466  GHPIVLRPVSSEDAM  IVLRPVSSE        0.5942         80.7          WB    16.00      Sequence
DRB1_0405  328  TAEFLVQGTLYPDVV  FLVQGTLYP        0.5910         83.6          WB    16.00      Sequence
DRB1_0405  449  LLADVRSVGVQGDGR  ADVRSVGVQ        0.5902         84.3          WB    16.00      Sequence
DRB1_0405  194  FLHDFAGLGAQWTPA  HDFAGLGAQ        0.5884         85.9          WB    16.00      Sequence
DRB1_0405  403  GPGLGIRIVGEVTAK  GIRIVGEVT        0.5854         88.7          WB    16.00      Sequence
DRB1_0405  418  RLDTLRHADSIVREE  TLRHADSIV        0.5838         90.3          WB    16.00      Sequence
DRB1_0405   90  GICYGFQAMAQALGG  YGFQAMAQA        0.5825         91.6          WB    16.00      Sequence
DRB1_0405  363  PDDLKFTLVEPLRLL  LKFTLVEPL        0.5825         91.6          WB    16.00      Sequence
DRB1_0405  417  KRLDTLRHADSIVRE  TLRHADSIV        0.5814         92.6          WB    16.00      Sequence
DRB1_0405   22  GAQYAQLIARRVREA  AQYAQLIAR        0.5792         94.9          WB    16.00      Sequence
DRB1_0405  364  DDLKFTLVEPLRLLF  LKFTLVEPL        0.5777         96.5          WB    16.00      Sequence
DRB1_0405   89  LGICYGFQAMAQALG  YGFQAMAQA        0.5774         96.8          WB    16.00      Sequence
DRB1_0405  419  LDTLRHADSIVREEL  TLRHADSIV        0.5745         99.8          WB    16.00      Sequence
DRB1_0405  362  LPDDLKFTLVEPLRL  LKFTLVEPL        0.5731        101.4          WB    16.00      Sequence
DRB1_0405  469  IVLRPVSSEDAMTAD  IVLRPVSSE        0.5726        101.9          WB    16.00      Sequence
DRB1_0405  443  WQCPVVLLADVRSVG  VVLLADVRS        0.5705        104.3          WB    16.00      Sequence
DRB1_0405  465  YGHPIVLRPVSSEDA  IVLRPVSSE        0.5683        106.8          WB    16.00      Sequence
DRB1_0405  368  FTLVEPLRLLFKDEV  FTLVEPLRL        0.5679        107.3          WB    16.00      Sequence
DRB1_0405  420  DTLRHADSIVREELT  TLRHADSIV        0.5669        108.4          WB    16.00      Sequence
DRB1_0405  365  DLKFTLVEPLRLLFK  LKFTLVEPL        0.5667        108.6          WB    16.00      Sequence
DRB1_0405  370  LVEPLRLLFKDEVRA  EPLRLLFKD        0.5651        110.6          WB    16.00      Sequence
DRB1_0405  371  VEPLRLLFKDEVRAV  LRLLFKDEV        0.5632        112.8          WB    32.00      Sequence
DRB1_0405   91  ICYGFQAMAQALGGI  YGFQAMAQA        0.5617        114.7          WB    32.00      Sequence
DRB1_0405  198  FAGLGAQWTPANIAN  GAQWTPANI        0.5608        115.8          WB    32.00      Sequence
DRB1_0405  406  LGIRIVGEVTAKRLD  GIRIVGEVT        0.5573        120.3          WB    32.00      Sequence
DRB1_0405   18  VVDFGAQYAQLIARR  GAQYAQLIA        0.5567        121.1          WB    32.00      Sequence
DRB1_0405  211  ANALIEQVRTQIGDG  ALIEQVRTQ        0.5558        122.3          WB    32.00      Sequence
DRB1_0405  372  EPLRLLFKDEVRAVG  LRLLFKDEV        0.5544        124.1          WB    32.00      Sequence
DRB1_0405  210  IANALIEQVRTQIGD  ALIEQVRTQ        0.5539        124.7          WB    32.00      Sequence
DRB1_0405  402  PGPGLGIRIVGEVTA  GIRIVGEVT        0.5531        125.9          WB    32.00      Sequence
DRB1_0405  366  LKFTLVEPLRLLFKD  FTLVEPLRL        0.5525        126.8          WB    32.00      Sequence
DRB1_0405  172  LAGVQYHPEVMHTPH  VQYHPEVMH        0.5496        130.7          WB    32.00      Sequence
DRB1_0405  369  TLVEPLRLLFKDEVR  EPLRLLFKD        0.5489        131.7          WB    32.00      Sequence
DRB1_0405  170  RRLAGVQYHPEVMHT  GVQYHPEVM        0.5488        131.8          WB    32.00      Sequence
DRB1_0405  327  KTAEFLVQGTLYPDV  FLVQGTLYP        0.5479        133.2          WB    32.00      Sequence
DRB1_0405  171  RLAGVQYHPEVMHTP  GVQYHPEVM        0.5476        133.6          WB    32.00      Sequence
DRB1_0405  197  DFAGLGAQWTPANIA  GAQWTPANI        0.5463        135.5          WB    32.00      Sequence
DRB1_0405  367  KFTLVEPLRLLFKDE  FTLVEPLRL        0.5456        136.6          WB    32.00      Sequence
DRB1_0405  450  LADVRSVGVQGDGRT  DVRSVGVQG        0.5452        137.1          WB    32.00      Sequence
DRB1_0405   88  VLGICYGFQAMAQAL  YGFQAMAQA        0.5430        140.5          WB    32.00      Sequence
DRB1_0405  212  NALIEQVRTQIGDGH  LIEQVRTQI        0.5426        141.1          WB    32.00      Sequence
DRB1_0405   34  REARVFSEVIPHTAS  RVFSEVIPH        0.5418        142.2          WB    32.00      Sequence
DRB1_0405  491  VLERISTRITNEVAE  LERISTRIT        0.5415        142.7          WB    32.00      Sequence
DRB1_0405  416  AKRLDTLRHADSIVR  TLRHADSIV        0.5381        148.0          WB    32.00      Sequence
DRB1_0405   33  VREARVFSEVIPHTA  RVFSEVIPH        0.5330        156.5          WB    32.00      Sequence
DRB1_0405  173  AGVQYHPEVMHTPHG  VQYHPEVMH        0.5328        156.7          WB    32.00      Sequence
DRB1_0405  490  EVLERISTRITNEVA  LERISTRIT        0.5321        158.0          WB    32.00      Sequence
DRB1_0405  199  AGLGAQWTPANIANA  GAQWTPANI        0.5309        160.0          WB    32.00      Sequence
DRB1_0405  200  GLGAQWTPANIANAL  GAQWTPANI        0.5304        161.0          WB    32.00      Sequence
DRB1_0405  487  VPYEVLERISTRITN  LERISTRIT        0.5294        162.7          WB    32.00      Sequence
DRB1_0405   17  LVVDFGAQYAQLIAR  GAQYAQLIA        0.5289        163.5          WB    32.00      Sequence
DRB1_0405  489  YEVLERISTRITNEV  LERISTRIT        0.5266        167.7          WB    32.00      Sequence
DRB1_0405  442  IWQCPVVLLADVRSV  VVLLADVRS        0.5265        167.8          WB    32.00      Sequence
DRB1_0405  407  GIRIVGEVTAKRLDT  GIRIVGEVT        0.5253        170.0          WB    32.00      Sequence
DRB1_0405  289  ETFLEALSGVSAPEG  FLEALSGVS        0.5252        170.3          WB    32.00      Sequence
DRB1_0405  191  LSRFLHDFAGLGAQW  FLHDFAGLG        0.5249        170.9          WB    32.00      Sequence
DRB1_0405  174  GVQYHPEVMHTPHGQ  VQYHPEVMH        0.5241        172.2          WB    32.00      Sequence
DRB1_0405  290  TFLEALSGVSAPEGK  FLEALSGVS        0.5233        173.8          WB    32.00      Sequence
DRB1_0405   35  EARVFSEVIPHTASI  RVFSEVIPH        0.5230        174.3          WB    32.00      Sequence
DRB1_0405  201  LGAQWTPANIANALI  GAQWTPANI        0.5223        175.7          WB    32.00      Sequence
DRB1_0405  488  PYEVLERISTRITNE  LERISTRIT        0.5217        176.7          WB    32.00      Sequence
DRB1_0405   92  CYGFQAMAQALGGIV  YGFQAMAQA        0.5196        180.8          WB    32.00      Sequence
DRB1_0405  288  AETFLEALSGVSAPE  FLEALSGVS        0.5195        181.1          WB    32.00      Sequence
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DRB1_0405  209  NIANALIEQVRTQIG  LIEQVRTQI        0.5171        185.9         WB    32.00      Sequence
DRB1_0405  169  DRRLAGVQYHPEVMH  GVQYHPEVM        0.5168        186.4         WB    32.00      Sequence
DRB1_0405  195  LHDFAGLGAQWTPAN  DFAGLGAQW        0.5162        187.6         WB    32.00      Sequence
DRB1_0405  486  RVPYEVLERISTRIT  LERISTRIT        0.5144        191.4         WB    32.00      Sequence
DRB1_0405   23  AQYAQLIARRVREAR  YAQLIARRV        0.5135        193.2         WB    32.00      Sequence
DRB1_0405  464  TYGHPIVLRPVSSED  IVLRPVSSE        0.5123        195.8         WB    32.00      Sequence
DRB1_0405  470  VLRPVSSEDAMTADW  VLRPVSSED        0.5114        197.6         WB    32.00      Sequence
DRB1_0405  326  GKTAEFLVQGTLYPD  FLVQGTLYP        0.5093        202.1         WB    32.00      Sequence
DRB1_0405  421  TLRHADSIVREELTA  TLRHADSIV        0.5086        203.6         WB    32.00      Sequence
DRB1_0405  492  LERISTRITNEVAEV  LERISTRIT        0.5081        204.7         WB    32.00      Sequence
DRB1_0405   87  PVLGICYGFQAMAQA  ICYGFQAMA        0.5069        207.5         WB    32.00      Sequence
DRB1_0405   37  RVFSEVIPHTASIEE  FSEVIPHTA        0.5051        211.6         WB    32.00      Sequence
DRB1_0405  332  LVQGTLYPDVVESGG  LVQGTLYPD        0.5051        211.7         WB    32.00      Sequence
DRB1_0405  309  GRQFIRAFEGAVRDV  FIRAFEGAV        0.5024        217.8         WB    32.00      Sequence
DRB1_0405   31  RRVREARVFSEVIPH  RVREARVFS        0.5012        220.7         WB    32.00      Sequence
DRB1_0405   32  RVREARVFSEVIPHT  EARVFSEVI        0.4985        227.2         WB    32.00      Sequence
DRB1_0405  308  IGRQFIRAFEGAVRD  FIRAFEGAV        0.4976        229.4         WB    32.00      Sequence
DRB1_0405  291  FLEALSGVSAPEGKR  FLEALSGVS        0.4960        233.6         WB    32.00      Sequence
DRB1_0405  287  AAETFLEALSGVSAP  FLEALSGVS        0.4957        234.4         WB    32.00      Sequence
DRB1_0405   36  ARVFSEVIPHTASIE  FSEVIPHTA        0.4955        234.7         WB    32.00      Sequence
DRB1_0405   39  FSEVIPHTASIEEIR  EVIPHTASI        0.4948        236.4         WB    32.00      Sequence
DRB1_0405   38  VFSEVIPHTASIEEI  EVIPHTASI        0.4944        237.6         WB    32.00      Sequence
DRB1_0405  190  VLSRFLHDFAGLGAQ  FLHDFAGLG        0.4939        238.9         WB    32.00      Sequence
DRB1_0405   16  VLVVDFGAQYAQLIA  VLVVDFGAQ        0.4937        239.5         WB    32.00      Sequence
DRB1_0405  451  ADVRSVGVQGDGRTY  DVRSVGVQG        0.4858        260.7         WB    32.00      Sequence
DRB1_0405  213  ALIEQVRTQIGDGHA  LIEQVRTQI        0.4855        261.5         WB    32.00      Sequence
DRB1_0405  307  IIGRQFIRAFEGAVR  FIRAFEGAV        0.4807        275.6         WB    32.00      Sequence
DRB1_0405  208  ANIANALIEQVRTQI  LIEQVRTQI        0.4789        280.9         WB    32.00      Sequence
DRB1_0405  463  RTYGHPIVLRPVSSE  IVLRPVSSE        0.4781        283.5         WB    32.00      Sequence
DRB1_0405  202  GAQWTPANIANALIE  GAQWTPANI        0.4780        283.8         WB    32.00      Sequence
DRB1_0405   93  YGFQAMAQALGGIVA  YGFQAMAQA        0.4764        288.7         WB    32.00      Sequence
DRB1_0405  373  PLRLLFKDEVRAVGR  LLFKDEVRA        0.4752        292.3         WB    50.00      Sequence
DRB1_0405   30  ARRVREARVFSEVIP  RVREARVFS        0.4751        292.6         WB    50.00      Sequence
DRB1_0405  441  QIWQCPVVLLADVRS  VVLLADVRS        0.4724        301.5         WB    50.00      Sequence
DRB1_0405  189  QVLSRFLHDFAGLGA  FLHDFAGLG        0.4723        301.6         WB    50.00      Sequence
DRB1_0405  361  GLPDDLKFTLVEPLR  LKFTLVEPL        0.4714        304.8         WB    50.00      Sequence
DRB1_0405  310  RQFIRAFEGAVRDVL  FIRAFEGAV        0.4706        307.3         WB    50.00      Sequence
DRB1_0405  401  FPGPGLGIRIVGEVT  GIRIVGEVT        0.4695        311.0         WB    50.00      Sequence
DRB1_0405  493  ERISTRITNEVAEVN  STRITNEVA        0.4654        325.2         WB    50.00      Sequence
DRB1_0405  306  KIIGRQFIRAFEGAV  FIRAFEGAV        0.4632        333.0         WB    50.00      Sequence
DRB1_0405  415  TAKRLDTLRHADSIV  TLRHADSIV        0.4628        334.6         WB    50.00      Sequence
DRB1_0405  311  QFIRAFEGAVRDVLD  FIRAFEGAV        0.4601        344.4         WB    50.00      Sequence
DRB1_0405  249  GDRLTCVFVDHGLLR  DRLTCVFVD        0.4585        350.5         WB    50.00      Sequence
DRB1_0405  277  ATGANLVTVDAAETF  GANLVTVDA        0.4584        350.7         WB    50.00      Sequence
DRB1_0405  248  IGDRLTCVFVDHGLL  DRLTCVFVD        0.4563        358.7         WB    50.00      Sequence
DRB1_0405  168  FDRRLAGVQYHPEVM  RRLAGVQYH        0.4554        362.4         WB    50.00      Sequence
DRB1_0405  276  AATGANLVTVDAAET  GANLVTVDA        0.4553        362.6         WB    50.00      Sequence
DRB1_0405  286  DAAETFLEALSGVSA  FLEALSGVS        0.4536        369.5         WB    50.00      Sequence
DRB1_0405   40  SEVIPHTASIEEIRA  EVIPHTASI        0.4521        375.5         WB    50.00      Sequence
DRB1_0405  278  TGANLVTVDAAETFL  ANLVTVDAA        0.4517        377.0         WB    50.00      Sequence
DRB1_0405   15  PVLVVDFGAQYAQLI  VLVVDFGAQ        0.4514        378.1         WB    50.00      Sequence
DRB1_0405  494  RISTRITNEVAEVNR  TRITNEVAE        0.4509        380.4         WB    50.00      Sequence
DRB1_0405  485  TRVPYEVLERISTRI  YEVLERIST        0.4497        385.1         WB    50.00      Sequence
DRB1_0405  481  TADWTRVPYEVLERI  WTRVPYEVL        0.4429        415.0         WB    50.00      Sequence
DRB1_0405  333  VQGTLYPDVVESGGG  GTLYPDVVE        0.4426        415.9         WB    50.00      Sequence
DRB1_0405  250  DRLTCVFVDHGLLRA  DRLTCVFVD        0.4408        424.3         WB    50.00      Sequence
DRB1_0405   79  PALLDLGVPVLGICY  DLGVPVLGI        0.4398        429.1         WB    50.00      Sequence
DRB1_0405  482  ADWTRVPYEVLERIS  WTRVPYEVL        0.4382        436.3         WB    50.00      Sequence
DRB1_0405  325  DGKTAEFLVQGTLYP  FLVQGTLYP        0.4375        439.9         WB    50.00      Sequence
DRB1_0405  312  FIRAFEGAVRDVLDG  FIRAFEGAV        0.4368        443.0         WB    50.00      Sequence
DRB1_0405  188  QQVLSRFLHDFAGLG  FLHDFAGLG        0.4358        447.7         WB    50.00      Sequence
DRB1_0405   29  IARRVREARVFSEVI  RVREARVFS        0.4357        448.2         WB    50.00      Sequence
DRB1_0405   41  EVIPHTASIEEIRAR  EVIPHTASI        0.4348        452.5         WB    50.00      Sequence
DRB1_0405  507  NRVVLDITSKPPATI  VVLDITSKP        0.4344        454.7         WB    50.00      Sequence
DRB1_0405  374  LRLLFKDEVRAVGRE  LRLLFKDEV        0.4332        460.7         WB    50.00      Sequence
DRB1_0405  506  VNRVVLDITSKPPAT  NRVVLDITS        0.4326        463.6         WB    50.00      Sequence
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DRB1_0405  462  GRTYGHPIVLRPVSS  RTYGHPIVL        0.4325        464.0        WB    50.00     Sequence
DRB1_0405   78  DPALLDLGVPVLGIC  ALLDLGVPV        0.4324        464.6        WB    50.00     Sequence
DRB1_0405  247  AIGDRLTCVFVDHGL  DRLTCVFVD        0.4319        467.0        WB    50.00     Sequence
DRB1_0405   14  RPVLVVDFGAQYAQL  LVVDFGAQY        0.4314        469.8        WB    50.00     Sequence
DRB1_0405  439  DNQIWQCPVVLLADV  NQIWQCPVV        0.4310        471.9        WB    50.00     Sequence
DRB1_0405  360  GGLPDDLKFTLVEPL  LKFTLVEPL        0.4306        474.0        WB    50.00     Sequence
DRB1_0405  495  ISTRITNEVAEVNRV  STRITNEVA        0.4302        475.7        WB    50.00     Sequence
DRB1_0405  505  EVNRVVLDITSKPPA  NRVVLDITS        0.4277        488.7        WB    50.00     Sequence
DRB1_0405  480  MTADWTRVPYEVLER  ADWTRVPYE        0.4273        490.8        WB    50.00     Sequence
DRB1_0405  483  DWTRVPYEVLERIST  VPYEVLERI        0.4264        495.9        WB    50.00     Sequence
DRB1_0405  279  GANLVTVDAAETFLE  ANLVTVDAA        0.4257        499.4        WB    50.00     Sequence
DRB1_0405  484  WTRVPYEVLERISTR  WTRVPYEVL        0.4252        502.2              50.00     Sequence
DRB1_0405  434  TAAGLDNQIWQCPVV  NQIWQCPVV        0.4250        503.4              50.00     Sequence
DRB1_0405  471  LRPVSSEDAMTADWT  PVSSEDAMT        0.4236        511.1              50.00     Sequence
DRB1_0405  246  RAIGDRLTCVFVDHG  DRLTCVFVD        0.4231        513.9              50.00     Sequence
DRB1_0405  275  VAATGANLVTVDAAE  GANLVTVDA        0.4231        514.0              50.00     Sequence
DRB1_0405  135  PVWMSHGDAVTAAPD  VWMSHGDAV        0.4226        516.7              50.00     Sequence
DRB1_0405   12  PARPVLVVDFGAQYA  VLVVDFGAQ        0.4213        523.7              50.00     Sequence
DRB1_0405  440  NQIWQCPVVLLADVR  NQIWQCPVV        0.4209        526.1              50.00     Sequence
DRB1_0405   86  VPVLGICYGFQAMAQ  ICYGFQAMA        0.4202        530.3              50.00     Sequence
DRB1_0405  274  FVAATGANLVTVDAA  FVAATGANL        0.4201        530.7              50.00     Sequence
DRB1_0405   77  LDPALLDLGVPVLGI  ALLDLGVPV        0.4199        531.7              50.00     Sequence
DRB1_0405  479  AMTADWTRVPYEVLE  ADWTRVPYE        0.4164        552.5              50.00     Sequence
DRB1_0405   13  ARPVLVVDFGAQYAQ  LVVDFGAQY        0.4163        552.8              50.00     Sequence
DRB1_0405  452  DVRSVGVQGDGRTYG  VRSVGVQGD        0.4163        553.4              50.00     Sequence
DRB1_0405   80  ALLDLGVPVLGICYG  DLGVPVLGI        0.4112        584.4              50.00     Sequence
DRB1_0405  478  DAMTADWTRVPYEVL  ADWTRVPYE        0.4110        585.5              50.00     Sequence
DRB1_0405   11  TPARPVLVVDFGAQY  PVLVVDFGA        0.4097        594.2              50.00     Sequence
DRB1_0405  334  QGTLYPDVVESGGGS  GTLYPDVVE        0.4085        601.7              50.00     Sequence
DRB1_0405  292  LEALSGVSAPEGKRK  EALSGVSAP        0.4056        621.3              50.00     Sequence
DRB1_0405  496  STRITNEVAEVNRVV  STRITNEVA        0.4041        631.3              50.00     Sequence
DRB1_0405  133  VQPVWMSHGDAVTAA  VWMSHGDAV        0.4034        635.6              50.00     Sequence
DRB1_0405  175  VQYHPEVMHTPHGQQ  VQYHPEVMH        0.4033        636.7              50.00     Sequence
DRB1_0405   57  PVALVLSGGPASVYA  LVLSGGPAS        0.4031        637.7              50.00     Sequence
DRB1_0405  207  PANIANALIEQVRTQ  IANALIEQV        0.4031        637.8              50.00     Sequence
DRB1_0405  273  DFVAATGANLVTVDA  FVAATGANL        0.4031        638.0              50.00     Sequence
DRB1_0405   56  QPVALVLSGGPASVY  LVLSGGPAS        0.4027        640.8              50.00     Sequence
DRB1_0405  136  VWMSHGDAVTAAPDG  VWMSHGDAV        0.3995        663.2              50.00     Sequence
DRB1_0405  504  AEVNRVVLDITSKPP  NRVVLDITS        0.3993        664.5              50.00     Sequence
DRB1_0405  437  GLDNQIWQCPVVLLA  NQIWQCPVV        0.3987        669.1              50.00     Sequence
DRB1_0405   58  VALVLSGGPASVYAD  LVLSGGPAS        0.3984        671.5              50.00     Sequence
DRB1_0405   59  ALVLSGGPASVYADG  LVLSGGPAS        0.3984        671.6              50.00     Sequence
DRB1_0405  426  DSIVREELTAAGLDN  IVREELTAA        0.3981        673.3              50.00     Sequence
DRB1_0405  134  QPVWMSHGDAVTAAP  VWMSHGDAV        0.3981        673.7              50.00     Sequence
DRB1_0405  131  PEVQPVWMSHGDAVT  VWMSHGDAV        0.3978        676.0              50.00     Sequence
DRB1_0405  508  RVVLDITSKPPATIE  VVLDITSKP        0.3965        685.1              50.00     Sequence
DRB1_0405  438  LDNQIWQCPVVLLAD  NQIWQCPVV        0.3965        685.3              50.00     Sequence
DRB1_0405  383  RAVGRELGLPEEIVA  GRELGLPEE        0.3962        687.2              50.00     Sequence
DRB1_0405   55  RQPVALVLSGGPASV  LVLSGGPAS        0.3961        688.2              50.00     Sequence
DRB1_0405  461  DGRTYGHPIVLRPVS  RTYGHPIVL        0.3954        693.2              50.00     Sequence
DRB1_0405  427  SIVREELTAAGLDNQ  IVREELTAA        0.3946        699.8              50.00     Sequence
DRB1_0405  253  TCVFVDHGLLRAGER  FVDHGLLRA        0.3936        706.9              50.00     Sequence
DRB1_0405  285  VDAAETFLEALSGVS  FLEALSGVS        0.3918        721.0              50.00     Sequence
DRB1_0405  254  CVFVDHGLLRAGERA  FVDHGLLRA        0.3917        721.7              50.00     Sequence
DRB1_0405  428  IVREELTAAGLDNQI  IVREELTAA        0.3916        722.5              50.00     Sequence
DRB1_0405  245  QRAIGDRLTCVFVDH  DRLTCVFVD        0.3912        725.8              50.00     Sequence
DRB1_0405  269  QVQRDFVAATGANLV  FVAATGANL        0.3908        728.8              50.00     Sequence
DRB1_0405   10  ETPARPVLVVDFGAQ  PVLVVDFGA        0.3893        740.7              50.00     Sequence
DRB1_0405  268  AQVQRDFVAATGANL  FVAATGANL        0.3872        758.1              50.00     Sequence
DRB1_0405  244  VQRAIGDRLTCVFVD  DRLTCVFVD        0.3853        773.5              50.00     Sequence
DRB1_0405  425  ADSIVREELTAAGLD  IVREELTAA        0.3850        775.6              50.00     Sequence
DRB1_0405  252  LTCVFVDHGLLRAGE  FVDHGLLRA        0.3848        777.4              50.00     Sequence
DRB1_0405  384  AVGRELGLPEEIVAR  VGRELGLPE        0.3848        778.0              50.00     Sequence
DRB1_0405  503  VAEVNRVVLDITSKP  NRVVLDITS        0.3836        787.9              50.00     Sequence
DRB1_0405  345  GGGSGTANIKSHHNV  GSGTANIKS        0.3831        792.5              50.00     Sequence
DRB1_0405   60  LVLSGGPASVYADGA  LVLSGGPAS        0.3808        812.5              50.00     Sequence
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DRB1_0405  184  TPHGQQVLSRFLHDF  GQQVLSRFL         0.3806         814.2                 50.00     Sequence
DRB1_0405  344  SGGGSGTANIKSHHN  GSGTANIKS         0.3801         818.3                 50.00     Sequence
DRB1_0405  132  EVQPVWMSHGDAVTA  VWMSHGDAV         0.3800         819.5                 50.00     Sequence
DRB1_0405  183  HTPHGQQVLSRFLHD  GQQVLSRFL         0.3797         821.4                 50.00     Sequence
DRB1_0405   73  GAPKLDPALLDLGVP  PKLDPALLD         0.3797         821.9                 50.00     Sequence
DRB1_0405  147  APDGFDVVASSAGAP  GFDVVASSA         0.3792         826.6                 50.00     Sequence
DRB1_0405  270  VQRDFVAATGANLVT  FVAATGANL         0.3780         837.2                 50.00     Sequence
DRB1_0405  130  LPEVQPVWMSHGDAV  VWMSHGDAV         0.3770         846.0                 50.00     Sequence
DRB1_0405  382  VRAVGRELGLPEEIV  VGRELGLPE         0.3753         862.3                 50.00     Sequence
DRB1_0405  187  GQQVLSRFLHDFAGL  GQQVLSRFL         0.3745         869.1                 50.00     Sequence
DRB1_0405  214  LIEQVRTQIGDGHAI  LIEQVRTQI         0.3739         874.6                 50.00     Sequence
DRB1_0405  460  GDGRTYGHPIVLRPV  RTYGHPIVL         0.3738         875.8                 50.00     Sequence
DRB1_0405   72  DGAPKLDPALLDLGV  PKLDPALLD         0.3731         882.7                 50.00     Sequence
DRB1_0405  255  VFVDHGLLRAGERAQ  FVDHGLLRA         0.3715         897.7                 50.00     Sequence
DRB1_0405   54  ARQPVALVLSGGPAS  LVLSGGPAS         0.3714         898.6                 50.00     Sequence
DRB1_0405  436  AGLDNQIWQCPVVLL  NQIWQCPVV         0.3714         898.6                 50.00     Sequence
DRB1_0405  408  IRIVGEVTAKRLDTL  IRIVGEVTA         0.3705         907.5                 50.00     Sequence
DRB1_0405  148  PDGFDVVASSAGAPV  GFDVVASSA         0.3700         913.0                 50.00     Sequence
DRB1_0405  122  LGGKLHSDLPEVQPV  KLHSDLPEV         0.3699         913.8                 50.00     Sequence
DRB1_0405   75  PKLDPALLDLGVPVL  ALLDLGVPV         0.3693         919.8                 50.00     Sequence
DRB1_0405  114  YGRTELKVLGGKLHS  YGRTELKVL         0.3693         920.0                 50.00     Sequence
DRB1_0405  113  EYGRTELKVLGGKLH  YGRTELKVL         0.3689         924.0                 50.00     Sequence
DRB1_0405  119  LKVLGGKLHSDLPEV  GGKLHSDLP         0.3683         929.9                 50.00     Sequence
DRB1_0405  123  GGKLHSDLPEVQPVW  GKLHSDLPE         0.3682         930.2                 50.00     Sequence
DRB1_0405  271  QRDFVAATGANLVTV  FVAATGANL         0.3681         931.8                 50.00     Sequence
DRB1_0405  400  PFPGPGLGIRIVGEV  GPGLGIRIV         0.3670         942.5                 50.00     Sequence
DRB1_0405  431  EELTAAGLDNQIWQC  TAAGLDNQI         0.3669         944.0                 50.00     Sequence
DRB1_0405  146  AAPDGFDVVASSAGA  DGFDVVASS         0.3655         957.9                 50.00     Sequence
DRB1_0405  121  VLGGKLHSDLPEVQP  GKLHSDLPE         0.3648         965.5                 50.00     Sequence
DRB1_0405  185  PHGQQVLSRFLHDFA  GQQVLSRFL         0.3643         970.9                 50.00     Sequence
DRB1_0405   47  ASIEEIRARQPVALV  SIEEIRARQ         0.3643         971.2                 50.00     Sequence
DRB1_0405  272  RDFVAATGANLVTVD  FVAATGANL         0.3642         972.0                 50.00     Sequence
DRB1_0405  385  VGRELGLPEEIVARQ  ELGLPEEIV         0.3642         972.2                 50.00     Sequence
DRB1_0405  120  KVLGGKLHSDLPEVQ  GGKLHSDLP         0.3634         980.6                 50.00     Sequence
DRB1_0405  430  REELTAAGLDNQIWQ  TAAGLDNQI         0.3632         982.3                 50.00     Sequence
DRB1_0405  346  GGSGTANIKSHHNVG  SGTANIKSH         0.3629         985.5                 50.00     Sequence
DRB1_0405  335  GTLYPDVVESGGGSG  GTLYPDVVE         0.3617         998.2                 50.00     Sequence
DRB1_0405  186  HGQQVLSRFLHDFAG  QVLSRFLHD         0.3617         998.4                 50.00     Sequence
DRB1_0405  375  RLLFKDEVRAVGREL  LLFKDEVRA         0.3617         998.7                 50.00     Sequence
DRB1_0405   42  VIPHTASIEEIRARQ  IPHTASIEE         0.3615        1000.5                 50.00     Sequence
DRB1_0405  472  RPVSSEDAMTADWTR  RPVSSEDAM         0.3614        1002.1                 50.00     Sequence
DRB1_0405   28  LIARRVREARVFSEV  RVREARVFS         0.3609        1007.3                 50.00     Sequence
DRB1_0405   74  APKLDPALLDLGVPV  PKLDPALLD         0.3597        1020.6                 50.00     Sequence
DRB1_0405  435  AAGLDNQIWQCPVVL  NQIWQCPVV         0.3592        1026.0                 50.00     Sequence
DRB1_0405  280  ANLVTVDAAETFLEA  NLVTVDAAE         0.3582        1037.5                 50.00     Sequence
DRB1_0405  343  ESGGGSGTANIKSHH  GSGTANIKS         0.3577        1043.2                 50.00     Sequence
DRB1_0405  414  VTAKRLDTLRHADSI  DTLRHADSI         0.3559        1063.6                 50.00     Sequence
DRB1_0405  424  HADSIVREELTAAGL  SIVREELTA         0.3525        1103.3                 50.00     Sequence
DRB1_0405  433  LTAAGLDNQIWQCPV  TAAGLDNQI         0.3518        1111.5                 50.00     Sequence
DRB1_0405   76  KLDPALLDLGVPVLG  ALLDLGVPV         0.3516        1114.4                 50.00     Sequence
DRB1_0405   85  GVPVLGICYGFQAMA  ICYGFQAMA         0.3515        1114.5                 50.00     Sequence
DRB1_0405  149  DGFDVVASSAGAPVA  GFDVVASSA         0.3513        1117.4                 50.00     Sequence
DRB1_0405  181  VMHTPHGQQVLSRFL  GQQVLSRFL         0.3509        1121.7                 50.00     Sequence
DRB1_0405   94  GFQAMAQALGGIVAH  GFQAMAQAL         0.3509        1122.0                 50.00     Sequence
DRB1_0405   71  ADGAPKLDPALLDLG  PKLDPALLD         0.3495        1139.6                 50.00     Sequence
DRB1_0405  509  VVLDITSKPPATIEW  VVLDITSKP         0.3495        1139.7                 50.00     Sequence
DRB1_0405   48  SIEEIRARQPVALVL  IRARQPVAL         0.3481        1156.3                 50.00     Sequence
DRB1_0405  182  MHTPHGQQVLSRFLH  GQQVLSRFL         0.3480        1157.5                 50.00     Sequence
DRB1_0405  251  RLTCVFVDHGLLRAG  CVFVDHGLL         0.3478        1161.2                 50.00     Sequence
DRB1_0405  112  REYGRTELKVLGGKL  YGRTELKVL         0.3476        1162.5                 50.00     Sequence
DRB1_0405  115  GRTELKVLGGKLHSD  ELKVLGGKL         0.3450        1196.8                 50.00     Sequence
DRB1_0405  293  EALSGVSAPEGKRKI  EALSGVSAP         0.3446        1200.9                 50.00     Sequence
DRB1_0405  381  EVRAVGRELGLPEEI  GRELGLPEE         0.3439        1210.7                 50.00     Sequence
DRB1_0405  429  VREELTAAGLDNQIW  EELTAAGLD         0.3427        1226.0                 50.00     Sequence
DRB1_0405   70  YADGAPKLDPALLDL  PKLDPALLD         0.3412        1246.1                 50.00     Sequence
DRB1_0405  129  DLPEVQPVWMSHGDA  PEVQPVWMS         0.3408        1251.8                 50.00     Sequence
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DRB1_0405	167	AFDRRLAGVQYHPEV	RRLAGVQYH	0.3408	1252.5	50.00	Sequence
DRB1_0405	432	ELTAAGLDNQIWQCP	TAAGLDNQI	0.3403	1258.2	50.00	Sequence
DRB1_0405	118	ELKVLGGKLHSDLPE	LKVLGGKLH	0.3401	1260.9	50.00	Sequence
DRB1_0405	111	TREYGRTELKVLGGK	YGRTELKVL	0.3376	1295.7	50.00	Sequence
DRB1_0405	9	PETPARPVLVVDFGA	PARPVLVVD	0.3375	1296.9	50.00	Sequence
DRB1_0405	52	IRARQPVALVLSGGP	RARQPVALV	0.3368	1306.9	50.00	Sequence
DRB1_0405	116	RTELKVLGGKLHSDL	ELKVLGGKL	0.3367	1308.4	50.00	Sequence
DRB1_0405	347	GSGTANIKSHHNVGG	SGTANIKSH	0.3366	1309.7	50.00	Sequence
DRB1_0405	81	LLDLGVPVLGICYGF	DLGVPVLGI	0.3361	1316.6	50.00	Sequence
DRB1_0405	117	TELKVLGGKLHSDLP	ELKVLGGKL	0.3358	1321.4	50.00	Sequence
DRB1_0405	267	RAQVQRDFVAATGAN	VQRDFVAAT	0.3358	1322.1	50.00	Sequence
DRB1_0405	459	QGDGRTYGHPIVLRP	RTYGHPIVL	0.3354	1326.7	50.00	Sequence
DRB1_0405	497	TRITNEVAEVNRVVL	TRITNEVAE	0.3346	1338.0	50.00	Sequence
DRB1_0405	422	LRHADSIVREELTAA	LRHADSIVR	0.3345	1340.8	50.00	Sequence
DRB1_0405	386	GRELGLPEEIVARQP	ELGLPEEIV	0.3342	1344.7	50.00	Sequence
DRB1_0405	502	EVAEVNRVVLDITSK	NRVVLDITS	0.3318	1380.6	50.00	Sequence
DRB1_0405	24	QYAQLIARRVREARV	YAQLIARRV	0.3311	1390.8	50.00	Sequence
DRB1_0405	206	TPANIANALIEQVRT	IANALIEQV	0.3296	1412.8	50.00	Sequence
DRB1_0405	49	IEEIRARQPVALVLS	IRARQPVAL	0.3291	1420.6	50.00	Sequence
DRB1_0405	110	GTREYGRTELKVLGG	YGRTELKVL	0.3291	1421.2	50.00	Sequence
DRB1_0405	124	GKLHSDLPEVQPVWM	KLHSDLPEV	0.3286	1429.0	50.00	Sequence
DRB1_0405	305	RKIIGRQFIRAFEGA	GRQFIRAFE	0.3282	1434.7	50.00	Sequence
DRB1_0405	50	EEIRARQPVALVLSG	RARQPVALV	0.3273	1448.5	50.00	Sequence
DRB1_0405	51	EIRARQPVALVLSGG	RARQPVALV	0.3272	1449.8	50.00	Sequence
DRB1_0405	43	IPHTASIEEIRARQP	IPHTASIEE	0.3266	1460.3	50.00	Sequence
DRB1_0405	125	KLHSDLPEVQPVWMS	KLHSDLPEV	0.3264	1462.9	50.00	Sequence
DRB1_0405	352	NIKSHHNVGGLPDDL	HHNVGGLPD	0.3254	1478.2	50.00	Sequence
DRB1_0405	69	VYADGAPKLDPALLD	PKLDPALLD	0.3251	1483.8	50.00	Sequence
DRB1_0405	145	TAAPDGFDVVASSAG	GFDVVASSA	0.3246	1492.3	50.00	Sequence
DRB1_0405	159	GAPVAAFEAFDRRLA	APVAAFEAF	0.3233	1513.0	50.00	Sequence
DRB1_0405	46	TASIEEIRARQPVAL	SIEEIRARQ	0.3224	1527.8	50.00	Sequence
DRB1_0405	137	WMSHGDAVTAAPDGF	GDAVTAAPD	0.3222	1530.5	50.00	Sequence
DRB1_0405	256	FVDHGLLRAGERAQV	FVDHGLLRA	0.3213	1545.8	50.00	Sequence
DRB1_0405	351	ANIKSHHNVGGLPDD	NIKSHHNVG	0.3211	1549.6	50.00	Sequence
DRB1_0405	53	RARQPVALVLSGGPA	RARQPVALV	0.3206	1557.3	50.00	Sequence
DRB1_0405	376	LLFKDEVRAVGRELG	LLFKDEVRA	0.3204	1561.8	50.00	Sequence
DRB1_0405	423	RHADSIVREELTAAG	SIVREELTA	0.3192	1580.7	50.00	Sequence
DRB1_0405	67	ASVYADGAPKLDPAL	YADGAPKLD	0.3189	1586.7	50.00	Sequence
DRB1_0405	25	YAQLIARRVREARVF	YAQLIARRV	0.3188	1588.1	50.00	Sequence
DRB1_0405	266	ERAQVQRDFVAATGA	VQRDFVAAT	0.3188	1588.2	50.00	Sequence
DRB1_0405	477	EDAMTADWTRVPYEV	ADWTRVPYE	0.3188	1589.0	50.00	Sequence
DRB1_0405	128	SDLPEVQPVWMSHGD	LPEVQPVWM	0.3171	1618.7	50.00	Sequence
DRB1_0405	160	APVAAFEAFDRRLAG	APVAAFEAF	0.3138	1677.3	50.00	Sequence
DRB1_0405	324	LDGKTAEFLVQGTLY	AEFLVQGTL	0.3127	1697.2	50.00	Sequence
DRB1_0405	342	VESGGGSGTANIKSH	GSGTANIKS	0.3122	1705.9	50.00	Sequence
DRB1_0405	150	GFDVVASSAGAPVAA	GFDVVASSA	0.3119	1711.4	50.00	Sequence
DRB1_0405	95	FQAMAQALGGIVAHT	MAQALGGIV	0.3113	1723.2	50.00	Sequence
DRB1_0405	261	LLRAGERAQVQRDFV	LLRAGERAQ	0.3099	1749.1	50.00	Sequence
DRB1_0405	27	QLIARRVREARVFSE	RVREARVFS	0.3084	1778.1	50.00	Sequence
DRB1_0405	260	GLLRAGERAQVQRDF	LLRAGERAQ	0.3079	1786.3	50.00	Sequence
DRB1_0405	103	GGIVAHTGTREYGRT	IVAHTGTRE	0.3069	1806.1	50.00	Sequence
DRB1_0405	265	GERAQVQRDFVAATG	RAQVQRDFV	0.3064	1816.1	50.00	Sequence
DRB1_0405	45	HTASIEEIRARQPVA	ASIEEIRAR	0.3060	1823.5	50.00	Sequence
DRB1_0405	501	NEVAEVNRVVLDITS	NRVVLDITS	0.3047	1850.9	50.00	Sequence
DRB1_0405	65	GPASVYADGAPKLDP	SVYADGAPK	0.3039	1867.1	50.00	Sequence
DRB1_0405	413	EVTAKRLDTLRHADS	KRLDTLRHA	0.3027	1890.4	50.00	Sequence
DRB1_0405	399	QPFPGPGLGIRIVGE	GPGLGIRIV	0.3023	1898.7	50.00	Sequence
DRB1_0405	82	LDLGVPVLGICYGFQ	DLGVPVLGI	0.3006	1935.0	50.00	Sequence
DRB1_0405	126	LHSDLPEVQPVWMSH	PEVQPVWMS	0.3002	1941.7	50.00	Sequence
DRB1_0405	259	HGLLRAGERAQVQRD	LLRAGERAQ	0.2999	1948.2	50.00	Sequence
DRB1_0405	66	PASVYADGAPKLDPA	SVYADGAPK	0.2999	1949.7	50.00	Sequence
DRB1_0405	359	VGGLPDDLKFTLVEP	DLKFTLVEP	0.2991	1965.4	50.00	Sequence
DRB1_0405	109	TGTREYGRTELKVLG	YGRTELKVL	0.2991	1965.4	50.00	Sequence
DRB1_0405	203	AQWTPANIANALIEQ	AQWTPANIA	0.2989	1969.6	50.00	Sequence
DRB1_0405	104	GIVAHTGTREYGRTE	IVAHTGTRE	0.2982	1984.8	50.00	Sequence
DRB1_0405	127	HSDLPEVQPVWMSHG	LPEVQPVWM	0.2982	1985.5	50.00	Sequence

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DRB1_0405  166  EAFDRRLAGVQYHPE  RRLAGVQYH       0.2978       1993.9                 50.00     Sequence
DRB1_0405  102  LGGIVAHTGTREYGR  IVAHTGTRE       0.2951       2053.7                 50.00     Sequence
DRB1_0405  281  NLVTVDAAETFLEAL  NLVTVDAAE       0.2950       2055.4                 50.00     Sequence
DRB1_0405  510  VLDITSKPPATIEWE  LDITSKPPA       0.2945       2065.5                 50.00     Sequence
DRB1_0405  348  SGTANIKSHHNVGGL  NIKSHHNVG       0.2941       2075.2                 50.00     Sequence
DRB1_0405  350  TANIKSHHNVGGLPD  NIKSHHNVG       0.2938       2082.5                 50.00     Sequence
DRB1_0405  354  KSHHNVGGLPDDLKF  HNVGGLPDD       0.2926       2108.1                 50.00     Sequence
DRB1_0405  304  KRKIIGRQFIRAFEG  IIGRQFIRA       0.2925       2112.2                 50.00     Sequence
DRB1_0405  264  AGERAQVQRDFVAAT  RAQVQRDFV       0.2922       2117.0                 50.00     Sequence
DRB1_0405   64  GGPASVYADGAPKLD  SVYADGAPK       0.2920       2123.3                 50.00     Sequence
DRB1_0405   44  PHTASIEEIRARQPV  SIEEIRARQ       0.2910       2146.8                 50.00     Sequence
DRB1_0405   68  SVYADGAPKLDPALL  SVYADGAPK       0.2898       2174.2                 50.00     Sequence
DRB1_0405  138  MSHGDAVTAAPDGFD  MSHGDAVTA       0.2887       2199.4                 50.00     Sequence
DRB1_0405  158  AGAPVAAFEAFDRRL  APVAAFEAF       0.2882       2211.5                 50.00     Sequence
DRB1_0405  353  IKSHHNVGGLPDDLK  HNVGGLPDD       0.2880       2216.6                 50.00     Sequence
DRB1_0405  476  SEDAMTADWTRVPYE  ADWTRVPYE       0.2875       2228.8                 50.00     Sequence
DRB1_0405  380  DEVRAVGRELGLPEE  EVRAVGREL       0.2867       2248.6                 50.00     Sequence
DRB1_0405  144  VTAAPDGFDVVASSA  GFDVVASSA       0.2861       2261.5                 50.00     Sequence
DRB1_0405   97  AMAQALGGIVAHTGT  MAQALGGIV       0.2853       2283.3                 50.00     Sequence
DRB1_0405  176  QYHPEVMHTPHGQQV  VMHTPHGQQ       0.2847       2297.4                 50.00     Sequence
DRB1_0405  205  WTPANIANALIEQVR  PANIANALI       0.2824       2356.2                 50.00     Sequence
DRB1_0405  458  VQGDGRTYGHPIVLR  RTYGHPIVL       0.2811       2387.3                 50.00     Sequence
DRB1_0405  313  IRAFEGAVRDVLDGK  FEGAVRDVL       0.2811       2388.2                 50.00     Sequence
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DRB1_0405  387  RELGLPEEIVARQPF  ELGLPEEIV       0.2786       2452.7                 50.00     Sequence
DRB1_0405   83  DLGVPVLGICYGFQA  DLGVPVLGI       0.2779       2473.2                 50.00     Sequence
DRB1_0405  453  VRSVGVQGDGRTYGH  VRSVGVQGD       0.2775       2482.4                 50.00     Sequence
DRB1_0405  179  PEVMHTPHGQQVLSR  VMHTPHGQQ       0.2761       2520.3                 50.00     Sequence
DRB1_0405    8  VPETPARPVLVVDFG  TPARPVLVV       0.2759       2526.6                 50.00     Sequence
DRB1_0405  101  ALGGIVAHTGTREYG  IVAHTGTRE       0.2747       2560.3                 50.00     Sequence
DRB1_0405  314  RAFEGAVRDVLDGKT  RAFEGAVRD       0.2743       2569.3                 50.00     Sequence
DRB1_0405   96  QAMAQALGGIVAHTG  MAQALGGIV       0.2737       2586.9                 50.00     Sequence
DRB1_0405  164  AFEAFDRRLAGVQYH  RRLAGVQYH       0.2733       2599.6                 50.00     Sequence
DRB1_0405  263  RAGERAQVQRDFVAA  GERAQVQRD       0.2724       2623.2                 50.00     Sequence
DRB1_0405  303  GKRKIIGRQFIRAFE  IIGRQFIRA       0.2719       2639.4                 50.00     Sequence
DRB1_0405  262  LRAGERAQVQRDFVA  GERAQVQRD       0.2703       2683.9                 50.00     Sequence
DRB1_0405  240  AAALVQRAIGDRLTC  VQRAIGDRL       0.2699       2695.7                 50.00     Sequence
DRB1_0405  165  FEAFDRRLAGVQYHP  RRLAGVQYH       0.2694       2709.9                 50.00     Sequence
DRB1_0405  355  SHHNVGGLPDDLKFT  HNVGGLPDD       0.2688       2727.7                 50.00     Sequence
DRB1_0405  204  QWTPANIANALIEQV  PANIANALI       0.2685       2738.1                 50.00     Sequence
DRB1_0405  412  GEVTAKRLDTLRHAD  TAKRLDTLR       0.2673       2772.2                 50.00     Sequence
DRB1_0405   98  MAQALGGIVAHTGTR  MAQALGGIV       0.2655       2826.0                 50.00     Sequence
DRB1_0405  180  EVMHTPHGQQVLSRF  VMHTPHGQQ       0.2634       2892.5                 50.00     Sequence
DRB1_0405  177  YHPEVMHTPHGQQVL  EVMHTPHGQ       0.2628       2910.1                 50.00     Sequence
DRB1_0405  241  AALVQRAIGDRLTCV  VQRAIGDRL       0.2621       2933.6                 50.00     Sequence
DRB1_0405  108  HTGTREYGRTELKVL  YGRTELKVL       0.2613       2958.3                 50.00     Sequence
DRB1_0405  215  IEQVRTQIGDGHAIC  IEQVRTQIG       0.2597       3009.2                 50.00     Sequence
DRB1_0405  178  HPEVMHTPHGQQVLS  VMHTPHGQQ       0.2597       3010.2                 50.00     Sequence
DRB1_0405  349  GTANIKSHHNVGGLP  NIKSHHNVG       0.2594       3019.6                 50.00     Sequence
DRB1_0405  243  LVQRAIGDRLTCVFV  VQRAIGDRL       0.2591       3031.2                 50.00     Sequence
DRB1_0405  377  LFKDEVRAVGRELGL  LFKDEVRAV       0.2587       3042.9                 50.00     Sequence
DRB1_0405   26  AQLIARRVREARVFS  RVREARVFS       0.2582       3060.1                 50.00     Sequence
DRB1_0405  356  HHNVGGLPDDLKFTL  HNVGGLPDD       0.2571       3096.0                 50.00     Sequence
DRB1_0405  258  DHGLLRAGERAQVQR  LLRAGERAQ       0.2557       3143.9                 50.00     Sequence
DRB1_0405  336  TLYPDVVESGGGSGT  TLYPDVVES       0.2555       3150.9                 50.00     Sequence
DRB1_0405  161  PVAAFEAFDRRLAGV  PVAAFEAFD       0.2542       3193.5                 50.00     Sequence
DRB1_0405  498  RITNEVAEVNRVVLD  RITNEVAEV       0.2539       3203.9                 50.00     Sequence
DRB1_0405  409  RIVGEVTAKRLDTLR  RIVGEVTAK       0.2537       3211.3                 50.00     Sequence
DRB1_0405  341  VVESGGGSGTANIKS  GGGSGTANI       0.2528       3244.0                 50.00     Sequence
DRB1_0405  242  ALVQRAIGDRLTCVF  VQRAIGDRL       0.2527       3247.4                 50.00     Sequence
DRB1_0405  323  VLDGKTAEFLVQGTL  AEFLVQGTL       0.2515       3290.7                 50.00     Sequence
DRB1_0405   84  LGVPVLGICYGFQAM  LGICYGFQA       0.2514       3293.4                 50.00     Sequence
DRB1_0405   99  AQALGGIVAHTGTRE  IVAHTGTRE       0.2510       3307.2                 50.00     Sequence
DRB1_0405  473  PVSSEDAMTADWTRV  PVSSEDAMT       0.2507       3317.9                 50.00     Sequence
DRB1_0405  388  ELGLPEEIVARQPFP  LPEEIVARQ       0.2502       3336.1                 50.00     Sequence
DRB1_0405    0  VVQPADIDVPETPAR  QPADIDVPE       0.2498       3350.8                 50.00     Sequence
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DRB1_0405    7  DVPETPARPVLVVDF  TPARPVLVV         0.2490        3380.8                  50.00     Sequence
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DRB1_0405  228  ICGLSGGVDSAVAAA  ICGLSGGVD         0.2466        3470.4                  50.00     Sequence
DRB1_0405  379  KDEVRAVGRELGLPE  EVRAVGREL         0.2448        3536.1                  50.00     Sequence
DRB1_0405  457  GVQGDGRTYGHPIVL  RTYGHPIVL         0.2445        3550.6                  50.00     Sequence
DRB1_0405  226  HAICGLSGGVDSAVA  ICGLSGGVD         0.2431        3601.7                  50.00     Sequence
DRB1_0405  282  LVTVDAAETFLEALS  LVTVDAAET         0.2428        3613.7                  50.00     Sequence
DRB1_0405    2  QPADIDVPETPARPV  DIDVPETPA         0.2428        3615.0                  50.00     Sequence
DRB1_0405  227  AICGLSGGVDSAVAA  ICGLSGGVD         0.2419        3650.2                  50.00     Sequence
DRB1_0405  411  VGEVTAKRLDTLRHA  TAKRLDTLR         0.2418        3653.9                  50.00     Sequence
DRB1_0405  257  VDHGLLRAGERAQVQ  LLRAGERAQ         0.2414        3670.3                  50.00     Sequence
DRB1_0405  157  SAGAPVAAFEAFDRR  PVAAFEAFD         0.2412        3677.2                  50.00     Sequence
DRB1_0405    1  VQPADIDVPETPARP  DIDVPETPA         0.2404        3709.2                  50.00     Sequence
DRB1_0405    5  DIDVPETPARPVLVV  DIDVPETPA         0.2395        3746.6                  50.00     Sequence
DRB1_0405  284  TVDAAETFLEALSGV  TVDAAETFL         0.2394        3749.7                  50.00     Sequence
DRB1_0405   61  VLSGGPASVYADGAP  GGPASVYAD         0.2390        3764.4                  50.00     Sequence
DRB1_0405  156  SSAGAPVAAFEAFDR  APVAAFEAF         0.2387        3778.4                  50.00     Sequence
DRB1_0405   63  SGGPASVYADGAPKL  ASVYADGAP         0.2380        3805.3                  50.00     Sequence
DRB1_0405  105  IVAHTGTREYGRTEL  IVAHTGTRE         0.2379        3809.8                  50.00     Sequence
DRB1_0405  475  SSEDAMTADWTRVPY  DAMTADWTR         0.2370        3847.4                  50.00     Sequence
DRB1_0405  315  AFEGAVRDVLDGKTA  FEGAVRDVL         0.2361        3885.4                  50.00     Sequence
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DRB1_0405  357  HNVGGLPDDLKFTLV  HNVGGLPDD         0.2359        3895.5                  50.00     Sequence
DRB1_0405  238  AVAAALVQRAIGDRL  AAALVQRAI         0.2356        3907.5                  50.00     Sequence
DRB1_0405   62  LSGGPASVYADGAPK  ASVYADGAP         0.2355        3910.3                  50.00     Sequence
DRB1_0405  389  LGLPEEIVARQPFPG  LGLPEEIVA         0.2351        3927.5                  50.00     Sequence
DRB1_0405  302  EGKRKIIGRQFIRAF  KRKIIGRQF         0.2347        3943.7                  50.00     Sequence
DRB1_0405  225  GHAICGLSGGVDSAV  ICGLSGGVD         0.2323        4051.1                  50.00     Sequence
DRB1_0405  162  VAAFEAFDRRLAGVQ  FEAFDRRLA         0.2302        4140.5                  50.00     Sequence
DRB1_0405  139  SHGDAVTAAPDGFDV  HGDAVTAAP         0.2297        4164.2                  50.00     Sequence
DRB1_0405  378  FKDEVRAVGRELGLP  EVRAVGREL         0.2289        4200.0                  50.00     Sequence
DRB1_0405  499  ITNEVAEVNRVVLDI  EVAEVNRVV         0.2289        4200.2                  50.00     Sequence
DRB1_0405  151  FDVVASSAGAPVAAF  FDVVASSAG         0.2279        4246.3                  50.00     Sequence
DRB1_0405    6  IDVPETPARPVLVVD  VPETPARPV         0.2271        4282.5                  50.00     Sequence
DRB1_0405    3  PADIDVPETPARPVL  DIDVPETPA         0.2269        4293.8                  50.00     Sequence
DRB1_0405  224  DGHAICGLSGGVDSA  ICGLSGGVD         0.2256        4354.3                  50.00     Sequence
DRB1_0405  155  ASSAGAPVAAFEAFD  GAPVAAFEA         0.2242        4418.9                  50.00     Sequence
DRB1_0405    4  ADIDVPETPARPVLV  DIDVPETPA         0.2231        4474.0                  50.00     Sequence
DRB1_0405  223  GDGHAICGLSGGVDS  ICGLSGGVD         0.2219        4533.3                  50.00     Sequence
DRB1_0405  474  VSSEDAMTADWTRVP  SSEDAMTAD         0.2200        4623.7                  50.00     Sequence
DRB1_0405  316  FEGAVRDVLDGKTAE  GAVRDVLDG         0.2200        4625.7                  50.00     Sequence
DRB1_0405  398  RQPFPGPGLGIRIVG  GPGLGIRIV         0.2197        4642.7                  50.00     Sequence
DRB1_0405  140  HGDAVTAAPDGFDVV  HGDAVTAAP         0.2177        4744.4                  50.00     Sequence
DRB1_0405  283  VTVDAAETFLEALSG  TVDAAETFL         0.2172        4770.5                  50.00     Sequence
DRB1_0405  358  NVGGLPDDLKFTLVE  DDLKFTLVE         0.2169        4781.8                  50.00     Sequence
DRB1_0405  237  SAVAAALVQRAIGDR  AAALVQRAI         0.2152        4872.3                  50.00     Sequence
DRB1_0405  390  GLPEEIVARQPFPGP  LPEEIVARQ         0.2139        4939.5                  50.00     Sequence
DRB1_0405  230  GLSGGVDSAVAAALV  LSGGVDSAV         0.2135        4964.3                  50.00     Sequence
DRB1_0405  222  IGDGHAICGLSGGVD  ICGLSGGVD         0.2117        5062.6                  50.00     Sequence
DRB1_0405  231  LSGGVDSAVAAALVQ  GVDSAVAAA         0.2112        5088.1                  50.00     Sequence
DRB1_0405  294  ALSGVSAPEGKRKII  LSGVSAPEG         0.2097        5170.5                  50.00     Sequence
DRB1_0405  410  IVGEVTAKRLDTLRH  IVGEVTAKR         0.2085        5236.2                  50.00     Sequence
DRB1_0405  394  EIVARQPFPGPGLGI  VARQPFPGP         0.2084        5245.9                  50.00     Sequence
DRB1_0405  456  VGVQGDGRTYGHPIV  DGRTYGHPI         0.2074        5304.4                  50.00     Sequence
DRB1_0405  393  EEIVARQPFPGPGLG  VARQPFPGP         0.2058        5394.7                  50.00     Sequence
DRB1_0405  391  LPEEIVARQPFPGPG  LPEEIVARQ         0.2033        5544.5                  50.00     Sequence
DRB1_0405  397  ARQPFPGPGLGIRIV  GPGLGIRIV         0.2025        5589.9                  50.00     Sequence
DRB1_0405  232  SGGVDSAVAAALVQR  GGVDSAVAA         0.2003        5727.0                  50.00     Sequence
DRB1_0405  152  DVVASSAGAPVAAFE  VVASSAGAP         0.1982        5858.9                  50.00     Sequence
DRB1_0405  392  PEEIVARQPFPGPGL  VARQPFPGP         0.1978        5884.2                  50.00     Sequence
DRB1_0405  216  EQVRTQIGDGHAICG  QVRTQIGDG         0.1973        5911.4                  50.00     Sequence
DRB1_0405  233  GGVDSAVAAALVQRA  GGVDSAVAA         0.1967        5951.2                  50.00     Sequence
DRB1_0405  236  DSAVAAALVQRAIGD  SAVAAALVQ         0.1963        5976.8                  50.00     Sequence
DRB1_0405  317  EGAVRDVLDGKTAEF  GAVRDVLDG         0.1953        6041.8                  50.00     Sequence
DRB1_0405  395  IVARQPFPGPGLGIR  VARQPFPGP         0.1934        6166.8                  50.00     Sequence
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   DRB1_0405  229  CGLSGGVDSAVAAAL  LSGGVDSAV        0.1918       6275.8               50.00     Sequence
   DRB1_0405  301  PEGKRKIIGRQFIRA  KRKIIGRQF        0.1918       6277.1               50.00     Sequence
   DRB1_0405  143  AVTAAPDGFDVVASS  DGFDVVASS        0.1880       6540.0               50.00     Sequence
   DRB1_0405  396  VARQPFPGPGLGIRI  VARQPFPGP        0.1846       6786.5               50.00     Sequence
   DRB1_0405  141  GDAVTAAPDGFDVVA  GDAVTAAPD        0.1814       7020.6               50.00     Sequence
   DRB1_0405  154  VASSAGAPVAAFEAF  VASSAGAPV        0.1789       7220.1               50.00     Sequence
   DRB1_0405  106  VAHTGTREYGRTELK  VAHTGTREY        0.1768       7381.3               50.00     Sequence
   DRB1_0405  234  GVDSAVAAALVQRAI  GVDSAVAAA        0.1750       7528.0               50.00     Sequence
   DRB1_0405  153  VVASSAGAPVAAFEA  VVASSAGAP        0.1708       7876.4               50.00     Sequence
   DRB1_0405  235  VDSAVAAALVQRAIG  SAVAAALVQ        0.1668       8224.4               50.00     Sequence
   DRB1_0405  322  DVLDGKTAEFLVQGT  DGKTAEFLV        0.1661       8288.0               50.00     Sequence
   DRB1_0405  107  AHTGTREYGRTELKV  GTREYGRTE        0.1657       8325.7               50.00     Sequence
   DRB1_0405  318  GAVRDVLDGKTAEFL  GAVRDVLDG        0.1641       8470.3               50.00     Sequence
   DRB1_0405  455  SVGVQGDGRTYGHPI  DGRTYGHPI        0.1613       8731.5               50.00     Sequence
   DRB1_0405  221  QIGDGHAICGLSGGV  DGHAICGLS        0.1613       8732.6               50.00     Sequence
   DRB1_0405  142  DAVTAAPDGFDVVAS  VTAAPDGFD        0.1594       8907.3               50.00     Sequence
   DRB1_0405  337  LYPDVVESGGGSGTA  LYPDVVESG        0.1570       9143.0               50.00     Sequence
   DRB1_0405  300  APEGKRKIIGRQFIR  RKIIGRQFI        0.1560       9247.5               50.00     Sequence
   DRB1_0405  220  TQIGDGHAICGLSGG  DGHAICGLS        0.1552       9321.0               50.00     Sequence
   DRB1_0405  340  DVVESGGGSGTANIK  GGGSGTANI        0.1552       9326.6               50.00     Sequence
   DRB1_0405  219  RTQIGDGHAICGLSG  DGHAICGLS        0.1505       9811.3               50.00     Sequence
   DRB1_0405  454  RSVGVQGDGRTYGHP  VGVQGDGRT        0.1479      10092.0               50.00     Sequence
   DRB1_0405  321  RDVLDGKTAEFLVQG  DGKTAEFLV        0.1474      10143.7               50.00     Sequence
   DRB1_0405  319  AVRDVLDGKTAEFLV  VRDVLDGKT        0.1430      10637.7               50.00     Sequence
   DRB1_0405  217  QVRTQIGDGHAICGL  QVRTQIGDG        0.1430      10646.5               50.00     Sequence
   DRB1_0405  299  SAPEGKRKIIGRQFI  RKIIGRQFI        0.1400      10997.9               50.00     Sequence
   DRB1_0405  320  VRDVLDGKTAEFLVQ  VRDVLDGKT        0.1365      11415.7               50.00     Sequence
   DRB1_0405  295  LSGVSAPEGKRKIIG  LSGVSAPEG        0.1298      12279.6               50.00     Sequence
   DRB1_0405  339  PDVVESGGGSGTANI  GGGSGTANI        0.1184      13887.4               50.00     Sequence
   DRB1_0405  218  VRTQIGDGHAICGLS  DGHAICGLS        0.1177      13996.5               50.00     Sequence
   DRB1_0405  298  VSAPEGKRKIIGRQF  KRKIIGRQF        0.1125      14796.4               50.00     Sequence
   DRB1_0405  338  YPDVVESGGGSGTAN  DVVESGGGS        0.1051      16035.6               50.00     Sequence
   DRB1_0405  297  GVSAPEGKRKIIGRQ  GKRKIIGRQ        0.0982      17277.3               50.00     Sequence
   DRB1_0405  296  SGVSAPEGKRKIIGR  EGKRKIIGR        0.0869      19533.3               50.00     Sequence
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Allele: DRB1_0405. Number of high binders 2. Number of weak binders 156. Number of peptides 511

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0701  363  PDDLKFTLVEPLRLL  FTLVEPLRL        0.9133          2.6         SB     0.30     Sequence
   DRB1_0701  362  LPDDLKFTLVEPLRL  FTLVEPLRL        0.9125          2.6         SB     0.30     Sequence
   DRB1_0701  364  DDLKFTLVEPLRLLF  FTLVEPLRL        0.9017          2.9         SB     0.40     Sequence
   DRB1_0701  365  DLKFTLVEPLRLLFK  FTLVEPLRL        0.8839          3.5         SB     0.80     Sequence
   DRB1_0701  269  QVQRDFVAATGANLV  FVAATGANL        0.8785          3.7         SB     0.80     Sequence
   DRB1_0701  306  KIIGRQFIRAFEGAV  FIRAFEGAV        0.8754          3.8         SB     0.80     Sequence
   DRB1_0701  366  LKFTLVEPLRLLFKD  FTLVEPLRL        0.8700          4.1         SB     1.00     Sequence
   DRB1_0701  270  VQRDFVAATGANLVT  FVAATGANL        0.8652          4.3         SB     2.00     Sequence
   DRB1_0701  307  IIGRQFIRAFEGAVR  FIRAFEGAV        0.8616          4.5         SB     2.00     Sequence
   DRB1_0701  268  AQVQRDFVAATGANL  FVAATGANL        0.8532          4.9         SB     2.00     Sequence
   DRB1_0701  271  QRDFVAATGANLVTV  FVAATGANL        0.8510          5.0         SB     2.00     Sequence
   DRB1_0701  367  KFTLVEPLRLLFKDE  FTLVEPLRL        0.8468          5.2         SB     2.00     Sequence
   DRB1_0701  308  IGRQFIRAFEGAVRD  FIRAFEGAV        0.8400          5.6         SB     2.00     Sequence
   DRB1_0701  272  RDFVAATGANLVTVD  FVAATGANL        0.8316          6.2         SB     2.00     Sequence
   DRB1_0701  485  TRVPYEVLERISTRI  VLERISTRI        0.8287          6.4         SB     4.00     Sequence
   DRB1_0701  486  RVPYEVLERISTRIT  VLERISTRI        0.8286          6.4         SB     4.00     Sequence
   DRB1_0701  310  RQFIRAFEGAVRDVL  FIRAFEGAV        0.8236          6.7         SB     4.00     Sequence
   DRB1_0701  309  GRQFIRAFEGAVRDV  FIRAFEGAV        0.8215          6.9         SB     4.00     Sequence
   DRB1_0701  368  FTLVEPLRLLFKDEV  FTLVEPLRL        0.8203          7.0         SB     4.00     Sequence
   DRB1_0701  181  VMHTPHGQQVLSRFL  GQQVLSRFL        0.8095          7.9         SB     4.00     Sequence
   DRB1_0701  273  DFVAATGANLVTVDA  FVAATGANL        0.8094          7.9         SB     4.00     Sequence
   DRB1_0701  487  VPYEVLERISTRITN  VLERISTRI        0.7992          8.8         SB     4.00     Sequence
   DRB1_0701  311  QFIRAFEGAVRDVLD  FIRAFEGAV        0.7963          9.1         SB     4.00     Sequence
   DRB1_0701  507  NRVVLDITSKPPATI  ITSKPPATI        0.7913          9.6         SB     4.00     Sequence
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DRB1_0701  274  FVAATGANLVTVDAA  FVAATGANL       0.7897         9.7         SB     4.00     Sequence
DRB1_0701  444  QCPVVLLADVRSVGV  LADVRSVGV       0.7797        10.8         SB     4.00     Sequence
DRB1_0701  182  MHTPHGQQVLSRFLH  GQQVLSRFL       0.7770        11.2         SB     4.00     Sequence
DRB1_0701  312  FIRAFEGAVRDVLDG  FIRAFEGAV       0.7661        12.6         SB     8.00     Sequence
DRB1_0701  416  AKRLDTLRHADSIVR  LRHADSIVR       0.7651        12.7         SB     8.00     Sequence
DRB1_0701  508  RVVLDITSKPPATIE  ITSKPPATI       0.7649        12.7         SB     8.00     Sequence
DRB1_0701  488  PYEVLERISTRITNE  VLERISTRI       0.7562        14.0         SB     8.00     Sequence
DRB1_0701  489  YEVLERISTRITNEV  VLERISTRI       0.7476        15.3         SB     8.00     Sequence
DRB1_0701  445  CPVVLLADVRSVGVQ  LADVRSVGV       0.7464        15.6         SB     8.00     Sequence
DRB1_0701  417  KRLDTLRHADSIVRE  LRHADSIVR       0.7401        16.6         SB     8.00     Sequence
DRB1_0701  405  GLGIRIVGEVTAKRL  VGEVTAKRL       0.7366        17.3         SB     8.00     Sequence
DRB1_0701  509  VVLDITSKPPATIEW  ITSKPPATI       0.7357        17.5         SB     8.00     Sequence
DRB1_0701  490  EVLERISTRITNEVA  VLERISTRI       0.7131        22.3         SB     8.00     Sequence
DRB1_0701  183  HTPHGQQVLSRFLHD  GQQVLSRFL       0.7090        23.3         SB     8.00     Sequence
DRB1_0701  446  PVVLLADVRSVGVQG  LADVRSVGV       0.7087        23.4         SB     8.00     Sequence
DRB1_0701  418  RLDTLRHADSIVREE  LRHADSIVR       0.7081        23.5         SB     8.00     Sequence
DRB1_0701  184  TPHGQQVLSRFLHDF  GQQVLSRFL       0.7070        23.8         SB     8.00     Sequence
DRB1_0701  478  DAMTADWTRVPYEVL  WTRVPYEVL       0.7045        24.5         SB    16.00     Sequence
DRB1_0701  238  AVAAALVQRAIGDRL  VQRAIGDRL       0.6992        25.9         SB    16.00     Sequence
DRB1_0701   19  VDFGAQYAQLIARRV  YAQLIARRV       0.6982        26.2         SB    16.00     Sequence
DRB1_0701  406  LGIRIVGEVTAKRLD  VGEVTAKRL       0.6970        26.5         SB    16.00     Sequence
DRB1_0701  510  VLDITSKPPATIEWE  ITSKPPATI       0.6926        27.8         SB    16.00     Sequence
DRB1_0701   15  PVLVVDFGAQYAQLI  FGAQYAQLI       0.6873        29.5         SB    16.00     Sequence
DRB1_0701  442  IWQCPVVLLADVRSV  VLLADVRSV       0.6871        29.5         SB    16.00     Sequence
DRB1_0701  185  PHGQQVLSRFLHDFA  GQQVLSRFL       0.6864        29.8         SB    16.00     Sequence
DRB1_0701  360  GGLPDDLKFTLVEPL  LKFTLVEPL       0.6857        30.0         SB    16.00     Sequence
DRB1_0701   29  IARRVREARVFSEVI  EARVFSEVI       0.6842        30.5         SB    16.00     Sequence
DRB1_0701  491  VLERISTRITNEVAE  VLERISTRI       0.6841        30.5         SB    16.00     Sequence
DRB1_0701  419  LDTLRHADSIVREEL  LRHADSIVR       0.6827        31.0         SB    16.00     Sequence
DRB1_0701  230  GLSGGVDSAVAAALV  VDSAVAAAL       0.6813        31.5         SB    16.00     Sequence
DRB1_0701  375  RLLFKDEVRAVGREL  EVRAVGREL       0.6792        32.2         SB    16.00     Sequence
DRB1_0701  479  AMTADWTRVPYEVLE  WTRVPYEVL       0.6773        32.9         SB    16.00     Sequence
DRB1_0701   48  SIEEIRARQPVALVL  ARQPVALVL       0.6737        34.1         SB    16.00     Sequence
DRB1_0701  229  CGLSGGVDSAVAAAL  VDSAVAAAL       0.6688        36.0         SB    16.00     Sequence
DRB1_0701   20  DFGAQYAQLIARRVR  YAQLIARRV       0.6662        37.0         SB    16.00     Sequence
DRB1_0701  239  VAAALVQRAIGDRLT  VQRAIGDRL       0.6658        37.2         SB    16.00     Sequence
DRB1_0701  447  VVLLADVRSVGVQGD  LADVRSVGV       0.6658        37.2         SB    16.00     Sequence
DRB1_0701   16  VLVVDFGAQYAQLIA  FGAQYAQLI       0.6607        39.3         SB    16.00     Sequence
DRB1_0701  186  HGQQVLSRFLHDFAG  GQQVLSRFL       0.6587        40.2         SB    16.00     Sequence
DRB1_0701  420  DTLRHADSIVREELT  LRHADSIVR       0.6584        40.3         SB    16.00     Sequence
DRB1_0701  231  LSGGVDSAVAAALVQ  VDSAVAAAL       0.6511        43.6         SB    16.00     Sequence
DRB1_0701  408  IRIVGEVTAKRLDTL  VGEVTAKRL       0.6508        43.7         SB    16.00     Sequence
DRB1_0701  407  GIRIVGEVTAKRLDT  VGEVTAKRL       0.6486        44.8         SB    16.00     Sequence
DRB1_0701  443  WQCPVVLLADVRSVG  VLLADVRSV       0.6418        48.2         SB    16.00     Sequence
DRB1_0701  448  VLLADVRSVGVQGDG  LADVRSVGV       0.6401        49.1         SB    16.00     Sequence
DRB1_0701   30  ARRVREARVFSEVIP  EARVFSEVI       0.6399        49.2         SB    16.00     Sequence
DRB1_0701  376  LLFKDEVRAVGRELG  EVRAVGREL       0.6390        49.7         SB    16.00     Sequence
DRB1_0701  285  VDAAETFLEALSGVS  FLEALSGVS       0.6370        50.8         WB    16.00     Sequence
DRB1_0701  278  TGANLVTVDAAETFL  TVDAAETFL       0.6369        50.9         WB    16.00     Sequence
DRB1_0701  421  TLRHADSIVREELTA  LRHADSIVR       0.6368        50.9         WB    16.00     Sequence
DRB1_0701   24  QYAQLIARRVREARV  ARRVREARV       0.6366        51.0         WB    16.00     Sequence
DRB1_0701   49  IEEIRARQPVALVLS  ARQPVALVL       0.6319        53.7         WB    16.00     Sequence
DRB1_0701  361  GLPDDLKFTLVEPLR  LKFTLVEPL       0.6287        55.5         WB    16.00     Sequence
DRB1_0701  480  MTADWTRVPYEVLER  WTRVPYEVL       0.6279        56.0         WB    16.00     Sequence
DRB1_0701   25  YAQLIARRVREARVF  ARRVREARV       0.6278        56.1         WB    16.00     Sequence
DRB1_0701  187  GQQVLSRFLHDFAGL  GQQVLSRFL       0.6266        56.8         WB    16.00     Sequence
DRB1_0701  148  PDGFDVVASSAGAPV  VASSAGAPV       0.6245        58.1         WB    16.00     Sequence
DRB1_0701  240  AAALVQRAIGDRLTC  VQRAIGDRL       0.6237        58.6         WB    16.00     Sequence
DRB1_0701  286  DAAETFLEALSGVSA  FLEALSGVS       0.6221        59.7         WB    16.00     Sequence
DRB1_0701   21  FGAQYAQLIARRVRE  YAQLIARRV       0.6219        59.8         WB    16.00     Sequence
DRB1_0701   17  LVVDFGAQYAQLIAR  FGAQYAQLI       0.6215        60.1         WB    16.00     Sequence
DRB1_0701  409  RIVGEVTAKRLDTLR  VGEVTAKRL       0.6175        62.7         WB    16.00     Sequence
DRB1_0701  243  LVQRAIGDRLTCVFV  VQRAIGDRL       0.6080        69.5         WB    16.00     Sequence
DRB1_0701  275  VAATGANLVTVDAAE  VAATGANLV       0.6038        72.7         WB    16.00     Sequence
DRB1_0701  377  LFKDEVRAVGRELGL  EVRAVGREL       0.6034        73.1         WB    16.00     Sequence
DRB1_0701  149  DGFDVVASSAGAPVA  VASSAGAPV       0.6018        74.3         WB    16.00     Sequence
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DRB1_0701    4  ADIDVPETPARPVLV  ETPARPVLV        0.6002        75.6        WB    32.00     Sequence
DRB1_0701  242  ALVQRAIGDRLTCVF  VQRAIGDRL        0.5991        76.5        WB    32.00     Sequence
DRB1_0701  232  SGGVDSAVAAALVQR  VDSAVAAAL        0.5975        77.8        WB    32.00     Sequence
DRB1_0701  188  QQVLSRFLHDFAGLG  FLHDFAGLG        0.5958        79.3        WB    32.00     Sequence
DRB1_0701  279  GANLVTVDAAETFLE  TVDAAETFL        0.5911        83.4        WB    32.00     Sequence
DRB1_0701  100  QALGGIVAHTGTREY  VAHTGTREY        0.5909        83.6        WB    32.00     Sequence
DRB1_0701  241  AALVQRAIGDRLTCV  VQRAIGDRL        0.5900        84.5        WB    32.00     Sequence
DRB1_0701  289  ETFLEALSGVSAPEG  FLEALSGVS        0.5886        85.7        WB    32.00     Sequence
DRB1_0701  287  AAETFLEALSGVSAP  FLEALSGVS        0.5858        88.3        WB    32.00     Sequence
DRB1_0701  422  LRHADSIVREELTAA  LRHADSIVR        0.5854        88.7        WB    32.00     Sequence
DRB1_0701  481  TADWTRVPYEVLERI  WTRVPYEVL        0.5840        90.1        WB    32.00     Sequence
DRB1_0701   50  EEIRARQPVALVLSG  ARQPVALVL        0.5822        91.9        WB    32.00     Sequence
DRB1_0701   26  AQLIARRVREARVFS  ARRVREARV        0.5786        95.5        WB    32.00     Sequence
DRB1_0701   46  TASIEEIRARQPVAL  IRARQPVAL        0.5779        96.3        WB    32.00     Sequence
DRB1_0701   18  VVDFGAQYAQLIARR  FGAQYAQLI        0.5730       101.5        WB    32.00     Sequence
DRB1_0701  410  IVGEVTAKRLDTLRH  VGEVTAKRL        0.5722       102.4        WB    32.00     Sequence
DRB1_0701  177  YHPEVMHTPHGQQVL  MHTPHGQQV        0.5711       103.6        WB    32.00     Sequence
DRB1_0701   92  CYGFQAMAQALGGIV  MAQALGGIV        0.5692       105.7        WB    32.00     Sequence
DRB1_0701  189  QVLSRFLHDFAGLGA  FLHDFAGLG        0.5666       108.8        WB    32.00     Sequence
DRB1_0701   31  RRVREARVFSEVIPH  EARVFSEVI        0.5653       110.3        WB    32.00     Sequence
DRB1_0701    5  DIDVPETPARPVLVV  ETPARPVLV        0.5642       111.7        WB    32.00     Sequence
DRB1_0701   47  ASIEEIRARQPVALV  IRARQPVAL        0.5640       111.9        WB    32.00     Sequence
DRB1_0701  244  VQRAIGDRLTCVFVD  VQRAIGDRL        0.5633       112.7        WB    32.00     Sequence
DRB1_0701  233  GGVDSAVAAALVQRA  VDSAVAAAL        0.5628       113.3        WB    32.00     Sequence
DRB1_0701  150  GFDVVASSAGAPVAA  VASSAGAPV        0.5624       113.8        WB    32.00     Sequence
DRB1_0701  482  ADWTRVPYEVLERIS  WTRVPYEVL        0.5623       114.0        WB    32.00     Sequence
DRB1_0701  248  IGDRLTCVFVDHGLL  CVFVDHGLL        0.5621       114.3        WB    32.00     Sequence
DRB1_0701  290  TFLEALSGVSAPEGK  FLEALSGVS        0.5611       115.4        WB    32.00     Sequence
DRB1_0701  277  ATGANLVTVDAAETF  LVTVDAAET        0.5520       127.4        WB    32.00     Sequence
DRB1_0701   27  QLIARRVREARVFSE  ARRVREARV        0.5519       127.6        WB    32.00     Sequence
DRB1_0701  449  LLADVRSVGVQGDGR  LADVRSVGV        0.5518       127.6        WB    32.00     Sequence
DRB1_0701  280  ANLVTVDAAETFLEA  TVDAAETFL        0.5517       127.8        WB    32.00     Sequence
DRB1_0701   22  GAQYAQLIARRVREA  LIARRVREA        0.5493       131.2        WB    32.00     Sequence
DRB1_0701  288  AETFLEALSGVSAPE  FLEALSGVS        0.5475       133.7        WB    32.00     Sequence
DRB1_0701  415  TAKRLDTLRHADSIV  TLRHADSIV        0.5467       135.0        WB    32.00     Sequence
DRB1_0701  108  HTGTREYGRTELKVL  YGRTELKVL        0.5457       136.4        WB    32.00     Sequence
DRB1_0701  176  QYHPEVMHTPHGQQV  MHTPHGQQV        0.5416       142.6        WB    32.00     Sequence
DRB1_0701  101  ALGGIVAHTGTREYG  VAHTGTREY        0.5380       148.3        WB    32.00     Sequence
DRB1_0701   93  YGFQAMAQALGGIVA  MAQALGGIV        0.5370       149.9        WB    32.00     Sequence
DRB1_0701  234  GVDSAVAAALVQRAI  VDSAVAAAL        0.5345       153.9        WB    32.00     Sequence
DRB1_0701  178  HPEVMHTPHGQQVLS  MHTPHGQQV        0.5339       154.9        WB    32.00     Sequence
DRB1_0701  378  FKDEVRAVGRELGLP  EVRAVGREL        0.5314       159.2        WB    32.00     Sequence
DRB1_0701  192  SRFLHDFAGLGAQWT  FLHDFAGLG        0.5310       159.9        WB    32.00     Sequence
DRB1_0701   33  VREARVFSEVIPHTA  EARVFSEVI        0.5310       160.0        WB    32.00     Sequence
DRB1_0701  483  DWTRVPYEVLERIST  WTRVPYEVL        0.5283       164.7        WB    32.00     Sequence
DRB1_0701  276  AATGANLVTVDAAET  LVTVDAAET        0.5273       166.5        WB    32.00     Sequence
DRB1_0701  318  GAVRDVLDGKTAEFL  LDGKTAEFL        0.5261       168.7        WB    32.00     Sequence
DRB1_0701  190  VLSRFLHDFAGLGAQ  FLHDFAGLG        0.5258       169.1        WB    32.00     Sequence
DRB1_0701   51  EIRARQPVALVLSGG  IRARQPVAL        0.5245       171.5        WB    32.00     Sequence
DRB1_0701  291  FLEALSGVSAPEGKR  FLEALSGVS        0.5238       172.8        WB    32.00     Sequence
DRB1_0701  151  FDVVASSAGAPVAAF  VASSAGAPV        0.5238       172.8        WB    32.00     Sequence
DRB1_0701  411  VGEVTAKRLDTLRHA  VGEVTAKRL        0.5224       175.5        WB    32.00     Sequence
DRB1_0701  281  NLVTVDAAETFLEAL  TVDAAETFL        0.5154       189.3        WB    32.00     Sequence
DRB1_0701  450  LADVRSVGVQGDGRT  LADVRSVGV        0.5148       190.6        WB    32.00     Sequence
DRB1_0701  249  GDRLTCVFVDHGLLR  CVFVDHGLL        0.5127       194.9        WB    32.00     Sequence
DRB1_0701    6  IDVPETPARPVLVVD  ETPARPVLV        0.5122       195.9        WB    32.00     Sequence
DRB1_0701   28  LIARRVREARVFSEV  ARRVREARV        0.5122       196.0        WB    32.00     Sequence
DRB1_0701   23  AQYAQLIARRVREAR  YAQLIARRV        0.5101       200.4        WB    32.00     Sequence
DRB1_0701  319  AVRDVLDGKTAEFLV  LDGKTAEFL        0.5066       208.2        WB    32.00     Sequence
DRB1_0701  131  PEVQPVWMSHGDAVT  WMSHGDAVT        0.5056       210.4        WB    32.00     Sequence
DRB1_0701  235  VDSAVAAALVQRAIG  VDSAVAAAL        0.5036       215.1        WB    32.00     Sequence
DRB1_0701    2  QPADIDVPETPARPV  VPETPARPV        0.4957       234.2        WB    32.00     Sequence
DRB1_0701   94  GFQAMAQALGGIVAH  MAQALGGIV        0.4953       235.2        WB    32.00     Sequence
DRB1_0701   32  RVREARVFSEVIPHT  EARVFSEVI        0.4931       240.8        WB    32.00     Sequence
DRB1_0701  109  TGTREYGRTELKVLG  YGRTELKVL        0.4923       242.9        WB    32.00     Sequence
DRB1_0701  132  EVQPVWMSHGDAVTA  WMSHGDAVT        0.4923       243.0        WB    32.00     Sequence
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DRB1_0701  484  WTRVPYEVLERISTR  WTRVPYEVL        0.4917        244.5         WB    32.00      Sequence
DRB1_0701  179  PEVMHTPHGQQVLSR  MHTPHGQQV        0.4912        246.0         WB    32.00      Sequence
DRB1_0701  193  RFLHDFAGLGAQWTP  FLHDFAGLG        0.4910        246.5         WB    32.00      Sequence
DRB1_0701  102  LGGIVAHTGTREYGR  VAHTGTREY        0.4904        248.0         WB    32.00      Sequence
DRB1_0701   34  REARVFSEVIPHTAS  EARVFSEVI        0.4864        259.0         WB    32.00      Sequence
DRB1_0701  497  TRITNEVAEVNRVVL  VAEVNRVVL        0.4844        264.7         WB    32.00      Sequence
DRB1_0701  282  LVTVDAAETFLEALS  TVDAAETFL        0.4834        267.7         WB    32.00      Sequence
DRB1_0701  250  DRLTCVFVDHGLLRA  CVFVDHGLL        0.4827        269.5         WB    32.00      Sequence
DRB1_0701  402  PGPGLGIRIVGEVTA  IRIVGEVTA        0.4817        272.5         WB    32.00      Sequence
DRB1_0701  379  KDEVRAVGRELGLPE  EVRAVGREL        0.4798        278.4         WB    32.00      Sequence
DRB1_0701   52  IRARQPVALVLSGGP  ARQPVALVL        0.4797        278.6         WB    32.00      Sequence
DRB1_0701  191  LSRFLHDFAGLGAQW  FLHDFAGLG        0.4752        292.3         WB    32.00      Sequence
DRB1_0701  112  REYGRTELKVLGGKL  YGRTELKVL        0.4732        298.9         WB    32.00      Sequence
DRB1_0701   89  LGICYGFQAMAQALG  GFQAMAQAL        0.4717        303.8         WB    32.00      Sequence
DRB1_0701  180  EVMHTPHGQQVLSRF  MHTPHGQQV        0.4713        305.1         WB    32.00      Sequence
DRB1_0701    7  DVPETPARPVLVVDF  VPETPARPV        0.4699        309.6         WB    32.00      Sequence
DRB1_0701  369  TLVEPLRLLFKDEVR  LRLLFKDEV        0.4664        321.7         WB    32.00      Sequence
DRB1_0701  320  VRDVLDGKTAEFLVQ  LDGKTAEFL        0.4644        328.8         WB    32.00      Sequence
DRB1_0701  147  APDGFDVVASSAGAP  FDVVASSAG        0.4631        333.5         WB    32.00      Sequence
DRB1_0701    3  PADIDVPETPARPVL  VPETPARPV        0.4611        340.4         WB    32.00      Sequence
DRB1_0701  113  EYGRTELKVLGGKLH  YGRTELKVL        0.4602        344.1         WB    32.00      Sequence
DRB1_0701  145  TAAPDGFDVVASSAG  FDVVASSAG        0.4593        347.2         WB    32.00      Sequence
DRB1_0701  492  LERISTRITNEVAEV  ISTRITNEV        0.4587        349.6         WB    32.00      Sequence
DRB1_0701  197  DFAGLGAQWTPANIA  AQWTPANIA        0.4583        351.0         WB    32.00      Sequence
DRB1_0701   98  MAQALGGIVAHTGTR  MAQALGGIV        0.4527        373.2         WB    50.00      Sequence
DRB1_0701  152  DVVASSAGAPVAAFE  VASSAGAPV        0.4515        378.1         WB    50.00      Sequence
DRB1_0701  133  VQPVWMSHGDAVTAA  WMSHGDAVT        0.4503        382.8         WB    50.00      Sequence
DRB1_0701   56  QPVALVLSGGPASVY  LSGGPASVY        0.4501        383.5         WB    50.00      Sequence
DRB1_0701  158  AGAPVAAFEAFDRRL  AFEAFDRRL        0.4500        384.2         WB    50.00      Sequence
DRB1_0701   35  EARVFSEVIPHTASI  EARVFSEVI        0.4465        398.8         WB    50.00      Sequence
DRB1_0701  103  GGIVAHTGTREYGRT  VAHTGTREY        0.4462        400.3         WB    50.00      Sequence
DRB1_0701  194  FLHDFAGLGAQWTPA  FLHDFAGLG        0.4460        401.1         WB    50.00      Sequence
DRB1_0701   95  FQAMAQALGGIVAHT  MAQALGGIV        0.4448        406.4         WB    50.00      Sequence
DRB1_0701  498  RITNEVAEVNRVVLD  VAEVNRVVL        0.4394        430.8         WB    50.00      Sequence
DRB1_0701  175  VQYHPEVMHTPHGQQ  VMHTPHGQQ        0.4379        437.8         WB    50.00      Sequence
DRB1_0701  380  DEVRAVGRELGLPEE  EVRAVGREL        0.4366        444.0         WB    50.00      Sequence
DRB1_0701  153  VVASSAGAPVAAFEA  VASSAGAPV        0.4365        444.5         WB    50.00      Sequence
DRB1_0701    8  VPETPARPVLVVDFG  VPETPARPV        0.4365        444.6         WB    50.00      Sequence
DRB1_0701  146  AAPDGFDVVASSAGA  FDVVASSAG        0.4337        458.4         WB    50.00      Sequence
DRB1_0701  110  GTREYGRTELKVLGG  YGRTELKVL        0.4322        465.5         WB    50.00      Sequence
DRB1_0701   36  ARVFSEVIPHTASIE  VIPHTASIE        0.4315        469.3         WB    50.00      Sequence
DRB1_0701  159  GAPVAAFEAFDRRLA  AFEAFDRRL        0.4275        489.9         WB    50.00      Sequence
DRB1_0701  198  FAGLGAQWTPANIAN  AQWTPANIA        0.4234        511.9               50.00      Sequence
DRB1_0701   88  VLGICYGFQAMAQAL  GFQAMAQAL        0.4228        515.3               50.00      Sequence
DRB1_0701  321  RDVLDGKTAEFLVQG  LDGKTAEFL        0.4224        517.9               50.00      Sequence
DRB1_0701  104  GIVAHTGTREYGRTE  VAHTGTREY        0.4209        526.2               50.00      Sequence
DRB1_0701  403  GPGLGIRIVGEVTAK  IRIVGEVTA        0.4181        542.6               50.00      Sequence
DRB1_0701  499  ITNEVAEVNRVVLDI  VAEVNRVVL        0.4180        542.7               50.00      Sequence
DRB1_0701   37  RVFSEVIPHTASIEE  FSEVIPHTA        0.4174        546.8               50.00      Sequence
DRB1_0701   57  PVALVLSGGPASVYA  LSGGPASVY        0.4165        551.8               50.00      Sequence
DRB1_0701  299  SAPEGKRKIIGRQFI  RKIIGRQFI        0.4130        573.5               50.00      Sequence
DRB1_0701  251  RLTCVFVDHGLLRAG  CVFVDHGLL        0.4124        576.7               50.00      Sequence
DRB1_0701  114  YGRTELKVLGGKLHS  YGRTELKVL        0.4089        599.5               50.00      Sequence
DRB1_0701   96  QAMAQALGGIVAHTG  MAQALGGIV        0.4069        612.2               50.00      Sequence
DRB1_0701   99  AQALGGIVAHTGTRE  IVAHTGTRE        0.4054        622.5               50.00      Sequence
DRB1_0701   90  GICYGFQAMAQALGG  GFQAMAQAL        0.4052        623.9               50.00      Sequence
DRB1_0701  500  TNEVAEVNRVVLDIT  VAEVNRVVL        0.4048        626.1               50.00      Sequence
DRB1_0701  381  EVRAVGRELGLPEEI  EVRAVGREL        0.4009        653.0               50.00      Sequence
DRB1_0701  436  AGLDNQIWQCPVVLL  IWQCPVVLL        0.3990        666.7               50.00      Sequence
DRB1_0701  134  QPVWMSHGDAVTAAP  WMSHGDAVT        0.3962        687.5               50.00      Sequence
DRB1_0701  322  DVLDGKTAEFLVQGT  LDGKTAEFL        0.3915        723.5               50.00      Sequence
DRB1_0701   38  VFSEVIPHTASIEEI  VIPHTASIE        0.3886        746.4               50.00      Sequence
DRB1_0701  154  VASSAGAPVAAFEAF  VASSAGAPV        0.3879        751.9               50.00      Sequence
DRB1_0701   63  SGGPASVYADGAPKL  VYADGAPKL        0.3875        755.5               50.00      Sequence
DRB1_0701  323  VLDGKTAEFLVQGTL  LDGKTAEFL        0.3873        757.0               50.00      Sequence
DRB1_0701  105  IVAHTGTREYGRTEL  VAHTGTREY        0.3872        757.6               50.00      Sequence
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DRB1_0701	437	GLDNQIWQCPVVLLA	IWQCPVVLL	0.3861	767.0	50.00	Sequence
DRB1_0701	283	VTVDAAETFLEALSG	TVDAAETFL	0.3831	791.7	50.00	Sequence
DRB1_0701	97	AMAQALGGIVAHTGT	MAQALGGIV	0.3829	793.8	50.00	Sequence
DRB1_0701	493	ERISTRITNEVAEVN	ISTRITNEV	0.3818	803.4	50.00	Sequence
DRB1_0701	468	PIVLRPVSSEDAMTA	VSSEDAMTA	0.3806	813.9	50.00	Sequence
DRB1_0701	91	ICYGFQAMAQALGGI	GFQAMAQAL	0.3796	822.3	50.00	Sequence
DRB1_0701	465	YGHPIVLRPVSSEDA	LRPVSSEDA	0.3793	825.5	50.00	Sequence
DRB1_0701	496	STRITNEVAEVNRVV	EVAEVNRVV	0.3784	833.1	50.00	Sequence
DRB1_0701	58	VALVLSGGPASVYAD	LSGGPASVY	0.3781	836.6	50.00	Sequence
DRB1_0701	201	LGAQWTPANIANALI	AQWTPANIA	0.3768	847.7	50.00	Sequence
DRB1_0701	404	PGLGIRIVGEVTAKR	IRIVGEVTA	0.3746	868.2	50.00	Sequence
DRB1_0701	111	TREYGRTELKVLGGK	YGRTELKVL	0.3734	879.6	50.00	Sequence
DRB1_0701	501	NEVAEVNRVVLDITS	VAEVNRVVL	0.3728	886.0	50.00	Sequence
DRB1_0701	300	APEGKRKIIGRQFIR	RKIIGRQFI	0.3725	888.1	50.00	Sequence
DRB1_0701	135	PVWMSHGDAVTAAPD	WMSHGDAVT	0.3705	908.0	50.00	Sequence
DRB1_0701	457	GVQGDGRTYGHPIVL	GRTYGHPIV	0.3684	928.2	50.00	Sequence
DRB1_0701	64	GGPASVYADGAPKLD	VYADGAPKL	0.3664	949.0	50.00	Sequence
DRB1_0701	199	AGLGAQWTPANIANA	AQWTPANIA	0.3640	973.5	50.00	Sequence
DRB1_0701	252	LTCVFVDHGLLRAGE	CVFVDHGLL	0.3633	981.4	50.00	Sequence
DRB1_0701	160	APVAAFEAFDRRLAG	AFEAFDRRL	0.3608	1008.0	50.00	Sequence
DRB1_0701	55	RQPVALVLSGGPASV	VLSGGPASV	0.3601	1015.6	50.00	Sequence
DRB1_0701	370	LVEPLRLLFKDEVRA	LVEPLRLLF	0.3600	1017.2	50.00	Sequence
DRB1_0701	284	TVDAAETFLEALSGV	TVDAAETFL	0.3594	1023.4	50.00	Sequence
DRB1_0701	138	MSHGDAVTAAPDGFD	VTAAPDGFD	0.3591	1027.0	50.00	Sequence
DRB1_0701	53	RARQPVALVLSGGPA	ARQPVALVL	0.3558	1064.6	50.00	Sequence
DRB1_0701	75	PKLDPALLDLGVPVL	LLDLGVPVL	0.3553	1070.4	50.00	Sequence
DRB1_0701	494	RISTRITNEVAEVNR	ISTRITNEV	0.3513	1117.6	50.00	Sequence
DRB1_0701	9	PETPARPVLVVDFGA	ETPARPVLV	0.3502	1131.0	50.00	Sequence
DRB1_0701	202	GAQWTPANIANALIE	AQWTPANIA	0.3495	1139.7	50.00	Sequence
DRB1_0701	466	GHPIVLRPVSSEDAM	LRPVSSEDA	0.3463	1180.1	50.00	Sequence
DRB1_0701	469	IVLRPVSSEDAMTAD	VSSEDAMTA	0.3456	1188.8	50.00	Sequence
DRB1_0701	39	FSEVIPHTASIEEIR	VIPHTASIE	0.3443	1205.7	50.00	Sequence
DRB1_0701	209	NIANALIEQVRTQIG	LIEQVRTQI	0.3423	1232.4	50.00	Sequence
DRB1_0701	438	LDNQIWQCPVVLLAD	IWQCPVVLL	0.3403	1259.3	50.00	Sequence
DRB1_0701	137	WMSHGDAVTAAPDGF	AVTAAPDGF	0.3399	1264.2	50.00	Sequence
DRB1_0701	502	EVAEVNRVVLDITSK	VAEVNRVVL	0.3378	1293.2	50.00	Sequence
DRB1_0701	136	VWMSHGDAVTAAPDG	WMSHGDAVT	0.3376	1295.5	50.00	Sequence
DRB1_0701	54	ARQPVALVLSGGPAS	ARQPVALVL	0.3373	1300.8	50.00	Sequence
DRB1_0701	139	SHGDAVTAAPDGFDV	VTAAPDGFD	0.3371	1302.8	50.00	Sequence
DRB1_0701	464	TYGHPIVLRPVSSED	IVLRPVSSE	0.3364	1312.5	50.00	Sequence
DRB1_0701	59	ALVLSGGPASVYADG	LSGGPASVY	0.3335	1354.6	50.00	Sequence
DRB1_0701	162	VAAFEAFDRRLAGVQ	AFEAFDRRL	0.3325	1369.1	50.00	Sequence
DRB1_0701	200	GLGAQWTPANIANAL	AQWTPANIA	0.3318	1380.1	50.00	Sequence
DRB1_0701	324	LDGKTAEFLVQGTLY	LDGKTAEFL	0.3307	1396.1	50.00	Sequence
DRB1_0701	301	PEGKRKIIGRQFIRA	RKIIGRQFI	0.3306	1397.3	50.00	Sequence
DRB1_0701	253	TCVFVDHGLLRAGER	CVFVDHGLL	0.3301	1406.1	50.00	Sequence
DRB1_0701	10	ETPARPVLVVDFGAQ	ETPARPVLV	0.3292	1419.9	50.00	Sequence
DRB1_0701	304	KRKIIGRQFIRAFEG	RKIIGRQFI	0.3291	1421.5	50.00	Sequence
DRB1_0701	456	VGVQGDGRTYGHPIV	GRTYGHPIV	0.3290	1423.0	50.00	Sequence
DRB1_0701	371	VEPLRLLFKDEVRAV	LFKDEVRAV	0.3286	1428.5	50.00	Sequence
DRB1_0701	467	HPIVLRPVSSEDAMT	LRPVSSEDA	0.3268	1456.1	50.00	Sequence
DRB1_0701	106	VAHTGTREYGRTELK	VAHTGTREY	0.3261	1467.8	50.00	Sequence
DRB1_0701	495	ISTRITNEVAEVNRV	ISTRITNEV	0.3252	1481.7	50.00	Sequence
DRB1_0701	130	LPEVQPVWMSHGDAV	VWMSHGDAV	0.3242	1498.2	50.00	Sequence
DRB1_0701	164	AFEAFDRRLAGVQYH	AFEAFDRRL	0.3231	1516.7	50.00	Sequence
DRB1_0701	401	FPGPGLGIRIVGEVT	GIRIVGEVT	0.3228	1521.8	50.00	Sequence
DRB1_0701	65	GPASVYADGAPKLDP	VYADGAPKL	0.3205	1559.8	50.00	Sequence
DRB1_0701	245	QRAIGDRLTCVFVDH	GDRLTCVFV	0.3197	1572.8	50.00	Sequence
DRB1_0701	302	EGKRKIIGRQFIRAF	RKIIGRQFI	0.3188	1588.4	50.00	Sequence
DRB1_0701	161	PVAAFEAFDRRLAGV	AFEAFDRRL	0.3187	1590.4	50.00	Sequence
DRB1_0701	256	FVDHGLLRAGERAQV	LLRAGERAQ	0.3185	1593.4	50.00	Sequence
DRB1_0701	463	RTYGHPIVLRPVSSE	IVLRPVSSE	0.3183	1597.2	50.00	Sequence
DRB1_0701	208	ANIANALIEQVRTQI	LIEQVRTQI	0.3170	1619.0	50.00	Sequence
DRB1_0701	327	KTAEFLVQGTLYPDV	FLVQGTLYP	0.3170	1619.2	50.00	Sequence
DRB1_0701	168	FDRRLAGVQYHPEVM	GVQYHPEVM	0.3134	1684.7	50.00	Sequence
DRB1_0701	76	KLDPALLDLGVPVLG	LLDLGVPVL	0.3133	1684.8	50.00	Sequence

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DRB1_0701  140  HGDAVTAAPDGFDVV  VTAAPDGFD        0.3113        1723.0                 50.00      Sequence
DRB1_0701  163  AAFEAFDRRLAGVQY  AFEAFDRRL        0.3104        1739.5                 50.00      Sequence
DRB1_0701   77  LDPALLDLGVPVLGI  LLDLGVPVL        0.3090        1766.1                 50.00      Sequence
DRB1_0701   60  LVLSGGPASVYADGA  LSGGPASVY        0.3089        1767.7                 50.00      Sequence
DRB1_0701  439  DNQIWQCPVVLLADV  IWQCPVVLL        0.3071        1803.5                 50.00      Sequence
DRB1_0701  255  VFVDHGLLRAGERAQ  LLRAGERAQ        0.3070        1804.0                 50.00      Sequence
DRB1_0701  203  AQWTPANIANALIEQ  AQWTPANIA        0.3064        1816.8                 50.00      Sequence
DRB1_0701  458  VQGDGRTYGHPIVLR  GRTYGHPIV        0.3037        1870.5                 50.00      Sequence
DRB1_0701  169  DRRLAGVQYHPEVMH  GVQYHPEVM        0.3032        1879.8                 50.00      Sequence
DRB1_0701  246  RAIGDRLTCVFVDHG  GDRLTCVFV        0.3004        1938.8                 50.00      Sequence
DRB1_0701  325  DGKTAEFLVQGTLYP  FLVQGTLYP        0.2990        1967.7                 50.00      Sequence
DRB1_0701  254  CVFVDHGLLRAGERA  CVFVDHGLL        0.2985        1978.7                 50.00      Sequence
DRB1_0701  328  TAEFLVQGTLYPDVV  VQGTLYPDV        0.2961        2030.6                 50.00      Sequence
DRB1_0701  460  GDGRTYGHPIVLRPV  GHPIVLRPV        0.2947        2061.2                 50.00      Sequence
DRB1_0701  313  IRAFEGAVRDVLDGK  FEGAVRDVL        0.2938        2082.5                 50.00      Sequence
DRB1_0701  292  LEALSGVSAPEGKRK  LSGVSAPEG        0.2927        2107.4                 50.00      Sequence
DRB1_0701  305  RKIIGRQFIRAFEGA  RQFIRAFEG        0.2926        2108.8                 50.00      Sequence
DRB1_0701  116  RTELKVLGGKLHSDL  LGGKLHSDL        0.2922        2118.8                 50.00      Sequence
DRB1_0701  372  EPLRLLFKDEVRAVG  LFKDEVRAV        0.2914        2137.6                 50.00      Sequence
DRB1_0701  303  GKRKIIGRQFIRAFE  RKIIGRQFI        0.2908        2151.0                 50.00      Sequence
DRB1_0701   66  PASVYADGAPKLDPA  VYADGAPKL        0.2895        2181.8                 50.00      Sequence
DRB1_0701  314  RAFEGAVRDVLDGKT  FEGAVRDVL        0.2867        2248.0                 50.00      Sequence
DRB1_0701  210  IANALIEQVRTQIGD  LIEQVRTQI        0.2855        2277.4                 50.00      Sequence
DRB1_0701  470  VLRPVSSEDAMTADW  VSSEDAMTA        0.2847        2298.3                 50.00      Sequence
DRB1_0701   61  VLSGGPASVYADGAP  LSGGPASVY        0.2841        2312.3                 50.00      Sequence
DRB1_0701  441  QIWQCPVVLLADVRS  IWQCPVVLL        0.2823        2357.9                 50.00      Sequence
DRB1_0701   67  ASVYADGAPKLDPAL  VYADGAPKL        0.2815        2378.3                 50.00      Sequence
DRB1_0701   79  PALLDLGVPVLGICY  LLDLGVPVL        0.2784        2458.7                 50.00      Sequence
DRB1_0701  141  GDAVTAAPDGFDVVA  VTAAPDGFD        0.2766        2508.4                 50.00      Sequence
DRB1_0701  317  EGAVRDVLDGKTAEF  VLDGKTAEF        0.2757        2530.9                 50.00      Sequence
DRB1_0701  247  AIGDRLTCVFVDHGL  GDRLTCVFV        0.2746        2563.5                 50.00      Sequence
DRB1_0701   68  SVYADGAPKLDPALL  VYADGAPKL        0.2684        2741.2                 50.00      Sequence
DRB1_0701   78  DPALLDLGVPVLGIC  LLDLGVPVL        0.2675        2767.4                 50.00      Sequence
DRB1_0701  440  NQIWQCPVVLLADVR  IWQCPVVLL        0.2674        2768.5                 50.00      Sequence
DRB1_0701  326  GKTAEFLVQGTLYPD  FLVQGTLYP        0.2672        2775.6                 50.00      Sequence
DRB1_0701  257  VDHGLLRAGERAQVQ  LLRAGERAQ        0.2659        2814.7                 50.00      Sequence
DRB1_0701  329  AEFLVQGTLYPDVVE  FLVQGTLYP        0.2651        2839.8                 50.00      Sequence
DRB1_0701  459  QGDGRTYGHPIVLRP  RTYGHPIVL        0.2641        2871.1                 50.00      Sequence
DRB1_0701  389  LGLPEEIVARQPFPG  IVARQPFPG        0.2639        2877.5                 50.00      Sequence
DRB1_0701  503  VAEVNRVVLDITSKP  VAEVNRVVL        0.2628        2909.7                 50.00      Sequence
DRB1_0701  170  RRLAGVQYHPEVMHT  GVQYHPEVM        0.2618        2941.6                 50.00      Sequence
DRB1_0701  293  EALSGVSAPEGKRKI  LSGVSAPEG        0.2616        2950.9                 50.00      Sequence
DRB1_0701   69  VYADGAPKLDPALLD  VYADGAPKL        0.2611        2963.9                 50.00      Sequence
DRB1_0701   40  SEVIPHTASIEEIRA  VIPHTASIE        0.2610        2968.8                 50.00      Sequence
DRB1_0701  348  SGTANIKSHHNVGGL  IKSHHNVGG        0.2606        2983.0                 50.00      Sequence
DRB1_0701  461  DGRTYGHPIVLRPVS  GHPIVLRPV        0.2594        3020.2                 50.00      Sequence
DRB1_0701  347  GSGTANIKSHHNVGG  IKSHHNVGG        0.2591        3029.9                 50.00      Sequence
DRB1_0701  142  DAVTAAPDGFDVVAS  VTAAPDGFD        0.2576        3080.8                 50.00      Sequence
DRB1_0701  115  GRTELKVLGGKLHSD  ELKVLGGKL        0.2561        3130.5                 50.00      Sequence
DRB1_0701  373  PLRLLFKDEVRAVGR  LFKDEVRAV        0.2558        3141.6                 50.00      Sequence
DRB1_0701  315  AFEGAVRDVLDGKTA  FEGAVRDVL        0.2551        3165.2                 50.00      Sequence
DRB1_0701   45  HTASIEEIRARQPVA  EIRARQPVA        0.2539        3203.9                 50.00      Sequence
DRB1_0701  117  TELKVLGGKLHSDLP  LGGKLHSDL        0.2481        3415.0                 50.00      Sequence
DRB1_0701  504  AEVNRVVLDITSKPP  VLDITSKPP        0.2452        3520.4                 50.00      Sequence
DRB1_0701   80  ALLDLGVPVLGICYG  LLDLGVPVL        0.2451        3526.3                 50.00      Sequence
DRB1_0701  471  LRPVSSEDAMTADWT  VSSEDAMTA        0.2447        3542.5                 50.00      Sequence
DRB1_0701   62  LSGGPASVYADGAPK  LSGGPASVY        0.2446        3546.7                 50.00      Sequence
DRB1_0701    0  VVQPADIDVPETPAR  VVQPADIDV        0.2409        3689.4                 50.00      Sequence
DRB1_0701  143  AVTAAPDGFDVVASS  VTAAPDGFD        0.2397        3737.8                 50.00      Sequence
DRB1_0701  330  EFLVQGTLYPDVVES  FLVQGTLYP        0.2355        3912.3                 50.00      Sequence
DRB1_0701  294  ALSGVSAPEGKRKII  LSGVSAPEG        0.2353        3921.9                 50.00      Sequence
DRB1_0701   41  EVIPHTASIEEIRAR  VIPHTASIE        0.2310        4108.6                 50.00      Sequence
DRB1_0701  412  GEVTAKRLDTLRHAD  VTAKRLDTL        0.2309        4110.0                 50.00      Sequence
DRB1_0701  462  GRTYGHPIVLRPVSS  GHPIVLRPV        0.2296        4170.8                 50.00      Sequence
DRB1_0701  316  FEGAVRDVLDGKTAE  FEGAVRDVL        0.2288        4205.9                 50.00      Sequence
DRB1_0701  195  LHDFAGLGAQWTPAN  FAGLGAQWT        0.2285        4221.7                 50.00      Sequence
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DRB1_0701  505  EVNRVVLDITSKPPA  VLDITSKPP        0.2281        4236.6                 50.00     Sequence
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DRB1_0701  473  PVSSEDAMTADWTRV  VSSEDAMTA        0.2264        4315.2                 50.00     Sequence
DRB1_0701  211  ANALIEQVRTQIGDG  IEQVRTQIG        0.2261        4332.0                 50.00     Sequence
DRB1_0701  435  AAGLDNQIWQCPVVL  QIWQCPVVL        0.2235        4453.8                 50.00     Sequence
DRB1_0701  258  DHGLLRAGERAQVQR  LLRAGERAQ        0.2234        4459.0                 50.00     Sequence
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DRB1_0701  374  LRLLFKDEVRAVGRE  LFKDEVRAV        0.2225        4503.8                 50.00     Sequence
DRB1_0701  196  HDFAGLGAQWTPANI  FAGLGAQWT        0.2215        4549.4                 50.00     Sequence
DRB1_0701  119  LKVLGGKLHSDLPEV  KLHSDLPEV        0.2212        4567.1                 50.00     Sequence
DRB1_0701  390  GLPEEIVARQPFPGP  IVARQPFPG        0.2208        4583.6                 50.00     Sequence
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DRB1_0701  295  LSGVSAPEGKRKIIG  LSGVSAPEG        0.2153        4869.8                 50.00     Sequence
DRB1_0701  261  LLRAGERAQVQRDFV  LLRAGERAQ        0.2148        4891.7                 50.00     Sequence
DRB1_0701  331  FLVQGTLYPDVVESG  FLVQGTLYP        0.2132        4979.3                 50.00     Sequence
DRB1_0701  204  QWTPANIANALIEQV  IANALIEQV        0.2128        5000.5                 50.00     Sequence
DRB1_0701  413  EVTAKRLDTLRHADS  VTAKRLDTL        0.2102        5141.0                 50.00     Sequence
DRB1_0701   42  VIPHTASIEEIRARQ  VIPHTASIE        0.2069        5327.6                 50.00     Sequence
DRB1_0701  474  VSSEDAMTADWTRVP  VSSEDAMTA        0.2066        5348.6                 50.00     Sequence
DRB1_0701  124  GKLHSDLPEVQPVWM  LPEVQPVWM        0.2058        5393.8                 50.00     Sequence
DRB1_0701  451  ADVRSVGVQGDGRTY  GVQGDGRTY        0.2050        5438.6                 50.00     Sequence
DRB1_0701  346  GGSGTANIKSHHNVG  NIKSHHNVG        0.2036        5524.4                 50.00     Sequence
DRB1_0701  506  VNRVVLDITSKPPAT  VLDITSKPP        0.2023        5602.4                 50.00     Sequence
DRB1_0701  171  RLAGVQYHPEVMHTP  GVQYHPEVM        0.2022        5609.8                 50.00     Sequence
DRB1_0701  213  ALIEQVRTQIGDGHA  LIEQVRTQI        0.2011        5677.9                 50.00     Sequence
DRB1_0701  400  PFPGPGLGIRIVGEV  LGIRIVGEV        0.2009        5686.1                 50.00     Sequence
DRB1_0701  350  TANIKSHHNVGGLPD  IKSHHNVGG        0.2006        5708.2                 50.00     Sequence
DRB1_0701  212  NALIEQVRTQIGDGH  LIEQVRTQI        0.1975        5900.3                 50.00     Sequence
DRB1_0701  225  GHAICGLSGGVDSAV  LSGGVDSAV        0.1961        5993.3                 50.00     Sequence
DRB1_0701  155  ASSAGAPVAAFEAFD  ASSAGAPVA        0.1960        5998.0                 50.00     Sequence
DRB1_0701  260  GLLRAGERAQVQRDF  LLRAGERAQ        0.1932        6181.5                 50.00     Sequence
DRB1_0701  455  SVGVQGDGRTYGHPI  DGRTYGHPI        0.1931        6189.0                 50.00     Sequence
DRB1_0701  391  LPEEIVARQPFPGPG  IVARQPFPG        0.1920        6262.1                 50.00     Sequence
DRB1_0701  392  PEEIVARQPFPGPGL  IVARQPFPG        0.1919        6269.6                 50.00     Sequence
DRB1_0701  236  DSAVAAALVQRAIGD  DSAVAAALV        0.1908        6344.4                 50.00     Sequence
DRB1_0701  120  KVLGGKLHSDLPEVQ  KLHSDLPEV        0.1888        6482.8                 50.00     Sequence
DRB1_0701  414  VTAKRLDTLRHADSI  VTAKRLDTL        0.1882        6525.7                 50.00     Sequence
DRB1_0701  214  LIEQVRTQIGDGHAI  LIEQVRTQI        0.1853        6733.9                 50.00     Sequence
DRB1_0701   13  ARPVLVVDFGAQYAQ  VVDFGAQYA        0.1827        6929.2                 50.00     Sequence
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DRB1_0701  452  DVRSVGVQGDGRTYG  GVQGDGRTY        0.1813        7031.6                 50.00     Sequence
DRB1_0701  345  GGGSGTANIKSHHNV  ANIKSHHNV        0.1811        7045.7                 50.00     Sequence
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DRB1_0701  394  EIVARQPFPGPGLGI  IVARQPFPG        0.1782        7272.5                 50.00     Sequence
DRB1_0701  226  HAICGLSGGVDSAVA  LSGGVDSAV        0.1770        7365.9                 50.00     Sequence
DRB1_0701  205  WTPANIANALIEQVR  IANALIEQV        0.1758        7458.8                 50.00     Sequence
DRB1_0701  351  ANIKSHHNVGGLPDD  IKSHHNVGG        0.1719        7785.5                 50.00     Sequence
DRB1_0701  125  KLHSDLPEVQPVWMS  LPEVQPVWM        0.1715        7819.9                 50.00     Sequence
DRB1_0701  172  LAGVQYHPEVMHTPH  GVQYHPEVM        0.1697        7974.9                 50.00     Sequence
DRB1_0701  393  EEIVARQPFPGPGLG  IVARQPFPG        0.1696        7980.1                 50.00     Sequence
DRB1_0701  144  VTAAPDGFDVVASSA  VTAAPDGFD        0.1689        8039.2                 50.00     Sequence
DRB1_0701  382  VRAVGRELGLPEEIV  ELGLPEEIV        0.1661        8287.3                 50.00     Sequence
DRB1_0701  127  HSDLPEVQPVWMSHG  VQPVWMSHG        0.1661        8288.8                 50.00     Sequence
DRB1_0701  388  ELGLPEEIVARQPFP  EIVARQPFP        0.1652        8372.5                 50.00     Sequence
DRB1_0701  453  VRSVGVQGDGRTYGH  GVQGDGRTY        0.1613        8726.3                 50.00     Sequence
DRB1_0701   11  TPARPVLVVDFGAQY  LVVDFGAQY        0.1606        8801.1                 50.00     Sequence
DRB1_0701  237  SAVAAALVQRAIGDR  LVQRAIGDR        0.1585        8996.0                 50.00     Sequence
DRB1_0701  121  VLGGKLHSDLPEVQP  KLHSDLPEV        0.1583        9023.0                 50.00     Sequence
DRB1_0701  434  TAAGLDNQIWQCPVV  DNQIWQCPV        0.1575        9092.9                 50.00     Sequence
DRB1_0701  383  RAVGRELGLPEEIVA  ELGLPEEIV        0.1571        9133.6                 50.00     Sequence
DRB1_0701  227  AICGLSGGVDSAVAA  LSGGVDSAV        0.1571        9134.2                 50.00     Sequence
DRB1_0701  344  SGGGSGTANIKSHHN  TANIKSHHN        0.1562        9222.8                 50.00     Sequence
DRB1_0701   74  APKLDPALLDLGVPV  ALLDLGVPV        0.1538        9465.5                 50.00     Sequence
DRB1_0701  262  LRAGERAQVQRDFVA  RAQVQRDFV        0.1535        9503.8                 50.00     Sequence
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DRB1_0701	14	RPVLVVDFGAQYAQL	VVDFGAQYA	0.1517	9689.7	50.00	Sequence
DRB1_0701	433	LTAAGLDNQIWQCPV	DNQIWQCPV	0.1515	9704.8	50.00	Sequence
DRB1_0701	298	VSAPEGKRKIIGRQF	KRKIIGRQF	0.1481	10070.1	50.00	Sequence
DRB1_0701	206	TPANIANALIEQVRT	IANALIEQV	0.1473	10160.6	50.00	Sequence
DRB1_0701	173	AGVQYHPEVMHTPHG	GVQYHPEVM	0.1463	10267.4	50.00	Sequence
DRB1_0701	128	SDLPEVQPVWMSHGD	VQPVWMSHG	0.1461	10293.8	50.00	Sequence
DRB1_0701	122	LGGKLHSDLPEVQPV	KLHSDLPEV	0.1460	10305.4	50.00	Sequence
DRB1_0701	352	NIKSHHNVGGLPDDL	IKSHHNVGG	0.1457	10335.7	50.00	Sequence
DRB1_0701	222	IGDGHAICGLSGGVD	ICGLSGGVD	0.1457	10335.8	50.00	Sequence
DRB1_0701	129	DLPEVQPVWMSHGDA	VQPVWMSHG	0.1451	10399.3	50.00	Sequence
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DRB1_0701	426	DSIVREELTAAGLDN	REELTAAGL	0.1418	10777.5	50.00	Sequence
DRB1_0701	167	AFDRRLAGVQYHPEV	FDRRLAGVQ	0.1418	10784.8	50.00	Sequence
DRB1_0701	228	ICGLSGGVDSAVAAA	LSGGVDSAV	0.1413	10839.6	50.00	Sequence
DRB1_0701	341	VVESGGGSGTANIKS	GGGSGTANI	0.1411	10868.1	50.00	Sequence
DRB1_0701	340	DVVESGGGSGTANIK	GGGSGTANI	0.1397	11033.3	50.00	Sequence
DRB1_0701	266	ERAQVQRDFVAATGA	RDFVAATGA	0.1394	11067.7	50.00	Sequence
DRB1_0701	43	IPHTASIEEIRARQP	IEEIRARQP	0.1386	11159.6	50.00	Sequence
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DRB1_0701	215	IEQVRTQIGDGHAIC	IEQVRTQIG	0.1369	11365.0	50.00	Sequence
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DRB1_0701	174	GVQYHPEVMHTPHGQ	GVQYHPEVM	0.1295	12311.0	50.00	Sequence
DRB1_0701	476	SEDAMTADWTRVPYE	MTADWTRVP	0.1295	12315.3	50.00	Sequence
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DRB1_0701	107	AHTGTREYGRTELKV	EYGRTELKV	0.1258	12823.0	50.00	Sequence
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DRB1_0701	263	RAGERAQVQRDFVAA	RAQVQRDFV	0.1213	13460.0	50.00	Sequence
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DRB1_0701	297	GVSAPEGKRKIIGRQ	GVSAPEGKR	0.1199	13669.2	50.00	Sequence
DRB1_0701	224	DGHAICGLSGGVDSA	ICGLSGGVD	0.1198	13672.1	50.00	Sequence
DRB1_0701	429	VREELTAAGLDNQIW	LTAAGLDNQ	0.1197	13698.8	50.00	Sequence
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DRB1_0701	337	LYPDVVESGGGSGTA	VVESGGGSG	0.1170	14102.9	50.00	Sequence
DRB1_0701	353	IKSHHNVGGLPDDLK	IKSHHNVGG	0.1169	14112.3	50.00	Sequence
DRB1_0701	332	LVQGTLYPDVVESGG	VQGTLYPDV	0.1168	14131.3	50.00	Sequence
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DRB1_0701	126	LHSDLPEVQPVWMSH	LPEVQPVWM	0.1151	14398.8	50.00	Sequence
DRB1_0701	221	QIGDGHAICGLSGGV	AICGLSGGV	0.1141	14546.0	50.00	Sequence
DRB1_0701	217	QVRTQIGDGHAICGL	GDGHAICGL	0.1139	14585.0	50.00	Sequence
DRB1_0701	396	VARQPFPGPGLGIRI	PFPGPGLGI	0.1092	15333.3	50.00	Sequence
DRB1_0701	342	VESGGGSGTANIKSH	GGGSGTANI	0.1086	15446.2	50.00	Sequence
DRB1_0701	430	REELTAAGLDNQIWQ	LTAAGLDNQ	0.1061	15868.0	50.00	Sequence
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DRB1_0701	84	LGVPVLGICYGFQAM	GVPVLGICY	0.1023	16534.2	50.00	Sequence
DRB1_0701	218	VRTQIGDGHAICGLS	GDGHAICGL	0.1017	16633.4	50.00	Sequence
DRB1_0701	265	GERAQVQRDFVAATG	GERAQVQRD	0.1009	16775.8	50.00	Sequence
DRB1_0701	333	VQGTLYPDVVESGGG	VQGTLYPDV	0.1007	16819.6	50.00	Sequence

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   DRB1_0701  431  EELTAAGLDNQIWQC  GLDNQIWQC        0.1004      16865.4                 50.00     Sequence
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   DRB1_0701  219  RTQIGDGHAICGLSG  GDGHAICGL        0.0952      17854.6                 50.00     Sequence
   DRB1_0701  385  VGRELGLPEEIVARQ  ELGLPEEIV        0.0949      17899.9                 50.00     Sequence
   DRB1_0701  423  RHADSIVREELTAAG  ADSIVREEL        0.0935      18180.0                 50.00     Sequence
   DRB1_0701   71  ADGAPKLDPALLDLG  KLDPALLDL        0.0930      18273.0                 50.00     Sequence
   DRB1_0701   86  VPVLGICYGFQAMAQ  ICYGFQAMA        0.0908      18723.8                 50.00     Sequence
   DRB1_0701  216  EQVRTQIGDGHAICG  RTQIGDGHA        0.0884      19212.2                 50.00     Sequence
   DRB1_0701  432  ELTAAGLDNQIWQCP  GLDNQIWQC        0.0838      20183.2                 50.00     Sequence
   DRB1_0701  386  GRELGLPEEIVARQP  ELGLPEEIV        0.0803      20971.5                 50.00     Sequence
   DRB1_0701   87  PVLGICYGFQAMAQA  ICYGFQAMA        0.0800      21044.0                 50.00     Sequence
   DRB1_0701  354  KSHHNVGGLPDDLKF  GGLPDDLKF        0.0788      21307.9                 50.00     Sequence
   DRB1_0701   72  DGAPKLDPALLDLGV  KLDPALLDL        0.0782      21458.3                 50.00     Sequence
   DRB1_0701  399  QPFPGPGLGIRIVGE  PFPGPGLGI        0.0776      21586.1                 50.00     Sequence
   DRB1_0701  356  HHNVGGLPDDLKFTL  HHNVGGLPD        0.0755      22078.9                 50.00     Sequence
   DRB1_0701  355  SHHNVGGLPDDLKFT  GGLPDDLKF        0.0710      23193.8                 50.00     Sequence
   DRB1_0701  220  TQIGDGHAICGLSGG  GDGHAICGL        0.0685      23827.1                 50.00     Sequence
   DRB1_0701   73  GAPKLDPALLDLGVP  KLDPALLDL        0.0681      23929.4                 50.00     Sequence
   DRB1_0701  357  HNVGGLPDDLKFTLV  LPDDLKFTL        0.0624      25440.4                 50.00     Sequence
   DRB1_0701  358  NVGGLPDDLKFTLVE  LPDDLKFTL        0.0601      26098.1                 50.00     Sequence
   DRB1_0701  334  QGTLYPDVVESGGGS  PDVVESGGG        0.0498      29177.7                 50.00     Sequence
   DRB1_0701  359  VGGLPDDLKFTLVEP  GGLPDDLKF        0.0496      29248.2                 50.00     Sequence
   DRB1_0701    1  VQPADIDVPETPARP  IDVPETPAR        0.0434      31274.4                 50.00     Sequence
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Allele: DRB1_0701. Number of high binders 71. Number of weak binders 127. Number of peptides 511

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0802   25  YAQLIARRVREARVF  LIARRVREA        0.5981         77.4          WB     4.00     Sequence
   DRB1_0802   26  AQLIARRVREARVFS  LIARRVREA        0.5919         82.7          WB     4.00     Sequence
   DRB1_0802   27  QLIARRVREARVFSE  LIARRVREA        0.5898         84.7          WB     4.00     Sequence
   DRB1_0802  306  KIIGRQFIRAFEGAV  IIGRQFIRA        0.5895         84.9          WB     4.00     Sequence
   DRB1_0802   28  LIARRVREARVFSEV  LIARRVREA        0.5885         85.8          WB     4.00     Sequence
   DRB1_0802  307  IIGRQFIRAFEGAVR  IIGRQFIRA        0.5779         96.3          WB     4.00     Sequence
   DRB1_0802   24  QYAQLIARRVREARV  YAQLIARRV        0.5774         96.8          WB     4.00     Sequence
   DRB1_0802  305  RKIIGRQFIRAFEGA  RKIIGRQFI        0.5665        108.9          WB     4.00     Sequence
   DRB1_0802   22  GAQYAQLIARRVREA  YAQLIARRV        0.5632        112.9          WB     4.00     Sequence
   DRB1_0802  303  GKRKIIGRQFIRAFE  RKIIGRQFI        0.5618        114.6          WB     4.00     Sequence
   DRB1_0802  304  KRKIIGRQFIRAFEG  RKIIGRQFI        0.5568        120.9          WB     4.00     Sequence
   DRB1_0802   23  AQYAQLIARRVREAR  YAQLIARRV        0.5543        124.2          WB     4.00     Sequence
   DRB1_0802   21  FGAQYAQLIARRVRE  YAQLIARRV        0.5440        138.9          WB     8.00     Sequence
   DRB1_0802  302  EGKRKIIGRQFIRAF  RKIIGRQFI        0.5380        148.2          WB     8.00     Sequence
   DRB1_0802  309  GRQFIRAFEGAVRDV  FIRAFEGAV        0.5354        152.5          WB     8.00     Sequence
   DRB1_0802   20  DFGAQYAQLIARRVR  YAQLIARRV        0.5344        154.1          WB     8.00     Sequence
   DRB1_0802  164  AFEAFDRRLAGVQYH  FEAFDRRLA        0.5341        154.6          WB     8.00     Sequence
   DRB1_0802  308  IGRQFIRAFEGAVRD  GRQFIRAFE        0.5334        155.7          WB     8.00     Sequence
   DRB1_0802  301  PEGKRKIIGRQFIRA  RKIIGRQFI        0.5214        177.5          WB     8.00     Sequence
   DRB1_0802  163  AAFEAFDRRLAGVQY  FEAFDRRLA        0.5190        182.0          WB     8.00     Sequence
   DRB1_0802  300  APEGKRKIIGRQFIR  RKIIGRQFI        0.5035        215.4          WB     8.00     Sequence
   DRB1_0802  162  VAAFEAFDRRLAGVQ  FEAFDRRLA        0.4975        229.9          WB     8.00     Sequence
   DRB1_0802   19  VDFGAQYAQLIARRV  YAQLIARRV        0.4963        232.8          WB     8.00     Sequence
   DRB1_0802  165  FEAFDRRLAGVQYHP  FEAFDRRLA        0.4895        250.6          WB     8.00     Sequence
   DRB1_0802   92  CYGFQAMAQALGGIV  GFQAMAQAL        0.4844        264.6          WB    16.00     Sequence
   DRB1_0802   93  YGFQAMAQALGGIVA  GFQAMAQAL        0.4816        272.8          WB    16.00     Sequence
   DRB1_0802  299  SAPEGKRKIIGRQFI  RKIIGRQFI        0.4812        273.9          WB    16.00     Sequence
   DRB1_0802   90  GICYGFQAMAQALGG  YGFQAMAQA        0.4774        285.6          WB    16.00     Sequence
   DRB1_0802  367  KFTLVEPLRLLFKDE  KFTLVEPLR        0.4770        286.8          WB    16.00     Sequence
   DRB1_0802  462  GRTYGHPIVLRPVSS  HPIVLRPVS        0.4738        297.0          WB    16.00     Sequence
   DRB1_0802  366  LKFTLVEPLRLLFKD  KFTLVEPLR        0.4735        297.9          WB    16.00     Sequence
   DRB1_0802   91  ICYGFQAMAQALGGI  YGFQAMAQA        0.4725        301.1          WB    16.00     Sequence
   DRB1_0802  465  YGHPIVLRPVSSEDA  YGHPIVLRP        0.4686        314.1          WB    16.00     Sequence
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DRB1_0802  365  DLKFTLVEPLRLLFK  KFTLVEPLR         0.4662         322.3          WB    16.00      Sequence
DRB1_0802   29  IARRVREARVFSEVI  IARRVREAR         0.4596         346.2          WB    16.00      Sequence
DRB1_0802  464  TYGHPIVLRPVSSED  YGHPIVLRP         0.4588         349.3          WB    16.00      Sequence
DRB1_0802  114  YGRTELKVLGGKLHS  GRTELKVLG         0.4575         354.3          WB    16.00      Sequence
DRB1_0802  463  RTYGHPIVLRPVSSE  HPIVLRPVS         0.4570         356.3          WB    16.00      Sequence
DRB1_0802  310  RQFIRAFEGAVRDVL  FIRAFEGAV         0.4528         372.7          WB    16.00      Sequence
DRB1_0802  486  RVPYEVLERISTRIT  YEVLERIST         0.4526         373.6          WB    16.00      Sequence
DRB1_0802  407  GIRIVGEVTAKRLDT  GIRIVGEVT         0.4524         374.1          WB    16.00      Sequence
DRB1_0802  256  FVDHGLLRAGERAQV  LLRAGERAQ         0.4514         378.4          WB    16.00      Sequence
DRB1_0802   89  LGICYGFQAMAQALG  YGFQAMAQA         0.4508         380.7          WB    16.00      Sequence
DRB1_0802  406  LGIRIVGEVTAKRLD  GIRIVGEVT         0.4494         386.7          WB    16.00      Sequence
DRB1_0802  404  PGLGIRIVGEVTAKR  GIRIVGEVT         0.4492         387.3          WB    16.00      Sequence
DRB1_0802  487  VPYEVLERISTRITN  YEVLERIST         0.4462         400.1          WB    16.00      Sequence
DRB1_0802  461  DGRTYGHPIVLRPVS  HPIVLRPVS         0.4442         408.8          WB    16.00      Sequence
DRB1_0802  186  HGQQVLSRFLHDFAG  GQQVLSRFL         0.4415         421.1          WB    16.00      Sequence
DRB1_0802  364  DDLKFTLVEPLRLLF  KFTLVEPLR         0.4414         421.5          WB    16.00      Sequence
DRB1_0802  187  GQQVLSRFLHDFAGL  GQQVLSRFL         0.4408         424.4          WB    16.00      Sequence
DRB1_0802  403  GPGLGIRIVGEVTAK  GIRIVGEVT         0.4383         435.9          WB    16.00      Sequence
DRB1_0802  484  WTRVPYEVLERISTR  WTRVPYEVL         0.4378         438.3          WB    16.00      Sequence
DRB1_0802  185  PHGQQVLSRFLHDFA  QQVLSRFLH         0.4353         450.4          WB    16.00      Sequence
DRB1_0802  402  PGPGLGIRIVGEVTA  GIRIVGEVT         0.4350         451.9          WB    16.00      Sequence
DRB1_0802  405  GLGIRIVGEVTAKRL  GIRIVGEVT         0.4340         456.6          WB    16.00      Sequence
DRB1_0802  188  QQVLSRFLHDFAGLG  QQVLSRFLH         0.4336         458.8          WB    16.00      Sequence
DRB1_0802  488  PYEVLERISTRITNE  YEVLERIST         0.4327         463.3          WB    16.00      Sequence
DRB1_0802  113  EYGRTELKVLGGKLH  LKVLGGKLH         0.4317         468.3          WB    16.00      Sequence
DRB1_0802  161  PVAAFEAFDRRLAGV  FEAFDRRLA         0.4265         495.3          WB    16.00      Sequence
DRB1_0802  375  RLLFKDEVRAVGREL  RLLFKDEVR         0.4260         497.8          WB    16.00      Sequence
DRB1_0802  466  GHPIVLRPVSSEDAM  HPIVLRPVS         0.4240         508.7                16.00      Sequence
DRB1_0802   94  GFQAMAQALGGIVAH  FQAMAQALG         0.4198         532.4                16.00      Sequence
DRB1_0802   18  VVDFGAQYAQLIARR  FGAQYAQLI         0.4196         533.7                16.00      Sequence
DRB1_0802  115  GRTELKVLGGKLHSD  GRTELKVLG         0.4189         537.7                16.00      Sequence
DRB1_0802  416  AKRLDTLRHADSIVR  RLDTLRHAD         0.4152         560.0                16.00      Sequence
DRB1_0802  485  TRVPYEVLERISTRI  YEVLERIST         0.4148         562.3                16.00      Sequence
DRB1_0802  483  DWTRVPYEVLERIST  WTRVPYEVL         0.4137         569.1                16.00      Sequence
DRB1_0802  311  QFIRAFEGAVRDVLD  FIRAFEGAV         0.4124         577.1                16.00      Sequence
DRB1_0802  260  GLLRAGERAQVQRDF  GLLRAGERA         0.4096         594.6                32.00      Sequence
DRB1_0802  257  VDHGLLRAGERAQVQ  LLRAGERAQ         0.4095         595.5                32.00      Sequence
DRB1_0802  255  VFVDHGLLRAGERAQ  LLRAGERAQ         0.4092         597.1                32.00      Sequence
DRB1_0802  259  HGLLRAGERAQVQRD  LLRAGERAQ         0.4066         614.6                32.00      Sequence
DRB1_0802  184  TPHGQQVLSRFLHDF  GQQVLSRFL         0.4063         616.0                32.00      Sequence
DRB1_0802   49  IEEIRARQPVALVLS  EIRARQPVA         0.4050         624.8                32.00      Sequence
DRB1_0802  312  FIRAFEGAVRDVLDG  FIRAFEGAV         0.4038         633.1                32.00      Sequence
DRB1_0802  363  PDDLKFTLVEPLRLL  KFTLVEPLR         0.4037         634.1                32.00      Sequence
DRB1_0802  376  LLFKDEVRAVGRELG  LFKDEVRAV         0.4028         640.4                32.00      Sequence
DRB1_0802   31  RRVREARVFSEVIPH  RVREARVFS         0.4009         653.1                32.00      Sequence
DRB1_0802  239  VAAALVQRAIGDRLT  VAAALVQRA         0.3970         681.9                32.00      Sequence
DRB1_0802   88  VLGICYGFQAMAQAL  YGFQAMAQA         0.3964         686.0                32.00      Sequence
DRB1_0802  258  DHGLLRAGERAQVQR  LLRAGERAQ         0.3950         696.4                32.00      Sequence
DRB1_0802  112  REYGRTELKVLGGKL  GRTELKVLG         0.3939         705.1                32.00      Sequence
DRB1_0802  183  HTPHGQQVLSRFLHD  GQQVLSRFL         0.3936         707.1                32.00      Sequence
DRB1_0802  369  TLVEPLRLLFKDEVR  TLVEPLRLL         0.3932         710.1                32.00      Sequence
DRB1_0802  392  PEEIVARQPFPGPGL  EIVARQPFP         0.3926         714.6                32.00      Sequence
DRB1_0802  168  FDRRLAGVQYHPEVM  RLAGVQYHP         0.3925         715.9                32.00      Sequence
DRB1_0802  368  FTLVEPLRLLFKDEV  TLVEPLRLL         0.3914         723.9                32.00      Sequence
DRB1_0802   50  EEIRARQPVALVLSG  EIRARQPVA         0.3914         723.9                32.00      Sequence
DRB1_0802  160  APVAAFEAFDRRLAG  FEAFDRRLA         0.3904         731.7                32.00      Sequence
DRB1_0802  489  YEVLERISTRITNEV  VLERISTRI         0.3899         735.7                32.00      Sequence
DRB1_0802  460  GDGRTYGHPIVLRPV  GRTYGHPIV         0.3879         752.3                32.00      Sequence
DRB1_0802  377  LFKDEVRAVGRELGL  FKDEVRAVG         0.3869         760.0                32.00      Sequence
DRB1_0802  415  TAKRLDTLRHADSIV  RLDTLRHAD         0.3868         761.3                32.00      Sequence
DRB1_0802   30  ARRVREARVFSEVIP  RVREARVFS         0.3863         765.3                32.00      Sequence
DRB1_0802  238  AVAAALVQRAIGDRL  VAAALVQRA         0.3851         775.5                32.00      Sequence
DRB1_0802  182  MHTPHGQQVLSRFLH  GQQVLSRFL         0.3849         777.2                32.00      Sequence
DRB1_0802   17  LVVDFGAQYAQLIAR  FGAQYAQLI         0.3842         782.4                32.00      Sequence
DRB1_0802  414  VTAKRLDTLRHADSI  RLDTLRHAD         0.3821         801.0                32.00      Sequence
DRB1_0802  393  EEIVARQPFPGPGLG  EIVARQPFP         0.3818         803.6                32.00      Sequence
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DRB1_0802  374  LRLLFKDEVRAVGRE  RLLFKDEVR         0.3808         811.9                    32.00      Sequence
DRB1_0802   48  SIEEIRARQPVALVL  EIRARQPVA         0.3792         826.4                    32.00      Sequence
DRB1_0802  167  AFDRRLAGVQYHPEV  FDRRLAGVQ         0.3773         843.5                    32.00      Sequence
DRB1_0802  373  PLRLLFKDEVRAVGR  RLLFKDEVR         0.3762         853.6                    32.00      Sequence
DRB1_0802  298  VSAPEGKRKIIGRQF  GKRKIIGRQ         0.3759         856.4                    32.00      Sequence
DRB1_0802  401  FPGPGLGIRIVGEVT  GIRIVGEVT         0.3752         862.8                    32.00      Sequence
DRB1_0802  417  KRLDTLRHADSIVRE  RLDTLRHAD         0.3734         879.4                    32.00      Sequence
DRB1_0802   32  RVREARVFSEVIPHT  RVREARVFS         0.3720         893.3                    32.00      Sequence
DRB1_0802  394  EIVARQPFPGPGLGI  EIVARQPFP         0.3682         930.4                    32.00      Sequence
DRB1_0802  391  LPEEIVARQPFPGPG  EIVARQPFP         0.3677         935.6                    32.00      Sequence
DRB1_0802  159  GAPVAAFEAFDRRLA  FEAFDRRLA         0.3677         935.7                    32.00      Sequence
DRB1_0802  491  VLERISTRITNEVAE  VLERISTRI         0.3675         937.4                    32.00      Sequence
DRB1_0802   51  EIRARQPVALVLSGG  EIRARQPVA         0.3648         965.1                    32.00      Sequence
DRB1_0802  479  AMTADWTRVPYEVLE  MTADWTRVP         0.3647         966.1                    32.00      Sequence
DRB1_0802  482  ADWTRVPYEVLERIS  WTRVPYEVL         0.3636         978.0                    32.00      Sequence
DRB1_0802  413  EVTAKRLDTLRHADS  RLDTLRHAD         0.3631         983.3                    32.00      Sequence
DRB1_0802  166  EAFDRRLAGVQYHPE  RLAGVQYHP         0.3629         985.3                    32.00      Sequence
DRB1_0802  408  IRIVGEVTAKRLDTL  IRIVGEVTA         0.3622         993.1                    32.00      Sequence
DRB1_0802  254  CVFVDHGLLRAGERA  GLLRAGERA         0.3601        1016.3                    32.00      Sequence
DRB1_0802  478  DAMTADWTRVPYEVL  MTADWTRVP         0.3595        1022.8                    32.00      Sequence
DRB1_0802   47  ASIEEIRARQPVALV  EIRARQPVA         0.3581        1037.7                    32.00      Sequence
DRB1_0802   16  VLVVDFGAQYAQLIA  FGAQYAQLI         0.3581        1038.1                    32.00      Sequence
DRB1_0802  372  EPLRLLFKDEVRAVG  RLLFKDEVR         0.3581        1038.4                    32.00      Sequence
DRB1_0802  170  RRLAGVQYHPEVMHT  RLAGVQYHP         0.3580        1038.9                    32.00      Sequence
DRB1_0802  189  QVLSRFLHDFAGLGA  LSRFLHDFA         0.3534        1092.4                    32.00      Sequence
DRB1_0802  412  GEVTAKRLDTLRHAD  GEVTAKRLD         0.3528        1099.3                    32.00      Sequence
DRB1_0802  509  VVLDITSKPPATIEW  LDITSKPPA         0.3525        1102.6                    32.00      Sequence
DRB1_0802  410  IVGEVTAKRLDTLRH  IVGEVTAKR         0.3522        1106.3                    32.00      Sequence
DRB1_0802  459  QGDGRTYGHPIVLRP  GRTYGHPIV         0.3516        1113.8                    32.00      Sequence
DRB1_0802  409  RIVGEVTAKRLDTLR  IVGEVTAKR         0.3509        1122.5                    32.00      Sequence
DRB1_0802  390  GLPEEIVARQPFPGP  EIVARQPFP         0.3508        1124.1                    32.00      Sequence
DRB1_0802  411  VGEVTAKRLDTLRHA  GEVTAKRLD         0.3491        1143.8                    32.00      Sequence
DRB1_0802  467  HPIVLRPVSSEDAMT  HPIVLRPVS         0.3476        1162.9                    32.00      Sequence
DRB1_0802  490  EVLERISTRITNEVA  VLERISTRI         0.3470        1170.3                    32.00      Sequence
DRB1_0802   46  TASIEEIRARQPVAL  EIRARQPVA         0.3444        1203.6                    32.00      Sequence
DRB1_0802  480  MTADWTRVPYEVLER  MTADWTRVP         0.3443        1205.6                    32.00      Sequence
DRB1_0802  190  VLSRFLHDFAGLGAQ  LSRFLHDFA         0.3439        1210.3                    32.00      Sequence
DRB1_0802  169  DRRLAGVQYHPEVMH  RLAGVQYHP         0.3437        1212.9                    32.00      Sequence
DRB1_0802  508  RVVLDITSKPPATIE  LDITSKPPA         0.3426        1228.0                    32.00      Sequence
DRB1_0802  237  SAVAAALVQRAIGDR  VAAALVQRA         0.3394        1271.1                    32.00      Sequence
DRB1_0802  111  TREYGRTELKVLGGK  GRTELKVLG         0.3387        1281.1                    32.00      Sequence
DRB1_0802  110  GTREYGRTELKVLGG  GRTELKVLG         0.3384        1285.4                    32.00      Sequence
DRB1_0802  362  LPDDLKFTLVEPLRL  KFTLVEPLR         0.3383        1286.8                    32.00      Sequence
DRB1_0802  510  VLDITSKPPATIEWE  LDITSKPPA         0.3378        1292.6                    32.00      Sequence
DRB1_0802  171  RLAGVQYHPEVMHTP  RLAGVQYHP         0.3374        1299.2                    32.00      Sequence
DRB1_0802   87  PVLGICYGFQAMAQA  YGFQAMAQA         0.3373        1300.6                    32.00      Sequence
DRB1_0802  378  FKDEVRAVGRELGLP  FKDEVRAVG         0.3330        1362.8                    32.00      Sequence
DRB1_0802  389  LGLPEEIVARQPFPG  EIVARQPFP         0.3295        1415.0                    32.00      Sequence
DRB1_0802  194  FLHDFAGLGAQWTPA  FLHDFAGLG         0.3274        1446.8                    32.00      Sequence
DRB1_0802  330  EFLVQGTLYPDVVES  FLVQGTLYP         0.3269        1454.4                    32.00      Sequence
DRB1_0802  211  ANALIEQVRTQIGDG  ALIEQVRTQ         0.3250        1486.1                    32.00      Sequence
DRB1_0802  240  AAALVQRAIGDRLTC  AAALVQRAI         0.3238        1504.4                    32.00      Sequence
DRB1_0802  297  GVSAPEGKRKIIGRQ  GKRKIIGRQ         0.3218        1537.5                    32.00      Sequence
DRB1_0802  118  ELKVLGGKLHSDLPE  LKVLGGKLH         0.3217        1539.8                    32.00      Sequence
DRB1_0802  507  NRVVLDITSKPPATI  VLDITSKPP         0.3215        1542.6                    32.00      Sequence
DRB1_0802  261  LLRAGERAQVQRDFV  LLRAGERAQ         0.3210        1551.5                    32.00      Sequence
DRB1_0802   95  FQAMAQALGGIVAHT  FQAMAQALG         0.3201        1567.0                    32.00      Sequence
DRB1_0802  446  PVVLLADVRSVGVQG  VLLADVRSV         0.3195        1577.0                    32.00      Sequence
DRB1_0802  331  FLVQGTLYPDVVESG  FLVQGTLYP         0.3189        1587.4                    50.00      Sequence
DRB1_0802  371  VEPLRLLFKDEVRAV  LRLLFKDEV         0.3166        1626.7                    50.00      Sequence
DRB1_0802   36  ARVFSEVIPHTASIE  VFSEVIPHT         0.3157        1642.9                    50.00      Sequence
DRB1_0802  212  NALIEQVRTQIGDGH  LIEQVRTQI         0.3150        1654.6                    50.00      Sequence
DRB1_0802  447  VVLLADVRSVGVQGD  VLLADVRSV         0.3146        1662.0                    50.00      Sequence
DRB1_0802  191  LSRFLHDFAGLGAQW  LSRFLHDFA         0.3132        1687.4                    50.00      Sequence
DRB1_0802  448  VLLADVRSVGVQGDG  VLLADVRSV         0.3127        1697.3                    50.00      Sequence
DRB1_0802  370  LVEPLRLLFKDEVRA  LVEPLRLLF         0.3119        1712.1                    50.00      Sequence
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DRB1_0802  116  RTELKVLGGKLHSDL  LKVLGGKLH        0.3112       1723.6                 50.00      Sequence
DRB1_0802  326  GKTAEFLVQGTLYPD  FLVQGTLYP        0.3098       1751.5                 50.00      Sequence
DRB1_0802  119  LKVLGGKLHSDLPEV  LKVLGGKLH        0.3094       1758.0                 50.00      Sequence
DRB1_0802  418  RLDTLRHADSIVREE  RLDTLRHAD        0.3091       1765.0                 50.00      Sequence
DRB1_0802  117  TELKVLGGKLHSDLP  LKVLGGKLH        0.3083       1778.8                 50.00      Sequence
DRB1_0802  329  AEFLVQGTLYPDVVE  FLVQGTLYP        0.3067       1810.5                 50.00      Sequence
DRB1_0802  197  DFAGLGAQWTPANIA  FAGLGAQWT        0.3038       1868.5                 50.00      Sequence
DRB1_0802  314  RAFEGAVRDVLDGKT  FEGAVRDVL        0.3036       1871.3                 50.00      Sequence
DRB1_0802  381  EVRAVGRELGLPEEI  VRAVGRELG        0.3033       1878.1                 50.00      Sequence
DRB1_0802  481  TADWTRVPYEVLERI  WTRVPYEVL        0.3018       1908.3                 50.00      Sequence
DRB1_0802   35  EARVFSEVIPHTASI  VFSEVIPHT        0.3016       1913.8                 50.00      Sequence
DRB1_0802  198  FAGLGAQWTPANIAN  FAGLGAQWT        0.3013       1920.0                 50.00      Sequence
DRB1_0802  213  ALIEQVRTQIGDGHA  LIEQVRTQI        0.3012       1920.9                 50.00      Sequence
DRB1_0802   98  MAQALGGIVAHTGTR  AQALGGIVA        0.3010       1925.5                 50.00      Sequence
DRB1_0802  315  AFEGAVRDVLDGKTA  FEGAVRDVL        0.3005       1936.1                 50.00      Sequence
DRB1_0802  313  IRAFEGAVRDVLDGK  FEGAVRDVL        0.2996       1954.4                 50.00      Sequence
DRB1_0802  327  KTAEFLVQGTLYPDV  FLVQGTLYP        0.2993       1961.5                 50.00      Sequence
DRB1_0802  325  DGKTAEFLVQGTLYP  FLVQGTLYP        0.2993       1962.0                 50.00      Sequence
DRB1_0802  109  TGTREYGRTELKVLG  GRTELKVLG        0.2989       1970.6                 50.00      Sequence
DRB1_0802   37  RVFSEVIPHTASIEE  VFSEVIPHT        0.2986       1975.7                 50.00      Sequence
DRB1_0802  236  DSAVAAALVQRAIGD  VAAALVQRA        0.2981       1987.2                 50.00      Sequence
DRB1_0802   55  RQPVALVLSGGPASV  QPVALVLSG        0.2978       1994.5                 50.00      Sequence
DRB1_0802  210  IANALIEQVRTQIGD  ALIEQVRTQ        0.2964       2023.4                 50.00      Sequence
DRB1_0802  291  FLEALSGVSAPEGKR  FLEALSGVS        0.2948       2058.8                 50.00      Sequence
DRB1_0802  492  LERISTRITNEVAEV  LERISTRIT        0.2933       2092.1                 50.00      Sequence
DRB1_0802  200  GLGAQWTPANIANAL  GLGAQWTPA        0.2921       2119.7                 50.00      Sequence
DRB1_0802  181  VMHTPHGQQVLSRFL  GQQVLSRFL        0.2919       2125.1                 50.00      Sequence
DRB1_0802  380  DEVRAVGRELGLPEE  VRAVGRELG        0.2919       2125.3                 50.00      Sequence
DRB1_0802  328  TAEFLVQGTLYPDVV  FLVQGTLYP        0.2911       2144.2                 50.00      Sequence
DRB1_0802  209  NIANALIEQVRTQIG  LIEQVRTQI        0.2903       2160.9                 50.00      Sequence
DRB1_0802   45  HTASIEEIRARQPVA  EIRARQPVA        0.2899       2170.5                 50.00      Sequence
DRB1_0802  101  ALGGIVAHTGTREYG  ALGGIVAHT        0.2886       2202.0                 50.00      Sequence
DRB1_0802   86  VPVLGICYGFQAMAQ  ICYGFQAMA        0.2884       2206.3                 50.00      Sequence
DRB1_0802  196  HDFAGLGAQWTPANI  FAGLGAQWT        0.2883       2208.6                 50.00      Sequence
DRB1_0802   85  GVPVLGICYGFQAMA  LGICYGFQA        0.2883       2210.1                 50.00      Sequence
DRB1_0802  193  RFLHDFAGLGAQWTP  FLHDFAGLG        0.2869       2242.2                 50.00      Sequence
DRB1_0802  443  WQCPVVLLADVRSVG  WQCPVVLLA        0.2865       2252.7                 50.00      Sequence
DRB1_0802  458  VQGDGRTYGHPIVLR  GRTYGHPIV        0.2855       2277.5                 50.00      Sequence
DRB1_0802  192  SRFLHDFAGLGAQWT  FLHDFAGLG        0.2848       2293.6                 50.00      Sequence
DRB1_0802  235  VDSAVAAALVQRAIG  VAAALVQRA        0.2841       2312.8                 50.00      Sequence
DRB1_0802  135  PVWMSHGDAVTAAPD  WMSHGDAVT        0.2837       2320.9                 50.00      Sequence
DRB1_0802  379  KDEVRAVGRELGLPE  VRAVGRELG        0.2833       2332.4                 50.00      Sequence
DRB1_0802  199  AGLGAQWTPANIANA  GLGAQWTPA        0.2825       2352.3                 50.00      Sequence
DRB1_0802  361  GLPDDLKFTLVEPLR  KFTLVEPLR        0.2822       2361.2                 50.00      Sequence
DRB1_0802   34  REARVFSEVIPHTAS  VFSEVIPHT        0.2812       2386.5                 50.00      Sequence
DRB1_0802  457  GVQGDGRTYGHPIVL  GRTYGHPIV        0.2804       2406.0                 50.00      Sequence
DRB1_0802   99  AQALGGIVAHTGTRE  LGGIVAHTG        0.2790       2442.1                 50.00      Sequence
DRB1_0802  195  LHDFAGLGAQWTPAN  FAGLGAQWT        0.2790       2444.3                 50.00      Sequence
DRB1_0802  133  VQPVWMSHGDAVTAA  WMSHGDAVT        0.2779       2473.0                 50.00      Sequence
DRB1_0802   38  VFSEVIPHTASIEEI  VFSEVIPHT        0.2772       2491.5                 50.00      Sequence
DRB1_0802  253  TCVFVDHGLLRAGER  FVDHGLLRA        0.2750       2550.6                 50.00      Sequence
DRB1_0802  100  QALGGIVAHTGTREY  ALGGIVAHT        0.2747       2560.5                 50.00      Sequence
DRB1_0802  150  GFDVVASSAGAPVAA  FDVVASSAG        0.2745       2563.9                 50.00      Sequence
DRB1_0802   54  ARQPVALVLSGGPAS  LVLSGGPAS        0.2743       2570.4                 50.00      Sequence
DRB1_0802  437  GLDNQIWQCPVVLLA  WQCPVVLLA        0.2733       2597.5                 50.00      Sequence
DRB1_0802  131  PEVQPVWMSHGDAVT  WMSHGDAVT        0.2732       2600.8                 50.00      Sequence
DRB1_0802  506  VNRVVLDITSKPPAT  LDITSKPPA        0.2728       2613.5                 50.00      Sequence
DRB1_0802   33  VREARVFSEVIPHTA  VFSEVIPHT        0.2711       2660.4                 50.00      Sequence
DRB1_0802  438  LDNQIWQCPVVLLAD  WQCPVVLLA        0.2702       2688.5                 50.00      Sequence
DRB1_0802  442  IWQCPVVLLADVRSV  WQCPVVLLA        0.2699       2695.4                 50.00      Sequence
DRB1_0802  102  LGGIVAHTGTREYGR  LGGIVAHTG        0.2699       2696.6                 50.00      Sequence
DRB1_0802  445  CPVVLLADVRSVGVQ  VLLADVRSV        0.2697       2703.1                 50.00      Sequence
DRB1_0802  290  TFLEALSGVSAPEGK  FLEALSGVS        0.2695       2706.7                 50.00      Sequence
DRB1_0802   56  QPVALVLSGGPASVY  ALVLSGGPA        0.2686       2734.4                 50.00      Sequence
DRB1_0802  214  LIEQVRTQIGDGHAI  LIEQVRTQI        0.2683       2743.4                 50.00      Sequence
DRB1_0802  132  EVQPVWMSHGDAVTA  WMSHGDAVT        0.2674       2769.7                 50.00      Sequence
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DRB1_0802	134	QPVWMSHGDAVTAAP	WMSHGDAVT	0.2670	2782.6	50.00	Sequence
DRB1_0802	208	ANIANALIEQVRTQI	LIEQVRTQI	0.2667	2791.6	50.00	Sequence
DRB1_0802	456	VGVQGDGRTYGHPIV	GRTYGHPIV	0.2660	2813.6	50.00	Sequence
DRB1_0802	505	EVNRVVLDITSKPPA	LDITSKPPA	0.2640	2874.1	50.00	Sequence
DRB1_0802	15	PVLVVDFGAQYAQLI	FGAQYAQLI	0.2634	2893.4	50.00	Sequence
DRB1_0802	349	GTANIKSHHNVGGLP	GTANIKSHH	0.2619	2939.7	50.00	Sequence
DRB1_0802	97	AMAQALGGIVAHTGT	AQALGGIVA	0.2612	2963.4	50.00	Sequence
DRB1_0802	104	GIVAHTGTREYGRTE	GIVAHTGTR	0.2611	2966.7	50.00	Sequence
DRB1_0802	252	LTCVFVDHGLLRAGE	FVDHGLLRA	0.2603	2990.3	50.00	Sequence
DRB1_0802	502	EVAEVNRVVLDITSK	EVAEVNRVV	0.2593	3022.0	50.00	Sequence
DRB1_0802	348	SGTANIKSHHNVGGL	GTANIKSHH	0.2593	3024.2	50.00	Sequence
DRB1_0802	289	ETFLEALSGVSAPEG	FLEALSGVS	0.2592	3026.5	50.00	Sequence
DRB1_0802	136	VWMSHGDAVTAAPDG	WMSHGDAVT	0.2589	3037.3	50.00	Sequence
DRB1_0802	347	GSGTANIKSHHNVGG	GTANIKSHH	0.2589	3038.0	50.00	Sequence
DRB1_0802	149	DGFDVVASSAGAPVA	FDVVASSAG	0.2583	3055.5	50.00	Sequence
DRB1_0802	251	RLTCVFVDHGLLRAG	FVDHGLLRA	0.2577	3077.1	50.00	Sequence
DRB1_0802	241	AALVQRAIGDRLTCV	AALVQRAIG	0.2565	3117.0	50.00	Sequence
DRB1_0802	441	QIWQCPVVLLADVRS	WQCPVVLLA	0.2557	3143.9	50.00	Sequence
DRB1_0802	103	GGIVAHTGTREYGRT	GIVAHTGTR	0.2524	3258.8	50.00	Sequence
DRB1_0802	288	AETFLEALSGVSAPE	FLEALSGVS	0.2507	3317.6	50.00	Sequence
DRB1_0802	382	VRAVGRELGLPEEIV	VRAVGRELG	0.2495	3362.9	50.00	Sequence
DRB1_0802	287	AAETFLEALSGVSAP	FLEALSGVS	0.2494	3366.7	50.00	Sequence
DRB1_0802	400	PFPGPGLGIRIVGEV	GPGLGIRIV	0.2492	3372.6	50.00	Sequence
DRB1_0802	148	PDGFDVVASSAGAPV	FDVVASSAG	0.2485	3399.0	50.00	Sequence
DRB1_0802	422	LRHADSIVREELTAA	LRHADSIVR	0.2483	3407.0	50.00	Sequence
DRB1_0802	388	ELGLPEEIVARQPFP	EIVARQPFP	0.2481	3414.0	50.00	Sequence
DRB1_0802	440	NQIWQCPVVLLADVR	WQCPVVLLA	0.2479	3422.3	50.00	Sequence
DRB1_0802	137	WMSHGDAVTAAPDGF	WMSHGDAVT	0.2467	3464.8	50.00	Sequence
DRB1_0802	421	TLRHADSIVREELTA	TLRHADSIV	0.2464	3477.4	50.00	Sequence
DRB1_0802	477	EDAMTADWTRVPYEV	MTADWTRVP	0.2461	3486.5	50.00	Sequence
DRB1_0802	52	IRARQPVALVLSGGP	IRARQPVAL	0.2439	3573.7	50.00	Sequence
DRB1_0802	501	NEVAEVNRVVLDITS	EVAEVNRVV	0.2435	3588.9	50.00	Sequence
DRB1_0802	316	FEGAVRDVLDGKTAE	FEGAVRDVL	0.2430	3607.3	50.00	Sequence
DRB1_0802	57	PVALVLSGGPASVYA	LVLSGGPAS	0.2429	3610.1	50.00	Sequence
DRB1_0802	53	RARQPVALVLSGGPA	QPVALVLSG	0.2429	3611.0	50.00	Sequence
DRB1_0802	234	GVDSAVAAALVQRAI	VAAALVQRA	0.2422	3637.8	50.00	Sequence
DRB1_0802	424	HADSIVREELTAAGL	HADSIVREE	0.2417	3658.7	50.00	Sequence
DRB1_0802	267	RAQVQRDFVAATGAN	RAQVQRDFV	0.2414	3671.6	50.00	Sequence
DRB1_0802	286	DAAETFLEALSGVSA	FLEALSGVS	0.2405	3704.5	50.00	Sequence
DRB1_0802	419	LDTLRHADSIVREEL	LDTLRHADS	0.2375	3827.1	50.00	Sequence
DRB1_0802	439	DNQIWQCPVVLLADV	WQCPVVLLA	0.2369	3851.5	50.00	Sequence
DRB1_0802	444	QCPVVLLADVRSVGV	VLLADVRSV	0.2367	3862.3	50.00	Sequence
DRB1_0802	346	GGSGTANIKSHHNVG	NIKSHHNVG	0.2360	3892.3	50.00	Sequence
DRB1_0802	84	LGVPVLGICYGFQAM	LGICYGFQA	0.2353	3918.3	50.00	Sequence
DRB1_0802	96	QAMAQALGGIVAHTG	AQALGGIVA	0.2349	3937.2	50.00	Sequence
DRB1_0802	449	LLADVRSVGVQGDGR	LLADVRSVG	0.2344	3959.7	50.00	Sequence
DRB1_0802	265	GERAQVQRDFVAATG	AQVQRDFVA	0.2342	3967.2	50.00	Sequence
DRB1_0802	147	APDGFDVVASSAGAP	GFDVVASSA	0.2341	3970.7	50.00	Sequence
DRB1_0802	423	RHADSIVREELTAAG	HADSIVREE	0.2336	3994.5	50.00	Sequence
DRB1_0802	399	QPFPGPGLGIRIVGE	GPGLGIRIV	0.2323	4050.3	50.00	Sequence
DRB1_0802	266	ERAQVQRDFVAATGA	RAQVQRDFV	0.2318	4071.7	50.00	Sequence
DRB1_0802	398	RQPFPGPGLGIRIVG	GPGLGIRIV	0.2310	4105.1	50.00	Sequence
DRB1_0802	295	LSGVSAPEGKRKIIG	GVSAPEGKR	0.2308	4114.4	50.00	Sequence
DRB1_0802	503	VAEVNRVVLDITSKP	VAEVNRVVL	0.2297	4167.0	50.00	Sequence
DRB1_0802	264	AGERAQVQRDFVAAT	RAQVQRDFV	0.2288	4205.0	50.00	Sequence
DRB1_0802	420	DTLRHADSIVREELT	LRHADSIVR	0.2287	4209.1	50.00	Sequence
DRB1_0802	58	VALVLSGGPASVYAD	LVLSGGPAS	0.2281	4238.3	50.00	Sequence
DRB1_0802	233	GGVDSAVAAALVQRA	VAAALVQRA	0.2268	4297.0	50.00	Sequence
DRB1_0802	249	GDRLTCVFVDHGLLR	GDRLTCVFV	0.2256	4354.7	50.00	Sequence
DRB1_0802	296	SGVSAPEGKRKIIGR	GVSAPEGKR	0.2241	4427.6	50.00	Sequence
DRB1_0802	494	RISTRITNEVAEVNR	ISTRITNEV	0.2236	4446.9	50.00	Sequence
DRB1_0802	395	IVARQPFPGPGLGIR	IVARQPFPG	0.2234	4457.9	50.00	Sequence
DRB1_0802	250	DRLTCVFVDHGLLRA	CVFVDHGLL	0.2224	4508.6	50.00	Sequence
DRB1_0802	59	ALVLSGGPASVYADG	LVLSGGPAS	0.2222	4516.2	50.00	Sequence
DRB1_0802	269	QVQRDFVAATGANLV	QVQRDFVAA	0.2220	4524.7	50.00	Sequence
DRB1_0802	120	KVLGGKLHSDLPEVQ	KVLGGKLHS	0.2203	4611.8	50.00	Sequence

DRB1_0802	504	AEVNRVVLDITSKPP	VLDITSKPP	0.2192	4666.8	50.00	Sequence
DRB1_0802	151	FDVVASSAGAPVAAF	FDVVASSAG	0.2182	4718.3	50.00	Sequence
DRB1_0802	268	AQVQRDFVAATGANL	QVQRDFVAA	0.2175	4753.8	50.00	Sequence
DRB1_0802	177	YHPEVMHTPHGQQVL	HPEVMHTPH	0.2174	4756.7	50.00	Sequence
DRB1_0802	285	VDAAETFLEALSGVS	FLEALSGVS	0.2171	4775.4	50.00	Sequence
DRB1_0802	476	SEDAMTADWTRVPYE	MTADWTRVP	0.2154	4861.0	50.00	Sequence
DRB1_0802	397	ARQPFPGPGLGIRIV	GPGLGIRIV	0.2149	4890.6	50.00	Sequence
DRB1_0802	146	AAPDGFDVVASSAGA	FDVVASSAG	0.2141	4932.1	50.00	Sequence
DRB1_0802	178	HPEVMHTPHGQQVLS	HPEVMHTPH	0.2139	4938.8	50.00	Sequence
DRB1_0802	80	ALLDLGVPVLGICYG	ALLDLGVPV	0.2133	4973.2	50.00	Sequence
DRB1_0802	321	RDVLDGKTAEFLVQG	RDVLDGKTA	0.2131	4985.0	50.00	Sequence
DRB1_0802	292	LEALSGVSAPEGKRK	ALSGVSAPE	0.2118	5054.4	50.00	Sequence
DRB1_0802	294	ALSGVSAPEGKRKII	ALSGVSAPE	0.2117	5059.9	50.00	Sequence
DRB1_0802	207	PANIANALIEQVRTQ	IANALIEQV	0.2110	5100.7	50.00	Sequence
DRB1_0802	179	PEVMHTPHGQQVLSR	HTPHGQQVL	0.2106	5121.5	50.00	Sequence
DRB1_0802	451	ADVRSVGVQGDGRTY	DVRSVGVQG	0.2104	5130.8	50.00	Sequence
DRB1_0802	81	LLDLGVPVLGICYGF	LLDLGVPVL	0.2103	5138.4	50.00	Sequence
DRB1_0802	493	ERISTRITNEVAEVN	STRITNEVA	0.2093	5191.6	50.00	Sequence
DRB1_0802	263	RAGERAQVQRDFVAA	RAGERAQVQ	0.2091	5202.6	50.00	Sequence
DRB1_0802	500	TNEVAEVNRVVLDIT	EVAEVNRVV	0.2081	5263.4	50.00	Sequence
DRB1_0802	452	DVRSVGVQGDGRTYG	DVRSVGVQG	0.2075	5297.7	50.00	Sequence
DRB1_0802	474	VSSEDAMTADWTRVP	MTADWTRVP	0.2071	5319.0	50.00	Sequence
DRB1_0802	105	IVAHTGTREYGRTEL	IVAHTGTRE	0.2069	5332.0	50.00	Sequence
DRB1_0802	425	ADSIVREELTAAGLD	ADSIVREEL	0.2067	5344.1	50.00	Sequence
DRB1_0802	44	PHTASIEEIRARQPV	HTASIEEIR	0.2062	5371.5	50.00	Sequence
DRB1_0802	324	LDGKTAEFLVQGTLY	KTAEFLVQG	0.2061	5377.9	50.00	Sequence
DRB1_0802	248	IGDRLTCVFVDHGLL	GDRLTCVFV	0.2059	5386.1	50.00	Sequence
DRB1_0802	243	LVQRAIGDRLTCVFV	VQRAIGDRL	0.2051	5438.0	50.00	Sequence
DRB1_0802	262	LRAGERAQVQRDFVA	LRAGERAQV	0.2043	5480.0	50.00	Sequence
DRB1_0802	176	QYHPEVMHTPHGQQV	YHPEVMHTP	0.2032	5548.0	50.00	Sequence
DRB1_0802	495	ISTRITNEVAEVNRV	ISTRITNEV	0.2031	5553.7	50.00	Sequence
DRB1_0802	205	WTPANIANALIEQVR	WTPANIANA	0.2030	5560.7	50.00	Sequence
DRB1_0802	201	LGAQWTPANIANALI	LGAQWTPAN	0.2025	5593.1	50.00	Sequence
DRB1_0802	79	PALLDLGVPVLGICY	ALLDLGVPV	0.2002	5728.2	50.00	Sequence
DRB1_0802	108	HTGTREYGRTELKVL	YGRTELKVL	0.1999	5751.5	50.00	Sequence
DRB1_0802	130	LPEVQPVWMSHGDAV	PEVQPVWMS	0.1974	5904.3	50.00	Sequence
DRB1_0802	475	SSEDAMTADWTRVPY	MTADWTRVP	0.1973	5914.8	50.00	Sequence
DRB1_0802	244	VQRAIGDRLTCVFVD	GDRLTCVFV	0.1968	5947.2	50.00	Sequence
DRB1_0802	172	LAGVQYHPEVMHTPH	AGVQYHPEV	0.1963	5981.1	50.00	Sequence
DRB1_0802	180	EVMHTPHGQQVLSRF	HTPHGQQVL	0.1956	6024.5	50.00	Sequence
DRB1_0802	204	QWTPANIANALIEQV	WTPANIANA	0.1954	6036.5	50.00	Sequence
DRB1_0802	293	EALSGVSAPEGKRKI	ALSGVSAPE	0.1953	6045.1	50.00	Sequence
DRB1_0802	14	RPVLVVDFGAQYAQL	LVVDFGAQY	0.1942	6113.0	50.00	Sequence
DRB1_0802	215	IEQVRTQIGDGHAIC	IEQVRTQIG	0.1939	6132.9	50.00	Sequence
DRB1_0802	106	VAHTGTREYGRTELK	VAHTGTREY	0.1937	6145.9	50.00	Sequence
DRB1_0802	173	AGVQYHPEVMHTPHG	AGVQYHPEV	0.1933	6172.9	50.00	Sequence
DRB1_0802	497	TRITNEVAEVNRVVL	EVAEVNRVV	0.1931	6185.7	50.00	Sequence
DRB1_0802	125	KLHSDLPEVQPVWMS	KLHSDLPEV	0.1924	6236.6	50.00	Sequence
DRB1_0802	39	FSEVIPHTASIEEIR	FSEVIPHTA	0.1912	6314.6	50.00	Sequence
DRB1_0802	498	RITNEVAEVNRVVLD	EVAEVNRVV	0.1909	6340.2	50.00	Sequence
DRB1_0802	129	DLPEVQPVWMSHGDA	PEVQPVWMS	0.1909	6340.7	50.00	Sequence
DRB1_0802	274	FVAATGANLVTVDAA	FVAATGANL	0.1901	6393.6	50.00	Sequence
DRB1_0802	426	DSIVREELTAAGLDN	SIVREELTA	0.1888	6486.2	50.00	Sequence
DRB1_0802	68	SVYADGAPKLDPALL	SVYADGAPK	0.1885	6506.0	50.00	Sequence
DRB1_0802	145	TAAPDGFDVVASSAG	FDVVASSAG	0.1883	6520.9	50.00	Sequence
DRB1_0802	107	AHTGTREYGRTELKV	AHTGTREYG	0.1873	6587.7	50.00	Sequence
DRB1_0802	158	AGAPVAAFEAFDRRL	AFEAFDRRL	0.1872	6599.9	50.00	Sequence
DRB1_0802	123	GGKLHSDLPEVQPVW	GGKLHSDLP	0.1871	6604.2	50.00	Sequence
DRB1_0802	345	GGGSGTANIKSHHNV	GSGTANIKS	0.1867	6632.1	50.00	Sequence
DRB1_0802	436	AGLDNQIWQCPVVLL	LDNQIWQCP	0.1867	6634.2	50.00	Sequence
DRB1_0802	350	TANIKSHHNVGGLPD	ANIKSHHNV	0.1847	6774.5	50.00	Sequence
DRB1_0802	127	HSDLPEVQPVWMSHG	PEVQPVWMS	0.1842	6812.9	50.00	Sequence
DRB1_0802	175	VQYHPEVMHTPHGQQ	YHPEVMHTP	0.1840	6829.6	50.00	Sequence
DRB1_0802	83	DLGVPVLGICYGFQA	GVPVLGICY	0.1839	6836.1	50.00	Sequence
DRB1_0802	320	VRDVLDGKTAEFLVQ	RDVLDGKTA	0.1839	6836.4	50.00	Sequence
DRB1_0802	318	GAVRDVLDGKTAEFL	RDVLDGKTA	0.1837	6854.9	50.00	Sequence

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DRB1_0802  273  DFVAATGANLVTVDA  FVAATGANL        0.1836       6856.1                  50.00     Sequence
DRB1_0802  232  SGGVDSAVAAALVQR  GVDSAVAAA        0.1834       6874.5                  50.00     Sequence
DRB1_0802  450  LADVRSVGVQGDGRT  DVRSVGVQG        0.1834       6875.5                  50.00     Sequence
DRB1_0802  272  RDFVAATGANLVTVD  FVAATGANL        0.1833       6878.7                  50.00     Sequence
DRB1_0802  454  RSVGVQGDGRTYGHP  GVQGDGRTY        0.1826       6936.1                  50.00     Sequence
DRB1_0802  323  VLDGKTAEFLVQGTL  GKTAEFLVQ        0.1826       6936.6                  50.00     Sequence
DRB1_0802  351  ANIKSHHNVGGLPDD  ANIKSHHNV        0.1824       6951.1                  50.00     Sequence
DRB1_0802  496  STRITNEVAEVNRVV  STRITNEVA        0.1822       6966.6                  50.00     Sequence
DRB1_0802   60  LVLSGGPASVYADGA  LVLSGGPAS        0.1821       6971.4                  50.00     Sequence
DRB1_0802  203  AQWTPANIANALIEQ  WTPANIANA        0.1820       6977.7                  50.00     Sequence
DRB1_0802   43  IPHTASIEEIRARQP  HTASIEEIR        0.1810       7054.7                  50.00     Sequence
DRB1_0802   67  ASVYADGAPKLDPAL  VYADGAPKL        0.1789       7218.2                  50.00     Sequence
DRB1_0802  247  AIGDRLTCVFVDHGL  GDRLTCVFV        0.1788       7222.2                  50.00     Sequence
DRB1_0802  499  ITNEVAEVNRVVLDI  EVAEVNRVV        0.1782       7269.4                  50.00     Sequence
DRB1_0802  435  AAGLDNQIWQCPVVL  QIWQCPVVL        0.1781       7276.1                  50.00     Sequence
DRB1_0802  124  GKLHSDLPEVQPVWM  KLHSDLPEV        0.1770       7368.3                  50.00     Sequence
DRB1_0802  276  AATGANLVTVDAAET  LVTVDAAET        0.1768       7380.5                  50.00     Sequence
DRB1_0802    8  VPETPARPVLVVDFG  PETPARPVL        0.1752       7514.8                  50.00     Sequence
DRB1_0802  206  TPANIANALIEQVRT  IANALIEQV        0.1749       7532.2                  50.00     Sequence
DRB1_0802  122  LGGKLHSDLPEVQPV  GGKLHSDLP        0.1749       7537.2                  50.00     Sequence
DRB1_0802  455  SVGVQGDGRTYGHPI  GVQGDGRTY        0.1746       7564.0                  50.00     Sequence
DRB1_0802  202  GAQWTPANIANALIE  WTPANIANA        0.1745       7568.7                  50.00     Sequence
DRB1_0802  322  DVLDGKTAEFLVQGT  GKTAEFLVQ        0.1731       7680.9                  50.00     Sequence
DRB1_0802  121  VLGGKLHSDLPEVQP  GGKLHSDLP        0.1722       7757.4                  50.00     Sequence
DRB1_0802  468  PIVLRPVSSEDAMTA  PIVLRPVSS        0.1703       7916.1                  50.00     Sequence
DRB1_0802   13  ARPVLVVDFGAQYAQ  LVVDFGAQY        0.1694       7995.7                  50.00     Sequence
DRB1_0802  270  VQRDFVAATGANLVT  FVAATGANL        0.1686       8070.4                  50.00     Sequence
DRB1_0802  219  RTQIGDGHAICGLSG  RTQIGDGHA        0.1681       8114.0                  50.00     Sequence
DRB1_0802  225  GHAICGLSGGVDSAV  GHAICGLSG        0.1680       8118.5                  50.00     Sequence
DRB1_0802  246  RAIGDRLTCVFVDHG  GDRLTCVFV        0.1680       8121.0                  50.00     Sequence
DRB1_0802  128  SDLPEVQPVWMSHGD  PEVQPVWMS        0.1675       8159.9                  50.00     Sequence
DRB1_0802  427  SIVREELTAAGLDNQ  SIVREELTA        0.1674       8173.5                  50.00     Sequence
DRB1_0802  453  VRSVGVQGDGRTYGH  GVQGDGRTY        0.1671       8203.1                  50.00     Sequence
DRB1_0802  271  QRDFVAATGANLVTV  FVAATGANL        0.1670       8209.9                  50.00     Sequence
DRB1_0802  317  EGAVRDVLDGKTAEF  RDVLDGKTA        0.1669       8220.1                  50.00     Sequence
DRB1_0802    6  IDVPETPARPVLVVD  IDVPETPAR        0.1662       8280.0                  50.00     Sequence
DRB1_0802   82  LDLGVPVLGICYGFQ  LDLGVPVLG        0.1657       8325.6                  50.00     Sequence
DRB1_0802  138  MSHGDAVTAAPDGFD  HGDAVTAAP        0.1654       8355.8                  50.00     Sequence
DRB1_0802  319  AVRDVLDGKTAEFLV  RDVLDGKTA        0.1641       8465.9                  50.00     Sequence
DRB1_0802  245  QRAIGDRLTCVFVDH  QRAIGDRLT        0.1639       8488.7                  50.00     Sequence
DRB1_0802  230  GLSGGVDSAVAAALV  GVDSAVAAA        0.1631       8557.9                  50.00     Sequence
DRB1_0802    9  PETPARPVLVVDFGA  PETPARPVL        0.1621       8650.6                  50.00     Sequence
DRB1_0802  384  AVGRELGLPEEIVAR  AVGRELGLP        0.1618       8679.1                  50.00     Sequence
DRB1_0802    7  DVPETPARPVLVVDF  PETPARPVL        0.1615       8713.1                  50.00     Sequence
DRB1_0802  242  ALVQRAIGDRLTCVF  LVQRAIGDR        0.1613       8731.9                  50.00     Sequence
DRB1_0802  396  VARQPFPGPGLGIRI  ARQPFPGPG        0.1608       8772.9                  50.00     Sequence
DRB1_0802  126  LHSDLPEVQPVWMSH  PEVQPVWMS        0.1605       8801.4                  50.00     Sequence
DRB1_0802  221  QIGDGHAICGLSGGV  GHAICGLSG        0.1598       8873.9                  50.00     Sequence
DRB1_0802  434  TAAGLDNQIWQCPVV  LDNQIWQCP        0.1593       8919.0                  50.00     Sequence
DRB1_0802  224  DGHAICGLSGGVDSA  GHAICGLSG        0.1592       8927.8                  50.00     Sequence
DRB1_0802  222  IGDGHAICGLSGGVD  GHAICGLSG        0.1584       9011.9                  50.00     Sequence
DRB1_0802   69  VYADGAPKLDPALLD  VYADGAPKL        0.1580       9047.9                  50.00     Sequence
DRB1_0802  344  SGGGSGTANIKSHHN  GSGTANIKS        0.1574       9109.1                  50.00     Sequence
DRB1_0802   12  PARPVLVVDFGAQYA  VVDFGAQYA        0.1571       9136.2                  50.00     Sequence
DRB1_0802  277  ATGANLVTVDAAETF  LVTVDAAET        0.1569       9151.4                  50.00     Sequence
DRB1_0802  153  VVASSAGAPVAAFEA  VVASSAGAP        0.1569       9154.8                  50.00     Sequence
DRB1_0802   78  DPALLDLGVPVLGIC  LLDLGVPVL        0.1568       9161.9                  50.00     Sequence
DRB1_0802  231  LSGGVDSAVAAALVQ  GVDSAVAAA        0.1563       9220.1                  50.00     Sequence
DRB1_0802  278  TGANLVTVDAAETFL  LVTVDAAET        0.1559       9258.4                  50.00     Sequence
DRB1_0802  229  CGLSGGVDSAVAAAL  GVDSAVAAA        0.1541       9433.8                  50.00     Sequence
DRB1_0802  383  RAVGRELGLPEEIVA  AVGRELGLP        0.1541       9441.7                  50.00     Sequence
DRB1_0802  352  NIKSHHNVGGLPDDL  NIKSHHNVG        0.1539       9459.6                  50.00     Sequence
DRB1_0802  217  QVRTQIGDGHAICGL  RTQIGDGHA        0.1538       9467.0                  50.00     Sequence
DRB1_0802   66  PASVYADGAPKLDPA  VYADGAPKL        0.1538       9467.6                  50.00     Sequence
DRB1_0802   76  KLDPALLDLGVPVLG  LLDLGVPVL        0.1536       9487.9                  50.00     Sequence
DRB1_0802    5  DIDVPETPARPVLVV  IDVPETPAR        0.1526       9587.2                  50.00     Sequence
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DRB1_0802	279	GANLVTVDAAETFLE	LVTVDAAET	0.1514	9715.7	50.00	Sequence
DRB1_0802	77	LDPALLDLGVPVLGI	LLDLGVPVL	0.1505	9807.8	50.00	Sequence
DRB1_0802	42	VIPHTASIEEIRARQ	HTASIEEIR	0.1503	9829.5	50.00	Sequence
DRB1_0802	65	GPASVYADGAPKLDP	SVYADGAPK	0.1500	9861.0	50.00	Sequence
DRB1_0802	154	VASSAGAPVAAFEAF	ASSAGAPVA	0.1496	9908.3	50.00	Sequence
DRB1_0802	473	PVSSEDAMTADWTRV	VSSEDAMTA	0.1491	9963.7	50.00	Sequence
DRB1_0802	469	IVLRPVSSEDAMTAD	VLRPVSSED	0.1488	9989.5	50.00	Sequence
DRB1_0802	223	GDGHAICGLSGGVDS	GHAICGLSG	0.1484	10043.3	50.00	Sequence
DRB1_0802	220	TQIGDGHAICGLSGG	GHAICGLSG	0.1482	10059.9	50.00	Sequence
DRB1_0802	63	SGGPASVYADGAPKL	SVYADGAPK	0.1476	10122.5	50.00	Sequence
DRB1_0802	40	SEVIPHTASIEEIRA	HTASIEEIR	0.1475	10140.8	50.00	Sequence
DRB1_0802	360	GGLPDDLKFTLVEPL	DLKFTLVEP	0.1469	10203.8	50.00	Sequence
DRB1_0802	64	GGPASVYADGAPKLD	VYADGAPKL	0.1465	10248.1	50.00	Sequence
DRB1_0802	152	DVVASSAGAPVAAFE	VVASSAGAP	0.1463	10271.7	50.00	Sequence
DRB1_0802	343	ESGGGSGTANIKSHH	GSGTANIKS	0.1459	10315.2	50.00	Sequence
DRB1_0802	355	SHHNVGGLPDDLKFT	HHNVGGLPD	0.1455	10354.3	50.00	Sequence
DRB1_0802	174	GVQYHPEVMHTPHGQ	YHPEVMHTP	0.1442	10504.7	50.00	Sequence
DRB1_0802	41	EVIPHTASIEEIRAR	HTASIEEIR	0.1441	10511.5	50.00	Sequence
DRB1_0802	282	LVTVDAAETFLEALS	LVTVDAAET	0.1418	10776.3	50.00	Sequence
DRB1_0802	387	RELGLPEEIVARQPF	PEEIVARQP	0.1414	10825.7	50.00	Sequence
DRB1_0802	218	VRTQIGDGHAICGLS	RTQIGDGHA	0.1387	11149.6	50.00	Sequence
DRB1_0802	10	ETPARPVLVVDFGAQ	RPVLVVDFG	0.1381	11222.4	50.00	Sequence
DRB1_0802	4	ADIDVPETPARPVLV	IDVPETPAR	0.1380	11230.4	50.00	Sequence
DRB1_0802	470	VLRPVSSEDAMTADW	VLRPVSSED	0.1380	11236.5	50.00	Sequence
DRB1_0802	216	EQVRTQIGDGHAICG	RTQIGDGHA	0.1358	11501.2	50.00	Sequence
DRB1_0802	472	RPVSSEDAMTADWTR	VSSEDAMTA	0.1348	11633.3	50.00	Sequence
DRB1_0802	356	HHNVGGLPDDLKFTL	HHNVGGLPD	0.1348	11633.7	50.00	Sequence
DRB1_0802	155	ASSAGAPVAAFEAFD	ASSAGAPVA	0.1346	11658.0	50.00	Sequence
DRB1_0802	140	HGDAVTAAPDGFDVV	HGDAVTAAP	0.1345	11664.1	50.00	Sequence
DRB1_0802	11	TPARPVLVVDFGAQY	RPVLVVDFG	0.1339	11739.5	50.00	Sequence
DRB1_0802	281	NLVTVDAAETFLEAL	LVTVDAAET	0.1331	11849.0	50.00	Sequence
DRB1_0802	139	SHGDAVTAAPDGFDV	HGDAVTAAP	0.1329	11865.4	50.00	Sequence
DRB1_0802	280	ANLVTVDAAETFLEA	LVTVDAAET	0.1329	11866.1	50.00	Sequence
DRB1_0802	353	IKSHHNVGGLPDDLK	IKSHHNVGG	0.1329	11873.4	50.00	Sequence
DRB1_0802	385	VGRELGLPEEIVARQ	VGRELGLPE	0.1324	11936.1	50.00	Sequence
DRB1_0802	428	IVREELTAAGLDNQI	IVREELTAA	0.1314	12066.0	50.00	Sequence
DRB1_0802	275	VAATGANLVTVDAAE	GANLVTVDA	0.1291	12372.8	50.00	Sequence
DRB1_0802	226	HAICGLSGGVDSAVA	HAICGLSGG	0.1283	12470.5	50.00	Sequence
DRB1_0802	386	GRELGLPEEIVARQP	PEEIVARQP	0.1278	12542.4	50.00	Sequence
DRB1_0802	228	ICGLSGGVDSAVAAA	GVDSAVAAA	0.1277	12556.9	50.00	Sequence
DRB1_0802	354	KSHHNVGGLPDDLKF	HHNVGGLPD	0.1263	12748.4	50.00	Sequence
DRB1_0802	283	VTVDAAETFLEALSG	AETFLEALS	0.1242	13043.1	50.00	Sequence
DRB1_0802	433	LTAAGLDNQIWQCPV	LTAAGLDNQ	0.1241	13051.2	50.00	Sequence
DRB1_0802	3	PADIDVPETPARPVL	IDVPETPAR	0.1238	13099.1	50.00	Sequence
DRB1_0802	284	TVDAAETFLEALSGV	AETFLEALS	0.1235	13140.3	50.00	Sequence
DRB1_0802	341	VVESGGGSGTANIKS	GSGTANIKS	0.1226	13264.8	50.00	Sequence
DRB1_0802	335	GTLYPDVVESGGGSG	VVESGGGSG	0.1188	13825.0	50.00	Sequence
DRB1_0802	227	AICGLSGGVDSAVAA	GLSGGVDSA	0.1168	14124.7	50.00	Sequence
DRB1_0802	75	PKLDPALLDLGVPVL	LLDLGVPVL	0.1159	14271.4	50.00	Sequence
DRB1_0802	359	VGGLPDDLKFTLVEP	GLPDDLKFT	0.1152	14372.3	50.00	Sequence
DRB1_0802	471	LRPVSSEDAMTADWT	PVSSEDAMT	0.1143	14521.1	50.00	Sequence
DRB1_0802	73	GAPKLDPALLDLGVP	GAPKLDPAL	0.1108	15081.1	50.00	Sequence
DRB1_0802	144	VTAAPDGFDVVASSA	GFDVVASSA	0.1106	15117.3	50.00	Sequence
DRB1_0802	336	TLYPDVVESGGGSGT	TLYPDVVES	0.1085	15457.9	50.00	Sequence
DRB1_0802	70	YADGAPKLDPALLDL	GAPKLDPAL	0.1084	15475.5	50.00	Sequence
DRB1_0802	61	VLSGGPASVYADGAP	VLSGGPASV	0.1081	15524.9	50.00	Sequence
DRB1_0802	342	VESGGGSGTANIKSH	GSGTANIKS	0.1080	15534.2	50.00	Sequence
DRB1_0802	62	LSGGPASVYADGAPK	SVYADGAPK	0.1076	15601.4	50.00	Sequence
DRB1_0802	334	QGTLYPDVVESGGGS	QGTLYPDVV	0.1024	16517.0	50.00	Sequence
DRB1_0802	432	ELTAAGLDNQIWQCP	AAGLDNQIW	0.1017	16632.5	50.00	Sequence
DRB1_0802	1	VQPADIDVPETPARP	IDVPETPAR	0.0987	17192.4	50.00	Sequence
DRB1_0802	0	VVQPADIDVPETPAR	IDVPETPAR	0.0981	17292.2	50.00	Sequence
DRB1_0802	2	QPADIDVPETPARPV	IDVPETPAR	0.0976	17389.6	50.00	Sequence
DRB1_0802	340	DVVESGGGSGTANIK	VVESGGGSG	0.0957	17754.8	50.00	Sequence
DRB1_0802	71	ADGAPKLDPALLDLG	GAPKLDPAL	0.0950	17883.6	50.00	Sequence
DRB1_0802	72	DGAPKLDPALLDLGV	GAPKLDPAL	0.0948	17927.4	50.00	Sequence

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   DRB1_0802  332  LVQGTLYPDVVESGG  LVQGTLYPD        0.0940      18074.8               50.00     Sequence
   DRB1_0802  156  SSAGAPVAAFEAFDR  GAPVAAFEA        0.0927      18333.4               50.00     Sequence
   DRB1_0802  337  LYPDVVESGGGSGTA  VVESGGGSG        0.0927      18333.8               50.00     Sequence
   DRB1_0802  333  VQGTLYPDVVESGGG  GTLYPDVVE        0.0917      18529.3               50.00     Sequence
   DRB1_0802  157  SAGAPVAAFEAFDRR  GAPVAAFEA        0.0898      18915.6               50.00     Sequence
   DRB1_0802  357  HNVGGLPDDLKFTLV  GLPDDLKFT        0.0896      18958.8               50.00     Sequence
   DRB1_0802  358  NVGGLPDDLKFTLVE  GLPDDLKFT        0.0895      18990.0               50.00     Sequence
   DRB1_0802  429  VREELTAAGLDNQIW  VREELTAAG        0.0869      19520.2               50.00     Sequence
   DRB1_0802   74  APKLDPALLDLGVPV  APKLDPALL        0.0843      20086.0               50.00     Sequence
   DRB1_0802  339  PDVVESGGGSGTANI  VVESGGGSG        0.0842      20103.8               50.00     Sequence
   DRB1_0802  338  YPDVVESGGGSGTAN  VVESGGGSG        0.0818      20643.9               50.00     Sequence
   DRB1_0802  141  GDAVTAAPDGFDVVA  GDAVTAAPD        0.0759      21990.0               50.00     Sequence
   DRB1_0802  431  EELTAAGLDNQIWQC  AAGLDNQIW        0.0712      23152.7               50.00     Sequence
   DRB1_0802  430  REELTAAGLDNQIWQ  AAGLDNQIW        0.0645      24885.0               50.00     Sequence
   DRB1_0802  142  DAVTAAPDGFDVVAS  DAVTAAPDG        0.0554      27458.1               50.00     Sequence
   DRB1_0802  143  AVTAAPDGFDVVASS  PDGFDVVAS        0.0493      29320.1               50.00     Sequence
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Allele: DRB1_0802. Number of high binders 0. Number of weak binders 60. Number of peptides 511

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0901   92  CYGFQAMAQALGGIV  YGFQAMAQA        0.7278         19.0         SB     0.20     Sequence
   DRB1_0901   91  ICYGFQAMAQALGGI  YGFQAMAQA        0.7230         20.0         SB     0.20     Sequence
   DRB1_0901   93  YGFQAMAQALGGIVA  YGFQAMAQA        0.7214         20.4         SB     0.30     Sequence
   DRB1_0901   90  GICYGFQAMAQALGG  YGFQAMAQA        0.7104         23.0         SB     0.30     Sequence
   DRB1_0901   89  LGICYGFQAMAQALG  YGFQAMAQA        0.6806         31.7         SB     0.80     Sequence
   DRB1_0901  366  LKFTLVEPLRLLFKD  FTLVEPLRL        0.6786         32.4         SB     0.80     Sequence
   DRB1_0901  310  RQFIRAFEGAVRDVL  FIRAFEGAV        0.6612         39.1         SB     2.00     Sequence
   DRB1_0901  365  DLKFTLVEPLRLLFK  FTLVEPLRL        0.6608         39.3         SB     2.00     Sequence
   DRB1_0901  136  VWMSHGDAVTAAPDG  WMSHGDAVT        0.6471         45.5         SB     2.00     Sequence
   DRB1_0901  135  PVWMSHGDAVTAAPD  WMSHGDAVT        0.6420         48.1         SB     2.00     Sequence
   DRB1_0901  309  GRQFIRAFEGAVRDV  FIRAFEGAV        0.6362         51.2         WB     2.00     Sequence
   DRB1_0901  311  QFIRAFEGAVRDVLD  FIRAFEGAV        0.6350         51.9         WB     2.00     Sequence
   DRB1_0901  364  DDLKFTLVEPLRLLF  FTLVEPLRL        0.6301         54.7         WB     2.00     Sequence
   DRB1_0901  367  KFTLVEPLRLLFKDE  FTLVEPLRL        0.6269         56.6         WB     4.00     Sequence
   DRB1_0901  308  IGRQFIRAFEGAVRD  FIRAFEGAV        0.6213         60.2         WB     4.00     Sequence
   DRB1_0901  134  QPVWMSHGDAVTAAP  WMSHGDAVT        0.6125         66.2         WB     4.00     Sequence
   DRB1_0901  307  IIGRQFIRAFEGAVR  FIRAFEGAV        0.6098         68.2         WB     4.00     Sequence
   DRB1_0901  468  PIVLRPVSSEDAMTA  IVLRPVSSE        0.6037         72.8         WB     4.00     Sequence
   DRB1_0901  467  HPIVLRPVSSEDAMT  IVLRPVSSE        0.6037         72.8         WB     4.00     Sequence
   DRB1_0901   88  VLGICYGFQAMAQAL  YGFQAMAQA        0.6017         74.4         WB     4.00     Sequence
   DRB1_0901   94  GFQAMAQALGGIVAH  FQAMAQALG        0.5962         79.0         WB     4.00     Sequence
   DRB1_0901  363  PDDLKFTLVEPLRLL  FTLVEPLRL        0.5922         82.5         WB     4.00     Sequence
   DRB1_0901  270  VQRDFVAATGANLVT  FVAATGANL        0.5911         83.5         WB     8.00     Sequence
   DRB1_0901  271  QRDFVAATGANLVTV  DFVAATGAN        0.5894         85.0         WB     8.00     Sequence
   DRB1_0901  368  FTLVEPLRLLFKDEV  TLVEPLRLL        0.5886         85.7         WB     8.00     Sequence
   DRB1_0901  272  RDFVAATGANLVTVD  FVAATGANL        0.5878         86.5         WB     8.00     Sequence
   DRB1_0901  137  WMSHGDAVTAAPDGF  WMSHGDAVT        0.5853         88.9         WB     8.00     Sequence
   DRB1_0901  133  VQPVWMSHGDAVTAA  WMSHGDAVT        0.5814         92.7         WB     8.00     Sequence
   DRB1_0901  269  QVQRDFVAATGANLV  FVAATGANL        0.5797         94.4         WB     8.00     Sequence
   DRB1_0901  469  IVLRPVSSEDAMTAD  IVLRPVSSE        0.5761         98.2         WB     8.00     Sequence
   DRB1_0901   20  DFGAQYAQLIARRVR  FGAQYAQLI        0.5745         99.9         WB     8.00     Sequence
   DRB1_0901   38  VFSEVIPHTASIEEI  VIPHTASIE        0.5744        100.0         WB     8.00     Sequence
   DRB1_0901  466  GHPIVLRPVSSEDAM  IVLRPVSSE        0.5738        100.6         WB     8.00     Sequence
   DRB1_0901  192  SRFLHDFAGLGAQWT  RFLHDFAGL        0.5714        103.3         WB     8.00     Sequence
   DRB1_0901  132  EVQPVWMSHGDAVTA  WMSHGDAVT        0.5699        105.0         WB     8.00     Sequence
   DRB1_0901  191  LSRFLHDFAGLGAQW  FLHDFAGLG        0.5687        106.4         WB     8.00     Sequence
   DRB1_0901  231  LSGGVDSAVAAALVQ  LSGGVDSAV        0.5651        110.5         WB     8.00     Sequence
   DRB1_0901  465  YGHPIVLRPVSSEDA  IVLRPVSSE        0.5646        111.1         WB     8.00     Sequence
   DRB1_0901   19  VDFGAQYAQLIARRV  YAQLIARRV        0.5633        112.8         WB     8.00     Sequence
   DRB1_0901   95  FQAMAQALGGIVAHT  FQAMAQALG        0.5632        112.9         WB     8.00     Sequence
   DRB1_0901  312  FIRAFEGAVRDVLDG  FIRAFEGAV        0.5611        115.4         WB     8.00     Sequence
   DRB1_0901   37  RVFSEVIPHTASIEE  VIPHTASIE        0.5607        115.9         WB     8.00     Sequence
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DRB1_0901   21  FGAQYAQLIARRVRE  YAQLIARRV        0.5597        117.2          WB     8.00      Sequence
DRB1_0901   39  FSEVIPHTASIEEIR  VIPHTASIE        0.5592        117.9          WB     8.00      Sequence
DRB1_0901  190  VLSRFLHDFAGLGAQ  RFLHDFAGL        0.5581        119.2          WB     8.00      Sequence
DRB1_0901  193  RFLHDFAGLGAQWTP  RFLHDFAGL        0.5525        126.7          WB     8.00      Sequence
DRB1_0901  233  GGVDSAVAAALVQRA  DSAVAAALV        0.5496        130.8          WB     8.00      Sequence
DRB1_0901  440  NQIWQCPVVLLADVR  IWQCPVVLL        0.5488        131.9          WB     8.00      Sequence
DRB1_0901  331  FLVQGTLYPDVVESG  QGTLYPDVV        0.5484        132.5          WB     8.00      Sequence
DRB1_0901  189  QVLSRFLHDFAGLGA  FLHDFAGLG        0.5446        138.0          WB    16.00      Sequence
DRB1_0901  149  DGFDVVASSAGAPVA  VASSAGAPV        0.5439        139.1          WB    16.00      Sequence
DRB1_0901  482  ADWTRVPYEVLERIS  WTRVPYEVL        0.5425        141.2          WB    16.00      Sequence
DRB1_0901   50  EEIRARQPVALVLSG  RARQPVALV        0.5416        142.6          WB    16.00      Sequence
DRB1_0901  232  SGGVDSAVAAALVQR  DSAVAAALV        0.5414        142.9          WB    16.00      Sequence
DRB1_0901  306  KIIGRQFIRAFEGAV  FIRAFEGAV        0.5397        145.5          WB    16.00      Sequence
DRB1_0901  441  QIWQCPVVLLADVRS  IWQCPVVLL        0.5385        147.5          WB    16.00      Sequence
DRB1_0901  202  GAQWTPANIANALIE  WTPANIANA        0.5375        149.1          WB    16.00      Sequence
DRB1_0901  114  YGRTELKVLGGKLHS  YGRTELKVL        0.5374        149.1          WB    16.00      Sequence
DRB1_0901   49  IEEIRARQPVALVLS  RARQPVALV        0.5371        149.6          WB    16.00      Sequence
DRB1_0901  131  PEVQPVWMSHGDAVT  WMSHGDAVT        0.5368        150.1          WB    16.00      Sequence
DRB1_0901  483  DWTRVPYEVLERIST  WTRVPYEVL        0.5356        152.2          WB    16.00      Sequence
DRB1_0901  234  GVDSAVAAALVQRAI  DSAVAAALV        0.5342        154.5          WB    16.00      Sequence
DRB1_0901  439  DNQIWQCPVVLLADV  IWQCPVVLL        0.5331        156.2          WB    16.00      Sequence
DRB1_0901  230  GLSGGVDSAVAAALV  DSAVAAALV        0.5329        156.6          WB    16.00      Sequence
DRB1_0901  330  EFLVQGTLYPDVVES  QGTLYPDVV        0.5328        156.7          WB    16.00      Sequence
DRB1_0901  463  RTYGHPIVLRPVSSE  IVLRPVSSE        0.5326        157.1          WB    16.00      Sequence
DRB1_0901   23  AQYAQLIARRVREAR  YAQLIARRV        0.5322        157.8          WB    16.00      Sequence
DRB1_0901   22  GAQYAQLIARRVREA  YAQLIARRV        0.5322        157.8          WB    16.00      Sequence
DRB1_0901   51  EIRARQPVALVLSGG  RARQPVALV        0.5316        158.9          WB    16.00      Sequence
DRB1_0901  240  AAALVQRAIGDRLTC  VQRAIGDRL        0.5314        159.3          WB    16.00      Sequence
DRB1_0901   25  YAQLIARRVREARVF  YAQLIARRV        0.5310        160.0          WB    16.00      Sequence
DRB1_0901  203  AQWTPANIANALIEQ  WTPANIANA        0.5308        160.2          WB    16.00      Sequence
DRB1_0901  369  TLVEPLRLLFKDEVR  TLVEPLRLL        0.5286        164.1          WB    16.00      Sequence
DRB1_0901  113  EYGRTELKVLGGKLH  YGRTELKVL        0.5285        164.2          WB    16.00      Sequence
DRB1_0901   87  PVLGICYGFQAMAQA  YGFQAMAQA        0.5280        165.2          WB    16.00      Sequence
DRB1_0901  484  WTRVPYEVLERISTR  WTRVPYEVL        0.5269        167.1          WB    16.00      Sequence
DRB1_0901  420  DTLRHADSIVREELT  TLRHADSIV        0.5260        168.7          WB    16.00      Sequence
DRB1_0901   40  SEVIPHTASIEEIRA  VIPHTASIE        0.5260        168.8          WB    16.00      Sequence
DRB1_0901  201  LGAQWTPANIANALI  WTPANIANA        0.5257        169.4          WB    16.00      Sequence
DRB1_0901  421  TLRHADSIVREELTA  TLRHADSIV        0.5255        169.8          WB    16.00      Sequence
DRB1_0901  268  AQVQRDFVAATGANL  FVAATGANL        0.5252        170.2          WB    16.00      Sequence
DRB1_0901  241  AALVQRAIGDRLTCV  VQRAIGDRL        0.5250        170.5          WB    16.00      Sequence
DRB1_0901   24  QYAQLIARRVREARV  YAQLIARRV        0.5248        171.0          WB    16.00      Sequence
DRB1_0901  150  GFDVVASSAGAPVAA  VASSAGAPV        0.5242        172.0          WB    16.00      Sequence
DRB1_0901  332  LVQGTLYPDVVESGG  GTLYPDVVE        0.5231        174.2          WB    16.00      Sequence
DRB1_0901   52  IRARQPVALVLSGGP  RARQPVALV        0.5227        175.0          WB    16.00      Sequence
DRB1_0901  242  ALVQRAIGDRLTCVF  VQRAIGDRL        0.5213        177.6          WB    16.00      Sequence
DRB1_0901  481  TADWTRVPYEVLERI  WTRVPYEVL        0.5204        179.2          WB    16.00      Sequence
DRB1_0901  148  PDGFDVVASSAGAPV  VASSAGAPV        0.5197        180.7          WB    16.00      Sequence
DRB1_0901  462  GRTYGHPIVLRPVSS  GRTYGHPIV        0.5188        182.5          WB    16.00      Sequence
DRB1_0901  329  AEFLVQGTLYPDVVE  QGTLYPDVV        0.5182        183.7          WB    16.00      Sequence
DRB1_0901  273  DFVAATGANLVTVDA  FVAATGANL        0.5180        184.0          WB    16.00      Sequence
DRB1_0901  235  VDSAVAAALVQRAIG  DSAVAAALV        0.5180        184.1          WB    16.00      Sequence
DRB1_0901   42  VIPHTASIEEIRARQ  VIPHTASIE        0.5178        184.4          WB    16.00      Sequence
DRB1_0901  442  IWQCPVVLLADVRSV  IWQCPVVLL        0.5166        186.8          WB    16.00      Sequence
DRB1_0901  464  TYGHPIVLRPVSSED  IVLRPVSSE        0.5165        187.0          WB    16.00      Sequence
DRB1_0901  290  TFLEALSGVSAPEGK  TFLEALSGV        0.5152        189.6          WB    16.00      Sequence
DRB1_0901  151  FDVVASSAGAPVAAF  VASSAGAPV        0.5141        192.0          WB    16.00      Sequence
DRB1_0901  479  AMTADWTRVPYEVLE  WTRVPYEVL        0.5132        193.9          WB    16.00      Sequence
DRB1_0901  480  MTADWTRVPYEVLER  WTRVPYEVL        0.5093        202.2          WB    16.00      Sequence
DRB1_0901  419  LDTLRHADSIVREEL  TLRHADSIV        0.5071        207.2          WB    16.00      Sequence
DRB1_0901  112  REYGRTELKVLGGKL  YGRTELKVL        0.5063        208.9          WB    16.00      Sequence
DRB1_0901   48  SIEEIRARQPVALVL  IRARQPVAL        0.5054        211.0          WB    16.00      Sequence
DRB1_0901   36  ARVFSEVIPHTASIE  VIPHTASIE        0.5046        212.7          WB    16.00      Sequence
DRB1_0901  239  VAAALVQRAIGDRLT  VQRAIGDRL        0.5043        213.3          WB    16.00      Sequence
DRB1_0901  152  DVVASSAGAPVAAFE  VASSAGAPV        0.5032        216.1          WB    16.00      Sequence
DRB1_0901  438  LDNQIWQCPVVLLAD  IWQCPVVLL        0.5030        216.4          WB    16.00      Sequence
DRB1_0901  461  DGRTYGHPIVLRPVS  RTYGHPIVL        0.5004        222.7          WB    16.00      Sequence
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DRB1_0901  333  VQGTLYPDVVESGGG  GTLYPDVVE         0.4979         228.6         WB    16.00      Sequence
DRB1_0901  418  RLDTLRHADSIVREE  TLRHADSIV         0.4979         228.7         WB    16.00      Sequence
DRB1_0901  228  ICGLSGGVDSAVAAA  LSGGVDSAV         0.4979         228.8         WB    16.00      Sequence
DRB1_0901  200  GLGAQWTPANIANAL  WTPANIANA         0.4955         234.8         WB    16.00      Sequence
DRB1_0901   41  EVIPHTASIEEIRAR  VIPHTASIE         0.4949         236.3         WB    16.00      Sequence
DRB1_0901  188  QQVLSRFLHDFAGLG  FLHDFAGLG         0.4927         242.1         WB    32.00      Sequence
DRB1_0901  375  RLLFKDEVRAVGREL  EVRAVGREL         0.4926         242.2         WB    32.00      Sequence
DRB1_0901  379  KDEVRAVGRELGLPE  EVRAVGREL         0.4910         246.5         WB    32.00      Sequence
DRB1_0901  289  ETFLEALSGVSAPEG  TFLEALSGV         0.4896         250.3         WB    32.00      Sequence
DRB1_0901  377  LFKDEVRAVGRELGL  EVRAVGREL         0.4890         251.8         WB    32.00      Sequence
DRB1_0901  229  CGLSGGVDSAVAAAL  LSGGVDSAV         0.4886         252.9         WB    32.00      Sequence
DRB1_0901  153  VVASSAGAPVAAFEA  VASSAGAPV         0.4874         256.1         WB    32.00      Sequence
DRB1_0901  111  TREYGRTELKVLGGK  YGRTELKVL         0.4871         257.0         WB    32.00      Sequence
DRB1_0901  380  DEVRAVGRELGLPEE  EVRAVGREL         0.4869         257.6         WB    32.00      Sequence
DRB1_0901  374  LRLLFKDEVRAVGRE  LRLLFKDEV         0.4858         260.7         WB    32.00      Sequence
DRB1_0901   18  VVDFGAQYAQLIARR  FGAQYAQLI         0.4837         266.9         WB    32.00      Sequence
DRB1_0901  378  FKDEVRAVGRELGLP  EVRAVGREL         0.4836         267.0         WB    32.00      Sequence
DRB1_0901  489  YEVLERISTRITNEV  VLERISTRI         0.4836         267.1         WB    32.00      Sequence
DRB1_0901  376  LLFKDEVRAVGRELG  EVRAVGREL         0.4836         267.1         WB    32.00      Sequence
DRB1_0901   69  VYADGAPKLDPALLD  YADGAPKLD         0.4830         268.8         WB    32.00      Sequence
DRB1_0901  109  TGTREYGRTELKVLG  YGRTELKVL         0.4802         277.0         WB    32.00      Sequence
DRB1_0901  291  FLEALSGVSAPEGKR  LSGVSAPEG         0.4802         277.0         WB    32.00      Sequence
DRB1_0901  406  LGIRIVGEVTAKRLD  LGIRIVGEV         0.4796         279.0         WB    32.00      Sequence
DRB1_0901  362  LPDDLKFTLVEPLRL  FTLVEPLRL         0.4788         281.3         WB    32.00      Sequence
DRB1_0901  236  DSAVAAALVQRAIGD  DSAVAAALV         0.4786         282.0         WB    32.00      Sequence
DRB1_0901  417  KRLDTLRHADSIVRE  TLRHADSIV         0.4783         282.8         WB    32.00      Sequence
DRB1_0901  328  TAEFLVQGTLYPDVV  QGTLYPDVV         0.4776         284.9         WB    32.00      Sequence
DRB1_0901  138  MSHGDAVTAAPDGFD  MSHGDAVTA         0.4773         286.0         WB    32.00      Sequence
DRB1_0901  408  IRIVGEVTAKRLDTL  IVGEVTAKR         0.4772         286.2         WB    32.00      Sequence
DRB1_0901  293  EALSGVSAPEGKRKI  LSGVSAPEG         0.4761         289.5         WB    32.00      Sequence
DRB1_0901  478  DAMTADWTRVPYEVL  WTRVPYEVL         0.4751         292.8         WB    32.00      Sequence
DRB1_0901   17  LVVDFGAQYAQLIAR  FGAQYAQLI         0.4740         296.3         WB    32.00      Sequence
DRB1_0901   16  VLVVDFGAQYAQLIA  FGAQYAQLI         0.4739         296.5         WB    32.00      Sequence
DRB1_0901  118  ELKVLGGKLHSDLPE  ELKVLGGKL         0.4732         298.7         WB    32.00      Sequence
DRB1_0901   47  ASIEEIRARQPVALV  EIRARQPVA         0.4730         299.5         WB    32.00      Sequence
DRB1_0901   64  GGPASVYADGAPKLD  YADGAPKLD         0.4705         307.7         WB    32.00      Sequence
DRB1_0901  181  VMHTPHGQQVLSRFL  VMHTPHGQQ         0.4686         314.1         WB    32.00      Sequence
DRB1_0901  259  HGLLRAGERAQVQRD  LRAGERAQV         0.4684         314.8         WB    32.00      Sequence
DRB1_0901   26  AQLIARRVREARVFS  AQLIARRVR         0.4682         315.3         WB    32.00      Sequence
DRB1_0901  256  FVDHGLLRAGERAQV  FVDHGLLRA         0.4682         315.4         WB    32.00      Sequence
DRB1_0901  313  IRAFEGAVRDVLDGK  RAFEGAVRD         0.4680         316.2         WB    32.00      Sequence
DRB1_0901   67  ASVYADGAPKLDPAL  YADGAPKLD         0.4669         319.9         WB    32.00      Sequence
DRB1_0901  110  GTREYGRTELKVLGG  YGRTELKVL         0.4666         321.0         WB    32.00      Sequence
DRB1_0901  294  ALSGVSAPEGKRKII  ALSGVSAPE         0.4666         321.1         WB    32.00      Sequence
DRB1_0901  199  AGLGAQWTPANIANA  WTPANIANA         0.4655         324.8         WB    32.00      Sequence
DRB1_0901   53  RARQPVALVLSGGPA  RARQPVALV         0.4651         326.3         WB    32.00      Sequence
DRB1_0901  292  LEALSGVSAPEGKRK  LSGVSAPEG         0.4649         327.0         WB    32.00      Sequence
DRB1_0901  460  GDGRTYGHPIVLRPV  RTYGHPIVL         0.4641         329.8         WB    32.00      Sequence
DRB1_0901  334  QGTLYPDVVESGGGS  QGTLYPDVV         0.4640         330.0         WB    32.00      Sequence
DRB1_0901   97  AMAQALGGIVAHTGT  MAQALGGIV         0.4624         335.8         WB    32.00      Sequence
DRB1_0901  407  GIRIVGEVTAKRLDT  VGEVTAKRL         0.4616         338.6         WB    32.00      Sequence
DRB1_0901  154  VASSAGAPVAAFEAF  VASSAGAPV         0.4610         341.1         WB    32.00      Sequence
DRB1_0901  204  QWTPANIANALIEQV  WTPANIANA         0.4600         344.7         WB    32.00      Sequence
DRB1_0901  260  GLLRAGERAQVQRDF  LRAGERAQV         0.4598         345.4         WB    32.00      Sequence
DRB1_0901   68  SVYADGAPKLDPALL  YADGAPKLD         0.4590         348.4         WB    32.00      Sequence
DRB1_0901  416  AKRLDTLRHADSIVR  TLRHADSIV         0.4586         349.9         WB    32.00      Sequence
DRB1_0901  387  RELGLPEEIVARQPF  ELGLPEEIV         0.4584         350.9         WB    32.00      Sequence
DRB1_0901   15  PVLVVDFGAQYAQLI  FGAQYAQLI         0.4581         351.8         WB    32.00      Sequence
DRB1_0901   61  VLSGGPASVYADGAP  VLSGGPASV         0.4581         351.9         WB    32.00      Sequence
DRB1_0901  437  GLDNQIWQCPVVLLA  QIWQCPVVL         0.4577         353.3         WB    32.00      Sequence
DRB1_0901  227  AICGLSGGVDSAVAA  LSGGVDSAV         0.4572         355.3         WB    32.00      Sequence
DRB1_0901  490  EVLERISTRITNEVA  VLERISTRI         0.4570         355.9         WB    32.00      Sequence
DRB1_0901  238  AVAAALVQRAIGDRL  VQRAIGDRL         0.4566         357.8         WB    32.00      Sequence
DRB1_0901  386  GRELGLPEEIVARQP  LGLPEEIVA         0.4563         358.9         WB    32.00      Sequence
DRB1_0901  108  HTGTREYGRTELKVL  YGRTELKVL         0.4528         372.5         WB    32.00      Sequence
DRB1_0901  314  RAFEGAVRDVLDGKT  RAFEGAVRD         0.4506         381.5         WB    32.00      Sequence
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DRB1_0901  405  GLGIRIVGEVTAKRL  LGIRIVGEV         0.4500         384.1          WB    32.00      Sequence
DRB1_0901  373  PLRLLFKDEVRAVGR  LRLLFKDEV         0.4499         384.6          WB    32.00      Sequence
DRB1_0901   35  EARVFSEVIPHTASI  VFSEVIPHT         0.4496         385.6          WB    32.00      Sequence
DRB1_0901  372  EPLRLLFKDEVRAVG  LRLLFKDEV         0.4495         386.2          WB    32.00      Sequence
DRB1_0901   60  LVLSGGPASVYADGA  VLSGGPASV         0.4495         386.3          WB    32.00      Sequence
DRB1_0901  409  RIVGEVTAKRLDTLR  VGEVTAKRL         0.4490         388.3          WB    32.00      Sequence
DRB1_0901  305  RKIIGRQFIRAFEGA  RKIIGRQFI         0.4484         390.7          WB    32.00      Sequence
DRB1_0901  119  LKVLGGKLHSDLPEV  LKVLGGKLH         0.4482         391.5          WB    32.00      Sequence
DRB1_0901  243  LVQRAIGDRLTCVFV  QRAIGDRLT         0.4482         391.8          WB    32.00      Sequence
DRB1_0901  388  ELGLPEEIVARQPFP  ELGLPEEIV         0.4475         394.8          WB    32.00      Sequence
DRB1_0901  117  TELKVLGGKLHSDLP  LKVLGGKLH         0.4469         397.4          WB    32.00      Sequence
DRB1_0901    8  VPETPARPVLVVDFG  TPARPVLVV         0.4451         404.9          WB    32.00      Sequence
DRB1_0901  488  PYEVLERISTRITNE  VLERISTRI         0.4439         410.2          WB    32.00      Sequence
DRB1_0901   34  REARVFSEVIPHTAS  VFSEVIPHT         0.4437         411.2          WB    32.00      Sequence
DRB1_0901  491  VLERISTRITNEVAE  VLERISTRI         0.4434         412.7          WB    32.00      Sequence
DRB1_0901  288  AETFLEALSGVSAPE  FLEALSGVS         0.4421         418.6          WB    32.00      Sequence
DRB1_0901  170  RRLAGVQYHPEVMHT  VQYHPEVMH         0.4398         428.7          WB    32.00      Sequence
DRB1_0901   66  PASVYADGAPKLDPA  YADGAPKLD         0.4395         430.1          WB    32.00      Sequence
DRB1_0901  180  EVMHTPHGQQVLSRF  MHTPHGQQV         0.4393         431.4          WB    32.00      Sequence
DRB1_0901   96  QAMAQALGGIVAHTG  AMAQALGGI         0.4389         433.2          WB    32.00      Sequence
DRB1_0901  194  FLHDFAGLGAQWTPA  HDFAGLGAQ         0.4368         443.1          WB    32.00      Sequence
DRB1_0901   65  GPASVYADGAPKLDP  YADGAPKLD         0.4328         462.8          WB    32.00      Sequence
DRB1_0901   98  MAQALGGIVAHTGTR  MAQALGGIV         0.4324         464.9          WB    32.00      Sequence
DRB1_0901  450  LADVRSVGVQGDGRT  LADVRSVGV         0.4313         470.0          WB    32.00      Sequence
DRB1_0901  121  VLGGKLHSDLPEVQP  KLHSDLPEV         0.4293         480.5          WB    32.00      Sequence
DRB1_0901  447  VVLLADVRSVGVQGD  VLLADVRSV         0.4292         481.2          WB    32.00      Sequence
DRB1_0901  385  VGRELGLPEEIVARQ  ELGLPEEIV         0.4289         482.5          WB    32.00      Sequence
DRB1_0901  370  LVEPLRLLFKDEVRA  LRLLFKDEV         0.4287         483.6          WB    32.00      Sequence
DRB1_0901  261  LLRAGERAQVQRDFV  LRAGERAQV         0.4287         483.7          WB    32.00      Sequence
DRB1_0901  171  RLAGVQYHPEVMHTP  VQYHPEVMH         0.4285         484.6          WB    32.00      Sequence
DRB1_0901  371  VEPLRLLFKDEVRAV  LRLLFKDEV         0.4277         488.8          WB    32.00      Sequence
DRB1_0901  384  AVGRELGLPEEIVAR  ELGLPEEIV         0.4276         489.6          WB    32.00      Sequence
DRB1_0901  116  RTELKVLGGKLHSDL  LKVLGGKLH         0.4273         490.9          WB    32.00      Sequence
DRB1_0901  172  LAGVQYHPEVMHTPH  VQYHPEVMH         0.4273         491.0          WB    32.00      Sequence
DRB1_0901  410  IVGEVTAKRLDTLRH  VGEVTAKRL         0.4270         492.6          WB    32.00      Sequence
DRB1_0901  258  DHGLLRAGERAQVQR  LRAGERAQV         0.4265         495.4          WB    32.00      Sequence
DRB1_0901  487  VPYEVLERISTRITN  VLERISTRI         0.4260         497.9          WB    32.00      Sequence
DRB1_0901   27  QLIARRVREARVFSE  RRVREARVF         0.4251         502.9                50.00      Sequence
DRB1_0901  459  QGDGRTYGHPIVLRP  GRTYGHPIV         0.4249         504.0                50.00      Sequence
DRB1_0901   59  ALVLSGGPASVYADG  VLSGGPASV         0.4236         511.3                50.00      Sequence
DRB1_0901  147  APDGFDVVASSAGAP  FDVVASSAG         0.4234         512.4                50.00      Sequence
DRB1_0901  404  PGLGIRIVGEVTAKR  LGIRIVGEV         0.4229         515.2                50.00      Sequence
DRB1_0901  173  AGVQYHPEVMHTPHG  VQYHPEVMH         0.4216         522.3                50.00      Sequence
DRB1_0901  498  RITNEVAEVNRVVLD  RITNEVAEV         0.4213         524.1                50.00      Sequence
DRB1_0901  381  EVRAVGRELGLPEEI  EVRAVGREL         0.4208         526.5                50.00      Sequence
DRB1_0901   33  VREARVFSEVIPHTA  EARVFSEVI         0.4198         532.7                50.00      Sequence
DRB1_0901  100  QALGGIVAHTGTREY  ALGGIVAHT         0.4189         537.8                50.00      Sequence
DRB1_0901  187  GQQVLSRFLHDFAGL  RFLHDFAGL         0.4185         539.9                50.00      Sequence
DRB1_0901    9  PETPARPVLVVDFGA  ETPARPVLV         0.4177         544.5                50.00      Sequence
DRB1_0901  179  PEVMHTPHGQQVLSR  MHTPHGQQV         0.4176         545.1                50.00      Sequence
DRB1_0901  422  LRHADSIVREELTAA  LRHADSIVR         0.4171         548.4                50.00      Sequence
DRB1_0901  446  PVVLLADVRSVGVQG  VLLADVRSV         0.4165         552.2                50.00      Sequence
DRB1_0901   10  ETPARPVLVVDFGAQ  ETPARPVLV         0.4164         552.4                50.00      Sequence
DRB1_0901  267  RAQVQRDFVAATGAN  DFVAATGAN         0.4160         554.7                50.00      Sequence
DRB1_0901  130  LPEVQPVWMSHGDAV  LPEVQPVWM         0.4158         556.0                50.00      Sequence
DRB1_0901    7  DVPETPARPVLVVDF  TPARPVLVV         0.4157         556.9                50.00      Sequence
DRB1_0901  120  KVLGGKLHSDLPEVQ  KLHSDLPEV         0.4155         557.9                50.00      Sequence
DRB1_0901  115  GRTELKVLGGKLHSD  LKVLGGKLH         0.4147         563.0                50.00      Sequence
DRB1_0901  159  GAPVAAFEAFDRRLA  GAPVAAFEA         0.4141         566.3                50.00      Sequence
DRB1_0901  274  FVAATGANLVTVDAA  FVAATGANL         0.4139         567.9                50.00      Sequence
DRB1_0901  497  TRITNEVAEVNRVVL  TRITNEVAE         0.4127         574.9                50.00      Sequence
DRB1_0901  198  FAGLGAQWTPANIAN  QWTPANIAN         0.4123         577.6                50.00      Sequence
DRB1_0901   99  AQALGGIVAHTGTRE  ALGGIVAHT         0.4106         588.4                50.00      Sequence
DRB1_0901  175  VQYHPEVMHTPHGQQ  VQYHPEVMH         0.4104         589.3                50.00      Sequence
DRB1_0901  169  DRRLAGVQYHPEVMH  VQYHPEVMH         0.4100         592.0                50.00      Sequence
DRB1_0901  494  RISTRITNEVAEVNR  ISTRITNEV         0.4099         592.6                50.00      Sequence
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DRB1_0901  226  HAICGLSGGVDSAVA  LSGGVDSAV       0.4093        596.7            50.00     Sequence
DRB1_0901   62  LSGGPASVYADGAPK  LSGGPASVY       0.4093        596.8            50.00     Sequence
DRB1_0901  250  DRLTCVFVDHGLLRA  DRLTCVFVD       0.4075        608.6            50.00     Sequence
DRB1_0901  486  RVPYEVLERISTRIT  VLERISTRI       0.4067        613.6            50.00     Sequence
DRB1_0901  448  VLLADVRSVGVQGDG  LADVRSVGV       0.4064        615.7            50.00     Sequence
DRB1_0901   43  IPHTASIEEIRARQP  IPHTASIEE       0.4060        618.3            50.00     Sequence
DRB1_0901  101  ALGGIVAHTGTREYG  ALGGIVAHT       0.4057        620.5            50.00     Sequence
DRB1_0901  470  VLRPVSSEDAMTADW  VLRPVSSED       0.4054        622.6            50.00     Sequence
DRB1_0901  495  ISTRITNEVAEVNRV  ISTRITNEV       0.4047        627.2            50.00     Sequence
DRB1_0901   58  VALVLSGGPASVYAD  LVLSGGPAS       0.4034        635.7            50.00     Sequence
DRB1_0901  383  RAVGRELGLPEEIVA  ELGLPEEIV       0.4025        642.4            50.00     Sequence
DRB1_0901  237  SAVAAALVQRAIGDR  SAVAAALVQ       0.4008        654.3            50.00     Sequence
DRB1_0901  493  ERISTRITNEVAEVN  ISTRITNEV       0.4004        656.9            50.00     Sequence
DRB1_0901  257  VDHGLLRAGERAQVQ  LRAGERAQV       0.4002        658.3            50.00     Sequence
DRB1_0901  244  VQRAIGDRLTCVFVD  VQRAIGDRL       0.4001        659.2            50.00     Sequence
DRB1_0901   70  YADGAPKLDPALLDL  YADGAPKLD       0.4001        659.3            50.00     Sequence
DRB1_0901  255  VFVDHGLLRAGERAQ  FVDHGLLRA       0.3998        661.1            50.00     Sequence
DRB1_0901  178  HPEVMHTPHGQQVLS  MHTPHGQQV       0.3993        664.8            50.00     Sequence
DRB1_0901  122  LGGKLHSDLPEVQPV  KLHSDLPEV       0.3991        666.4            50.00     Sequence
DRB1_0901   32  RVREARVFSEVIPHT  EARVFSEVI       0.3976        677.4            50.00     Sequence
DRB1_0901  205  WTPANIANALIEQVR  WTPANIANA       0.3973        679.1            50.00     Sequence
DRB1_0901  335  GTLYPDVVESGGGSG  GTLYPDVVE       0.3957        691.0            50.00     Sequence
DRB1_0901  139  SHGDAVTAAPDGFDV  VTAAPDGFD       0.3953        694.4            50.00     Sequence
DRB1_0901    6  IDVPETPARPVLVVD  ETPARPVLV       0.3947        698.5            50.00     Sequence
DRB1_0901  315  AFEGAVRDVLDGKTA  AFEGAVRDV       0.3930        711.5            50.00     Sequence
DRB1_0901  287  AAETFLEALSGVSAP  FLEALSGVS       0.3929        712.3            50.00     Sequence
DRB1_0901  207  PANIANALIEQVRTQ  IANALIEQV       0.3924        716.5            50.00     Sequence
DRB1_0901   86  VPVLGICYGFQAMAQ  ICYGFQAMA       0.3921        718.4            50.00     Sequence
DRB1_0901  492  LERISTRITNEVAEV  LERISTRIT       0.3921        718.8            50.00     Sequence
DRB1_0901  174  GVQYHPEVMHTPHGQ  VQYHPEVMH       0.3912        725.7            50.00     Sequence
DRB1_0901  225  GHAICGLSGGVDSAV  LSGGVDSAV       0.3903        732.8            50.00     Sequence
DRB1_0901  182  MHTPHGQQVLSRFLH  MHTPHGQQV       0.3902        733.8            50.00     Sequence
DRB1_0901  295  LSGVSAPEGKRKIIG  LSGVSAPEG       0.3900        735.5            50.00     Sequence
DRB1_0901   63  SGGPASVYADGAPKL  VYADGAPKL       0.3884        747.6            50.00     Sequence
DRB1_0901  445  CPVVLLADVRSVGVQ  VLLADVRSV       0.3883        749.2            50.00     Sequence
DRB1_0901   30  ARRVREARVFSEVIP  RRVREARVF       0.3878        752.4            50.00     Sequence
DRB1_0901  124  GKLHSDLPEVQPVWM  KLHSDLPEV       0.3870        759.1            50.00     Sequence
DRB1_0901  496  STRITNEVAEVNRVV  TRITNEVAE       0.3869        760.0            50.00     Sequence
DRB1_0901  449  LLADVRSVGVQGDGR  LADVRSVGV       0.3868        760.8            50.00     Sequence
DRB1_0901  509  VVLDITSKPPATIEW  ITSKPPATI       0.3864        764.5            50.00     Sequence
DRB1_0901  208  ANIANALIEQVRTQI  IANALIEQV       0.3856        770.9            50.00     Sequence
DRB1_0901  195  LHDFAGLGAQWTPAN  HDFAGLGAQ       0.3854        772.9            50.00     Sequence
DRB1_0901  163  AAFEAFDRRLAGVQY  FEAFDRRLA       0.3845        780.3            50.00     Sequence
DRB1_0901   29  IARRVREARVFSEVI  RRVREARVF       0.3841        783.9            50.00     Sequence
DRB1_0901  396  VARQPFPGPGLGIRI  RQPFPGPGL       0.3839        785.0            50.00     Sequence
DRB1_0901  323  VLDGKTAEFLVQGTL  DGKTAEFLV       0.3839        785.5            50.00     Sequence
DRB1_0901  415  TAKRLDTLRHADSIV  TLRHADSIV       0.3832        791.6            50.00     Sequence
DRB1_0901  403  GPGLGIRIVGEVTAK  LGIRIVGEV       0.3826        796.0            50.00     Sequence
DRB1_0901  325  DGKTAEFLVQGTLYP  DGKTAEFLV       0.3820        801.4            50.00     Sequence
DRB1_0901  485  TRVPYEVLERISTRI  VLERISTRI       0.3819        802.4            50.00     Sequence
DRB1_0901   28  LIARRVREARVFSEV  LIARRVREA       0.3818        803.3            50.00     Sequence
DRB1_0901  436  AGLDNQIWQCPVVLL  IWQCPVVLL       0.3810        810.1            50.00     Sequence
DRB1_0901  160  APVAAFEAFDRRLAG  FEAFDRRLA       0.3808        812.4            50.00     Sequence
DRB1_0901  158  AGAPVAAFEAFDRRL  GAPVAAFEA       0.3797        821.7            50.00     Sequence
DRB1_0901  382  VRAVGRELGLPEEIV  ELGLPEEIV       0.3785        832.4            50.00     Sequence
DRB1_0901  209  NIANALIEQVRTQIG  IANALIEQV       0.3781        836.6            50.00     Sequence
DRB1_0901  499  ITNEVAEVNRVVLDI  ITNEVAEVN       0.3776        840.4            50.00     Sequence
DRB1_0901  395  IVARQPFPGPGLGIR  RQPFPGPGL       0.3771        845.2            50.00     Sequence
DRB1_0901  183  HTPHGQQVLSRFLHD  HTPHGQQVL       0.3767        849.0            50.00     Sequence
DRB1_0901  458  VQGDGRTYGHPIVLR  GRTYGHPIV       0.3765        850.8            50.00     Sequence
DRB1_0901  123  GGKLHSDLPEVQPVW  KLHSDLPEV       0.3760        855.4            50.00     Sequence
DRB1_0901  177  YHPEVMHTPHGQQVL  MHTPHGQQV       0.3754        860.8            50.00     Sequence
DRB1_0901  508  RVVLDITSKPPATIE  ITSKPPATI       0.3752        863.2            50.00     Sequence
DRB1_0901  164  AFEAFDRRLAGVQYH  FEAFDRRLA       0.3751        863.6            50.00     Sequence
DRB1_0901  393  EEIVARQPFPGPGLG  RQPFPGPGL       0.3735        878.8            50.00     Sequence
DRB1_0901  327  KTAEFLVQGTLYPDV  VQGTLYPDV       0.3733        880.7            50.00     Sequence
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DRB1_0901	426	DSIVREELTAAGLDN	EELTAAGLD	0.3733	880.8	50.00	Sequence
DRB1_0901	176	QYHPEVMHTPHGQQV	MHTPHGQQV	0.3733	880.9	50.00	Sequence
DRB1_0901	304	KRKIIGRQFIRAFEG	RKIIGRQFI	0.3705	907.7	50.00	Sequence
DRB1_0901	46	TASIEEIRARQPVAL	EIRARQPVA	0.3704	908.5	50.00	Sequence
DRB1_0901	510	VLDITSKPPATIEWE	ITSKPPATI	0.3697	916.1	50.00	Sequence
DRB1_0901	146	AAPDGFDVVASSAGA	FDVVASSAG	0.3684	928.5	50.00	Sequence
DRB1_0901	321	RDVLDGKTAEFLVQG	DGKTAEFLV	0.3669	943.5	50.00	Sequence
DRB1_0901	286	DAAETFLEALSGVSA	FLEALSGVS	0.3665	948.3	50.00	Sequence
DRB1_0901	210	IANALIEQVRTQIGD	IANALIEQV	0.3655	957.9	50.00	Sequence
DRB1_0901	254	CVFVDHGLLRAGERA	FVDHGLLRA	0.3650	963.0	50.00	Sequence
DRB1_0901	140	HGDAVTAAPDGFDVV	VTAAPDGFD	0.3647	967.1	50.00	Sequence
DRB1_0901	162	VAAFEAFDRRLAGVQ	AFEAFDRRL	0.3644	969.5	50.00	Sequence
DRB1_0901	322	DVLDGKTAEFLVQGT	DGKTAEFLV	0.3641	972.5	50.00	Sequence
DRB1_0901	31	RRVREARVFSEVIPH	EARVFSEVI	0.3640	973.6	50.00	Sequence
DRB1_0901	161	PVAAFEAFDRRLAGV	PVAAFEAFD	0.3638	975.6	50.00	Sequence
DRB1_0901	155	ASSAGAPVAAFEAFD	ASSAGAPVA	0.3632	982.2	50.00	Sequence
DRB1_0901	451	ADVRSVGVQGDGRTY	VGVQGDGRT	0.3632	982.3	50.00	Sequence
DRB1_0901	85	GVPVLGICYGFQAMA	ICYGFQAMA	0.3625	990.4	50.00	Sequence
DRB1_0901	186	HGQQVLSRFLHDFAG	QVLSRFLHD	0.3615	1000.3	50.00	Sequence
DRB1_0901	501	NEVAEVNRVVLDITS	VAEVNRVVL	0.3613	1002.6	50.00	Sequence
DRB1_0901	452	DVRSVGVQGDGRTYG	VGVQGDGRT	0.3604	1012.4	50.00	Sequence
DRB1_0901	103	GGIVAHTGTREYGRT	GIVAHTGTR	0.3597	1020.7	50.00	Sequence
DRB1_0901	389	LGLPEEIVARQPFPG	LGLPEEIVA	0.3586	1032.2	50.00	Sequence
DRB1_0901	394	EIVARQPFPGPGLGI	RQPFPGPGL	0.3585	1033.1	50.00	Sequence
DRB1_0901	502	EVAEVNRVVLDITSK	VAEVNRVVL	0.3581	1038.6	50.00	Sequence
DRB1_0901	262	LRAGERAQVQRDFVA	LRAGERAQV	0.3577	1042.8	50.00	Sequence
DRB1_0901	443	WQCPVVLLADVRSVG	WQCPVVLLA	0.3574	1046.2	50.00	Sequence
DRB1_0901	397	ARQPFPGPGLGIRIV	RQPFPGPGL	0.3572	1048.8	50.00	Sequence
DRB1_0901	197	DFAGLGAQWTPANIA	AQWTPANIA	0.3570	1050.1	50.00	Sequence
DRB1_0901	57	PVALVLSGGPASVYA	LSGGPASVY	0.3541	1084.5	50.00	Sequence
DRB1_0901	212	NALIEQVRTQIGDGH	LIEQVRTQI	0.3537	1089.2	50.00	Sequence
DRB1_0901	411	VGEVTAKRLDTLRHA	VGEVTAKRL	0.3532	1094.8	50.00	Sequence
DRB1_0901	320	VRDVLDGKTAEFLVQ	VLDGKTAEF	0.3524	1104.2	50.00	Sequence
DRB1_0901	398	RQPFPGPGLGIRIVG	RQPFPGPGL	0.3508	1124.1	50.00	Sequence
DRB1_0901	251	RLTCVFVDHGLLRAG	FVDHGLLRA	0.3502	1130.8	50.00	Sequence
DRB1_0901	425	ADSIVREELTAAGLD	EELTAAGLD	0.3489	1146.5	50.00	Sequence
DRB1_0901	45	HTASIEEIRARQPVA	EIRARQPVA	0.3485	1151.4	50.00	Sequence
DRB1_0901	5	DIDVPETPARPVLVV	VPETPARPV	0.3464	1178.7	50.00	Sequence
DRB1_0901	144	VTAAPDGFDVVASSA	VTAAPDGFD	0.3452	1194.3	50.00	Sequence
DRB1_0901	423	RHADSIVREELTAAG	HADSIVREE	0.3447	1199.5	50.00	Sequence
DRB1_0901	102	LGGIVAHTGTREYGR	GGIVAHTGT	0.3447	1199.9	50.00	Sequence
DRB1_0901	185	PHGQQVLSRFLHDFA	LSRFLHDFA	0.3443	1205.6	50.00	Sequence
DRB1_0901	196	HDFAGLGAQWTPANI	FAGLGAQWT	0.3441	1208.5	50.00	Sequence
DRB1_0901	252	LTCVFVDHGLLRAGE	FVDHGLLRA	0.3422	1232.8	50.00	Sequence
DRB1_0901	326	GKTAEFLVQGTLYPD	EFLVQGTLY	0.3422	1233.3	50.00	Sequence
DRB1_0901	253	TCVFVDHGLLRAGER	FVDHGLLRA	0.3418	1238.7	50.00	Sequence
DRB1_0901	168	FDRRLAGVQYHPEVM	DRRLAGVQY	0.3413	1244.9	50.00	Sequence
DRB1_0901	392	PEEIVARQPFPGPGL	RQPFPGPGL	0.3403	1258.6	50.00	Sequence
DRB1_0901	11	TPARPVLVVDFGAQY	TPARPVLVV	0.3403	1259.0	50.00	Sequence
DRB1_0901	427	SIVREELTAAGLDNQ	EELTAAGLD	0.3400	1262.5	50.00	Sequence
DRB1_0901	444	QCPVVLLADVRSVGV	LADVRSVGV	0.3384	1285.4	50.00	Sequence
DRB1_0901	211	ANALIEQVRTQIGDG	LIEQVRTQI	0.3382	1288.1	50.00	Sequence
DRB1_0901	157	SAGAPVAAFEAFDRR	PVAAFEAFD	0.3379	1291.1	50.00	Sequence
DRB1_0901	428	IVREELTAAGLDNQI	EELTAAGLD	0.3379	1291.2	50.00	Sequence
DRB1_0901	156	SSAGAPVAAFEAFDR	SSAGAPVAA	0.3375	1297.2	50.00	Sequence
DRB1_0901	324	LDGKTAEFLVQGTLY	DGKTAEFLV	0.3370	1304.0	50.00	Sequence
DRB1_0901	125	KLHSDLPEVQPVWMS	KLHSDLPEV	0.3369	1305.4	50.00	Sequence
DRB1_0901	184	TPHGQQVLSRFLHDF	GQQVLSRFL	0.3364	1312.3	50.00	Sequence
DRB1_0901	285	VDAAETFLEALSGVS	FLEALSGVS	0.3361	1317.4	50.00	Sequence
DRB1_0901	500	TNEVAEVNRVVLDIT	VAEVNRVVL	0.3355	1326.1	50.00	Sequence
DRB1_0901	402	PGPGLGIRIVGEVTA	LGIRIVGEV	0.3347	1337.7	50.00	Sequence
DRB1_0901	55	RQPVALVLSGGPASV	VLSGGPASV	0.3345	1340.1	50.00	Sequence
DRB1_0901	303	GKRKIIGRQFIRAFE	RKIIGRQFI	0.3341	1346.3	50.00	Sequence
DRB1_0901	503	VAEVNRVVLDITSKP	VAEVNRVVL	0.3331	1359.9	50.00	Sequence
DRB1_0901	206	TPANIANALIEQVRT	IANALIEQV	0.3325	1369.9	50.00	Sequence
DRB1_0901	361	GLPDDLKFTLVEPLR	LKFTLVEPL	0.3312	1388.2	50.00	Sequence

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DRB1_0901  316  FEGAVRDVLDGKTAE  FEGAVRDVL        0.3311       1391.1                50.00     Sequence
DRB1_0901  266  ERAQVQRDFVAATGA  VQRDFVAAT        0.3309       1393.6                50.00     Sequence
DRB1_0901  129  DLPEVQPVWMSHGDA  LPEVQPVWM        0.3297       1411.0                50.00     Sequence
DRB1_0901  424  HADSIVREELTAAGL  HADSIVREE        0.3295       1415.4                50.00     Sequence
DRB1_0901   56  QPVALVLSGGPASVY  LSGGPASVY        0.3280       1437.1                50.00     Sequence
DRB1_0901  223  GDGHAICGLSGGVDS  ICGLSGGVD        0.3280       1438.3                50.00     Sequence
DRB1_0901  222  IGDGHAICGLSGGVD  IGDGHAICG        0.3277       1443.0                50.00     Sequence
DRB1_0901  507  NRVVLDITSKPPATI  ITSKPPATI        0.3265       1461.0                50.00     Sequence
DRB1_0901  145  TAAPDGFDVVASSAG  FDVVASSAG        0.3264       1463.3                50.00     Sequence
DRB1_0901   44  PHTASIEEIRARQPV  PHTASIEEI        0.3262       1465.6                50.00     Sequence
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DRB1_0901  249  GDRLTCVFVDHGLLR  DRLTCVFVD        0.3248       1488.5                50.00     Sequence
DRB1_0901  353  IKSHHNVGGLPDDLK  KSHHNVGGL        0.3245       1492.7                50.00     Sequence
DRB1_0901  354  KSHHNVGGLPDDLKF  KSHHNVGGL        0.3231       1515.9                50.00     Sequence
DRB1_0901  213  ALIEQVRTQIGDGHA  LIEQVRTQI        0.3216       1540.4                50.00     Sequence
DRB1_0901  224  DGHAICGLSGGVDSA  ICGLSGGVD        0.3206       1558.2                50.00     Sequence
DRB1_0901   75  PKLDPALLDLGVPVL  PKLDPALLD        0.3181       1600.0                50.00     Sequence
DRB1_0901  143  AVTAAPDGFDVVASS  VTAAPDGFD        0.3178       1604.7                50.00     Sequence
DRB1_0901  457  GVQGDGRTYGHPIVL  GRTYGHPIV        0.3173       1613.7                50.00     Sequence
DRB1_0901   14  RPVLVVDFGAQYAQL  DFGAQYAQL        0.3159       1638.5                50.00     Sequence
DRB1_0901   54  ARQPVALVLSGGPAS  RQPVALVLS        0.3154       1647.3                50.00     Sequence
DRB1_0901  319  AVRDVLDGKTAEFLV  VLDGKTAEF        0.3153       1649.9                50.00     Sequence
DRB1_0901  302  EGKRKIIGRQFIRAF  RKIIGRQFI        0.3147       1660.4                50.00     Sequence
DRB1_0901  429  VREELTAAGLDNQIW  EELTAAGLD        0.3141       1670.8                50.00     Sequence
DRB1_0901  165  FEAFDRRLAGVQYHP  FEAFDRRLA        0.3136       1680.9                50.00     Sequence
DRB1_0901  280  ANLVTVDAAETFLEA  LVTVDAAET        0.3134       1684.4                50.00     Sequence
DRB1_0901  296  SGVSAPEGKRKIIGR  SGVSAPEGK        0.3121       1708.1                50.00     Sequence
DRB1_0901  390  GLPEEIVARQPFPGP  EEIVARQPF        0.3118       1714.0                50.00     Sequence
DRB1_0901  336  TLYPDVVESGGGSGT  TLYPDVVES        0.3114       1721.6                50.00     Sequence
DRB1_0901  128  SDLPEVQPVWMSHGD  LPEVQPVWM        0.3110       1727.8                50.00     Sequence
DRB1_0901  248  IGDRLTCVFVDHGLL  DRLTCVFVD        0.3103       1740.8                50.00     Sequence
DRB1_0901    4  ADIDVPETPARPVLV  VPETPARPV        0.3097       1752.9                50.00     Sequence
DRB1_0901  456  VGVQGDGRTYGHPIV  VGVQGDGRT        0.3096       1753.7                50.00     Sequence
DRB1_0901  355  SHHNVGGLPDDLKFT  VGGLPDDLK        0.3094       1757.8                50.00     Sequence
DRB1_0901  281  NLVTVDAAETFLEAL  LVTVDAAET        0.3076       1792.9                50.00     Sequence
DRB1_0901  357  HNVGGLPDDLKFTLV  VGGLPDDLK        0.3070       1803.6                50.00     Sequence
DRB1_0901  142  DAVTAAPDGFDVVAS  VTAAPDGFD        0.3044       1855.9                50.00     Sequence
DRB1_0901   74  APKLDPALLDLGVPV  APKLDPALL        0.3037       1869.7                50.00     Sequence
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DRB1_0901  356  HHNVGGLPDDLKFTL  VGGLPDDLK        0.3018       1909.9                50.00     Sequence
DRB1_0901  317  EGAVRDVLDGKTAEF  VLDGKTAEF        0.2997       1952.6                50.00     Sequence
DRB1_0901  279  GANLVTVDAAETFLE  NLVTVDAAE        0.2987       1973.7                50.00     Sequence
DRB1_0901  167  AFDRRLAGVQYHPEV  FDRRLAGVQ        0.2981       1987.4                50.00     Sequence
DRB1_0901  401  FPGPGLGIRIVGEVT  LGIRIVGEV        0.2972       2007.2                50.00     Sequence
DRB1_0901   84  LGVPVLGICYGFQAM  LGICYGFQA        0.2964       2025.0                50.00     Sequence
DRB1_0901  275  VAATGANLVTVDAAE  VAATGANLV        0.2956       2040.9                50.00     Sequence
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DRB1_0901  221  QIGDGHAICGLSGGV  DGHAICGLS        0.2930       2099.7                50.00     Sequence
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DRB1_0901  127  HSDLPEVQPVWMSHG  LPEVQPVWM        0.2891       2189.4                50.00     Sequence
DRB1_0901  245  QRAIGDRLTCVFVDH  QRAIGDRLT        0.2891       2190.8                50.00     Sequence
DRB1_0901  453  VRSVGVQGDGRTYGH  VGVQGDGRT        0.2887       2200.9                50.00     Sequence
DRB1_0901  278  TGANLVTVDAAETFL  NLVTVDAAE        0.2883       2210.1                50.00     Sequence
DRB1_0901  282  LVTVDAAETFLEALS  LVTVDAAET        0.2868       2244.8                50.00     Sequence
DRB1_0901  471  LRPVSSEDAMTADWT  LRPVSSEDA        0.2862       2259.8                50.00     Sequence
DRB1_0901  345  GGGSGTANIKSHHNV  GGGSGTANI        0.2858       2269.7                50.00     Sequence
DRB1_0901  455  SVGVQGDGRTYGHPI  VGVQGDGRT        0.2857       2271.4                50.00     Sequence
DRB1_0901  104  GIVAHTGTREYGRTE  IVAHTGTRE        0.2820       2365.6                50.00     Sequence
DRB1_0901  358  NVGGLPDDLKFTLVE  VGGLPDDLK        0.2813       2384.0                50.00     Sequence
DRB1_0901   72  DGAPKLDPALLDLGV  APKLDPALL        0.2809       2394.2                50.00     Sequence
DRB1_0901  220  TQIGDGHAICGLSGG  IGDGHAICG        0.2808       2396.2                50.00     Sequence
DRB1_0901   83  DLGVPVLGICYGFQA  LGICYGFQA        0.2807       2399.1                50.00     Sequence
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DRB1_0901   81  LLDLGVPVLGICYGF  LLDLGVPVL         0.2762        2519.0                  50.00      Sequence
DRB1_0901  344  SGGGSGTANIKSHHN  GGGSGTANI         0.2755        2536.3                  50.00      Sequence
DRB1_0901  126  LHSDLPEVQPVWMSH  LPEVQPVWM         0.2747        2558.5                  50.00      Sequence
DRB1_0901  400  PFPGPGLGIRIVGEV  LGIRIVGEV         0.2747        2558.7                  50.00      Sequence
DRB1_0901  343  ESGGGSGTANIKSHH  GGSGTANIK         0.2727        2615.3                  50.00      Sequence
DRB1_0901  105  IVAHTGTREYGRTEL  IVAHTGTRE         0.2725        2622.3                  50.00      Sequence
DRB1_0901  247  AIGDRLTCVFVDHGL  DRLTCVFVD         0.2724        2623.4                  50.00      Sequence
DRB1_0901  265  GERAQVQRDFVAATG  QRDFVAATG         0.2722        2630.0                  50.00      Sequence
DRB1_0901  352  NIKSHHNVGGLPDDL  KSHHNVGGL         0.2720        2634.4                  50.00      Sequence
DRB1_0901  342  VESGGGSGTANIKSH  GGGSGTANI         0.2708        2670.8                  50.00      Sequence
DRB1_0901  300  APEGKRKIIGRQFIR  RKIIGRQFI         0.2681        2748.0                  50.00      Sequence
DRB1_0901   71  ADGAPKLDPALLDLG  APKLDPALL         0.2669        2786.2                  50.00      Sequence
DRB1_0901   13  ARPVLVVDFGAQYAQ  VVDFGAQYA         0.2668        2788.0                  50.00      Sequence
DRB1_0901  341  VVESGGGSGTANIKS  GGSGTANIK         0.2663        2804.2                  50.00      Sequence
DRB1_0901  106  VAHTGTREYGRTELK  VAHTGTREY         0.2661        2809.4                  50.00      Sequence
DRB1_0901   76  KLDPALLDLGVPVLG  KLDPALLDL         0.2654        2830.2                  50.00      Sequence
DRB1_0901   82  LDLGVPVLGICYGFQ  LDLGVPVLG         0.2649        2846.9                  50.00      Sequence
DRB1_0901  219  RTQIGDGHAICGLSG  DGHAICGLS         0.2635        2890.1                  50.00      Sequence
DRB1_0901  454  RSVGVQGDGRTYGHP  VGVQGDGRT         0.2634        2891.4                  50.00      Sequence
DRB1_0901  214  LIEQVRTQIGDGHAI  LIEQVRTQI         0.2617        2946.9                  50.00      Sequence
DRB1_0901  505  EVNRVVLDITSKPPA  LDITSKPPA         0.2615        2953.3                  50.00      Sequence
DRB1_0901  297  GVSAPEGKRKIIGRQ  GVSAPEGKR         0.2609        2971.2                  50.00      Sequence
DRB1_0901  264  AGERAQVQRDFVAAT  AGERAQVQR         0.2599        3003.4                  50.00      Sequence
DRB1_0901  318  GAVRDVLDGKTAEFL  VLDGKTAEF         0.2592        3026.7                  50.00      Sequence
DRB1_0901  166  EAFDRRLAGVQYHPE  FDRRLAGVQ         0.2584        3054.2                  50.00      Sequence
DRB1_0901  435  AAGLDNQIWQCPVVL  QIWQCPVVL         0.2584        3054.7                  50.00      Sequence
DRB1_0901  340  DVVESGGGSGTANIK  GGGSGTANI         0.2572        3092.6                  50.00      Sequence
DRB1_0901   80  ALLDLGVPVLGICYG  LLDLGVPVL         0.2559        3137.3                  50.00      Sequence
DRB1_0901  431  EELTAAGLDNQIWQC  EELTAAGLD         0.2550        3167.7                  50.00      Sequence
DRB1_0901  263  RAGERAQVQRDFVAA  GERAQVQRD         0.2528        3242.4                  50.00      Sequence
DRB1_0901  399  QPFPGPGLGIRIVGE  QPFPGPGLG         0.2528        3244.3                  50.00      Sequence
DRB1_0901  299  SAPEGKRKIIGRQFI  RKIIGRQFI         0.2525        3255.9                  50.00      Sequence
DRB1_0901  284  TVDAAETFLEALSGV  TVDAAETFL         0.2522        3265.8                  50.00      Sequence
DRB1_0901  351  ANIKSHHNVGGLPDD  KSHHNVGGL         0.2499        3349.0                  50.00      Sequence
DRB1_0901  506  VNRVVLDITSKPPAT  LDITSKPPA         0.2481        3412.6                  50.00      Sequence
DRB1_0901  477  EDAMTADWTRVPYEV  AMTADWTRV         0.2467        3465.4                  50.00      Sequence
DRB1_0901  277  ATGANLVTVDAAETF  NLVTVDAAE         0.2456        3506.2                  50.00      Sequence
DRB1_0901  473  PVSSEDAMTADWTRV  PVSSEDAMT         0.2437        3577.8                  50.00      Sequence
DRB1_0901  359  VGGLPDDLKFTLVEP  VGGLPDDLK         0.2421        3643.0                  50.00      Sequence
DRB1_0901    3  PADIDVPETPARPVL  VPETPARPV         0.2418        3653.9                  50.00      Sequence
DRB1_0901    0  VVQPADIDVPETPAR  VVQPADIDV         0.2405        3706.6                  50.00      Sequence
DRB1_0901  472  RPVSSEDAMTADWTR  PVSSEDAMT         0.2398        3735.4                  50.00      Sequence
DRB1_0901  346  GGSGTANIKSHHNVG  GGSGTANIK         0.2395        3747.7                  50.00      Sequence
DRB1_0901  218  VRTQIGDGHAICGLS  DGHAICGLS         0.2392        3757.1                  50.00      Sequence
DRB1_0901  337  LYPDVVESGGGSGTA  LYPDVVESG         0.2371        3842.5                  50.00      Sequence
DRB1_0901  246  RAIGDRLTCVFVDHG  DRLTCVFVD         0.2368        3856.0                  50.00      Sequence
DRB1_0901  216  EQVRTQIGDGHAICG  EQVRTQIGD         0.2367        3861.4                  50.00      Sequence
DRB1_0901  360  GGLPDDLKFTLVEPL  LKFTLVEPL         0.2366        3864.8                  50.00      Sequence
DRB1_0901  276  AATGANLVTVDAAET  NLVTVDAAE         0.2333        4007.6                  50.00      Sequence
DRB1_0901  350  TANIKSHHNVGGLPD  KSHHNVGGL         0.2299        4157.1                  50.00      Sequence
DRB1_0901  217  QVRTQIGDGHAICGL  QVRTQIGDG         0.2281        4239.1                  50.00      Sequence
DRB1_0901  475  SSEDAMTADWTRVPY  SSEDAMTAD         0.2280        4241.4                  50.00      Sequence
DRB1_0901  283  VTVDAAETFLEALSG  TVDAAETFL         0.2275        4265.1                  50.00      Sequence
DRB1_0901  476  SEDAMTADWTRVPYE  EDAMTADWT         0.2274        4271.4                  50.00      Sequence
DRB1_0901  348  SGTANIKSHHNVGGL  KSHHNVGGL         0.2221        4522.7                  50.00      Sequence
DRB1_0901   79  PALLDLGVPVLGICY  LLDLGVPVL         0.2215        4553.3                  50.00      Sequence
DRB1_0901  412  GEVTAKRLDTLRHAD  GEVTAKRLD         0.2195        4650.0                  50.00      Sequence
DRB1_0901  474  VSSEDAMTADWTRVP  SSEDAMTAD         0.2181        4724.1                  50.00      Sequence
DRB1_0901    2  QPADIDVPETPARPV  VPETPARPV         0.2162        4822.0                  50.00      Sequence
DRB1_0901   78  DPALLDLGVPVLGIC  LLDLGVPVL         0.2148        4895.6                  50.00      Sequence
DRB1_0901  339  PDVVESGGGSGTANI  VVESGGGSG         0.2139        4939.7                  50.00      Sequence
DRB1_0901  215  IEQVRTQIGDGHAIC  IEQVRTQIG         0.2082        5256.9                  50.00      Sequence
DRB1_0901  298  VSAPEGKRKIIGRQF  APEGKRKII         0.2045        5472.4                  50.00      Sequence
DRB1_0901  347  GSGTANIKSHHNVGG  SGTANIKSH         0.2017        5641.5                  50.00      Sequence
DRB1_0901  349  GTANIKSHHNVGGLP  KSHHNVGGL         0.2012        5670.0                  50.00      Sequence
DRB1_0901  338  YPDVVESGGGSGTAN  ESGGGSGTA         0.1998        5755.3                  50.00      Sequence
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   DRB1_0901   77  LDPALLDLGVPVLGI  LLDLGVPVL        0.1995       5772.8                50.00     Sequence
   DRB1_0901  434  TAAGLDNQIWQCPVV  NQIWQCPVV        0.1917       6282.5                50.00     Sequence
   DRB1_0901  414  VTAKRLDTLRHADSI  KRLDTLRHA        0.1782       7275.2                50.00     Sequence
   DRB1_0901  413  EVTAKRLDTLRHADS  KRLDTLRHA        0.1764       7410.6                50.00     Sequence
   DRB1_0901  432  ELTAAGLDNQIWQCP  ELTAAGLDN        0.1621       8650.7                50.00     Sequence
   DRB1_0901    1  VQPADIDVPETPARP  DIDVPETPA        0.1258      12814.1                50.00     Sequence
   DRB1_0901  433  LTAAGLDNQIWQCPV  LTAAGLDNQ        0.1175      14029.2                50.00     Sequence
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Allele: DRB1_0901. Number of high binders 10. Number of weak binders 201. Number of peptides 511

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1101  486  RVPYEVLERISTRIT  YEVLERIST        0.6569         40.9         SB     4.00     Sequence
   DRB1_1101  487  VPYEVLERISTRITN  YEVLERIST        0.6527         42.9         SB     4.00     Sequence
   DRB1_1101  405  GLGIRIVGEVTAKRL  IRIVGEVTA        0.6472         45.5         SB     4.00     Sequence
   DRB1_1101  304  KRKIIGRQFIRAFEG  RKIIGRQFI        0.6454         46.4         SB     4.00     Sequence
   DRB1_1101  488  PYEVLERISTRITNE  YEVLERIST        0.6354         51.7         WB     8.00     Sequence
   DRB1_1101   92  CYGFQAMAQALGGIV  FQAMAQALG        0.6274         56.3         WB     8.00     Sequence
   DRB1_1101  406  LGIRIVGEVTAKRLD  IRIVGEVTA        0.6236         58.7         WB     8.00     Sequence
   DRB1_1101   23  AQYAQLIARRVREAR  YAQLIARRV        0.6230         59.1         WB     8.00     Sequence
   DRB1_1101  303  GKRKIIGRQFIRAFE  RKIIGRQFI        0.6223         59.6         WB     8.00     Sequence
   DRB1_1101   93  YGFQAMAQALGGIVA  FQAMAQALG        0.6217         59.9         WB     8.00     Sequence
   DRB1_1101  485  TRVPYEVLERISTRI  YEVLERIST        0.6209         60.4         WB     8.00     Sequence
   DRB1_1101   91  ICYGFQAMAQALGGI  FQAMAQALG        0.6174         62.8         WB     8.00     Sequence
   DRB1_1101  302  EGKRKIIGRQFIRAF  RKIIGRQFI        0.6167         63.2         WB     8.00     Sequence
   DRB1_1101   24  QYAQLIARRVREARV  YAQLIARRV        0.6162         63.6         WB     8.00     Sequence
   DRB1_1101  255  VFVDHGLLRAGERAQ  HGLLRAGER        0.6069         70.3         WB     8.00     Sequence
   DRB1_1101  163  AAFEAFDRRLAGVQY  FEAFDRRLA        0.6039         72.7         WB     8.00     Sequence
   DRB1_1101  404  PGLGIRIVGEVTAKR  IRIVGEVTA        0.6038         72.7         WB     8.00     Sequence
   DRB1_1101   25  YAQLIARRVREARVF  YAQLIARRV        0.6029         73.5         WB     8.00     Sequence
   DRB1_1101   22  GAQYAQLIARRVREA  YAQLIARRV        0.6027         73.6         WB     8.00     Sequence
   DRB1_1101  164  AFEAFDRRLAGVQYH  EAFDRRLAG        0.5972         78.1         WB     8.00     Sequence
   DRB1_1101  256  FVDHGLLRAGERAQV  HGLLRAGER        0.5963         78.9         WB     8.00     Sequence
   DRB1_1101  162  VAAFEAFDRRLAGVQ  FEAFDRRLA        0.5913         83.2         WB     8.00     Sequence
   DRB1_1101   90  GICYGFQAMAQALGG  YGFQAMAQA        0.5888         85.5         WB     8.00     Sequence
   DRB1_1101  305  RKIIGRQFIRAFEGA  RKIIGRQFI        0.5881         86.2         WB     8.00     Sequence
   DRB1_1101  257  VDHGLLRAGERAQVQ  HGLLRAGER        0.5862         88.0         WB     8.00     Sequence
   DRB1_1101  407  GIRIVGEVTAKRLDT  IRIVGEVTA        0.5834         90.7         WB     8.00     Sequence
   DRB1_1101  367  KFTLVEPLRLLFKDE  VEPLRLLFK        0.5831         91.0         WB     8.00     Sequence
   DRB1_1101  307  IIGRQFIRAFEGAVR  RQFIRAFEG        0.5829         91.2         WB     8.00     Sequence
   DRB1_1101  254  CVFVDHGLLRAGERA  HGLLRAGER        0.5777         96.5         WB     8.00     Sequence
   DRB1_1101  489  YEVLERISTRITNEV  YEVLERIST        0.5766         97.6         WB     8.00     Sequence
   DRB1_1101  309  GRQFIRAFEGAVRDV  RQFIRAFEG        0.5674        107.8         WB     8.00     Sequence
   DRB1_1101  366  LKFTLVEPLRLLFKD  FTLVEPLRL        0.5658        109.8         WB    16.00     Sequence
   DRB1_1101  308  IGRQFIRAFEGAVRD  RQFIRAFEG        0.5638        112.1         WB    16.00     Sequence
   DRB1_1101  306  KIIGRQFIRAFEGAV  RQFIRAFEG        0.5614        115.0         WB    16.00     Sequence
   DRB1_1101  301  PEGKRKIIGRQFIRA  RKIIGRQFI        0.5596        117.3         WB    16.00     Sequence
   DRB1_1101   89  LGICYGFQAMAQALG  YGFQAMAQA        0.5593        117.7         WB    16.00     Sequence
   DRB1_1101  368  FTLVEPLRLLFKDEV  VEPLRLLFK        0.5588        118.3         WB    16.00     Sequence
   DRB1_1101  484  WTRVPYEVLERISTR  YEVLERIST        0.5579        119.5         WB    16.00     Sequence
   DRB1_1101   94  GFQAMAQALGGIVAH  FQAMAQALG        0.5529        126.2         WB    16.00     Sequence
   DRB1_1101   21  FGAQYAQLIARRVRE  YAQLIARRV        0.5507        129.2         WB    16.00     Sequence
   DRB1_1101  365  DLKFTLVEPLRLLFK  FTLVEPLRL        0.5477        133.4         WB    16.00     Sequence
   DRB1_1101  161  PVAAFEAFDRRLAGV  FEAFDRRLA        0.5414        142.8         WB    16.00     Sequence
   DRB1_1101  310  RQFIRAFEGAVRDVL  RQFIRAFEG        0.5387        147.1         WB    16.00     Sequence
   DRB1_1101  258  DHGLLRAGERAQVQR  HGLLRAGER        0.5333        156.0         WB    16.00     Sequence
   DRB1_1101  403  GPGLGIRIVGEVTAK  IRIVGEVTA        0.5319        158.3         WB    16.00     Sequence
   DRB1_1101  373  PLRLLFKDEVRAVGR  LRLLFKDEV        0.5265        167.9         WB    16.00     Sequence
   DRB1_1101  369  TLVEPLRLLFKDEVR  VEPLRLLFK        0.5256        169.6         WB    16.00     Sequence
   DRB1_1101  371  VEPLRLLFKDEVRAV  VEPLRLLFK        0.5196        180.9         WB    16.00     Sequence
   DRB1_1101  374  LRLLFKDEVRAVGRE  LFKDEVRAV        0.5183        183.4         WB    16.00     Sequence
   DRB1_1101   88  VLGICYGFQAMAQAL  YGFQAMAQA        0.5153        189.5         WB    16.00     Sequence
   DRB1_1101  165  FEAFDRRLAGVQYHP  FEAFDRRLA        0.5125        195.2         WB    16.00     Sequence
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DRB1_1101  253  TCVFVDHGLLRAGER  HGLLRAGER         0.5116         197.2          WB    16.00      Sequence
DRB1_1101  370  LVEPLRLLFKDEVRA  VEPLRLLFK         0.5095         201.8          WB    16.00      Sequence
DRB1_1101  114  YGRTELKVLGGKLHS  LKVLGGKLH         0.5023         218.1          WB    16.00      Sequence
DRB1_1101  115  GRTELKVLGGKLHSD  LKVLGGKLH         0.5019         219.1          WB    16.00      Sequence
DRB1_1101  372  EPLRLLFKDEVRAVG  LRLLFKDEV         0.4996         224.5          WB    16.00      Sequence
DRB1_1101   20  DFGAQYAQLIARRVR  YAQLIARRV         0.4962         232.9          WB    16.00      Sequence
DRB1_1101  117  TELKVLGGKLHSDLP  LKVLGGKLH         0.4934         240.3          WB    16.00      Sequence
DRB1_1101  116  RTELKVLGGKLHSDL  LKVLGGKLH         0.4934         240.3          WB    16.00      Sequence
DRB1_1101  375  RLLFKDEVRAVGREL  FKDEVRAVG         0.4923         243.1          WB    16.00      Sequence
DRB1_1101  490  EVLERISTRITNEVA  LERISTRIT         0.4893         251.0          WB    16.00      Sequence
DRB1_1101  483  DWTRVPYEVLERIST  YEVLERIST         0.4847         263.9          WB    16.00      Sequence
DRB1_1101  118  ELKVLGGKLHSDLPE  LKVLGGKLH         0.4780         283.6          WB    16.00      Sequence
DRB1_1101  465  YGHPIVLRPVSSEDA  HPIVLRPVS         0.4775         285.2          WB    16.00      Sequence
DRB1_1101   26  AQLIARRVREARVFS  QLIARRVRE         0.4773         285.9          WB    16.00      Sequence
DRB1_1101  300  APEGKRKIIGRQFIR  RKIIGRQFI         0.4757         290.9          WB    16.00      Sequence
DRB1_1101  491  VLERISTRITNEVAE  LERISTRIT         0.4736         297.7          WB    16.00      Sequence
DRB1_1101  113  EYGRTELKVLGGKLH  RTELKVLGG         0.4673         318.6          WB    32.00      Sequence
DRB1_1101  288  AETFLEALSGVSAPE  FLEALSGVS         0.4672         318.8          WB    32.00      Sequence
DRB1_1101  259  HGLLRAGERAQVQRD  HGLLRAGER         0.4661         322.8          WB    32.00      Sequence
DRB1_1101  376  LLFKDEVRAVGRELG  FKDEVRAVG         0.4659         323.2          WB    32.00      Sequence
DRB1_1101  464  TYGHPIVLRPVSSED  HPIVLRPVS         0.4640         330.2          WB    32.00      Sequence
DRB1_1101  364  DDLKFTLVEPLRLLF  FTLVEPLRL         0.4635         332.0          WB    32.00      Sequence
DRB1_1101  291  FLEALSGVSAPEGKR  FLEALSGVS         0.4623         336.3          WB    32.00      Sequence
DRB1_1101  377  LFKDEVRAVGRELGL  FKDEVRAVG         0.4608         341.6          WB    32.00      Sequence
DRB1_1101  160  APVAAFEAFDRRLAG  AFEAFDRRL         0.4607         342.1          WB    32.00      Sequence
DRB1_1101  289  ETFLEALSGVSAPEG  FLEALSGVS         0.4597         346.0          WB    32.00      Sequence
DRB1_1101   95  FQAMAQALGGIVAHT  FQAMAQALG         0.4547         365.2          WB    32.00      Sequence
DRB1_1101  416  AKRLDTLRHADSIVR  LDTLRHADS         0.4517         377.1          WB    32.00      Sequence
DRB1_1101  290  TFLEALSGVSAPEGK  FLEALSGVS         0.4505         382.0          WB    32.00      Sequence
DRB1_1101  466  GHPIVLRPVSSEDAM  HPIVLRPVS         0.4469         397.1          WB    32.00      Sequence
DRB1_1101  402  PGPGLGIRIVGEVTA  IRIVGEVTA         0.4461         400.8          WB    32.00      Sequence
DRB1_1101   27  QLIARRVREARVFSE  QLIARRVRE         0.4391         432.2          WB    32.00      Sequence
DRB1_1101  378  FKDEVRAVGRELGLP  EVRAVGREL         0.4384         435.3          WB    32.00      Sequence
DRB1_1101  287  AAETFLEALSGVSAP  FLEALSGVS         0.4373         440.5          WB    32.00      Sequence
DRB1_1101  379  KDEVRAVGRELGLPE  VRAVGRELG         0.4345         454.1          WB    32.00      Sequence
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DRB1_1101  381  EVRAVGRELGLPEEI  VRAVGRELG         0.4254         501.4                32.00      Sequence
DRB1_1101  292  LEALSGVSAPEGKRK  ALSGVSAPE         0.4252         502.2                32.00      Sequence
DRB1_1101  463  RTYGHPIVLRPVSSE  HPIVLRPVS         0.4249         503.8                32.00      Sequence
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DRB1_1101  194  FLHDFAGLGAQWTPA  FAGLGAQWT         0.4242         507.6                32.00      Sequence
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DRB1_1101  119  LKVLGGKLHSDLPEV  LKVLGGKLH         0.4233         512.9                32.00      Sequence
DRB1_1101   19  VDFGAQYAQLIARRV  YAQLIARRV         0.4176         545.1                32.00      Sequence
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DRB1_1101  186  HGQQVLSRFLHDFAG  QQVLSRFLH         0.4139         567.3                32.00      Sequence
DRB1_1101  192  SRFLHDFAGLGAQWT  FLHDFAGLG         0.4137         568.9                32.00      Sequence
DRB1_1101  467  HPIVLRPVSSEDAMT  PIVLRPVSS         0.4115         582.7                32.00      Sequence
DRB1_1101  187  GQQVLSRFLHDFAGL  QQVLSRFLH         0.4106         588.1                32.00      Sequence
DRB1_1101  185  PHGQQVLSRFLHDFA  QQVLSRFLH         0.4075         608.4                32.00      Sequence
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DRB1_1101   36  ARVFSEVIPHTASIE  FSEVIPHTA         0.4052         623.7                32.00      Sequence
DRB1_1101   58  VALVLSGGPASVYAD  LVLSGGPAS         0.4045         628.1                32.00      Sequence
DRB1_1101  312  FIRAFEGAVRDVLDG  AFEGAVRDV         0.4023         643.6                32.00      Sequence
DRB1_1101  492  LERISTRITNEVAEV  LERISTRIT         0.4019         646.6                32.00      Sequence
DRB1_1101   37  RVFSEVIPHTASIEE  FSEVIPHTA         0.3985         670.8                32.00      Sequence
DRB1_1101   28  LIARRVREARVFSEV  IARRVREAR         0.3978         675.4                32.00      Sequence
DRB1_1101   57  PVALVLSGGPASVYA  VALVLSGGP         0.3954         693.3                32.00      Sequence
DRB1_1101  286  DAAETFLEALSGVSA  ETFLEALSG         0.3942         702.3                32.00      Sequence
DRB1_1101  417  KRLDTLRHADSIVRE  LDTLRHADS         0.3916         722.7                32.00      Sequence
DRB1_1101  252  LTCVFVDHGLLRAGE  VFVDHGLLR         0.3911         726.7                32.00      Sequence
DRB1_1101  382  VRAVGRELGLPEEIV  VRAVGRELG         0.3886         746.4                32.00      Sequence
DRB1_1101  363  PDDLKFTLVEPLRLL  FTLVEPLRL         0.3864         764.6                32.00      Sequence
DRB1_1101  413  EVTAKRLDTLRHADS  AKRLDTLRH         0.3861         766.6                32.00      Sequence
DRB1_1101  191  LSRFLHDFAGLGAQW  LSRFLHDFA         0.3853         773.4                32.00      Sequence
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DRB1_1101	299	SAPEGKRKIIGRQFI	RKIIGRQFI	0.3838	786.1	32.00	Sequence
DRB1_1101	29	IARRVREARVFSEVI	RVREARVFS	0.3791	827.0	32.00	Sequence
DRB1_1101	112	REYGRTELKVLGGKL	RTELKVLGG	0.3789	829.3	32.00	Sequence
DRB1_1101	188	QQVLSRFLHDFAGLG	QQVLSRFLH	0.3785	832.2	32.00	Sequence
DRB1_1101	87	PVLGICYGFQAMAQA	YGFQAMAQA	0.3784	833.7	32.00	Sequence
DRB1_1101	184	TPHGQQVLSRFLHDF	QQVLSRFLH	0.3778	838.6	32.00	Sequence
DRB1_1101	462	GRTYGHPIVLRPVSS	HPIVLRPVS	0.3765	851.0	32.00	Sequence
DRB1_1101	328	TAEFLVQGTLYPDVV	FLVQGTLYP	0.3743	871.2	32.00	Sequence
DRB1_1101	329	AEFLVQGTLYPDVVE	FLVQGTLYP	0.3727	886.4	32.00	Sequence
DRB1_1101	56	QPVALVLSGGPASVY	VALVLSGGP	0.3713	900.2	32.00	Sequence
DRB1_1101	35	EARVFSEVIPHTASI	FSEVIPHTA	0.3686	926.6	32.00	Sequence
DRB1_1101	195	LHDFAGLGAQWTPAN	FAGLGAQWT	0.3661	951.9	32.00	Sequence
DRB1_1101	414	VTAKRLDTLRHADSI	AKRLDTLRH	0.3660	953.1	32.00	Sequence
DRB1_1101	418	RLDTLRHADSIVREE	LDTLRHADS	0.3657	956.7	32.00	Sequence
DRB1_1101	419	LDTLRHADSIVREEL	LRHADSIVR	0.3570	1050.6	32.00	Sequence
DRB1_1101	293	EALSGVSAPEGKRKI	LSGVSAPEG	0.3554	1069.4	32.00	Sequence
DRB1_1101	327	KTAEFLVQGTLYPDV	EFLVQGTLY	0.3541	1084.3	32.00	Sequence
DRB1_1101	190	VLSRFLHDFAGLGAQ	LSRFLHDFA	0.3531	1095.7	50.00	Sequence
DRB1_1101	189	QVLSRFLHDFAGLGA	LSRFLHDFA	0.3529	1098.1	50.00	Sequence
DRB1_1101	412	GEVTAKRLDTLRHAD	AKRLDTLRH	0.3520	1108.8	50.00	Sequence
DRB1_1101	447	VVLLADVRSVGVQGD	VVLLADVRS	0.3482	1155.5	50.00	Sequence
DRB1_1101	251	RLTCVFVDHGLLRAG	VFVDHGLLR	0.3481	1156.7	50.00	Sequence
DRB1_1101	167	AFDRRLAGVQYHPEV	RRLAGVQYH	0.3467	1174.2	50.00	Sequence
DRB1_1101	159	GAPVAAFEAFDRRLA	FEAFDRRLA	0.3457	1187.6	50.00	Sequence
DRB1_1101	59	ALVLSGGPASVYADG	LVLSGGPAS	0.3455	1189.7	50.00	Sequence
DRB1_1101	330	EFLVQGTLYPDVVES	EFLVQGTLY	0.3454	1190.6	50.00	Sequence
DRB1_1101	411	VGEVTAKRLDTLRHA	AKRLDTLRH	0.3442	1206.1	50.00	Sequence
DRB1_1101	446	PVVLLADVRSVGVQG	VVLLADVRS	0.3438	1211.9	50.00	Sequence
DRB1_1101	30	ARRVREARVFSEVIP	RVREARVFS	0.3434	1216.8	50.00	Sequence
DRB1_1101	285	VDAAETFLEALSGVS	ETFLEALSG	0.3364	1312.5	50.00	Sequence
DRB1_1101	410	IVGEVTAKRLDTLRH	AKRLDTLRH	0.3359	1320.5	50.00	Sequence
DRB1_1101	313	IRAFEGAVRDVLDGK	AFEGAVRDV	0.3314	1385.3	50.00	Sequence
DRB1_1101	34	REARVFSEVIPHTAS	FSEVIPHTA	0.3305	1399.3	50.00	Sequence
DRB1_1101	183	HTPHGQQVLSRFLHD	QQVLSRFLH	0.3282	1434.3	50.00	Sequence
DRB1_1101	445	CPVVLLADVRSVGVQ	VVLLADVRS	0.3281	1436.4	50.00	Sequence
DRB1_1101	38	VFSEVIPHTASIEEI	FSEVIPHTA	0.3242	1498.5	50.00	Sequence
DRB1_1101	238	AVAAALVQRAIGDRL	AALVQRAIG	0.3233	1512.2	50.00	Sequence
DRB1_1101	326	GKTAEFLVQGTLYPD	EFLVQGTLY	0.3216	1540.6	50.00	Sequence
DRB1_1101	31	RRVREARVFSEVIPH	RVREARVFS	0.3212	1547.6	50.00	Sequence
DRB1_1101	55	RQPVALVLSGGPASV	VALVLSGGP	0.3193	1580.2	50.00	Sequence
DRB1_1101	362	LPDDLKFTLVEPLRL	FTLVEPLRL	0.3181	1599.6	50.00	Sequence
DRB1_1101	224	DGHAICGLSGGVDSA	AICGLSGGV	0.3164	1630.5	50.00	Sequence
DRB1_1101	196	HDFAGLGAQWTPANI	FAGLGAQWT	0.3147	1659.6	50.00	Sequence
DRB1_1101	444	QCPVVLLADVRSVGV	VVLLADVRS	0.3140	1672.7	50.00	Sequence
DRB1_1101	294	ALSGVSAPEGKRKII	LSGVSAPEG	0.3136	1679.8	50.00	Sequence
DRB1_1101	111	TREYGRTELKVLGGK	RTELKVLGG	0.3115	1718.3	50.00	Sequence
DRB1_1101	98	MAQALGGIVAHTGTR	LGGIVAHTG	0.3105	1736.9	50.00	Sequence
DRB1_1101	33	VREARVFSEVIPHTA	FSEVIPHTA	0.3098	1751.4	50.00	Sequence
DRB1_1101	225	GHAICGLSGGVDSAV	AICGLSGGV	0.3081	1782.9	50.00	Sequence
DRB1_1101	168	FDRRLAGVQYHPEVM	RRLAGVQYH	0.3051	1843.0	50.00	Sequence
DRB1_1101	507	NRVVLDITSKPPATI	VLDITSKPP	0.3040	1864.7	50.00	Sequence
DRB1_1101	96	QAMAQALGGIVAHTG	AQALGGIVA	0.3032	1880.9	50.00	Sequence
DRB1_1101	97	AMAQALGGIVAHTGT	MAQALGGIV	0.3013	1920.3	50.00	Sequence
DRB1_1101	86	VPVLGICYGFQAMAQ	VPVLGICYG	0.3005	1935.6	50.00	Sequence
DRB1_1101	209	NIANALIEQVRTQIG	NALIEQVRT	0.2987	1974.4	50.00	Sequence
DRB1_1101	461	DGRTYGHPIVLRPVS	HPIVLRPVS	0.2982	1985.9	50.00	Sequence
DRB1_1101	239	VAAALVQRAIGDRLT	AALVQRAIG	0.2973	2003.3	50.00	Sequence
DRB1_1101	420	DTLRHADSIVREELT	LRHADSIVR	0.2962	2029.2	50.00	Sequence
DRB1_1101	32	RVREARVFSEVIPHT	RVREARVFS	0.2951	2051.5	50.00	Sequence
DRB1_1101	493	ERISTRITNEVAEVN	ERISTRITN	0.2932	2095.7	50.00	Sequence
DRB1_1101	237	SAVAAALVQRAIGDR	AAALVQRAI	0.2931	2098.3	50.00	Sequence
DRB1_1101	260	GLLRAGERAQVQRDF	LLRAGERAQ	0.2926	2108.4	50.00	Sequence
DRB1_1101	223	GDGHAICGLSGGVDS	AICGLSGGV	0.2926	2108.7	50.00	Sequence
DRB1_1101	250	DRLTCVFVDHGLLRA	VFVDHGLLR	0.2924	2113.0	50.00	Sequence
DRB1_1101	210	IANALIEQVRTQIGD	NALIEQVRT	0.2914	2136.4	50.00	Sequence
DRB1_1101	169	DRRLAGVQYHPEVMH	RRLAGVQYH	0.2891	2189.9	50.00	Sequence

DRB1_1101	506	VNRVVLDITSKPPAT	NRVVLDITS	0.2880	2217.1	50.00	Sequence
DRB1_1101	170	RRLAGVQYHPEVMHT	RRLAGVQYH	0.2842	2310.6	50.00	Sequence
DRB1_1101	182	MHTPHGQQVLSRFLH	GQQVLSRFL	0.2837	2320.8	50.00	Sequence
DRB1_1101	85	GVPVLGICYGFQAMA	VPVLGICYG	0.2834	2330.5	50.00	Sequence
DRB1_1101	508	RVVLDITSKPPATIE	VLDITSKPP	0.2804	2406.6	50.00	Sequence
DRB1_1101	421	TLRHADSIVREELTA	LRHADSIVR	0.2799	2418.5	50.00	Sequence
DRB1_1101	226	HAICGLSGGVDSAVA	AICGLSGGV	0.2792	2439.1	50.00	Sequence
DRB1_1101	99	AQALGGIVAHTGTRE	LGGIVAHTG	0.2779	2471.3	50.00	Sequence
DRB1_1101	409	RIVGEVTAKRLDTLR	EVTAKRLDT	0.2771	2492.8	50.00	Sequence
DRB1_1101	197	DFAGLGAQWTPANIA	FAGLGAQWT	0.2768	2503.1	50.00	Sequence
DRB1_1101	100	QALGGIVAHTGTREY	LGGIVAHTG	0.2754	2539.8	50.00	Sequence
DRB1_1101	455	SVGVQGDGRTYGHPI	GVQGDGRTY	0.2744	2568.6	50.00	Sequence
DRB1_1101	39	FSEVIPHTASIEEIR	FSEVIPHTA	0.2739	2582.8	50.00	Sequence
DRB1_1101	401	FPGPGLGIRIVGEVT	GIRIVGEVT	0.2717	2642.7	50.00	Sequence
DRB1_1101	325	DGKTAEFLVQGTLYP	EFLVQGTLY	0.2717	2644.0	50.00	Sequence
DRB1_1101	454	RSVGVQGDGRTYGHP	GVQGDGRTY	0.2705	2677.4	50.00	Sequence
DRB1_1101	48	SIEEIRARQPVALVL	IEEIRARQP	0.2696	2703.6	50.00	Sequence
DRB1_1101	174	GVQYHPEVMHTPHGQ	VQYHPEVMH	0.2692	2717.8	50.00	Sequence
DRB1_1101	60	LVLSGGPASVYADGA	LVLSGGPAS	0.2673	2773.2	50.00	Sequence
DRB1_1101	212	NALIEQVRTQIGDGH	IEQVRTQIG	0.2673	2774.1	50.00	Sequence
DRB1_1101	211	ANALIEQVRTQIGDG	NALIEQVRT	0.2665	2797.6	50.00	Sequence
DRB1_1101	120	KVLGGKLHSDLPEVQ	KVLGGKLHS	0.2658	2819.3	50.00	Sequence
DRB1_1101	173	AGVQYHPEVMHTPHG	VQYHPEVMH	0.2647	2853.1	50.00	Sequence
DRB1_1101	172	LAGVQYHPEVMHTPH	VQYHPEVMH	0.2634	2891.1	50.00	Sequence
DRB1_1101	331	FLVQGTLYPDVVESG	FLVQGTLYP	0.2631	2902.9	50.00	Sequence
DRB1_1101	456	VGVQGDGRTYGHPIV	GVQGDGRTY	0.2611	2966.2	50.00	Sequence
DRB1_1101	198	FAGLGAQWTPANIAN	FAGLGAQWT	0.2582	3060.4	50.00	Sequence
DRB1_1101	505	EVNRVVLDITSKPPA	NRVVLDITS	0.2579	3071.4	50.00	Sequence
DRB1_1101	509	VVLDITSKPPATIEW	LDITSKPPA	0.2578	3073.1	50.00	Sequence
DRB1_1101	314	RAFEGAVRDVLDGKT	RAFEGAVRD	0.2577	3075.6	50.00	Sequence
DRB1_1101	240	AAALVQRAIGDRLTC	AALVQRAIG	0.2575	3082.2	50.00	Sequence
DRB1_1101	208	ANIANALIEQVRTQI	NALIEQVRT	0.2574	3085.4	50.00	Sequence
DRB1_1101	101	ALGGIVAHTGTREYG	LGGIVAHTG	0.2568	3107.8	50.00	Sequence
DRB1_1101	84	LGVPVLGICYGFQAM	VPVLGICYG	0.2559	3135.5	50.00	Sequence
DRB1_1101	468	PIVLRPVSSEDAMTA	PIVLRPVSS	0.2555	3150.4	50.00	Sequence
DRB1_1101	80	ALLDLGVPVLGICYG	ALLDLGVPV	0.2555	3152.2	50.00	Sequence
DRB1_1101	222	IGDGHAICGLSGGVD	AICGLSGGV	0.2546	3179.8	50.00	Sequence
DRB1_1101	49	IEEIRARQPVALVLS	EIRARQPVA	0.2542	3194.3	50.00	Sequence
DRB1_1101	227	AICGLSGGVDSAVAA	AICGLSGGV	0.2534	3224.6	50.00	Sequence
DRB1_1101	110	GTREYGRTELKVLGG	GRTELKVLG	0.2516	3287.6	50.00	Sequence
DRB1_1101	47	ASIEEIRARQPVALV	IEEIRARQP	0.2501	3338.7	50.00	Sequence
DRB1_1101	102	LGGIVAHTGTREYGR	LGGIVAHTG	0.2496	3357.7	50.00	Sequence
DRB1_1101	82	LDLGVPVLGICYGFQ	VPVLGICYG	0.2489	3385.5	50.00	Sequence
DRB1_1101	104	GIVAHTGTREYGRTE	VAHTGTREY	0.2486	3394.9	50.00	Sequence
DRB1_1101	438	LDNQIWQCPVVLLAD	IWQCPVVLL	0.2482	3410.8	50.00	Sequence
DRB1_1101	482	ADWTRVPYEVLERIS	PYEVLERIS	0.2458	3498.4	50.00	Sequence
DRB1_1101	443	WQCPVVLLADVRSVG	VVLLADVRS	0.2457	3503.2	50.00	Sequence
DRB1_1101	448	VLLADVRSVGVQGDG	VLLADVRSV	0.2447	3542.7	50.00	Sequence
DRB1_1101	54	ARQPVALVLSGGPAS	VALVLSGGP	0.2434	3589.7	50.00	Sequence
DRB1_1101	150	GFDVVASSAGAPVAA	FDVVASSAG	0.2431	3604.3	50.00	Sequence
DRB1_1101	171	RLAGVQYHPEVMHTP	VQYHPEVMH	0.2428	3613.5	50.00	Sequence
DRB1_1101	453	VRSVGVQGDGRTYGH	GVQGDGRTY	0.2423	3634.4	50.00	Sequence
DRB1_1101	103	GGIVAHTGTREYGRT	VAHTGTREY	0.2421	3643.5	50.00	Sequence
DRB1_1101	249	GDRLTCVFVDHGLLR	VFVDHGLLR	0.2410	3685.4	50.00	Sequence
DRB1_1101	439	DNQIWQCPVVLLADV	IWQCPVVLL	0.2409	3689.5	50.00	Sequence
DRB1_1101	149	DGFDVVASSAGAPVA	FDVVASSAG	0.2393	3752.5	50.00	Sequence
DRB1_1101	83	DLGVPVLGICYGFQA	VPVLGICYG	0.2383	3793.3	50.00	Sequence
DRB1_1101	437	GLDNQIWQCPVVLLA	NQIWQCPVV	0.2380	3806.3	50.00	Sequence
DRB1_1101	46	TASIEEIRARQPVAL	IEEIRARQP	0.2358	3898.4	50.00	Sequence
DRB1_1101	175	VQYHPEVMHTPHGQQ	VQYHPEVMH	0.2344	3957.6	50.00	Sequence
DRB1_1101	15	PVLVVDFGAQYAQLI	VVDFGAQYA	0.2335	3995.6	50.00	Sequence
DRB1_1101	79	PALLDLGVPVLGICY	ALLDLGVPV	0.2328	4028.7	50.00	Sequence
DRB1_1101	236	DSAVAAALVQRAIGD	VAAALVQRA	0.2322	4054.3	50.00	Sequence
DRB1_1101	148	PDGFDVVASSAGAPV	FDVVASSAG	0.2320	4060.5	50.00	Sequence
DRB1_1101	442	IWQCPVVLLADVRSV	VVLLADVRS	0.2300	4149.9	50.00	Sequence
DRB1_1101	18	VVDFGAQYAQLIARR	VVDFGAQYA	0.2290	4198.5	50.00	Sequence

DRB1_1101	504	AEVNRVVLDITSKPP	NRVVLDITS	0.2279	4247.3	50.00	Sequence
DRB1_1101	440	NQIWQCPVVLLADVR	IWQCPVVLL	0.2271	4283.8	50.00	Sequence
DRB1_1101	295	LSGVSAPEGKRKIIG	LSGVSAPEG	0.2267	4303.1	50.00	Sequence
DRB1_1101	241	AALVQRAIGDRLTCV	AALVQRAIG	0.2262	4323.9	50.00	Sequence
DRB1_1101	14	RPVLVVDFGAQYAQL	VLVVDFGAQ	0.2249	4385.0	50.00	Sequence
DRB1_1101	105	IVAHTGTREYGRTEL	VAHTGTREY	0.2244	4408.6	50.00	Sequence
DRB1_1101	81	LLDLGVPVLGICYGF	VPVLGICYG	0.2224	4509.6	50.00	Sequence
DRB1_1101	13	ARPVLVVDFGAQYAQ	VLVVDFGAQ	0.2213	4562.2	50.00	Sequence
DRB1_1101	221	QIGDGHAICGLSGGV	AICGLSGGV	0.2195	4650.5	50.00	Sequence
DRB1_1101	422	LRHADSIVREELTAA	LRHADSIVR	0.2194	4656.5	50.00	Sequence
DRB1_1101	510	VLDITSKPPATIEWE	LDITSKPPA	0.2192	4667.2	50.00	Sequence
DRB1_1101	441	QIWQCPVVLLADVRS	IWQCPVVLL	0.2175	4754.6	50.00	Sequence
DRB1_1101	284	TVDAAETFLEALSGV	ETFLEALSG	0.2173	4763.5	50.00	Sequence
DRB1_1101	452	DVRSVGVQGDGRTYG	GVQGDGRTY	0.2169	4782.6	50.00	Sequence
DRB1_1101	503	VAEVNRVVLDITSKP	VNRVVLDIT	0.2168	4787.2	50.00	Sequence
DRB1_1101	207	PANIANALIEQVRTQ	NALIEQVRT	0.2162	4817.9	50.00	Sequence
DRB1_1101	78	DPALLDLGVPVLGIC	ALLDLGVPV	0.2159	4837.9	50.00	Sequence
DRB1_1101	16	VLVVDFGAQYAQLIA	VVDFGAQYA	0.2153	4866.3	50.00	Sequence
DRB1_1101	17	LVVDFGAQYAQLIAR	VVDFGAQYA	0.2150	4881.4	50.00	Sequence
DRB1_1101	77	LDPALLDLGVPVLGI	ALLDLGVPV	0.2127	5007.6	50.00	Sequence
DRB1_1101	298	VSAPEGKRKIIGRQF	KRKIIGRQF	0.2091	5203.4	50.00	Sequence
DRB1_1101	457	GVQGDGRTYGHPIVL	GVQGDGRTY	0.2082	5255.4	50.00	Sequence
DRB1_1101	392	PEEIVARQPFPGPGL	IVARQPFPG	0.2037	5515.1	50.00	Sequence
DRB1_1101	349	GTANIKSHHNVGGLP	NIKSHHNVG	0.2028	5570.5	50.00	Sequence
DRB1_1101	181	VMHTPHGQQVLSRFL	GQQVLSRFL	0.2017	5641.4	50.00	Sequence
DRB1_1101	383	RAVGRELGLPEEIVA	RAVGRELGL	0.2013	5661.9	50.00	Sequence
DRB1_1101	393	EEIVARQPFPGPGLG	IVARQPFPG	0.2008	5692.8	50.00	Sequence
DRB1_1101	500	TNEVAEVNRVVLDIT	VAEVNRVVL	0.1999	5752.6	50.00	Sequence
DRB1_1101	45	HTASIEEIRARQPVA	SIEEIRARQ	0.1987	5826.3	50.00	Sequence
DRB1_1101	436	AGLDNQIWQCPVVLL	IWQCPVVLL	0.1981	5865.8	50.00	Sequence
DRB1_1101	394	EIVARQPFPGPGLGI	IVARQPFPG	0.1977	5888.7	50.00	Sequence
DRB1_1101	53	RARQPVALVLSGGPA	VALVLSGGP	0.1953	6042.7	50.00	Sequence
DRB1_1101	499	ITNEVAEVNRVVLDI	VAEVNRVVL	0.1952	6049.9	50.00	Sequence
DRB1_1101	481	TADWTRVPYEVLERI	WTRVPYEVL	0.1945	6098.6	50.00	Sequence
DRB1_1101	449	LLADVRSVGVQGDGR	LADVRSVGV	0.1942	6117.3	50.00	Sequence
DRB1_1101	106	VAHTGTREYGRTELK	VAHTGTREY	0.1936	6153.8	50.00	Sequence
DRB1_1101	261	LLRAGERAQVQRDFV	LLRAGERAQ	0.1935	6163.8	50.00	Sequence
DRB1_1101	502	EVAEVNRVVLDITSK	VAEVNRVVL	0.1934	6170.6	50.00	Sequence
DRB1_1101	348	SGTANIKSHHNVGGL	NIKSHHNVG	0.1933	6177.7	50.00	Sequence
DRB1_1101	460	GDGRTYGHPIVLRPV	RTYGHPIVL	0.1930	6195.5	50.00	Sequence
DRB1_1101	134	QPVWMSHGDAVTAAP	MSHGDAVTA	0.1919	6268.9	50.00	Sequence
DRB1_1101	147	APDGFDVVASSAGAP	FDVVASSAG	0.1918	6275.7	50.00	Sequence
DRB1_1101	350	TANIKSHHNVGGLPD	IKSHHNVGG	0.1918	6279.5	50.00	Sequence
DRB1_1101	178	HPEVMHTPHGQQVLS	VMHTPHGQQ	0.1915	6296.1	50.00	Sequence
DRB1_1101	243	LVQRAIGDRLTCVFV	RAIGDRLTC	0.1911	6326.3	50.00	Sequence
DRB1_1101	501	NEVAEVNRVVLDITS	VAEVNRVVL	0.1908	6347.2	50.00	Sequence
DRB1_1101	151	FDVVASSAGAPVAAF	FDVVASSAG	0.1904	6369.9	50.00	Sequence
DRB1_1101	177	YHPEVMHTPHGQQVL	VMHTPHGQQ	0.1892	6455.1	50.00	Sequence
DRB1_1101	352	NIKSHHNVGGLPDDL	HHNVGGLPD	0.1890	6471.7	50.00	Sequence
DRB1_1101	176	QYHPEVMHTPHGQQV	HPEVMHTPH	0.1883	6516.2	50.00	Sequence
DRB1_1101	50	EEIRARQPVALVLSG	EIRARQPVA	0.1877	6562.0	50.00	Sequence
DRB1_1101	133	VQPVWMSHGDAVTAA	MSHGDAVTA	0.1875	6572.5	50.00	Sequence
DRB1_1101	315	AFEGAVRDVLDGKTA	AFEGAVRDV	0.1875	6575.8	50.00	Sequence
DRB1_1101	135	PVWMSHGDAVTAAPD	MSHGDAVTA	0.1866	6637.6	50.00	Sequence
DRB1_1101	391	LPEEIVARQPFPGPG	EIVARQPFP	0.1865	6644.2	50.00	Sequence
DRB1_1101	451	ADVRSVGVQGDGRTY	GVQGDGRTY	0.1858	6698.3	50.00	Sequence
DRB1_1101	12	PARPVLVVDFGAQYA	VLVVDFGAQ	0.1854	6724.0	50.00	Sequence
DRB1_1101	351	ANIKSHHNVGGLPDD	IKSHHNVGG	0.1849	6761.3	50.00	Sequence
DRB1_1101	494	RISTRITNEVAEVNR	STRITNEVA	0.1841	6823.7	50.00	Sequence
DRB1_1101	271	QRDFVAATGANLVTV	FVAATGANL	0.1840	6831.8	50.00	Sequence
DRB1_1101	76	KLDPALLDLGVPVLG	ALLDLGVPV	0.1834	6871.0	50.00	Sequence
DRB1_1101	235	VDSAVAAALVQRAIG	VAAALVQRA	0.1834	6872.3	50.00	Sequence
DRB1_1101	109	TGTREYGRTELKVLG	GRTELKVLG	0.1825	6938.3	50.00	Sequence
DRB1_1101	213	ALIEQVRTQIGDGHA	IEQVRTQIG	0.1815	7013.2	50.00	Sequence
DRB1_1101	244	VQRAIGDRLTCVFVD	RAIGDRLTC	0.1810	7056.0	50.00	Sequence
DRB1_1101	200	GLGAQWTPANIANAL	AQWTPANIA	0.1805	7091.3	50.00	Sequence

DRB1_1101	384	AVGRELGLPEEIVAR	RELGLPEEI	0.1799	7140.3	50.00	Sequence
DRB1_1101	480	MTADWTRVPYEVLER	WTRVPYEVL	0.1788	7225.6	50.00	Sequence
DRB1_1101	498	RITNEVAEVNRVVLD	VAEVNRVVL	0.1781	7277.8	50.00	Sequence
DRB1_1101	199	AGLGAQWTPANIANA	LGAQWTPAN	0.1777	7310.1	50.00	Sequence
DRB1_1101	132	EVQPVWMSHGDAVTA	PVWMSHGDA	0.1775	7324.0	50.00	Sequence
DRB1_1101	201	LGAQWTPANIANALI	AQWTPANIA	0.1774	7332.8	50.00	Sequence
DRB1_1101	51	EIRARQPVALVLSGG	EIRARQPVA	0.1771	7354.5	50.00	Sequence
DRB1_1101	478	DAMTADWTRVPYEVL	TADWTRVPY	0.1754	7491.9	50.00	Sequence
DRB1_1101	479	AMTADWTRVPYEVLE	WTRVPYEVL	0.1750	7530.5	50.00	Sequence
DRB1_1101	347	GSGTANIKSHHNVGG	TANIKSHHN	0.1744	7577.3	50.00	Sequence
DRB1_1101	242	ALVQRAIGDRLTCVF	RAIGDRLTC	0.1735	7652.0	50.00	Sequence
DRB1_1101	206	TPANIANALIEQVRT	NALIEQVRT	0.1734	7659.7	50.00	Sequence
DRB1_1101	52	IRARQPVALVLSGGP	RQPVALVLS	0.1717	7798.8	50.00	Sequence
DRB1_1101	270	VQRDFVAATGANLVT	FVAATGANL	0.1713	7837.4	50.00	Sequence
DRB1_1101	269	QVQRDFVAATGANLV	RDFVAATGA	0.1707	7884.9	50.00	Sequence
DRB1_1101	245	QRAIGDRLTCVFVDH	GDRLTCVFV	0.1700	7943.4	50.00	Sequence
DRB1_1101	214	LIEQVRTQIGDGHAI	IEQVRTQIG	0.1695	7992.0	50.00	Sequence
DRB1_1101	385	VGRELGLPEEIVARQ	RELGLPEEI	0.1677	8144.6	50.00	Sequence
DRB1_1101	279	GANLVTVDAAETFLE	LVTVDAAET	0.1675	8167.3	50.00	Sequence
DRB1_1101	136	VWMSHGDAVTAAPDG	MSHGDAVTA	0.1674	8169.8	50.00	Sequence
DRB1_1101	423	RHADSIVREELTAAG	DSIVREELT	0.1667	8237.4	50.00	Sequence
DRB1_1101	158	AGAPVAAFEAFDRRL	VAAFEAFDR	0.1659	8308.6	50.00	Sequence
DRB1_1101	246	RAIGDRLTCVFVDHG	GDRLTCVFV	0.1635	8527.5	50.00	Sequence
DRB1_1101	353	IKSHHNVGGLPDDLK	HHNVGGLPD	0.1632	8557.0	50.00	Sequence
DRB1_1101	424	HADSIVREELTAAGL	SIVREELTA	0.1631	8559.3	50.00	Sequence
DRB1_1101	450	LADVRSVGVQGDGRT	LADVRSVGV	0.1630	8568.2	50.00	Sequence
DRB1_1101	459	QGDGRTYGHPIVLRP	RTYGHPIVL	0.1628	8592.5	50.00	Sequence
DRB1_1101	390	GLPEEIVARQPFPGP	EEIVARQPF	0.1618	8684.1	50.00	Sequence
DRB1_1101	202	GAQWTPANIANALIE	WTPANIANA	0.1596	8895.7	50.00	Sequence
DRB1_1101	432	ELTAAGLDNQIWQCP	AAGLDNQIW	0.1585	8999.3	50.00	Sequence
DRB1_1101	435	AAGLDNQIWQCPVVL	QIWQCPVVL	0.1582	9027.7	50.00	Sequence
DRB1_1101	386	GRELGLPEEIVARQP	LGLPEEIVA	0.1566	9183.2	50.00	Sequence
DRB1_1101	469	IVLRPVSSEDAMTAD	VSSEDAMTA	0.1561	9237.7	50.00	Sequence
DRB1_1101	44	PHTASIEEIRARQPV	SIEEIRARQ	0.1559	9258.4	50.00	Sequence
DRB1_1101	283	VTVDAAETFLEALSG	AETFLEALS	0.1544	9405.7	50.00	Sequence
DRB1_1101	108	HTGTREYGRTELKVL	YGRTELKVL	0.1533	9523.1	50.00	Sequence
DRB1_1101	361	GLPDDLKFTLVEPLR	KFTLVEPLR	0.1531	9536.5	50.00	Sequence
DRB1_1101	497	TRITNEVAEVNRVVL	VAEVNRVVL	0.1528	9571.9	50.00	Sequence
DRB1_1101	431	EELTAAGLDNQIWQC	ELTAAGLDN	0.1528	9576.3	50.00	Sequence
DRB1_1101	495	ISTRITNEVAEVNRV	STRITNEVA	0.1525	9597.7	50.00	Sequence
DRB1_1101	470	VLRPVSSEDAMTADW	VSSEDAMTA	0.1523	9618.9	50.00	Sequence
DRB1_1101	107	AHTGTREYGRTELKV	AHTGTREYG	0.1521	9644.8	50.00	Sequence
DRB1_1101	354	KSHHNVGGLPDDLKF	HHNVGGLPD	0.1514	9722.5	50.00	Sequence
DRB1_1101	215	IEQVRTQIGDGHAIC	IEQVRTQIG	0.1505	9807.2	50.00	Sequence
DRB1_1101	272	RDFVAATGANLVTVD	FVAATGANL	0.1504	9820.2	50.00	Sequence
DRB1_1101	395	IVARQPFPGPGLGIR	IVARQPFPG	0.1499	9880.0	50.00	Sequence
DRB1_1101	425	ADSIVREELTAAGLD	SIVREELTA	0.1498	9882.3	50.00	Sequence
DRB1_1101	434	TAAGLDNQIWQCPVV	NQIWQCPVV	0.1495	9918.8	50.00	Sequence
DRB1_1101	268	AQVQRDFVAATGANL	QRDFVAATG	0.1489	9980.7	50.00	Sequence
DRB1_1101	248	IGDRLTCVFVDHGLL	RLTCVFVDH	0.1488	9997.1	50.00	Sequence
DRB1_1101	400	PFPGPGLGIRIVGEV	PGLGIRIVG	0.1485	10027.8	50.00	Sequence
DRB1_1101	387	RELGLPEEIVARQPF	RELGLPEEI	0.1477	10113.9	50.00	Sequence
DRB1_1101	234	GVDSAVAAALVQRAI	VAAALVQRA	0.1477	10118.2	50.00	Sequence
DRB1_1101	278	TGANLVTVDAAETFL	LVTVDAAET	0.1472	10168.8	50.00	Sequence
DRB1_1101	471	LRPVSSEDAMTADWT	VSSEDAMTA	0.1449	10428.6	50.00	Sequence
DRB1_1101	137	WMSHGDAVTAAPDGF	MSHGDAVTA	0.1448	10434.1	50.00	Sequence
DRB1_1101	75	PKLDPALLDLGVPVL	ALLDLGVPV	0.1428	10660.6	50.00	Sequence
DRB1_1101	280	ANLVTVDAAETFLEA	LVTVDAAET	0.1422	10730.8	50.00	Sequence
DRB1_1101	146	AAPDGFDVVASSAGA	FDVVASSAG	0.1411	10861.7	50.00	Sequence
DRB1_1101	228	ICGLSGGVDSAVAAA	CGLSGGVDS	0.1407	10905.5	50.00	Sequence
DRB1_1101	131	PEVQPVWMSHGDAVT	VQPVWMSHG	0.1406	10920.9	50.00	Sequence
DRB1_1101	355	SHHNVGGLPDDLKFT	HHNVGGLPD	0.1404	10940.6	50.00	Sequence
DRB1_1101	220	TQIGDGHAICGLSGG	GHAICGLSG	0.1400	10997.0	50.00	Sequence
DRB1_1101	346	GGSGTANIKSHHNVG	TANIKSHHN	0.1399	11005.8	50.00	Sequence
DRB1_1101	324	LDGKTAEFLVQGTLY	EFLVQGTLY	0.1392	11092.2	50.00	Sequence
DRB1_1101	433	LTAAGLDNQIWQCPV	AAGLDNQIW	0.1389	11129.1	50.00	Sequence

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DRB1_1101  247  AIGDRLTCVFVDHGL  GDRLTCVFV         0.1387       11150.5                  50.00      Sequence
DRB1_1101   11  TPARPVLVVDFGAQY  PVLVVDFGA         0.1383       11200.8                  50.00      Sequence
DRB1_1101  267  RAQVQRDFVAATGAN  RDFVAATGA         0.1377       11275.9                  50.00      Sequence
DRB1_1101  203  AQWTPANIANALIEQ  WTPANIANA         0.1373       11322.3                  50.00      Sequence
DRB1_1101  204  QWTPANIANALIEQV  WTPANIANA         0.1371       11342.9                  50.00      Sequence
DRB1_1101  430  REELTAAGLDNQIWQ  ELTAAGLDN         0.1358       11498.3                  50.00      Sequence
DRB1_1101  426  DSIVREELTAAGLDN  SIVREELTA         0.1340       11728.0                  50.00      Sequence
DRB1_1101  429  VREELTAAGLDNQIW  ELTAAGLDN         0.1339       11748.4                  50.00      Sequence
DRB1_1101  180  EVMHTPHGQQVLSRF  VMHTPHGQQ         0.1335       11797.9                  50.00      Sequence
DRB1_1101  389  LGLPEEIVARQPFPG  EEIVARQPF         0.1331       11842.0                  50.00      Sequence
DRB1_1101   43  IPHTASIEEIRARQP  SIEEIRARQ         0.1330       11854.0                  50.00      Sequence
DRB1_1101  320  VRDVLDGKTAEFLVQ  RDVLDGKTA         0.1326       11915.8                  50.00      Sequence
DRB1_1101  273  DFVAATGANLVTVDA  FVAATGANL         0.1325       11918.9                  50.00      Sequence
DRB1_1101  282  LVTVDAAETFLEALS  LVTVDAAET         0.1303       12213.8                  50.00      Sequence
DRB1_1101  281  NLVTVDAAETFLEAL  LVTVDAAET         0.1289       12401.0                  50.00      Sequence
DRB1_1101  266  ERAQVQRDFVAATGA  RAQVQRDFV         0.1285       12443.3                  50.00      Sequence
DRB1_1101  318  GAVRDVLDGKTAEFL  RDVLDGKTA         0.1277       12562.0                  50.00      Sequence
DRB1_1101   40  SEVIPHTASIEEIRA  SEVIPHTAS         0.1259       12804.7                  50.00      Sequence
DRB1_1101  477  EDAMTADWTRVPYEV  TADWTRVPY         0.1258       12814.3                  50.00      Sequence
DRB1_1101  319  AVRDVLDGKTAEFLV  RDVLDGKTA         0.1255       12855.2                  50.00      Sequence
DRB1_1101  458  VQGDGRTYGHPIVLR  RTYGHPIVL         0.1254       12872.5                  50.00      Sequence
DRB1_1101  179  PEVMHTPHGQQVLSR  VMHTPHGQQ         0.1254       12880.3                  50.00      Sequence
DRB1_1101  356  HHNVGGLPDDLKFTL  HHNVGGLPD         0.1237       13107.3                  50.00      Sequence
DRB1_1101  205  WTPANIANALIEQVR  WTPANIANA         0.1215       13433.3                  50.00      Sequence
DRB1_1101  219  RTQIGDGHAICGLSG  DGHAICGLS         0.1210       13500.0                  50.00      Sequence
DRB1_1101  472  RPVSSEDAMTADWTR  VSSEDAMTA         0.1210       13506.9                  50.00      Sequence
DRB1_1101   61  VLSGGPASVYADGAP  VLSGGPASV         0.1199       13663.7                  50.00      Sequence
DRB1_1101  496  STRITNEVAEVNRVV  STRITNEVA         0.1192       13762.4                  50.00      Sequence
DRB1_1101  274  FVAATGANLVTVDAA  FVAATGANL         0.1180       13942.5                  50.00      Sequence
DRB1_1101  233  GGVDSAVAAALVQRA  VAAALVQRA         0.1175       14016.9                  50.00      Sequence
DRB1_1101  297  GVSAPEGKRKIIGRQ  PEGKRKIIG         0.1175       14024.2                  50.00      Sequence
DRB1_1101  124  GKLHSDLPEVQPVWM  HSDLPEVQP         0.1174       14044.4                  50.00      Sequence
DRB1_1101  138  MSHGDAVTAAPDGFD  MSHGDAVTA         0.1150       14412.0                  50.00      Sequence
DRB1_1101  265  GERAQVQRDFVAATG  RAQVQRDFV         0.1146       14476.1                  50.00      Sequence
DRB1_1101  229  CGLSGGVDSAVAAAL  CGLSGGVDS         0.1142       14536.7                  50.00      Sequence
DRB1_1101  428  IVREELTAAGLDNQI  IVREELTAA         0.1139       14578.9                  50.00      Sequence
DRB1_1101  427  SIVREELTAAGLDNQ  IVREELTAA         0.1133       14681.3                  50.00      Sequence
DRB1_1101   10  ETPARPVLVVDFGAQ  VLVVDFGAQ         0.1132       14685.1                  50.00      Sequence
DRB1_1101  277  ATGANLVTVDAAETF  LVTVDAAET         0.1126       14781.4                  50.00      Sequence
DRB1_1101  123  GGKLHSDLPEVQPVW  KLHSDLPEV         0.1124       14821.8                  50.00      Sequence
DRB1_1101  264  AGERAQVQRDFVAAT  RAQVQRDFV         0.1120       14886.0                  50.00      Sequence
DRB1_1101  388  ELGLPEEIVARQPFP  EEIVARQPF         0.1105       15127.2                  50.00      Sequence
DRB1_1101  125  KLHSDLPEVQPVWMS  HSDLPEVQP         0.1102       15182.3                  50.00      Sequence
DRB1_1101  473  PVSSEDAMTADWTRV  VSSEDAMTA         0.1090       15375.8                  50.00      Sequence
DRB1_1101  218  VRTQIGDGHAICGLS  RTQIGDGHA         0.1069       15729.0                  50.00      Sequence
DRB1_1101  130  LPEVQPVWMSHGDAV  VQPVWMSHG         0.1068       15738.2                  50.00      Sequence
DRB1_1101  321  RDVLDGKTAEFLVQG  RDVLDGKTA         0.1066       15775.2                  50.00      Sequence
DRB1_1101  317  EGAVRDVLDGKTAEF  RDVLDGKTA         0.1054       15992.6                  50.00      Sequence
DRB1_1101  316  FEGAVRDVLDGKTAE  RDVLDGKTA         0.1047       16100.4                  50.00      Sequence
DRB1_1101  122  LGGKLHSDLPEVQPV  KLHSDLPEV         0.1046       16123.3                  50.00      Sequence
DRB1_1101  231  LSGGVDSAVAAALVQ  GVDSAVAAA         0.1041       16213.2                  50.00      Sequence
DRB1_1101  276  AATGANLVTVDAAET  LVTVDAAET         0.1018       16616.3                  50.00      Sequence
DRB1_1101  332  LVQGTLYPDVVESGG  LVQGTLYPD         0.1017       16635.2                  50.00      Sequence
DRB1_1101  217  QVRTQIGDGHAICGL  QVRTQIGDG         0.1013       16710.1                  50.00      Sequence
DRB1_1101  476  SEDAMTADWTRVPYE  TADWTRVPY         0.1003       16899.9                  50.00      Sequence
DRB1_1101  296  SGVSAPEGKRKIIGR  PEGKRKIIG         0.0995       17030.2                  50.00      Sequence
DRB1_1101   74  APKLDPALLDLGVPV  ALLDLGVPV         0.0994       17059.7                  50.00      Sequence
DRB1_1101  121  VLGGKLHSDLPEVQP  HSDLPEVQP         0.0991       17109.5                  50.00      Sequence
DRB1_1101   42  VIPHTASIEEIRARQ  TASIEEIRA         0.0982       17275.0                  50.00      Sequence
DRB1_1101  145  TAAPDGFDVVASSAG  FDVVASSAG         0.0964       17619.1                  50.00      Sequence
DRB1_1101  230  GLSGGVDSAVAAALV  GGVDSAVAA         0.0962       17664.2                  50.00      Sequence
DRB1_1101  399  QPFPGPGLGIRIVGE  PGLGIRIVG         0.0961       17671.1                  50.00      Sequence
DRB1_1101  263  RAGERAQVQRDFVAA  RAQVQRDFV         0.0950       17881.5                  50.00      Sequence
DRB1_1101  216  EQVRTQIGDGHAICG  QVRTQIGDG         0.0947       17950.7                  50.00      Sequence
DRB1_1101   68  SVYADGAPKLDPALL  SVYADGAPK         0.0945       17994.0                  50.00      Sequence
DRB1_1101  232  SGGVDSAVAAALVQR  VDSAVAAAL         0.0931       18260.8                  50.00      Sequence
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   DRB1_1101   70  YADGAPKLDPALLDL  ADGAPKLDP        0.0911      18666.3                 50.00     Sequence
   DRB1_1101  474  VSSEDAMTADWTRVP  VSSEDAMTA        0.0909      18707.5                 50.00     Sequence
   DRB1_1101   71  ADGAPKLDPALLDLG  APKLDPALL        0.0900      18876.9                 50.00     Sequence
   DRB1_1101  323  VLDGKTAEFLVQGTL  VLDGKTAEF        0.0887      19141.0                 50.00     Sequence
   DRB1_1101   69  VYADGAPKLDPALLD  ADGAPKLDP        0.0879      19316.6                 50.00     Sequence
   DRB1_1101  345  GGGSGTANIKSHHNV  GTANIKSHH        0.0869      19527.2                 50.00     Sequence
   DRB1_1101  152  DVVASSAGAPVAAFE  VVASSAGAP        0.0841      20131.9                 50.00     Sequence
   DRB1_1101  262  LRAGERAQVQRDFVA  LRAGERAQV        0.0836      20243.1                 50.00     Sequence
   DRB1_1101   72  DGAPKLDPALLDLGV  APKLDPALL        0.0834      20284.1                 50.00     Sequence
   DRB1_1101  126  LHSDLPEVQPVWMSH  HSDLPEVQP        0.0830      20367.7                 50.00     Sequence
   DRB1_1101   67  ASVYADGAPKLDPAL  SVYADGAPK        0.0821      20561.2                 50.00     Sequence
   DRB1_1101   73  GAPKLDPALLDLGVP  APKLDPALL        0.0814      20714.4                 50.00     Sequence
   DRB1_1101  398  RQPFPGPGLGIRIVG  PGLGIRIVG        0.0804      20951.5                 50.00     Sequence
   DRB1_1101  129  DLPEVQPVWMSHGDA  VQPVWMSHG        0.0802      21006.0                 50.00     Sequence
   DRB1_1101   41  EVIPHTASIEEIRAR  IPHTASIEE        0.0796      21128.8                 50.00     Sequence
   DRB1_1101  396  VARQPFPGPGLGIRI  RQPFPGPGL        0.0774      21629.6                 50.00     Sequence
   DRB1_1101  127  HSDLPEVQPVWMSHG  HSDLPEVQP        0.0774      21636.2                 50.00     Sequence
   DRB1_1101  475  SSEDAMTADWTRVPY  TADWTRVPY        0.0764      21869.7                 50.00     Sequence
   DRB1_1101  360  GGLPDDLKFTLVEPL  LKFTLVEPL        0.0739      22478.0                 50.00     Sequence
   DRB1_1101  275  VAATGANLVTVDAAE  AATGANLVT        0.0729      22727.7                 50.00     Sequence
   DRB1_1101  322  DVLDGKTAEFLVQGT  VLDGKTAEF        0.0704      23341.0                 50.00     Sequence
   DRB1_1101  397  ARQPFPGPGLGIRIV  PFPGPGLGI        0.0693      23623.6                 50.00     Sequence
   DRB1_1101   66  PASVYADGAPKLDPA  SVYADGAPK        0.0691      23663.2                 50.00     Sequence
   DRB1_1101  153  VVASSAGAPVAAFEA  VVASSAGAP        0.0686      23797.8                 50.00     Sequence
   DRB1_1101  344  SGGGSGTANIKSHHN  GSGTANIKS        0.0686      23802.1                 50.00     Sequence
   DRB1_1101  338  YPDVVESGGGSGTAN  VVESGGGSG        0.0672      24169.9                 50.00     Sequence
   DRB1_1101    5  DIDVPETPARPVLVV  VPETPARPV        0.0671      24196.8                 50.00     Sequence
   DRB1_1101  341  VVESGGGSGTANIKS  VVESGGGSG        0.0670      24208.1                 50.00     Sequence
   DRB1_1101  128  SDLPEVQPVWMSHGD  PEVQPVWMS        0.0652      24701.5                 50.00     Sequence
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   DRB1_1101  340  DVVESGGGSGTANIK  VVESGGGSG        0.0617      25638.8                 50.00     Sequence
   DRB1_1101  337  LYPDVVESGGGSGTA  VVESGGGSG        0.0616      25670.7                 50.00     Sequence
   DRB1_1101    7  DVPETPARPVLVVDF  VPETPARPV        0.0604      26023.1                 50.00     Sequence
   DRB1_1101    6  IDVPETPARPVLVVD  VPETPARPV        0.0599      26150.1                 50.00     Sequence
   DRB1_1101  140  HGDAVTAAPDGFDVV  AVTAAPDGF        0.0597      26202.2                 50.00     Sequence
   DRB1_1101    9  PETPARPVLVVDFGA  ETPARPVLV        0.0597      26207.3                 50.00     Sequence
   DRB1_1101    4  ADIDVPETPARPVLV  VPETPARPV        0.0596      26229.5                 50.00     Sequence
   DRB1_1101    8  VPETPARPVLVVDFG  VPETPARPV        0.0589      26440.3                 50.00     Sequence
   DRB1_1101  157  SAGAPVAAFEAFDRR  VAAFEAFDR        0.0576      26804.4                 50.00     Sequence
   DRB1_1101  357  HNVGGLPDDLKFTLV  VGGLPDDLK        0.0573      26897.7                 50.00     Sequence
   DRB1_1101  336  TLYPDVVESGGGSGT  YPDVVESGG        0.0555      27419.8                 50.00     Sequence
   DRB1_1101  335  GTLYPDVVESGGGSG  YPDVVESGG        0.0553      27485.2                 50.00     Sequence
   DRB1_1101  339  PDVVESGGGSGTANI  VVESGGGSG        0.0536      27985.4                 50.00     Sequence
   DRB1_1101  342  VESGGGSGTANIKSH  ESGGGSGTA        0.0535      28015.4                 50.00     Sequence
   DRB1_1101   62  LSGGPASVYADGAPK  LSGGPASVY        0.0528      28250.1                 50.00     Sequence
   DRB1_1101   64  GGPASVYADGAPKLD  SVYADGAPK        0.0526      28313.1                 50.00     Sequence
   DRB1_1101  139  SHGDAVTAAPDGFDV  HGDAVTAAP        0.0512      28744.9                 50.00     Sequence
   DRB1_1101  156  SSAGAPVAAFEAFDR  SSAGAPVAA        0.0509      28821.5                 50.00     Sequence
   DRB1_1101  358  NVGGLPDDLKFTLVE  VGGLPDDLK        0.0505      28966.9                 50.00     Sequence
   DRB1_1101    3  PADIDVPETPARPVL  VPETPARPV        0.0482      29679.2                 50.00     Sequence
   DRB1_1101  141  GDAVTAAPDGFDVVA  VTAAPDGFD        0.0457      30493.6                 50.00     Sequence
   DRB1_1101  143  AVTAAPDGFDVVASS  AVTAAPDGF        0.0446      30843.6                 50.00     Sequence
   DRB1_1101  334  QGTLYPDVVESGGGS  TLYPDVVES        0.0441      31013.0                 50.00     Sequence
   DRB1_1101  359  VGGLPDDLKFTLVEP  LPDDLKFTL        0.0437      31155.2                 50.00     Sequence
   DRB1_1101  154  VASSAGAPVAAFEAF  VASSAGAPV        0.0437      31156.2                 50.00     Sequence
   DRB1_1101  142  DAVTAAPDGFDVVAS  AVTAAPDGF        0.0426      31545.0                 50.00     Sequence
   DRB1_1101  144  VTAAPDGFDVVASSA  GFDVVASSA        0.0425      31581.9                 50.00     Sequence
   DRB1_1101    2  QPADIDVPETPARPV  VPETPARPV        0.0423      31621.5                 50.00     Sequence
   DRB1_1101  333  VQGTLYPDVVESGGG  YPDVVESGG        0.0416      31867.8                 50.00     Sequence
   DRB1_1101    0  VVQPADIDVPETPAR  VVQPADIDV        0.0397      32537.4                 50.00     Sequence
   DRB1_1101   63  SGGPASVYADGAPKL  SVYADGAPK        0.0338      34670.2                 50.00     Sequence
   DRB1_1101    1  VQPADIDVPETPARP  DIDVPETPA        0.0309      35797.8                 50.00     Sequence
   DRB1_1101  155  ASSAGAPVAAFEAFD  ASSAGAPVA        0.0291      36505.0                 50.00     Sequence
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Allele: DRB1_1101. Number of high binders 4. Number of weak binders 84. Number of peptides 511

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1302   92  CYGFQAMAQALGGIV  MAQALGGIV         0.5987          76.9          WB     8.00     Sequence
   DRB1_1302   93  YGFQAMAQALGGIVA  MAQALGGIV         0.5792          95.0          WB     8.00     Sequence
   DRB1_1302  497  TRITNEVAEVNRVVL  VAEVNRVVL         0.5631         113.0          WB     8.00     Sequence
   DRB1_1302   38  VFSEVIPHTASIEEI  EVIPHTASI         0.5566         121.2          WB     8.00     Sequence
   DRB1_1302   94  GFQAMAQALGGIVAH  MAQALGGIV         0.5562         121.8          WB     8.00     Sequence
   DRB1_1302  445  CPVVLLADVRSVGVQ  LADVRSVGV         0.5523         127.0          WB     8.00     Sequence
   DRB1_1302  498  RITNEVAEVNRVVLD  VAEVNRVVL         0.5474         133.9          WB     8.00     Sequence
   DRB1_1302  444  QCPVVLLADVRSVGV  LADVRSVGV         0.5467         134.9          WB     8.00     Sequence
   DRB1_1302  446  PVVLLADVRSVGVQG  LADVRSVGV         0.5455         136.7          WB     8.00     Sequence
   DRB1_1302  204  QWTPANIANALIEQV  PANIANALI         0.5447         137.9          WB     8.00     Sequence
   DRB1_1302   39  FSEVIPHTASIEEIR  EVIPHTASI         0.5392         146.3          WB     8.00     Sequence
   DRB1_1302   37  RVFSEVIPHTASIEE  EVIPHTASI         0.5353         152.6          WB     8.00     Sequence
   DRB1_1302  489  YEVLERISTRITNEV  VLERISTRI         0.5317         158.7          WB    16.00     Sequence
   DRB1_1302  447  VVLLADVRSVGVQGD  LADVRSVGV         0.5307         160.4          WB    16.00     Sequence
   DRB1_1302  486  RVPYEVLERISTRIT  VLERISTRI         0.5295         162.5          WB    16.00     Sequence
   DRB1_1302  487  VPYEVLERISTRITN  VLERISTRI         0.5232         173.9          WB    16.00     Sequence
   DRB1_1302  205  WTPANIANALIEQVR  PANIANALI         0.5217         176.9          WB    16.00     Sequence
   DRB1_1302   40  SEVIPHTASIEEIRA  EVIPHTASI         0.5216         176.9          WB    16.00     Sequence
   DRB1_1302   36  ARVFSEVIPHTASIE  EVIPHTASI         0.5204         179.2          WB    16.00     Sequence
   DRB1_1302  202  GAQWTPANIANALIE  PANIANALI         0.5175         184.9          WB    16.00     Sequence
   DRB1_1302  113  EYGRTELKVLGGKLH  ELKVLGGKL         0.5127         194.8          WB    16.00     Sequence
   DRB1_1302  114  YGRTELKVLGGKLHS  ELKVLGGKL         0.5121         196.2          WB    16.00     Sequence
   DRB1_1302   13  ARPVLVVDFGAQYAQ  LVVDFGAQY         0.5121         196.2          WB    16.00     Sequence
   DRB1_1302  448  VLLADVRSVGVQGDG  LADVRSVGV         0.5117         197.0          WB    16.00     Sequence
   DRB1_1302  132  EVQPVWMSHGDAVTA  MSHGDAVTA         0.5099         200.8          WB    16.00     Sequence
   DRB1_1302  203  AQWTPANIANALIEQ  PANIANALI         0.5075         206.1          WB    16.00     Sequence
   DRB1_1302   12  PARPVLVVDFGAQYA  LVVDFGAQY         0.5072         206.7          WB    16.00     Sequence
   DRB1_1302  133  VQPVWMSHGDAVTAA  MSHGDAVTA         0.5051         211.5          WB    16.00     Sequence
   DRB1_1302  201  LGAQWTPANIANALI  PANIANALI         0.5037         214.9          WB    16.00     Sequence
   DRB1_1302  485  TRVPYEVLERISTRI  VLERISTRI         0.5023         218.0          WB    16.00     Sequence
   DRB1_1302  488  PYEVLERISTRITNE  VLERISTRI         0.4997         224.5          WB    16.00     Sequence
   DRB1_1302  277  ATGANLVTVDAAETF  LVTVDAAET         0.4991         225.9          WB    16.00     Sequence
   DRB1_1302   16  VLVVDFGAQYAQLIA  LVVDFGAQY         0.4977         229.3          WB    16.00     Sequence
   DRB1_1302  490  EVLERISTRITNEVA  VLERISTRI         0.4975         229.7          WB    16.00     Sequence
   DRB1_1302   11  TPARPVLVVDFGAQY  LVVDFGAQY         0.4969         231.3          WB    16.00     Sequence
   DRB1_1302   14  RPVLVVDFGAQYAQL  LVVDFGAQY         0.4946         237.0          WB    16.00     Sequence
   DRB1_1302  115  GRTELKVLGGKLHSD  ELKVLGGKL         0.4930         241.2          WB    16.00     Sequence
   DRB1_1302   98  MAQALGGIVAHTGTR  MAQALGGIV         0.4921         243.6          WB    16.00     Sequence
   DRB1_1302   95  FQAMAQALGGIVAHT  MAQALGGIV         0.4898         249.8          WB    16.00     Sequence
   DRB1_1302  492  LERISTRITNEVAEV  RITNEVAEV         0.4897         249.9          WB    16.00     Sequence
   DRB1_1302  134  QPVWMSHGDAVTAAP  MSHGDAVTA         0.4873         256.6          WB    16.00     Sequence
   DRB1_1302   15  PVLVVDFGAQYAQLI  LVVDFGAQY         0.4855         261.7          WB    16.00     Sequence
   DRB1_1302   41  EVIPHTASIEEIRAR  EVIPHTASI         0.4846         264.1          WB    16.00     Sequence
   DRB1_1302  278  TGANLVTVDAAETFL  LVTVDAAET         0.4834         267.5          WB    16.00     Sequence
   DRB1_1302  206  TPANIANALIEQVRT  PANIANALI         0.4815         273.3          WB    16.00     Sequence
   DRB1_1302  239  VAAALVQRAIGDRLT  VQRAIGDRL         0.4789         280.9          WB    16.00     Sequence
   DRB1_1302   89  LGICYGFQAMAQALG  GFQAMAQAL         0.4773         285.8          WB    16.00     Sequence
   DRB1_1302   91  ICYGFQAMAQALGGI  GFQAMAQAL         0.4773         286.0          WB    16.00     Sequence
   DRB1_1302  182  MHTPHGQQVLSRFLH  GQQVLSRFL         0.4766         288.1          WB    16.00     Sequence
   DRB1_1302   17  LVVDFGAQYAQLIAR  LVVDFGAQY         0.4750         293.0          WB    16.00     Sequence
   DRB1_1302  417  KRLDTLRHADSIVRE  LRHADSIVR         0.4749         293.5          WB    16.00     Sequence
   DRB1_1302  302  EGKRKIIGRQFIRAF  KRKIIGRQF         0.4748         293.6          WB    16.00     Sequence
   DRB1_1302   96  QAMAQALGGIVAHTG  MAQALGGIV         0.4742         295.8          WB    16.00     Sequence
   DRB1_1302  491  VLERISTRITNEVAE  VLERISTRI         0.4723         301.9          WB    16.00     Sequence
   DRB1_1302  416  AKRLDTLRHADSIVR  LRHADSIVR         0.4719         303.1          WB    16.00     Sequence
   DRB1_1302  181  VMHTPHGQQVLSRFL  GQQVLSRFL         0.4708         306.6          WB    16.00     Sequence
   DRB1_1302  240  AAALVQRAIGDRLTC  VQRAIGDRL         0.4708         306.7          WB    16.00     Sequence
   DRB1_1302   88  VLGICYGFQAMAQAL  GFQAMAQAL         0.4706         307.4          WB    16.00     Sequence
   DRB1_1302  279  GANLVTVDAAETFLE  LVTVDAAET         0.4676         317.5          WB    16.00     Sequence
   DRB1_1302  493  ERISTRITNEVAEVN  RITNEVAEV         0.4669         319.8          WB    16.00     Sequence
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DRB1_1302  418  RLDTLRHADSIVREE  LRHADSIVR        0.4663        321.9          WB    16.00      Sequence
DRB1_1302  116  RTELKVLGGKLHSDL  ELKVLGGKL        0.4659        323.4          WB    16.00      Sequence
DRB1_1302  405  GLGIRIVGEVTAKRL  VGEVTAKRL        0.4647        327.6          WB    16.00      Sequence
DRB1_1302   56  QPVALVLSGGPASVY  VLSGGPASV        0.4634        332.4          WB    16.00      Sequence
DRB1_1302   97  AMAQALGGIVAHTGT  MAQALGGIV        0.4612        340.2          WB    16.00      Sequence
DRB1_1302  406  LGIRIVGEVTAKRLD  VGEVTAKRL        0.4607        342.1          WB    16.00      Sequence
DRB1_1302  135  PVWMSHGDAVTAAPD  MSHGDAVTA        0.4603        343.5          WB    16.00      Sequence
DRB1_1302  303  GKRKIIGRQFIRAFE  KRKIIGRQF        0.4598        345.5          WB    16.00      Sequence
DRB1_1302  269  QVQRDFVAATGANLV  VAATGANLV        0.4595        346.7          WB    16.00      Sequence
DRB1_1302  241  AALVQRAIGDRLTCV  VQRAIGDRL        0.4585        350.4          WB    16.00      Sequence
DRB1_1302   35  EARVFSEVIPHTASI  EVIPHTASI        0.4579        352.5          WB    16.00      Sequence
DRB1_1302  270  VQRDFVAATGANLVT  VAATGANLV        0.4551        363.4          WB    16.00      Sequence
DRB1_1302  301  PEGKRKIIGRQFIRA  KRKIIGRQF        0.4538        368.5          WB    16.00      Sequence
DRB1_1302  271  QRDFVAATGANLVTV  VAATGANLV        0.4534        370.4          WB    16.00      Sequence
DRB1_1302  230  GLSGGVDSAVAAALV  DSAVAAALV        0.4528        372.7          WB    16.00      Sequence
DRB1_1302   90  GICYGFQAMAQALGG  GFQAMAQAL        0.4518        376.7          WB    16.00      Sequence
DRB1_1302   58  VALVLSGGPASVYAD  VLSGGPASV        0.4515        378.1          WB    16.00      Sequence
DRB1_1302   57  PVALVLSGGPASVYA  VLSGGPASV        0.4509        380.4          WB    16.00      Sequence
DRB1_1302   48  SIEEIRARQPVALVL  IRARQPVAL        0.4502        383.1          WB    16.00      Sequence
DRB1_1302  419  LDTLRHADSIVREEL  LRHADSIVR        0.4485        390.3          WB    16.00      Sequence
DRB1_1302  136  VWMSHGDAVTAAPDG  MSHGDAVTA        0.4484        390.8          WB    16.00      Sequence
DRB1_1302  276  AATGANLVTVDAAET  LVTVDAAET        0.4470        396.8          WB    16.00      Sequence
DRB1_1302  495  ISTRITNEVAEVNRV  RITNEVAEV        0.4469        397.3          WB    16.00      Sequence
DRB1_1302   49  IEEIRARQPVALVLS  IRARQPVAL        0.4462        400.2          WB    16.00      Sequence
DRB1_1302  499  ITNEVAEVNRVVLDI  VAEVNRVVL        0.4460        401.0          WB    16.00      Sequence
DRB1_1302  300  APEGKRKIIGRQFIR  KRKIIGRQF        0.4459        401.7          WB    16.00      Sequence
DRB1_1302  242  ALVQRAIGDRLTCVF  VQRAIGDRL        0.4452        404.7          WB    16.00      Sequence
DRB1_1302  494  RISTRITNEVAEVNR  RITNEVAEV        0.4445        407.8          WB    32.00      Sequence
DRB1_1302  299  SAPEGKRKIIGRQFI  KRKIIGRQF        0.4438        410.7          WB    32.00      Sequence
DRB1_1302  148  PDGFDVVASSAGAPV  VASSAGAPV        0.4421        418.3          WB    32.00      Sequence
DRB1_1302  407  GIRIVGEVTAKRLDT  VGEVTAKRL        0.4418        419.6          WB    32.00      Sequence
DRB1_1302  238  AVAAALVQRAIGDRL  VQRAIGDRL        0.4413        421.8          WB    32.00      Sequence
DRB1_1302   29  IARRVREARVFSEVI  ARRVREARV        0.4411        423.1          WB    32.00      Sequence
DRB1_1302  500  TNEVAEVNRVVLDIT  VAEVNRVVL        0.4410        423.4          WB    32.00      Sequence
DRB1_1302  280  ANLVTVDAAETFLEA  LVTVDAAET        0.4403        426.5          WB    32.00      Sequence
DRB1_1302  304  KRKIIGRQFIRAFEG  KRKIIGRQF        0.4401        427.4          WB    32.00      Sequence
DRB1_1302   47  ASIEEIRARQPVALV  IRARQPVAL        0.4393        431.4          WB    32.00      Sequence
DRB1_1302  117  TELKVLGGKLHSDLP  ELKVLGGKL        0.4372        441.2          WB    32.00      Sequence
DRB1_1302  420  DTLRHADSIVREELT  LRHADSIVR        0.4368        442.8          WB    32.00      Sequence
DRB1_1302   50  EEIRARQPVALVLSG  IRARQPVAL        0.4366        444.2          WB    32.00      Sequence
DRB1_1302  208  ANIANALIEQVRTQI  LIEQVRTQI        0.4349        452.2          WB    32.00      Sequence
DRB1_1302  272  RDFVAATGANLVTVD  VAATGANLV        0.4346        453.5          WB    32.00      Sequence
DRB1_1302  149  DGFDVVASSAGAPVA  VASSAGAPV        0.4346        453.7          WB    32.00      Sequence
DRB1_1302  207  PANIANALIEQVRTQ  PANIANALI        0.4345        454.3          WB    32.00      Sequence
DRB1_1302  231  LSGGVDSAVAAALVQ  DSAVAAALV        0.4325        464.0          WB    32.00      Sequence
DRB1_1302   59  ALVLSGGPASVYADG  VLSGGPASV        0.4308        472.9          WB    32.00      Sequence
DRB1_1302  408  IRIVGEVTAKRLDTL  VGEVTAKRL        0.4283        485.7          WB    32.00      Sequence
DRB1_1302  243  LVQRAIGDRLTCVFV  VQRAIGDRL        0.4265        495.2          WB    32.00      Sequence
DRB1_1302  118  ELKVLGGKLHSDLPE  ELKVLGGKL        0.4262        497.1          WB    32.00      Sequence
DRB1_1302   30  ARRVREARVFSEVIP  ARRVREARV        0.4232        513.3                32.00      Sequence
DRB1_1302  501  NEVAEVNRVVLDITS  VAEVNRVVL        0.4225        516.9                32.00      Sequence
DRB1_1302  150  GFDVVASSAGAPVAA  VASSAGAPV        0.4221        519.2                32.00      Sequence
DRB1_1302   55  RQPVALVLSGGPASV  VLSGGPASV        0.4213        524.1                32.00      Sequence
DRB1_1302   25  YAQLIARRVREARVF  ARRVREARV        0.4192        535.9                32.00      Sequence
DRB1_1302  421  TLRHADSIVREELTA  LRHADSIVR        0.4183        541.3                32.00      Sequence
DRB1_1302  244  VQRAIGDRLTCVFVD  VQRAIGDRL        0.4179        543.7                32.00      Sequence
DRB1_1302  449  LLADVRSVGVQGDGR  LADVRSVGV        0.4154        558.4                32.00      Sequence
DRB1_1302  422  LRHADSIVREELTAA  LRHADSIVR        0.4140        567.2                32.00      Sequence
DRB1_1302  209  NIANALIEQVRTQIG  LIEQVRTQI        0.4122        577.9                32.00      Sequence
DRB1_1302  232  SGGVDSAVAAALVQR  DSAVAAALV        0.4120        579.1                32.00      Sequence
DRB1_1302   51  EIRARQPVALVLSGG  IRARQPVAL        0.4118        580.9                32.00      Sequence
DRB1_1302   20  DFGAQYAQLIARRVR  YAQLIARRV        0.4102        591.0                32.00      Sequence
DRB1_1302  281  NLVTVDAAETFLEAL  LVTVDAAET        0.4097        593.8                32.00      Sequence
DRB1_1302  151  FDVVASSAGAPVAAF  VASSAGAPV        0.4083        603.1                32.00      Sequence
DRB1_1302  233  GGVDSAVAAALVQRA  DSAVAAALV        0.4071        611.1                32.00      Sequence
DRB1_1302   27  QLIARRVREARVFSE  ARRVREARV        0.4068        613.0                32.00      Sequence
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DRB1_1302  503  VAEVNRVVLDITSKP  VAEVNRVVL        0.4055        621.4             32.00     Sequence
DRB1_1302   52  IRARQPVALVLSGGP  IRARQPVAL        0.4024        642.7             32.00     Sequence
DRB1_1302  112  REYGRTELKVLGGKL  ELKVLGGKL        0.4023        643.3             32.00     Sequence
DRB1_1302  273  DFVAATGANLVTVDA  VAATGANLV        0.4018        647.0             32.00     Sequence
DRB1_1302   24  QYAQLIARRVREARV  ARRVREARV        0.4016        648.1             32.00     Sequence
DRB1_1302  496  STRITNEVAEVNRVV  RITNEVAEV        0.4007        654.7             32.00     Sequence
DRB1_1302  450  LADVRSVGVQGDGRT  LADVRSVGV        0.3975        677.5             32.00     Sequence
DRB1_1302   60  LVLSGGPASVYADGA  VLSGGPASV        0.3970        681.8             32.00     Sequence
DRB1_1302   19  VDFGAQYAQLIARRV  YAQLIARRV        0.3955        692.7             32.00     Sequence
DRB1_1302   28  LIARRVREARVFSEV  ARRVREARV        0.3951        696.0             32.00     Sequence
DRB1_1302   26  AQLIARRVREARVFS  ARRVREARV        0.3937        706.1             32.00     Sequence
DRB1_1302  409  RIVGEVTAKRLDTLR  VGEVTAKRL        0.3913        724.6             32.00     Sequence
DRB1_1302  436  AGLDNQIWQCPVVLL  IWQCPVVLL        0.3898        736.8             32.00     Sequence
DRB1_1302  229  CGLSGGVDSAVAAAL  VDSAVAAAL        0.3892        741.4             32.00     Sequence
DRB1_1302  502  EVAEVNRVVLDITSK  VAEVNRVVL        0.3879        751.9             32.00     Sequence
DRB1_1302   21  FGAQYAQLIARRVRE  YAQLIARRV        0.3864        764.3             32.00     Sequence
DRB1_1302  210  IANALIEQVRTQIGD  LIEQVRTQI        0.3843        782.2             32.00     Sequence
DRB1_1302  152  DVVASSAGAPVAAFE  VASSAGAPV        0.3834        789.7             32.00     Sequence
DRB1_1302  317  EGAVRDVLDGKTAEF  VLDGKTAEF        0.3823        799.3             32.00     Sequence
DRB1_1302  282  LVTVDAAETFLEALS  LVTVDAAET        0.3822        800.2             32.00     Sequence
DRB1_1302  234  GVDSAVAAALVQRAI  DSAVAAALV        0.3818        803.1             32.00     Sequence
DRB1_1302   61  VLSGGPASVYADGAP  VLSGGPASV        0.3800        819.2             32.00     Sequence
DRB1_1302  274  FVAATGANLVTVDAA  VAATGANLV        0.3748        866.3             32.00     Sequence
DRB1_1302  183  HTPHGQQVLSRFLHD  GQQVLSRFL        0.3726        887.2             32.00     Sequence
DRB1_1302  318  GAVRDVLDGKTAEFL  VLDGKTAEF        0.3712        901.5             32.00     Sequence
DRB1_1302  137  WMSHGDAVTAAPDGF  MSHGDAVTA        0.3686        926.2             32.00     Sequence
DRB1_1302  437  GLDNQIWQCPVVLLA  QIWQCPVVL        0.3684        928.5             32.00     Sequence
DRB1_1302  130  LPEVQPVWMSHGDAV  VWMSHGDAV        0.3681        931.6             32.00     Sequence
DRB1_1302  214  LIEQVRTQIGDGHAI  TQIGDGHAI        0.3627        987.4             32.00     Sequence
DRB1_1302   22  GAQYAQLIARRVREA  YAQLIARRV        0.3611       1004.6             32.00     Sequence
DRB1_1302  227  AICGLSGGVDSAVAA  AICGLSGGV        0.3605       1011.2             32.00     Sequence
DRB1_1302  507  NRVVLDITSKPPATI  ITSKPPATI        0.3595       1022.5             32.00     Sequence
DRB1_1302  319  AVRDVLDGKTAEFLV  VLDGKTAEF        0.3585       1033.6             32.00     Sequence
DRB1_1302  147  APDGFDVVASSAGAP  DVVASSAGA        0.3582       1037.3             32.00     Sequence
DRB1_1302  320  VRDVLDGKTAEFLVQ  VLDGKTAEF        0.3569       1051.9             32.00     Sequence
DRB1_1302  460  GDGRTYGHPIVLRPV  RTYGHPIVL        0.3559       1062.8             32.00     Sequence
DRB1_1302  457  GVQGDGRTYGHPIVL  RTYGHPIVL        0.3549       1074.7             32.00     Sequence
DRB1_1302  200  GLGAQWTPANIANAL  WTPANIANA        0.3546       1078.2             32.00     Sequence
DRB1_1302  184  TPHGQQVLSRFLHDF  GQQVLSRFL        0.3542       1082.9             32.00     Sequence
DRB1_1302  442  IWQCPVVLLADVRSV  VLLADVRSV        0.3526       1101.9             32.00     Sequence
DRB1_1302   46  TASIEEIRARQPVAL  IRARQPVAL        0.3510       1121.4             32.00     Sequence
DRB1_1302  100  QALGGIVAHTGTREY  VAHTGTREY        0.3488       1147.8             32.00     Sequence
DRB1_1302  268  AQVQRDFVAATGANL  FVAATGANL        0.3461       1182.3             32.00     Sequence
DRB1_1302  185  PHGQQVLSRFLHDFA  GQQVLSRFL        0.3449       1197.5             32.00     Sequence
DRB1_1302  508  RVVLDITSKPPATIE  ITSKPPATI        0.3427       1226.1             32.00     Sequence
DRB1_1302  410  IVGEVTAKRLDTLRH  VGEVTAKRL        0.3412       1246.5             32.00     Sequence
DRB1_1302  321  RDVLDGKTAEFLVQG  VLDGKTAEF        0.3411       1247.8             32.00     Sequence
DRB1_1302   53  RARQPVALVLSGGPA  RARQPVALV        0.3406       1254.1             32.00     Sequence
DRB1_1302  402  PGPGLGIRIVGEVTA  IRIVGEVTA        0.3398       1265.9             32.00     Sequence
DRB1_1302  364  DDLKFTLVEPLRLLF  FTLVEPLRL        0.3389       1277.6             32.00     Sequence
DRB1_1302  458  VQGDGRTYGHPIVLR  RTYGHPIVL        0.3383       1285.7             32.00     Sequence
DRB1_1302   31  RRVREARVFSEVIPH  EARVFSEVI        0.3379       1292.4             32.00     Sequence
DRB1_1302   23  AQYAQLIARRVREAR  YAQLIARRV        0.3365       1311.3             32.00     Sequence
DRB1_1302  459  QGDGRTYGHPIVLRP  RTYGHPIVL        0.3360       1318.9             32.00     Sequence
DRB1_1302  363  PDDLKFTLVEPLRLL  FTLVEPLRL        0.3352       1330.2             32.00     Sequence
DRB1_1302  461  DGRTYGHPIVLRPVS  RTYGHPIVL        0.3344       1341.1             32.00     Sequence
DRB1_1302  365  DLKFTLVEPLRLLFK  FTLVEPLRL        0.3343       1342.6             32.00     Sequence
DRB1_1302  211  ANALIEQVRTQIGDG  LIEQVRTQI        0.3317       1381.1             32.00     Sequence
DRB1_1302  216  EQVRTQIGDGHAICG  TQIGDGHAI        0.3305       1399.8             32.00     Sequence
DRB1_1302  235  VDSAVAAALVQRAIG  DSAVAAALV        0.3297       1412.0             50.00     Sequence
DRB1_1302  131  PEVQPVWMSHGDAVT  VWMSHGDAV        0.3281       1435.7             50.00     Sequence
DRB1_1302  411  VGEVTAKRLDTLRHA  VGEVTAKRL        0.3280       1437.8             50.00     Sequence
DRB1_1302  101  ALGGIVAHTGTREYG  GIVAHTGTR        0.3270       1454.3             50.00     Sequence
DRB1_1302  180  EVMHTPHGQQVLSRF  MHTPHGQQV        0.3260       1468.9             50.00     Sequence
DRB1_1302  403  GPGLGIRIVGEVTAK  IRIVGEVTA        0.3258       1472.1             50.00     Sequence
DRB1_1302  138  MSHGDAVTAAPDGFD  MSHGDAVTA        0.3255       1477.4             50.00     Sequence
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DRB1_1302	275	VAATGANLVTVDAAE	VAATGANLV	0.3244	1495.6	50.00	Sequence
DRB1_1302	305	RKIIGRQFIRAFEGA	IGRQFIRAF	0.3230	1517.9	50.00	Sequence
DRB1_1302	404	PGLGIRIVGEVTAKR	IRIVGEVTA	0.3226	1523.8	50.00	Sequence
DRB1_1302	348	SGTANIKSHHNVGGL	KSHHNVGGL	0.3222	1531.0	50.00	Sequence
DRB1_1302	178	HPEVMHTPHGQQVLS	MHTPHGQQV	0.3220	1534.4	50.00	Sequence
DRB1_1302	443	WQCPVVLLADVRSVG	VLLADVRSV	0.3217	1539.0	50.00	Sequence
DRB1_1302	217	QVRTQIGDGHAICGL	TQIGDGHAI	0.3215	1542.5	50.00	Sequence
DRB1_1302	179	PEVMHTPHGQQVLSR	MHTPHGQQV	0.3213	1545.9	50.00	Sequence
DRB1_1302	153	VVASSAGAPVAAFEA	VASSAGAPV	0.3212	1548.1	50.00	Sequence
DRB1_1302	438	LDNQIWQCPVVLLAD	QIWQCPVVL	0.3201	1566.5	50.00	Sequence
DRB1_1302	509	VVLDITSKPPATIEW	ITSKPPATI	0.3196	1575.3	50.00	Sequence
DRB1_1302	176	QYHPEVMHTPHGQQV	MHTPHGQQV	0.3182	1598.0	50.00	Sequence
DRB1_1302	323	VLDGKTAEFLVQGTL	VLDGKTAEF	0.3156	1643.7	50.00	Sequence
DRB1_1302	186	HGQQVLSRFLHDFAG	GQQVLSRFL	0.3153	1650.4	50.00	Sequence
DRB1_1302	177	YHPEVMHTPHGQQVL	MHTPHGQQV	0.3143	1668.3	50.00	Sequence
DRB1_1302	212	NALIEQVRTQIGDGH	LIEQVRTQI	0.3134	1684.7	50.00	Sequence
DRB1_1302	322	DVLDGKTAEFLVQGT	VLDGKTAEF	0.3116	1717.6	50.00	Sequence
DRB1_1302	225	GHAICGLSGGVDSAV	AICGLSGGV	0.3110	1728.7	50.00	Sequence
DRB1_1302	102	LGGIVAHTGTREYGR	GIVAHTGTR	0.3102	1743.3	50.00	Sequence
DRB1_1302	18	VVDFGAQYAQLIARR	FGAQYAQLI	0.3097	1751.9	50.00	Sequence
DRB1_1302	435	AAGLDNQIWQCPVVL	QIWQCPVVL	0.3089	1767.9	50.00	Sequence
DRB1_1302	439	DNQIWQCPVVLLADV	QIWQCPVVL	0.3079	1787.7	50.00	Sequence
DRB1_1302	32	RVREARVFSEVIPHT	EARVFSEVI	0.3075	1794.5	50.00	Sequence
DRB1_1302	215	IEQVRTQIGDGHAIC	TQIGDGHAI	0.3060	1823.8	50.00	Sequence
DRB1_1302	218	VRTQIGDGHAICGLS	TQIGDGHAI	0.3056	1831.9	50.00	Sequence
DRB1_1302	306	KIIGRQFIRAFEGAV	FIRAFEGAV	0.3051	1842.5	50.00	Sequence
DRB1_1302	228	ICGLSGGVDSAVAAA	LSGGVDSAV	0.3046	1852.2	50.00	Sequence
DRB1_1302	366	LKFTLVEPLRLLFKD	FTLVEPLRL	0.3040	1864.7	50.00	Sequence
DRB1_1302	298	VSAPEGKRKIIGRQF	KRKIIGRQF	0.3038	1867.8	50.00	Sequence
DRB1_1302	213	ALIEQVRTQIGDGHA	LIEQVRTQI	0.3034	1876.5	50.00	Sequence
DRB1_1302	377	LFKDEVRAVGRELGL	LFKDEVRAV	0.3020	1904.3	50.00	Sequence
DRB1_1302	221	QIGDGHAICGLSGGV	AICGLSGGV	0.3009	1927.0	50.00	Sequence
DRB1_1302	124	GKLHSDLPEVQPVWM	LPEVQPVWM	0.3004	1938.1	50.00	Sequence
DRB1_1302	33	VREARVFSEVIPHTA	EARVFSEVI	0.3000	1947.1	50.00	Sequence
DRB1_1302	154	VASSAGAPVAAFEAF	VASSAGAPV	0.2997	1953.3	50.00	Sequence
DRB1_1302	510	VLDITSKPPATIEWE	ITSKPPATI	0.2992	1963.3	50.00	Sequence
DRB1_1302	349	GTANIKSHHNVGGLP	KSHHNVGGL	0.2992	1964.2	50.00	Sequence
DRB1_1302	219	RTQIGDGHAICGLSG	TQIGDGHAI	0.2974	2001.8	50.00	Sequence
DRB1_1302	187	GQQVLSRFLHDFAGL	GQQVLSRFL	0.2974	2002.3	50.00	Sequence
DRB1_1302	5	DIDVPETPARPVLVV	ETPARPVLV	0.2973	2004.3	50.00	Sequence
DRB1_1302	456	VGVQGDGRTYGHPIV	DGRTYGHPI	0.2972	2005.7	50.00	Sequence
DRB1_1302	375	RLLFKDEVRAVGREL	LFKDEVRAV	0.2972	2006.7	50.00	Sequence
DRB1_1302	328	TAEFLVQGTLYPDVV	EFLVQGTLY	0.2962	2027.4	50.00	Sequence
DRB1_1302	103	GGIVAHTGTREYGRT	VAHTGTREY	0.2961	2029.6	50.00	Sequence
DRB1_1302	307	IIGRQFIRAFEGAVR	FIRAFEGAV	0.2924	2114.4	50.00	Sequence
DRB1_1302	441	QIWQCPVVLLADVRS	QIWQCPVVL	0.2922	2118.9	50.00	Sequence
DRB1_1302	376	LLFKDEVRAVGRELG	LFKDEVRAV	0.2911	2142.7	50.00	Sequence
DRB1_1302	440	NQIWQCPVVLLADVR	QIWQCPVVL	0.2906	2155.5	50.00	Sequence
DRB1_1302	199	AGLGAQWTPANIANA	WTPANIANA	0.2896	2179.5	50.00	Sequence
DRB1_1302	329	AEFLVQGTLYPDVVE	EFLVQGTLY	0.2891	2190.5	50.00	Sequence
DRB1_1302	226	HAICGLSGGVDSAVA	AICGLSGGV	0.2884	2206.7	50.00	Sequence
DRB1_1302	350	TANIKSHHNVGGLPD	KSHHNVGGL	0.2878	2221.1	50.00	Sequence
DRB1_1302	99	AQALGGIVAHTGTRE	GIVAHTGTR	0.2875	2228.9	50.00	Sequence
DRB1_1302	10	ETPARPVLVVDFGAQ	ETPARPVLV	0.2868	2246.4	50.00	Sequence
DRB1_1302	222	IGDGHAICGLSGGVD	AICGLSGGV	0.2867	2247.6	50.00	Sequence
DRB1_1302	146	AAPDGFDVVASSAGA	DVVASSAGA	0.2853	2282.3	50.00	Sequence
DRB1_1302	397	ARQPFPGPGLGIRIV	PGPGLGIRI	0.2844	2303.9	50.00	Sequence
DRB1_1302	4	ADIDVPETPARPVLV	ETPARPVLV	0.2827	2346.1	50.00	Sequence
DRB1_1302	6	IDVPETPARPVLVVD	ETPARPVLV	0.2825	2351.8	50.00	Sequence
DRB1_1302	462	GRTYGHPIVLRPVSS	RTYGHPIVL	0.2819	2366.9	50.00	Sequence
DRB1_1302	326	GKTAEFLVQGTLYPD	EFLVQGTLY	0.2807	2398.0	50.00	Sequence
DRB1_1302	34	REARVFSEVIPHTAS	EARVFSEVI	0.2802	2410.5	50.00	Sequence
DRB1_1302	127	HSDLPEVQPVWMSHG	LPEVQPVWM	0.2800	2417.7	50.00	Sequence
DRB1_1302	236	DSAVAAALVQRAIGD	DSAVAAALV	0.2797	2425.1	50.00	Sequence
DRB1_1302	224	DGHAICGLSGGVDSA	AICGLSGGV	0.2793	2434.5	50.00	Sequence
DRB1_1302	368	FTLVEPLRLLFKDEV	LRLLFKDEV	0.2783	2462.3	50.00	Sequence

DRB1_1302	401	FPGPGLGIRIVGEVT	PGPGLGIRI	0.2767	2504.7	50.00	Sequence
DRB1_1302	367	KFTLVEPLRLLFKDE	FTLVEPLRL	0.2765	2509.5	50.00	Sequence
DRB1_1302	7	DVPETPARPVLVVDF	ETPARPVLV	0.2753	2542.6	50.00	Sequence
DRB1_1302	308	IGRQFIRAFEGAVRD	FIRAFEGAV	0.2731	2604.5	50.00	Sequence
DRB1_1302	223	GDGHAICGLSGGVDS	AICGLSGGV	0.2724	2622.6	50.00	Sequence
DRB1_1302	330	EFLVQGTLYPDVVES	EFLVQGTLY	0.2709	2667.6	50.00	Sequence
DRB1_1302	125	KLHSDLPEVQPVWMS	LPEVQPVWM	0.2707	2673.7	50.00	Sequence
DRB1_1302	104	GIVAHTGTREYGRTE	GIVAHTGTR	0.2689	2725.6	50.00	Sequence
DRB1_1302	84	LGVPVLGICYGFQAM	LGICYGFQA	0.2681	2749.8	50.00	Sequence
DRB1_1302	220	TQIGDGHAICGLSGG	TQIGDGHAI	0.2680	2750.6	50.00	Sequence
DRB1_1302	398	RQPFPGPGLGIRIVG	PGPGLGIRI	0.2670	2781.6	50.00	Sequence
DRB1_1302	351	ANIKSHHNVGGLPDD	KSHHNVGGL	0.2656	2825.8	50.00	Sequence
DRB1_1302	325	DGKTAEFLVQGTLYP	EFLVQGTLY	0.2653	2834.4	50.00	Sequence
DRB1_1302	327	KTAEFLVQGTLYPDV	EFLVQGTLY	0.2650	2841.4	50.00	Sequence
DRB1_1302	400	PFPGPGLGIRIVGEV	PGPGLGIRI	0.2637	2883.6	50.00	Sequence
DRB1_1302	79	PALLDLGVPVLGICY	ALLDLGVPV	0.2625	2920.2	50.00	Sequence
DRB1_1302	371	VEPLRLLFKDEVRAV	LFKDEVRAV	0.2617	2946.5	50.00	Sequence
DRB1_1302	85	GVPVLGICYGFQAMA	LGICYGFQA	0.2614	2954.8	50.00	Sequence
DRB1_1302	8	VPETPARPVLVVDFG	ETPARPVLV	0.2599	3005.6	50.00	Sequence
DRB1_1302	362	LPDDLKFTLVEPLRL	FTLVEPLRL	0.2595	3017.0	50.00	Sequence
DRB1_1302	80	ALLDLGVPVLGICYG	ALLDLGVPV	0.2595	3018.5	50.00	Sequence
DRB1_1302	83	DLGVPVLGICYGFQA	LGICYGFQA	0.2581	3062.2	50.00	Sequence
DRB1_1302	373	PLRLLFKDEVRAVGR	LFKDEVRAV	0.2578	3073.7	50.00	Sequence
DRB1_1302	128	SDLPEVQPVWMSHGD	LPEVQPVWM	0.2578	3074.5	50.00	Sequence
DRB1_1302	372	EPLRLLFKDEVRAVG	LFKDEVRAV	0.2578	3074.6	50.00	Sequence
DRB1_1302	264	AGERAQVQRDFVAAT	VQRDFVAAT	0.2536	3216.3	50.00	Sequence
DRB1_1302	262	LRAGERAQVQRDFVA	LRAGERAQV	0.2531	3231.7	50.00	Sequence
DRB1_1302	463	RTYGHPIVLRPVSSE	RTYGHPIVL	0.2519	3274.5	50.00	Sequence
DRB1_1302	54	ARQPVALVLSGGPAS	ALVLSGGPA	0.2518	3279.2	50.00	Sequence
DRB1_1302	126	LHSDLPEVQPVWMSH	LPEVQPVWM	0.2496	3359.6	50.00	Sequence
DRB1_1302	119	LKVLGGKLHSDLPEV	KLHSDLPEV	0.2495	3363.5	50.00	Sequence
DRB1_1302	168	FDRRLAGVQYHPEVM	DRRLAGVQY	0.2488	3386.7	50.00	Sequence
DRB1_1302	374	LRLLFKDEVRAVGRE	LFKDEVRAV	0.2480	3415.7	50.00	Sequence
DRB1_1302	261	LLRAGERAQVQRDFV	LRAGERAQV	0.2480	3417.9	50.00	Sequence
DRB1_1302	324	LDGKTAEFLVQGTLY	EFLVQGTLY	0.2472	3447.1	50.00	Sequence
DRB1_1302	75	PKLDPALLDLGVPVL	ALLDLGVPV	0.2454	3515.6	50.00	Sequence
DRB1_1302	164	AFEAFDRRLAGVQYH	DRRLAGVQY	0.2451	3525.3	50.00	Sequence
DRB1_1302	265	GERAQVQRDFVAATG	VQRDFVAAT	0.2437	3577.7	50.00	Sequence
DRB1_1302	63	SGGPASVYADGAPKL	VYADGAPKL	0.2435	3585.7	50.00	Sequence
DRB1_1302	267	RAQVQRDFVAATGAN	VQRDFVAAT	0.2427	3619.8	50.00	Sequence
DRB1_1302	64	GGPASVYADGAPKLD	VYADGAPKL	0.2419	3651.0	50.00	Sequence
DRB1_1302	399	QPFPGPGLGIRIVGE	PGPGLGIRI	0.2418	3653.6	50.00	Sequence
DRB1_1302	309	GRQFIRAFEGAVRDV	FIRAFEGAV	0.2417	3658.0	50.00	Sequence
DRB1_1302	455	SVGVQGDGRTYGHPI	DGRTYGHPI	0.2407	3699.1	50.00	Sequence
DRB1_1302	129	DLPEVQPVWMSHGDA	LPEVQPVWM	0.2406	3701.4	50.00	Sequence
DRB1_1302	87	PVLGICYGFQAMAQA	LGICYGFQA	0.2399	3729.8	50.00	Sequence
DRB1_1302	430	REELTAAGLDNQIWQ	REELTAAGL	0.2394	3750.9	50.00	Sequence
DRB1_1302	76	KLDPALLDLGVPVLG	ALLDLGVPV	0.2393	3754.3	50.00	Sequence
DRB1_1302	169	DRRLAGVQYHPEVMH	DRRLAGVQY	0.2373	3837.3	50.00	Sequence
DRB1_1302	396	VARQPFPGPGLGIRI	PGPGLGIRI	0.2370	3849.1	50.00	Sequence
DRB1_1302	434	TAAGLDNQIWQCPVV	NQIWQCPVV	0.2365	3867.8	50.00	Sequence
DRB1_1302	62	LSGGPASVYADGAPK	LSGGPASVY	0.2351	3929.8	50.00	Sequence
DRB1_1302	9	PETPARPVLVVDFGA	ETPARPVLV	0.2348	3942.0	50.00	Sequence
DRB1_1302	504	AEVNRVVLDITSKPP	VVLDITSKP	0.2345	3955.9	50.00	Sequence
DRB1_1302	166	EAFDRRLAGVQYHPE	DRRLAGVQY	0.2339	3981.7	50.00	Sequence
DRB1_1302	256	FVDHGLLRAGERAQV	LRAGERAQV	0.2322	4055.0	50.00	Sequence
DRB1_1302	266	ERAQVQRDFVAATGA	VQRDFVAAT	0.2295	4174.0	50.00	Sequence
DRB1_1302	167	AFDRRLAGVQYHPEV	DRRLAGVQY	0.2294	4178.8	50.00	Sequence
DRB1_1302	42	VIPHTASIEEIRARQ	IPHTASIEE	0.2291	4190.1	50.00	Sequence
DRB1_1302	165	FEAFDRRLAGVQYHP	DRRLAGVQY	0.2291	4193.3	50.00	Sequence
DRB1_1302	352	NIKSHHNVGGLPDDL	KSHHNVGGL	0.2283	4230.4	50.00	Sequence
DRB1_1302	81	LLDLGVPVLGICYGF	GVPVLGICY	0.2249	4385.0	50.00	Sequence
DRB1_1302	257	VDHGLLRAGERAQVQ	LRAGERAQV	0.2245	4404.2	50.00	Sequence
DRB1_1302	74	APKLDPALLDLGVPV	ALLDLGVPV	0.2231	4475.5	50.00	Sequence
DRB1_1302	78	DPALLDLGVPVLGIC	ALLDLGVPV	0.2223	4510.7	50.00	Sequence
DRB1_1302	86	VPVLGICYGFQAMAQ	LGICYGFQA	0.2196	4643.5	50.00	Sequence

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DRB1_1302  424  HADSIVREELTAAGL  REELTAAGL        0.2182       4719.1                50.00     Sequence
DRB1_1302  428  IVREELTAAGLDNQI  REELTAAGL        0.2175       4750.4                50.00     Sequence
DRB1_1302  505  EVNRVVLDITSKPPA  VVLDITSKP        0.2174       4760.2                50.00     Sequence
DRB1_1302  506  VNRVVLDITSKPPAT  VVLDITSKP        0.2166       4797.2                50.00     Sequence
DRB1_1302  310  RQFIRAFEGAVRDVL  FIRAFEGAV        0.2156       4850.8                50.00     Sequence
DRB1_1302  353  IKSHHNVGGLPDDLK  KSHHNVGGL        0.2150       4884.8                50.00     Sequence
DRB1_1302   77  LDPALLDLGVPVLGI  ALLDLGVPV        0.2145       4910.0                50.00     Sequence
DRB1_1302  433  LTAAGLDNQIWQCPV  TAAGLDNQI        0.2140       4937.8                50.00     Sequence
DRB1_1302  429  VREELTAAGLDNQIW  REELTAAGL        0.2121       5037.5                50.00     Sequence
DRB1_1302   65  GPASVYADGAPKLDP  VYADGAPKL        0.2121       5040.3                50.00     Sequence
DRB1_1302   82  LDLGVPVLGICYGFQ  GVPVLGICY        0.2117       5059.4                50.00     Sequence
DRB1_1302  431  EELTAAGLDNQIWQC  TAAGLDNQI        0.2101       5148.8                50.00     Sequence
DRB1_1302  378  FKDEVRAVGRELGLP  RAVGRELGL        0.2099       5162.8                50.00     Sequence
DRB1_1302  170  RRLAGVQYHPEVMHT  QYHPEVMHT        0.2097       5173.8                50.00     Sequence
DRB1_1302  473  PVSSEDAMTADWTRV  AMTADWTRV        0.2096       5179.2                50.00     Sequence
DRB1_1302  258  DHGLLRAGERAQVQR  LRAGERAQV        0.2088       5221.0                50.00     Sequence
DRB1_1302  251  RLTCVFVDHGLLRAG  VFVDHGLLR        0.2084       5244.3                50.00     Sequence
DRB1_1302  432  ELTAAGLDNQIWQCP  TAAGLDNQI        0.2076       5290.4                50.00     Sequence
DRB1_1302  425  ADSIVREELTAAGLD  REELTAAGL        0.2063       5366.5                50.00     Sequence
DRB1_1302  354  KSHHNVGGLPDDLKF  KSHHNVGGL        0.2056       5404.2                50.00     Sequence
DRB1_1302  369  TLVEPLRLLFKDEVR  LRLLFKDEV        0.2050       5442.2                50.00     Sequence
DRB1_1302  347  GSGTANIKSHHNVGG  TANIKSHHN        0.2048       5451.3                50.00     Sequence
DRB1_1302  259  HGLLRAGERAQVQRD  LRAGERAQV        0.2037       5518.9                50.00     Sequence
DRB1_1302  331  FLVQGTLYPDVVESG  QGTLYPDVV        0.2024       5596.1                50.00     Sequence
DRB1_1302  311  QFIRAFEGAVRDVLD  FIRAFEGAV        0.2021       5612.5                50.00     Sequence
DRB1_1302  426  DSIVREELTAAGLDN  REELTAAGL        0.2008       5696.6                50.00     Sequence
DRB1_1302  345  GGGSGTANIKSHHNV  TANIKSHHN        0.2005       5710.9                50.00     Sequence
DRB1_1302   66  PASVYADGAPKLDPA  VYADGAPKL        0.1998       5756.5                50.00     Sequence
DRB1_1302   68  SVYADGAPKLDPALL  VYADGAPKL        0.1990       5802.9                50.00     Sequence
DRB1_1302  379  KDEVRAVGRELGLPE  RAVGRELGL        0.1990       5807.7                50.00     Sequence
DRB1_1302  344  SGGGSGTANIKSHHN  TANIKSHHN        0.1986       5828.4                50.00     Sequence
DRB1_1302  468  PIVLRPVSSEDAMTA  VSSEDAMTA        0.1970       5932.2                50.00     Sequence
DRB1_1302  250  DRLTCVFVDHGLLRA  VFVDHGLLR        0.1963       5977.9                50.00     Sequence
DRB1_1302  263  RAGERAQVQRDFVAA  RAQVQRDFV        0.1949       6072.2                50.00     Sequence
DRB1_1302  427  SIVREELTAAGLDNQ  REELTAAGL        0.1939       6135.3                50.00     Sequence
DRB1_1302  474  VSSEDAMTADWTRVP  AMTADWTRV        0.1939       6137.9                50.00     Sequence
DRB1_1302  252  LTCVFVDHGLLRAGE  VFVDHGLLR        0.1928       6207.5                50.00     Sequence
DRB1_1302  380  DEVRAVGRELGLPEE  RAVGRELGL        0.1919       6269.4                50.00     Sequence
DRB1_1302   43  IPHTASIEEIRARQP  IPHTASIEE        0.1903       6379.7                50.00     Sequence
DRB1_1302  286  DAAETFLEALSGVSA  LEALSGVSA        0.1893       6446.5                50.00     Sequence
DRB1_1302  260  GLLRAGERAQVQRDF  LRAGERAQV        0.1875       6571.7                50.00     Sequence
DRB1_1302  237  SAVAAALVQRAIGDR  VAAALVQRA        0.1874       6584.7                50.00     Sequence
DRB1_1302  283  VTVDAAETFLEALSG  VTVDAAETF        0.1869       6618.1                50.00     Sequence
DRB1_1302  105  IVAHTGTREYGRTEL  VAHTGTREY        0.1862       6666.2                50.00     Sequence
DRB1_1302  312  FIRAFEGAVRDVLDG  FIRAFEGAV        0.1849       6762.8                50.00     Sequence
DRB1_1302   67  ASVYADGAPKLDPAL  VYADGAPKL        0.1839       6834.6                50.00     Sequence
DRB1_1302  163  AAFEAFDRRLAGVQY  DRRLAGVQY        0.1837       6848.3                50.00     Sequence
DRB1_1302  346  GGSGTANIKSHHNVG  TANIKSHHN        0.1835       6864.2                50.00     Sequence
DRB1_1302   69  VYADGAPKLDPALLD  VYADGAPKL        0.1832       6885.6                50.00     Sequence
DRB1_1302  475  SSEDAMTADWTRVPY  AMTADWTRV        0.1830       6901.2                50.00     Sequence
DRB1_1302  288  AETFLEALSGVSAPE  LEALSGVSA        0.1829       6912.1                50.00     Sequence
DRB1_1302  381  EVRAVGRELGLPEEI  RAVGRELGL        0.1828       6914.8                50.00     Sequence
DRB1_1302  478  DAMTADWTRVPYEVL  AMTADWTRV        0.1824       6946.6                50.00     Sequence
DRB1_1302  249  GDRLTCVFVDHGLLR  VFVDHGLLR        0.1809       7059.2                50.00     Sequence
DRB1_1302  198  FAGLGAQWTPANIAN  GAQWTPANI        0.1809       7062.3                50.00     Sequence
DRB1_1302  192  SRFLHDFAGLGAQWT  DFAGLGAQW        0.1805       7093.1                50.00     Sequence
DRB1_1302  253  TCVFVDHGLLRAGER  VFVDHGLLR        0.1805       7093.8                50.00     Sequence
DRB1_1302  197  DFAGLGAQWTPANIA  GAQWTPANI        0.1799       7140.4                50.00     Sequence
DRB1_1302  289  ETFLEALSGVSAPEG  LEALSGVSA        0.1798       7144.4                50.00     Sequence
DRB1_1302  287  AAETFLEALSGVSAP  LEALSGVSA        0.1796       7159.0                50.00     Sequence
DRB1_1302  370  LVEPLRLLFKDEVRA  LRLLFKDEV        0.1765       7407.7                50.00     Sequence
DRB1_1302  120  KVLGGKLHSDLPEVQ  KLHSDLPEV        0.1764       7412.3                50.00     Sequence
DRB1_1302  254  CVFVDHGLLRAGERA  VFVDHGLLR        0.1758       7459.7                50.00     Sequence
DRB1_1302  415  TAKRLDTLRHADSIV  TLRHADSIV        0.1754       7494.0                50.00     Sequence
DRB1_1302  196  HDFAGLGAQWTPANI  GAQWTPANI        0.1754       7498.3                50.00     Sequence
DRB1_1302  188  QQVLSRFLHDFAGLG  FLHDFAGLG        0.1753       7504.4                50.00     Sequence
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DRB1_1302	476	SEDAMTADWTRVPYE	AMTADWTRV	0.1750	7527.9		50.00	Sequence
DRB1_1302	191	LSRFLHDFAGLGAQW	DFAGLGAQW	0.1725	7730.0		50.00	Sequence
DRB1_1302	466	GHPIVLRPVSSEDAM	LRPVSSEDA	0.1710	7860.8		50.00	Sequence
DRB1_1302	479	AMTADWTRVPYEVLE	AMTADWTRV	0.1696	7982.0		50.00	Sequence
DRB1_1302	290	TFLEALSGVSAPEGK	LEALSGVSA	0.1693	8002.9		50.00	Sequence
DRB1_1302	332	LVQGTLYPDVVESGG	QGTLYPDVV	0.1688	8051.6		50.00	Sequence
DRB1_1302	469	IVLRPVSSEDAMTAD	VSSEDAMTA	0.1686	8065.5		50.00	Sequence
DRB1_1302	451	ADVRSVGVQGDGRTY	GVQGDGRTY	0.1685	8072.2		50.00	Sequence
DRB1_1302	193	RFLHDFAGLGAQWTP	DFAGLGAQW	0.1665	8248.6		50.00	Sequence
DRB1_1302	342	VESGGGSGTANIKSH	GGGSGTANI	0.1649	8398.1		50.00	Sequence
DRB1_1302	255	VFVDHGLLRAGERAQ	VFVDHGLLR	0.1647	8411.5		50.00	Sequence
DRB1_1302	171	RLAGVQYHPEVMHTP	GVQYHPEVM	0.1628	8590.3		50.00	Sequence
DRB1_1302	174	GVQYHPEVMHTPHGQ	GVQYHPEVM	0.1624	8624.7		50.00	Sequence
DRB1_1302	452	DVRSVGVQGDGRTYG	GVQGDGRTY	0.1619	8669.8		50.00	Sequence
DRB1_1302	470	VLRPVSSEDAMTADW	VSSEDAMTA	0.1606	8797.3		50.00	Sequence
DRB1_1302	465	YGHPIVLRPVSSEDA	PIVLRPVSS	0.1604	8814.6		50.00	Sequence
DRB1_1302	44	PHTASIEEIRARQPV	IEEIRARQP	0.1588	8965.6		50.00	Sequence
DRB1_1302	423	RHADSIVREELTAAG	IVREELTAA	0.1586	8993.0		50.00	Sequence
DRB1_1302	106	VAHTGTREYGRTELK	VAHTGTREY	0.1583	9017.7		50.00	Sequence
DRB1_1302	173	AGVQYHPEVMHTPHG	GVQYHPEVM	0.1563	9218.7		50.00	Sequence
DRB1_1302	477	EDAMTADWTRVPYEV	AMTADWTRV	0.1562	9230.1		50.00	Sequence
DRB1_1302	175	VQYHPEVMHTPHGQQ	VMHTPHGQQ	0.1553	9312.7		50.00	Sequence
DRB1_1302	333	VQGTLYPDVVESGGG	QGTLYPDVV	0.1551	9331.8		50.00	Sequence
DRB1_1302	453	VRSVGVQGDGRTYGH	GVQGDGRTY	0.1531	9540.5		50.00	Sequence
DRB1_1302	471	LRPVSSEDAMTADWT	VSSEDAMTA	0.1513	9732.6		50.00	Sequence
DRB1_1302	172	LAGVQYHPEVMHTPH	GVQYHPEVM	0.1510	9762.6		50.00	Sequence
DRB1_1302	343	ESGGGSGTANIKSHH	GGGSGTANI	0.1509	9771.8		50.00	Sequence
DRB1_1302	481	TADWTRVPYEVLERI	VPYEVLERI	0.1507	9791.7		50.00	Sequence
DRB1_1302	467	HPIVLRPVSSEDAMT	LRPVSSEDA	0.1498	9888.8		50.00	Sequence
DRB1_1302	121	VLGGKLHSDLPEVQP	KLHSDLPEV	0.1496	9909.3		50.00	Sequence
DRB1_1302	334	QGTLYPDVVESGGGS	QGTLYPDVV	0.1478	10101.7		50.00	Sequence
DRB1_1302	122	LGGKLHSDLPEVQPV	KLHSDLPEV	0.1460	10301.1		50.00	Sequence
DRB1_1302	45	HTASIEEIRARQPVA	IEEIRARQP	0.1458	10322.6		50.00	Sequence
DRB1_1302	291	FLEALSGVSAPEGKR	LEALSGVSA	0.1454	10370.9		50.00	Sequence
DRB1_1302	340	DVVESGGGSGTANIK	GGGSGTANI	0.1454	10371.2		50.00	Sequence
DRB1_1302	70	YADGAPKLDPALLDL	APKLDPALL	0.1437	10562.4		50.00	Sequence
DRB1_1302	464	TYGHPIVLRPVSSED	PIVLRPVSS	0.1436	10568.5		50.00	Sequence
DRB1_1302	339	PDVVESGGGSGTANI	GGGSGTANI	0.1435	10585.5		50.00	Sequence
DRB1_1302	341	VVESGGGSGTANIKS	GGGSGTANI	0.1432	10624.0		50.00	Sequence
DRB1_1302	245	QRAIGDRLTCVFVDH	GDRLTCVFV	0.1429	10649.8		50.00	Sequence
DRB1_1302	189	QVLSRFLHDFAGLGA	FLHDFAGLG	0.1426	10683.2		50.00	Sequence
DRB1_1302	484	WTRVPYEVLERISTR	WTRVPYEVL	0.1412	10856.3		50.00	Sequence
DRB1_1302	383	RAVGRELGLPEEIVA	RAVGRELGL	0.1407	10915.7		50.00	Sequence
DRB1_1302	123	GGKLHSDLPEVQPVW	KLHSDLPEV	0.1402	10973.0		50.00	Sequence
DRB1_1302	382	VRAVGRELGLPEEIV	RAVGRELGL	0.1390	11112.1		50.00	Sequence
DRB1_1302	71	ADGAPKLDPALLDLG	APKLDPALL	0.1369	11371.1		50.00	Sequence
DRB1_1302	190	VLSRFLHDFAGLGAQ	FLHDFAGLG	0.1358	11500.5		50.00	Sequence
DRB1_1302	454	RSVGVQGDGRTYGHP	GVQGDGRTY	0.1341	11721.9		50.00	Sequence
DRB1_1302	194	FLHDFAGLGAQWTPA	FLHDFAGLG	0.1319	11997.0		50.00	Sequence
DRB1_1302	412	GEVTAKRLDTLRHAD	AKRLDTLRH	0.1308	12139.2		50.00	Sequence
DRB1_1302	482	ADWTRVPYEVLERIS	VPYEVLERI	0.1300	12244.6		50.00	Sequence
DRB1_1302	285	VDAAETFLEALSGVS	TFLEALSGV	0.1300	12254.8		50.00	Sequence
DRB1_1302	292	LEALSGVSAPEGKRK	LEALSGVSA	0.1297	12290.8		50.00	Sequence
DRB1_1302	483	DWTRVPYEVLERIST	VPYEVLERI	0.1284	12464.3		50.00	Sequence
DRB1_1302	72	DGAPKLDPALLDLGV	APKLDPALL	0.1266	12702.6		50.00	Sequence
DRB1_1302	155	ASSAGAPVAAFEAFD	GAPVAAFEA	0.1266	12710.7		50.00	Sequence
DRB1_1302	480	MTADWTRVPYEVLER	WTRVPYEVL	0.1264	12739.2		50.00	Sequence
DRB1_1302	158	AGAPVAAFEAFDRRL	AFEAFDRRL	0.1249	12941.5		50.00	Sequence
DRB1_1302	388	ELGLPEEIVARQPFP	EEIVARQPF	0.1237	13115.3		50.00	Sequence
DRB1_1302	248	IGDRLTCVFVDHGLL	CVFVDHGLL	0.1226	13263.6		50.00	Sequence
DRB1_1302	159	GAPVAAFEAFDRRLA	AFEAFDRRL	0.1219	13367.6		50.00	Sequence
DRB1_1302	414	VTAKRLDTLRHADSI	AKRLDTLRH	0.1212	13480.0		50.00	Sequence
DRB1_1302	389	LGLPEEIVARQPFPG	EEIVARQPF	0.1211	13484.8		50.00	Sequence
DRB1_1302	387	RELGLPEEIVARQPF	EEIVARQPF	0.1207	13552.4		50.00	Sequence
DRB1_1302	472	RPVSSEDAMTADWTR	VSSEDAMTA	0.1205	13578.2		50.00	Sequence
DRB1_1302	156	SSAGAPVAAFEAFDR	SAGAPVAAF	0.1194	13733.5		50.00	Sequence

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   DRB1_1302   73  GAPKLDPALLDLGVP  APKLDPALL        0.1188      13833.4               50.00     Sequence
   DRB1_1302  195  LHDFAGLGAQWTPAN  DFAGLGAQW        0.1161      14231.5               50.00     Sequence
   DRB1_1302    0  VVQPADIDVPETPAR  VVQPADIDV        0.1149      14426.7               50.00     Sequence
   DRB1_1302    2  QPADIDVPETPARPV  VPETPARPV        0.1141      14552.9               50.00     Sequence
   DRB1_1302  360  GGLPDDLKFTLVEPL  LKFTLVEPL        0.1122      14858.2               50.00     Sequence
   DRB1_1302    3  PADIDVPETPARPVL  VPETPARPV        0.1118      14919.9               50.00     Sequence
   DRB1_1302  413  EVTAKRLDTLRHADS  VTAKRLDTL        0.1110      15040.2               50.00     Sequence
   DRB1_1302  246  RAIGDRLTCVFVDHG  GDRLTCVFV        0.1105      15122.2               50.00     Sequence
   DRB1_1302  284  TVDAAETFLEALSGV  TFLEALSGV        0.1099      15226.3               50.00     Sequence
   DRB1_1302  160  APVAAFEAFDRRLAG  AFEAFDRRL        0.1066      15776.1               50.00     Sequence
   DRB1_1302  157  SAGAPVAAFEAFDRR  SAGAPVAAF        0.1060      15889.3               50.00     Sequence
   DRB1_1302  394  EIVARQPFPGPGLGI  PFPGPGLGI        0.1058      15908.2               50.00     Sequence
   DRB1_1302  384  AVGRELGLPEEIVAR  RELGLPEEI        0.1044      16150.2               50.00     Sequence
   DRB1_1302  390  GLPEEIVARQPFPGP  EEIVARQPF        0.1041      16217.9               50.00     Sequence
   DRB1_1302  385  VGRELGLPEEIVARQ  RELGLPEEI        0.1030      16397.5               50.00     Sequence
   DRB1_1302  337  LYPDVVESGGGSGTA  VESGGGSGT        0.1026      16471.3               50.00     Sequence
   DRB1_1302  145  TAAPDGFDVVASSAG  GFDVVASSA        0.1024      16512.6               50.00     Sequence
   DRB1_1302  392  PEEIVARQPFPGPGL  EEIVARQPF        0.1014      16683.9               50.00     Sequence
   DRB1_1302  361  GLPDDLKFTLVEPLR  LKFTLVEPL        0.1008      16797.6               50.00     Sequence
   DRB1_1302  338  YPDVVESGGGSGTAN  VESGGGSGT        0.0996      17024.0               50.00     Sequence
   DRB1_1302  247  AIGDRLTCVFVDHGL  GDRLTCVFV        0.0995      17037.8               50.00     Sequence
   DRB1_1302  395  IVARQPFPGPGLGIR  PFPGPGLGI        0.0994      17047.6               50.00     Sequence
   DRB1_1302  393  EEIVARQPFPGPGLG  EEIVARQPF        0.0977      17372.7               50.00     Sequence
   DRB1_1302  316  FEGAVRDVLDGKTAE  VRDVLDGKT        0.0967      17566.2               50.00     Sequence
   DRB1_1302  139  SHGDAVTAAPDGFDV  AVTAAPDGF        0.0964      17627.0               50.00     Sequence
   DRB1_1302  294  ALSGVSAPEGKRKII  APEGKRKII        0.0950      17895.4               50.00     Sequence
   DRB1_1302  140  HGDAVTAAPDGFDVV  AVTAAPDGF        0.0919      18488.8               50.00     Sequence
   DRB1_1302  336  TLYPDVVESGGGSGT  VESGGGSGT        0.0906      18770.4               50.00     Sequence
   DRB1_1302  315  AFEGAVRDVLDGKTA  VRDVLDGKT        0.0894      19010.4               50.00     Sequence
   DRB1_1302  386  GRELGLPEEIVARQP  RELGLPEEI        0.0878      19346.3               50.00     Sequence
   DRB1_1302  335  GTLYPDVVESGGGSG  VVESGGGSG        0.0872      19464.5               50.00     Sequence
   DRB1_1302  313  IRAFEGAVRDVLDGK  IRAFEGAVR        0.0872      19471.7               50.00     Sequence
   DRB1_1302  391  LPEEIVARQPFPGPG  EEIVARQPF        0.0869      19527.8               50.00     Sequence
   DRB1_1302  109  TGTREYGRTELKVLG  YGRTELKVL        0.0866      19600.4               50.00     Sequence
   DRB1_1302  108  HTGTREYGRTELKVL  YGRTELKVL        0.0862      19684.1               50.00     Sequence
   DRB1_1302  161  PVAAFEAFDRRLAGV  AFEAFDRRL        0.0835      20253.0               50.00     Sequence
   DRB1_1302  293  EALSGVSAPEGKRKI  SAPEGKRKI        0.0820      20590.6               50.00     Sequence
   DRB1_1302  141  GDAVTAAPDGFDVVA  AVTAAPDGF        0.0803      20971.0               50.00     Sequence
   DRB1_1302  314  RAFEGAVRDVLDGKT  VRDVLDGKT        0.0800      21041.0               50.00     Sequence
   DRB1_1302  110  GTREYGRTELKVLGG  RTELKVLGG        0.0798      21077.7               50.00     Sequence
   DRB1_1302  162  VAAFEAFDRRLAGVQ  AFEAFDRRL        0.0789      21297.1               50.00     Sequence
   DRB1_1302  107  AHTGTREYGRTELKV  REYGRTELK        0.0752      22152.8               50.00     Sequence
   DRB1_1302  295  LSGVSAPEGKRKIIG  APEGKRKII        0.0748      22268.2               50.00     Sequence
   DRB1_1302  111  TREYGRTELKVLGGK  RTELKVLGG        0.0702      23390.1               50.00     Sequence
   DRB1_1302  142  DAVTAAPDGFDVVAS  AVTAAPDGF        0.0701      23407.1               50.00     Sequence
   DRB1_1302  297  GVSAPEGKRKIIGRQ  APEGKRKII        0.0699      23471.7               50.00     Sequence
   DRB1_1302  143  AVTAAPDGFDVVASS  AVTAAPDGF        0.0657      24566.1               50.00     Sequence
   DRB1_1302  356  HHNVGGLPDDLKFTL  LPDDLKFTL        0.0646      24846.8               50.00     Sequence
   DRB1_1302  144  VTAAPDGFDVVASSA  GFDVVASSA        0.0644      24898.2               50.00     Sequence
   DRB1_1302  296  SGVSAPEGKRKIIGR  APEGKRKII        0.0633      25215.1               50.00     Sequence
   DRB1_1302  357  HNVGGLPDDLKFTLV  LPDDLKFTL        0.0621      25528.6               50.00     Sequence
   DRB1_1302  359  VGGLPDDLKFTLVEP  LPDDLKFTL        0.0594      26292.8               50.00     Sequence
   DRB1_1302  358  NVGGLPDDLKFTLVE  LPDDLKFTL        0.0578      26749.1               50.00     Sequence
   DRB1_1302    1  VQPADIDVPETPARP  IDVPETPAR        0.0532      28129.3               50.00     Sequence
   DRB1_1302  355  SHHNVGGLPDDLKFT  GGLPDDLKF        0.0502      29034.4               50.00     Sequence
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Allele: DRB1_1302. Number of high binders 0. Number of weak binders 109. Number of peptides 511

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      Allele  pos          peptide      core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1501  488  PYEVLERISTRITNE  VLERISTRI        0.7731         11.7         SB     0.40     Sequence
   DRB1_1501  489  YEVLERISTRITNEV  VLERISTRI        0.7636         12.9         SB     0.40     Sequence
   DRB1_1501  490  EVLERISTRITNEVA  VLERISTRI        0.7612         13.3         SB     0.80     Sequence
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DRB1_1501  487  VPYEVLERISTRITN  VLERISTRI        0.7607        13.3       SB    0.80     Sequence
DRB1_1501  486  RVPYEVLERISTRIT  VLERISTRI        0.7322        18.1       SB    0.80     Sequence
DRB1_1501  306  KIIGRQFIRAFEGAV  KIIGRQFIR        0.6874        29.4       SB    2.00     Sequence
DRB1_1501  303  GKRKIIGRQFIRAFE  KIIGRQFIR        0.6845        30.4       SB    2.00     Sequence
DRB1_1501  304  KRKIIGRQFIRAFEG  KIIGRQFIR        0.6800        31.9       SB    2.00     Sequence
DRB1_1501   14  RPVLVVDFGAQYAQL  LVVDFGAQY        0.6743        33.9       SB    4.00     Sequence
DRB1_1501  305  RKIIGRQFIRAFEGA  KIIGRQFIR        0.6740        34.0       SB    4.00     Sequence
DRB1_1501   15  PVLVVDFGAQYAQLI  LVVDFGAQY        0.6605        39.4       SB    4.00     Sequence
DRB1_1501  302  EGKRKIIGRQFIRAF  KIIGRQFIR        0.6594        39.9       SB    4.00     Sequence
DRB1_1501  307  IIGRQFIRAFEGAVR  IIGRQFIRA        0.6556        41.5       SB    4.00     Sequence
DRB1_1501   88  VLGICYGFQAMAQAL  ICYGFQAMA        0.6536        42.5       SB    4.00     Sequence
DRB1_1501  485  TRVPYEVLERISTRI  VLERISTRI        0.6532        42.6       SB    4.00     Sequence
DRB1_1501   13  ARPVLVVDFGAQYAQ  LVVDFGAQY        0.6523        43.1       SB    4.00     Sequence
DRB1_1501   87  PVLGICYGFQAMAQA  ICYGFQAMA        0.6494        44.4       SB    4.00     Sequence
DRB1_1501   16  VLVVDFGAQYAQLIA  LVVDFGAQY        0.6475        45.3       SB    4.00     Sequence
DRB1_1501   89  LGICYGFQAMAQALG  ICYGFQAMA        0.6462        46.0       SB    4.00     Sequence
DRB1_1501   12  PARPVLVVDFGAQYA  LVVDFGAQY        0.6283        55.8       WB    4.00     Sequence
DRB1_1501   90  GICYGFQAMAQALGG  ICYGFQAMA        0.6227        59.3       WB    8.00     Sequence
DRB1_1501   86  VPVLGICYGFQAMAQ  ICYGFQAMA        0.6211        60.3       WB    8.00     Sequence
DRB1_1501  100  QALGGIVAHTGTREY  GIVAHTGTR        0.6089        68.8       WB    8.00     Sequence
DRB1_1501  491  VLERISTRITNEVAE  VLERISTRI        0.6075        69.9       WB    8.00     Sequence
DRB1_1501  101  ALGGIVAHTGTREYG  GIVAHTGTR        0.6065        70.6       WB    8.00     Sequence
DRB1_1501  308  IGRQFIRAFEGAVRD  FIRAFEGAV        0.6045        72.2       WB    8.00     Sequence
DRB1_1501  408  IRIVGEVTAKRLDTL  IVGEVTAKR        0.5998        76.0       WB    8.00     Sequence
DRB1_1501  409  RIVGEVTAKRLDTLR  RIVGEVTAK        0.5994        76.3       WB    8.00     Sequence
DRB1_1501   17  LVVDFGAQYAQLIAR  LVVDFGAQY        0.5988        76.8       WB    8.00     Sequence
DRB1_1501  406  LGIRIVGEVTAKRLD  IVGEVTAKR        0.5983        77.2       WB    8.00     Sequence
DRB1_1501  407  GIRIVGEVTAKRLDT  IVGEVTAKR        0.5927        82.0       WB    8.00     Sequence
DRB1_1501  301  PEGKRKIIGRQFIRA  KIIGRQFIR        0.5911        83.4       WB    8.00     Sequence
DRB1_1501  405  GLGIRIVGEVTAKRL  IVGEVTAKR        0.5837        90.4       WB    8.00     Sequence
DRB1_1501  116  RTELKVLGGKLHSDL  ELKVLGGKL        0.5810        93.1       WB    8.00     Sequence
DRB1_1501  115  GRTELKVLGGKLHSD  ELKVLGGKL        0.5810        93.1       WB    8.00     Sequence
DRB1_1501   56  QPVALVLSGGPASVY  ALVLSGGPA        0.5719       102.7       WB    8.00     Sequence
DRB1_1501  114  YGRTELKVLGGKLHS  ELKVLGGKL        0.5709       103.8       WB    8.00     Sequence
DRB1_1501   91  ICYGFQAMAQALGGI  ICYGFQAMA        0.5708       103.9       WB    8.00     Sequence
DRB1_1501   99  AQALGGIVAHTGTRE  GIVAHTGTR        0.5683       106.8       WB    8.00     Sequence
DRB1_1501  117  TELKVLGGKLHSDLP  ELKVLGGKL        0.5646       111.2       WB   16.00     Sequence
DRB1_1501   98  MAQALGGIVAHTGTR  ALGGIVAHT        0.5626       113.5       WB   16.00     Sequence
DRB1_1501   85  GVPVLGICYGFQAMA  ICYGFQAMA        0.5619       114.5       WB   16.00     Sequence
DRB1_1501   57  PVALVLSGGPASVYA  ALVLSGGPA        0.5619       114.5       WB   16.00     Sequence
DRB1_1501  446  PVVLLADVRSVGVQG  PVVLLADVR        0.5596       117.3       WB   16.00     Sequence
DRB1_1501  309  GRQFIRAFEGAVRDV  FIRAFEGAV        0.5554       122.8       WB   16.00     Sequence
DRB1_1501   55  RQPVALVLSGGPASV  VALVLSGGP        0.5544       124.2       WB   16.00     Sequence
DRB1_1501  310  RQFIRAFEGAVRDVL  FIRAFEGAV        0.5504       129.7       WB   16.00     Sequence
DRB1_1501   58  VALVLSGGPASVYAD  ALVLSGGPA        0.5487       132.0       WB   16.00     Sequence
DRB1_1501  102  LGGIVAHTGTREYGR  GIVAHTGTR        0.5483       132.6       WB   16.00     Sequence
DRB1_1501  212  NALIEQVRTQIGDGH  LIEQVRTQI        0.5476       133.6       WB   16.00     Sequence
DRB1_1501  131  PEVQPVWMSHGDAVT  EVQPVWMSH        0.5463       135.5       WB   16.00     Sequence
DRB1_1501  211  ANALIEQVRTQIGDG  LIEQVRTQI        0.5462       135.6       WB   16.00     Sequence
DRB1_1501  103  GGIVAHTGTREYGRT  GIVAHTGTR        0.5447       137.8       WB   16.00     Sequence
DRB1_1501  130  LPEVQPVWMSHGDAV  EVQPVWMSH        0.5419       142.2       WB   16.00     Sequence
DRB1_1501  113  EYGRTELKVLGGKLH  ELKVLGGKL        0.5390       146.6       WB   16.00     Sequence
DRB1_1501  445  CPVVLLADVRSVGVQ  PVVLLADVR        0.5381       148.1       WB   16.00     Sequence
DRB1_1501  210  IANALIEQVRTQIGD  LIEQVRTQI        0.5305       160.8       WB   16.00     Sequence
DRB1_1501  507  NRVVLDITSKPPATI  VVLDITSKP        0.5302       161.3       WB   16.00     Sequence
DRB1_1501  118  ELKVLGGKLHSDLPE  ELKVLGGKL        0.5295       162.6       WB   16.00     Sequence
DRB1_1501  444  QCPVVLLADVRSVGV  PVVLLADVR        0.5265       167.9       WB   16.00     Sequence
DRB1_1501  404  PGLGIRIVGEVTAKR  RIVGEVTAK        0.5245       171.6       WB   16.00     Sequence
DRB1_1501  506  VNRVVLDITSKPPAT  VVLDITSKP        0.5244       171.8       WB   16.00     Sequence
DRB1_1501  104  GIVAHTGTREYGRTE  GIVAHTGTR        0.5215       177.1       WB   16.00     Sequence
DRB1_1501  209  NIANALIEQVRTQIG  LIEQVRTQI        0.5167       186.6       WB   16.00     Sequence
DRB1_1501  365  DLKFTLVEPLRLLFK  LVEPLRLLF        0.5161       187.8       WB   16.00     Sequence
DRB1_1501  508  RVVLDITSKPPATIE  VVLDITSKP        0.5155       189.1       WB   16.00     Sequence
DRB1_1501  213  ALIEQVRTQIGDGHA  LIEQVRTQI        0.5152       189.7       WB   16.00     Sequence
DRB1_1501  132  EVQPVWMSHGDAVTA  EVQPVWMSH        0.5116       197.1       WB   16.00     Sequence
DRB1_1501  194  FLHDFAGLGAQWTPA  FLHDFAGLG        0.5097       201.4       WB   16.00     Sequence
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DRB1_1501   11  TPARPVLVVDFGAQY  LVVDFGAQY        0.5093        202.1         WB    16.00      Sequence
DRB1_1501   25  YAQLIARRVREARVF  IARRVREAR        0.5062        209.0         WB    16.00      Sequence
DRB1_1501  505  EVNRVVLDITSKPPA  RVVLDITSK        0.5054        210.8         WB    16.00      Sequence
DRB1_1501   96  QAMAQALGGIVAHTG  ALGGIVAHT        0.5036        215.0         WB    16.00      Sequence
DRB1_1501  129  DLPEVQPVWMSHGDA  EVQPVWMSH        0.4995        224.7         WB    16.00      Sequence
DRB1_1501  311  QFIRAFEGAVRDVLD  FIRAFEGAV        0.4993        225.4         WB    16.00      Sequence
DRB1_1501   54  ARQPVALVLSGGPAS  VALVLSGGP        0.4974        230.0         WB    16.00      Sequence
DRB1_1501  370  LVEPLRLLFKDEVRA  RLLFKDEVR        0.4969        231.2         WB    16.00      Sequence
DRB1_1501   97  AMAQALGGIVAHTGT  ALGGIVAHT        0.4967        231.9         WB    16.00      Sequence
DRB1_1501   23  AQYAQLIARRVREAR  QYAQLIARR        0.4960        233.4         WB    16.00      Sequence
DRB1_1501  410  IVGEVTAKRLDTLRH  IVGEVTAKR        0.4936        239.6         WB    16.00      Sequence
DRB1_1501   47  ASIEEIRARQPVALV  EIRARQPVA        0.4935        239.9         WB    16.00      Sequence
DRB1_1501  371  VEPLRLLFKDEVRAV  RLLFKDEVR        0.4933        240.4         WB    16.00      Sequence
DRB1_1501  366  LKFTLVEPLRLLFKD  LVEPLRLLF        0.4899        249.3         WB    32.00      Sequence
DRB1_1501  193  RFLHDFAGLGAQWTP  FLHDFAGLG        0.4897        250.0         WB    32.00      Sequence
DRB1_1501  443  WQCPVVLLADVRSVG  PVVLLADVR        0.4893        251.0         WB    32.00      Sequence
DRB1_1501  447  VVLLADVRSVGVQGD  DVRSVGVQG        0.4889        252.2         WB    32.00      Sequence
DRB1_1501  369  TLVEPLRLLFKDEVR  LVEPLRLLF        0.4882        254.2         WB    32.00      Sequence
DRB1_1501  128  SDLPEVQPVWMSHGD  EVQPVWMSH        0.4878        255.2         WB    32.00      Sequence
DRB1_1501   95  FQAMAQALGGIVAHT  ALGGIVAHT        0.4875        255.9         WB    32.00      Sequence
DRB1_1501   26  AQLIARRVREARVFS  IARRVREAR        0.4875        255.9         WB    32.00      Sequence
DRB1_1501   22  GAQYAQLIARRVREA  QYAQLIARR        0.4854        262.0         WB    32.00      Sequence
DRB1_1501   59  ALVLSGGPASVYADG  ALVLSGGPA        0.4849        263.3         WB    32.00      Sequence
DRB1_1501  191  LSRFLHDFAGLGAQW  DFAGLGAQW        0.4846        264.0         WB    32.00      Sequence
DRB1_1501   24  QYAQLIARRVREARV  QYAQLIARR        0.4828        269.4         WB    32.00      Sequence
DRB1_1501  190  VLSRFLHDFAGLGAQ  RFLHDFAGL        0.4824        270.6         WB    32.00      Sequence
DRB1_1501  372  EPLRLLFKDEVRAVG  RLLFKDEVR        0.4791        280.4         WB    32.00      Sequence
DRB1_1501  195  LHDFAGLGAQWTPAN  GLGAQWTPA        0.4760        289.8         WB    32.00      Sequence
DRB1_1501  373  PLRLLFKDEVRAVGR  RLLFKDEVR        0.4754        291.7         WB    32.00      Sequence
DRB1_1501   20  DFGAQYAQLIARRVR  QYAQLIARR        0.4745        294.5         WB    32.00      Sequence
DRB1_1501  189  QVLSRFLHDFAGLGA  RFLHDFAGL        0.4744        295.1         WB    32.00      Sequence
DRB1_1501  127  HSDLPEVQPVWMSHG  EVQPVWMSH        0.4735        297.9         WB    32.00      Sequence
DRB1_1501  448  VLLADVRSVGVQGDG  DVRSVGVQG        0.4713        305.0         WB    32.00      Sequence
DRB1_1501  364  DDLKFTLVEPLRLLF  LVEPLRLLF        0.4702        308.6         WB    32.00      Sequence
DRB1_1501  504  AEVNRVVLDITSKPP  RVVLDITSK        0.4697        310.5         WB    32.00      Sequence
DRB1_1501  374  LRLLFKDEVRAVGRE  RLLFKDEVR        0.4663        322.2         WB    32.00      Sequence
DRB1_1501  466  GHPIVLRPVSSEDAM  IVLRPVSSE        0.4660        323.0         WB    32.00      Sequence
DRB1_1501   53  RARQPVALVLSGGPA  VALVLSGGP        0.4643        329.1         WB    32.00      Sequence
DRB1_1501  465  YGHPIVLRPVSSEDA  IVLRPVSSE        0.4642        329.3         WB    32.00      Sequence
DRB1_1501  192  SRFLHDFAGLGAQWT  FLHDFAGLG        0.4642        329.5         WB    32.00      Sequence
DRB1_1501   32  RVREARVFSEVIPHT  EARVFSEVI        0.4621        337.0         WB    32.00      Sequence
DRB1_1501   92  CYGFQAMAQALGGIV  GFQAMAQAL        0.4614        339.4         WB    32.00      Sequence
DRB1_1501   48  SIEEIRARQPVALVL  EIRARQPVA        0.4605        342.8         WB    32.00      Sequence
DRB1_1501   21  FGAQYAQLIARRVRE  QYAQLIARR        0.4600        344.7         WB    32.00      Sequence
DRB1_1501  442  IWQCPVVLLADVRSV  PVVLLADVR        0.4590        348.6         WB    32.00      Sequence
DRB1_1501  196  HDFAGLGAQWTPANI  GLGAQWTPA        0.4582        351.5         WB    32.00      Sequence
DRB1_1501  188  QQVLSRFLHDFAGLG  LSRFLHDFA        0.4568        356.9         WB    32.00      Sequence
DRB1_1501  240  AAALVQRAIGDRLTC  LVQRAIGDR        0.4567        357.3         WB    32.00      Sequence
DRB1_1501  367  KFTLVEPLRLLFKDE  LVEPLRLLF        0.4561        359.4         WB    32.00      Sequence
DRB1_1501   46  TASIEEIRARQPVAL  EIRARQPVA        0.4559        360.2         WB    32.00      Sequence
DRB1_1501  238  AVAAALVQRAIGDRL  LVQRAIGDR        0.4545        366.0         WB    32.00      Sequence
DRB1_1501   31  RRVREARVFSEVIPH  EARVFSEVI        0.4530        371.9         WB    32.00      Sequence
DRB1_1501  300  APEGKRKIIGRQFIR  KIIGRQFIR        0.4496        385.6         WB    32.00      Sequence
DRB1_1501   19  VDFGAQYAQLIARRV  QYAQLIARR        0.4492        387.4         WB    32.00      Sequence
DRB1_1501  239  VAAALVQRAIGDRLT  LVQRAIGDR        0.4485        390.5         WB    32.00      Sequence
DRB1_1501  112  REYGRTELKVLGGKL  ELKVLGGKL        0.4478        393.5         WB    32.00      Sequence
DRB1_1501  463  RTYGHPIVLRPVSSE  IVLRPVSSE        0.4477        394.0         WB    32.00      Sequence
DRB1_1501  161  PVAAFEAFDRRLAGV  AFEAFDRRL        0.4475        394.7         WB    32.00      Sequence
DRB1_1501   84  LGVPVLGICYGFQAM  PVLGICYGF        0.4458        402.1         WB    32.00      Sequence
DRB1_1501  159  GAPVAAFEAFDRRLA  AFEAFDRRL        0.4454        403.6         WB    32.00      Sequence
DRB1_1501  197  DFAGLGAQWTPANIA  GLGAQWTPA        0.4454        403.8         WB    32.00      Sequence
DRB1_1501   27  QLIARRVREARVFSE  IARRVREAR        0.4444        408.3         WB    32.00      Sequence
DRB1_1501  241  AALVQRAIGDRLTCV  AALVQRAIG        0.4442        408.8         WB    32.00      Sequence
DRB1_1501  160  APVAAFEAFDRRLAG  AFEAFDRRL        0.4432        413.4         WB    32.00      Sequence
DRB1_1501   33  VREARVFSEVIPHTA  RVFSEVIPH        0.4425        416.7         WB    32.00      Sequence
DRB1_1501  187  GQQVLSRFLHDFAGL  VLSRFLHDF        0.4424        417.1         WB    32.00      Sequence
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DRB1_1501  312  FIRAFEGAVRDVLDG  FIRAFEGAV       0.4406       425.3       WB   32.00     Sequence
DRB1_1501  162  VAAFEAFDRRLAGVQ  AFEAFDRRL       0.4397       429.4       WB   32.00     Sequence
DRB1_1501   77  LDPALLDLGVPVLGI  ALLDLGVPV       0.4394       430.9       WB   32.00     Sequence
DRB1_1501  208  ANIANALIEQVRTQI  ALIEQVRTQ       0.4372       441.3       WB   32.00     Sequence
DRB1_1501  503  VAEVNRVVLDITSKP  RVVLDITSK       0.4352       450.9       WB   32.00     Sequence
DRB1_1501   78  DPALLDLGVPVLGIC  ALLDLGVPV       0.4346       453.7       WB   32.00     Sequence
DRB1_1501  464  TYGHPIVLRPVSSED  IVLRPVSSE       0.4328       462.4       WB   32.00     Sequence
DRB1_1501   94  GFQAMAQALGGIVAH  GFQAMAQAL       0.4316       468.6       WB   32.00     Sequence
DRB1_1501   35  EARVFSEVIPHTASI  EVIPHTASI       0.4302       475.8       WB   32.00     Sequence
DRB1_1501   93  YGFQAMAQALGGIVA  GFQAMAQAL       0.4301       476.3       WB   32.00     Sequence
DRB1_1501   34  REARVFSEVIPHTAS  RVFSEVIPH       0.4288       483.1       WB   32.00     Sequence
DRB1_1501   49  IEEIRARQPVALVLS  EIRARQPVA       0.4282       486.4       WB   32.00     Sequence
DRB1_1501  163  AAFEAFDRRLAGVQY  AFEAFDRRL       0.4274       490.4       WB   32.00     Sequence
DRB1_1501  186  HGQQVLSRFLHDFAG  LSRFLHDFA       0.4266       494.7       WB   32.00     Sequence
DRB1_1501   41  EVIPHTASIEEIRAR  EVIPHTASI       0.4259       498.6       WB   32.00     Sequence
DRB1_1501  368  FTLVEPLRLLFKDEV  LVEPLRLLF       0.4242       508.0            32.00     Sequence
DRB1_1501   76  KLDPALLDLGVPVLG  ALLDLGVPV       0.4236       511.1            32.00     Sequence
DRB1_1501  449  LLADVRSVGVQGDGR  DVRSVGVQG       0.4209       526.5            32.00     Sequence
DRB1_1501  185  PHGQQVLSRFLHDFA  VLSRFLHDF       0.4201       530.6            32.00     Sequence
DRB1_1501   29  IARRVREARVFSEVI  IARRVREAR       0.4201       530.8            32.00     Sequence
DRB1_1501  198  FAGLGAQWTPANIAN  GLGAQWTPA       0.4195       534.5            32.00     Sequence
DRB1_1501  158  AGAPVAAFEAFDRRL  AFEAFDRRL       0.4186       539.5            32.00     Sequence
DRB1_1501  184  TPHGQQVLSRFLHDF  GQQVLSRFL       0.4185       540.2            32.00     Sequence
DRB1_1501   45  HTASIEEIRARQPVA  ASIEEIRAR       0.4175       545.8            32.00     Sequence
DRB1_1501   50  EEIRARQPVALVLSG  EIRARQPVA       0.4170       548.8            32.00     Sequence
DRB1_1501   75  PKLDPALLDLGVPVL  ALLDLGVPV       0.4169       549.4            32.00     Sequence
DRB1_1501   18  VVDFGAQYAQLIARR  VVDFGAQYA       0.4164       552.5            32.00     Sequence
DRB1_1501   51  EIRARQPVALVLSGG  EIRARQPVA       0.4133       571.5            32.00     Sequence
DRB1_1501  467  HPIVLRPVSSEDAMT  IVLRPVSSE       0.4132       571.7            32.00     Sequence
DRB1_1501   79  PALLDLGVPVLGICY  ALLDLGVPV       0.4118       580.6            32.00     Sequence
DRB1_1501   36  ARVFSEVIPHTASIE  EVIPHTASI       0.4095       595.4            32.00     Sequence
DRB1_1501  126  LHSDLPEVQPVWMSH  EVQPVWMSH       0.4093       596.4            32.00     Sequence
DRB1_1501  242  ALVQRAIGDRLTCVF  LVQRAIGDR       0.4073       609.5            32.00     Sequence
DRB1_1501  441  QIWQCPVVLLADVRS  PVVLLADVR       0.4060       618.4            32.00     Sequence
DRB1_1501   37  RVFSEVIPHTASIEE  EVIPHTASI       0.4053       622.8            32.00     Sequence
DRB1_1501  375  RLLFKDEVRAVGREL  RLLFKDEVR       0.4049       625.6            32.00     Sequence
DRB1_1501  415  TAKRLDTLRHADSIV  TAKRLDTLR       0.4021       645.0            32.00     Sequence
DRB1_1501  237  SAVAAALVQRAIGDR  AVAAALVQR       0.4004       656.9            32.00     Sequence
DRB1_1501   28  LIARRVREARVFSEV  IARRVREAR       0.4003       657.9            32.00     Sequence
DRB1_1501  164  AFEAFDRRLAGVQYH  AFEAFDRRL       0.4001       658.9            32.00     Sequence
DRB1_1501  411  VGEVTAKRLDTLRHA  TAKRLDTLR       0.4001       659.2            32.00     Sequence
DRB1_1501  348  SGTANIKSHHNVGGL  NIKSHHNVG       0.3992       665.8            32.00     Sequence
DRB1_1501  468  PIVLRPVSSEDAMTA  IVLRPVSSE       0.3982       672.7            32.00     Sequence
DRB1_1501  363  PDDLKFTLVEPLRLL  KFTLVEPLR       0.3964       685.7            32.00     Sequence
DRB1_1501   30  ARRVREARVFSEVIP  EARVFSEVI       0.3945       700.4            32.00     Sequence
DRB1_1501   40  SEVIPHTASIEEIRA  EVIPHTASI       0.3943       701.6            32.00     Sequence
DRB1_1501  243  LVQRAIGDRLTCVFV  LVQRAIGDR       0.3916       722.9            32.00     Sequence
DRB1_1501  349  GTANIKSHHNVGGLP  NIKSHHNVG       0.3906       730.1            32.00     Sequence
DRB1_1501  414  VTAKRLDTLRHADSI  TAKRLDTLR       0.3895       738.8            32.00     Sequence
DRB1_1501   52  IRARQPVALVLSGGP  RARQPVALV       0.3884       748.2            32.00     Sequence
DRB1_1501  412  GEVTAKRLDTLRHAD  TAKRLDTLR       0.3871       758.8            32.00     Sequence
DRB1_1501  251  RLTCVFVDHGLLRAG  VFVDHGLLR       0.3858       768.9            50.00     Sequence
DRB1_1501   38  VFSEVIPHTASIEEI  EVIPHTASI       0.3845       780.0            50.00     Sequence
DRB1_1501  403  GPGLGIRIVGEVTAK  RIVGEVTAK       0.3839       785.1            50.00     Sequence
DRB1_1501   39  FSEVIPHTASIEEIR  EVIPHTASI       0.3838       785.8            50.00     Sequence
DRB1_1501  199  AGLGAQWTPANIANA  GLGAQWTPA       0.3823       799.4            50.00     Sequence
DRB1_1501  250  DRLTCVFVDHGLLRA  VFVDHGLLR       0.3820       801.3            50.00     Sequence
DRB1_1501  469  IVLRPVSSEDAMTAD  IVLRPVSSE       0.3817       804.7            50.00     Sequence
DRB1_1501  214  LIEQVRTQIGDGHAI  LIEQVRTQI       0.3796       822.3            50.00     Sequence
DRB1_1501   80  ALLDLGVPVLGICYG  ALLDLGVPV       0.3792       826.2            50.00     Sequence
DRB1_1501  183  HTPHGQQVLSRFLHD  GQQVLSRFL       0.3758       857.3            50.00     Sequence
DRB1_1501  461  DGRTYGHPIVLRPVS  TYGHPIVLR       0.3735       878.6            50.00     Sequence
DRB1_1501  462  GRTYGHPIVLRPVSS  TYGHPIVLR       0.3734       880.2            50.00     Sequence
DRB1_1501  249  GDRLTCVFVDHGLLR  VFVDHGLLR       0.3724       889.2            50.00     Sequence
DRB1_1501  350  TANIKSHHNVGGLPD  NIKSHHNVG       0.3722       891.0            50.00     Sequence
DRB1_1501   83  DLGVPVLGICYGFQA  PVLGICYGF       0.3695       918.0            50.00     Sequence
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DRB1_1501  440  NQIWQCPVVLLADVR  PVVLLADVR       0.3644       969.5              50.00     Sequence
DRB1_1501  289  ETFLEALSGVSAPEG  FLEALSGVS       0.3628       986.9              50.00     Sequence
DRB1_1501  287  AAETFLEALSGVSAP  FLEALSGVS       0.3623       992.0              50.00     Sequence
DRB1_1501  288  AETFLEALSGVSAPE  FLEALSGVS       0.3589      1029.4              50.00     Sequence
DRB1_1501  460  GDGRTYGHPIVLRPV  RTYGHPIVL       0.3587      1031.1              50.00     Sequence
DRB1_1501  255  VFVDHGLLRAGERAQ  VFVDHGLLR       0.3579      1040.8              50.00     Sequence
DRB1_1501  413  EVTAKRLDTLRHADS  TAKRLDTLR       0.3578      1041.1              50.00     Sequence
DRB1_1501  290  TFLEALSGVSAPEGK  FLEALSGVS       0.3578      1041.8              50.00     Sequence
DRB1_1501  484  WTRVPYEVLERISTR  EVLERISTR       0.3565      1055.9              50.00     Sequence
DRB1_1501  347  GSGTANIKSHHNVGG  NIKSHHNVG       0.3562      1059.6              50.00     Sequence
DRB1_1501  170  RRLAGVQYHPEVMHT  RRLAGVQYH       0.3553      1070.6              50.00     Sequence
DRB1_1501  291  FLEALSGVSAPEGKR  EALSGVSAP       0.3524      1103.8              50.00     Sequence
DRB1_1501  169  DRRLAGVQYHPEVMH  RRLAGVQYH       0.3515      1114.8              50.00     Sequence
DRB1_1501  381  EVRAVGRELGLPEEI  AVGRELGLP       0.3515      1115.1              50.00     Sequence
DRB1_1501  225  GHAICGLSGGVDSAV  AICGLSGGV       0.3514      1116.7              50.00     Sequence
DRB1_1501  380  DEVRAVGRELGLPEE  AVGRELGLP       0.3491      1144.0              50.00     Sequence
DRB1_1501  450  LADVRSVGVQGDGRT  DVRSVGVQG       0.3471      1168.8              50.00     Sequence
DRB1_1501  327  KTAEFLVQGTLYPDV  FLVQGTLYP       0.3465      1177.2              50.00     Sequence
DRB1_1501  351  ANIKSHHNVGGLPDD  NIKSHHNVG       0.3448      1198.9              50.00     Sequence
DRB1_1501   74  APKLDPALLDLGVPV  ALLDLGVPV       0.3446      1201.1              50.00     Sequence
DRB1_1501   44  PHTASIEEIRARQPV  SIEEIRARQ       0.3433      1218.1              50.00     Sequence
DRB1_1501  379  KDEVRAVGRELGLPE  AVGRELGLP       0.3431      1220.6              50.00     Sequence
DRB1_1501  416  AKRLDTLRHADSIVR  TLRHADSIV       0.3424      1230.9              50.00     Sequence
DRB1_1501  252  LTCVFVDHGLLRAGE  VFVDHGLLR       0.3422      1232.4              50.00     Sequence
DRB1_1501  259  HGLLRAGERAQVQRD  GLLRAGERA       0.3407      1253.5              50.00     Sequence
DRB1_1501  328  TAEFLVQGTLYPDVV  EFLVQGTLY       0.3384      1284.3              50.00     Sequence
DRB1_1501  221  QIGDGHAICGLSGGV  QIGDGHAIC       0.3382      1287.8              50.00     Sequence
DRB1_1501  509  VVLDITSKPPATIEW  VVLDITSKP       0.3381      1289.2              50.00     Sequence
DRB1_1501  236  DSAVAAALVQRAIGD  AVAAALVQR       0.3380      1290.8              50.00     Sequence
DRB1_1501  417  KRLDTLRHADSIVRE  TLRHADSIV       0.3366      1309.4              50.00     Sequence
DRB1_1501  326  GKTAEFLVQGTLYPD  FLVQGTLYP       0.3366      1309.6              50.00     Sequence
DRB1_1501  224  DGHAICGLSGGVDSA  AICGLSGGV       0.3362      1315.1              50.00     Sequence
DRB1_1501   60  LVLSGGPASVYADGA  LVLSGGPAS       0.3355      1325.6              50.00     Sequence
DRB1_1501  226  HAICGLSGGVDSAVA  AICGLSGGV       0.3315      1384.4              50.00     Sequence
DRB1_1501   82  LDLGVPVLGICYGFQ  PVLGICYGF       0.3314      1385.5              50.00     Sequence
DRB1_1501  382  VRAVGRELGLPEEIV  AVGRELGLP       0.3300      1407.2              50.00     Sequence
DRB1_1501  254  CVFVDHGLLRAGERA  VFVDHGLLR       0.3291      1421.4              50.00     Sequence
DRB1_1501  362  LPDDLKFTLVEPLRL  KFTLVEPLR       0.3280      1438.0              50.00     Sequence
DRB1_1501  383  RAVGRELGLPEEIVA  AVGRELGLP       0.3275      1446.4              50.00     Sequence
DRB1_1501  267  RAQVQRDFVAATGAN  QVQRDFVAA       0.3272      1450.5              50.00     Sequence
DRB1_1501  325  DGKTAEFLVQGTLYP  FLVQGTLYP       0.3261      1467.2              50.00     Sequence
DRB1_1501  119  LKVLGGKLHSDLPEV  LKVLGGKLH       0.3256      1475.1              50.00     Sequence
DRB1_1501  329  AEFLVQGTLYPDVVE  EFLVQGTLY       0.3250      1485.8              50.00     Sequence
DRB1_1501  418  RLDTLRHADSIVREE  TLRHADSIV       0.3244      1495.5              50.00     Sequence
DRB1_1501  149  DGFDVVASSAGAPVA  DGFDVVASS       0.3239      1502.6              50.00     Sequence
DRB1_1501  157  SAGAPVAAFEAFDRR  PVAAFEAFD       0.3237      1505.7              50.00     Sequence
DRB1_1501  258  DHGLLRAGERAQVQR  GLLRAGERA       0.3237      1507.0              50.00     Sequence
DRB1_1501  286  DAAETFLEALSGVSA  FLEALSGVS       0.3229      1519.9              50.00     Sequence
DRB1_1501  168  FDRRLAGVQYHPEVM  RRLAGVQYH       0.3221      1533.2              50.00     Sequence
DRB1_1501  502  EVAEVNRVVLDITSK  RVVLDITSK       0.3214      1543.5              50.00     Sequence
DRB1_1501  182  MHTPHGQQVLSRFLH  GQQVLSRFL       0.3199      1569.6              50.00     Sequence
DRB1_1501  253  TCVFVDHGLLRAGER  VFVDHGLLR       0.3190      1585.5              50.00     Sequence
DRB1_1501  148  PDGFDVVASSAGAPV  GFDVVASSA       0.3188      1588.3              50.00     Sequence
DRB1_1501  269  QVQRDFVAATGANLV  DFVAATGAN       0.3138      1676.5              50.00     Sequence
DRB1_1501  419  LDTLRHADSIVREEL  TLRHADSIV       0.3120      1710.3              50.00     Sequence
DRB1_1501  133  VQPVWMSHGDAVTAA  VWMSHGDAV       0.3118      1713.3              50.00     Sequence
DRB1_1501  378  FKDEVRAVGRELGLP  AVGRELGLP       0.3105      1736.8              50.00     Sequence
DRB1_1501  147  APDGFDVVASSAGAP  DGFDVVASS       0.3095      1755.7              50.00     Sequence
DRB1_1501  346  GGSGTANIKSHHNVG  NIKSHHNVG       0.3093      1760.9              50.00     Sequence
DRB1_1501  246  RAIGDRLTCVFVDHG  AIGDRLTCV       0.3087      1771.6              50.00     Sequence
DRB1_1501   81  LLDLGVPVLGICYGF  PVLGICYGF       0.3082      1781.1              50.00     Sequence
DRB1_1501  244  VQRAIGDRLTCVFVD  AIGDRLTCV       0.3076      1792.2              50.00     Sequence
DRB1_1501  492  LERISTRITNEVAEV  ISTRITNEV       0.3072      1800.4              50.00     Sequence
DRB1_1501  257  VDHGLLRAGERAQVQ  GLLRAGERA       0.3070      1805.5              50.00     Sequence
DRB1_1501  223  GDGHAICGLSGGVDS  AICGLSGGV       0.3067      1811.1              50.00     Sequence
DRB1_1501  352  NIKSHHNVGGLPDDL  NIKSHHNVG       0.3060      1824.1              50.00     Sequence
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DRB1_1501  167  AFDRRLAGVQYHPEV  FDRRLAGVQ         0.3049       1845.5                 50.00     Sequence
DRB1_1501  165  FEAFDRRLAGVQYHP  AFDRRLAGV         0.3034       1875.6                 50.00     Sequence
DRB1_1501  266  ERAQVQRDFVAATGA  QVQRDFVAA         0.3031       1882.3                 50.00     Sequence
DRB1_1501  392  PEEIVARQPFPGPGL  IVARQPFPG         0.3023       1899.8                 50.00     Sequence
DRB1_1501  393  EEIVARQPFPGPGLG  IVARQPFPG         0.3020       1906.0                 50.00     Sequence
DRB1_1501  292  LEALSGVSAPEGKRK  ALSGVSAPE         0.3016       1912.8                 50.00     Sequence
DRB1_1501  245  QRAIGDRLTCVFVDH  AIGDRLTCV         0.3016       1913.7                 50.00     Sequence
DRB1_1501  394  EIVARQPFPGPGLGI  ARQPFPGPG         0.3004       1937.9                 50.00     Sequence
DRB1_1501  265  GERAQVQRDFVAATG  QVQRDFVAA         0.3003       1941.0                 50.00     Sequence
DRB1_1501   42  VIPHTASIEEIRARQ  VIPHTASIE         0.2995       1956.3                 50.00     Sequence
DRB1_1501  330  EFLVQGTLYPDVVES  EFLVQGTLY         0.2990       1967.3                 50.00     Sequence
DRB1_1501  166  EAFDRRLAGVQYHPE  AFDRRLAGV         0.2976       1997.9                 50.00     Sequence
DRB1_1501  451  ADVRSVGVQGDGRTY  DVRSVGVQG         0.2973       2004.9                 50.00     Sequence
DRB1_1501  256  FVDHGLLRAGERAQV  LLRAGERAQ         0.2969       2012.5                 50.00     Sequence
DRB1_1501  420  DTLRHADSIVREELT  TLRHADSIV         0.2962       2028.9                 50.00     Sequence
DRB1_1501  268  AQVQRDFVAATGANL  QVQRDFVAA         0.2951       2053.2                 50.00     Sequence
DRB1_1501  150  GFDVVASSAGAPVAA  GFDVVASSA         0.2942       2073.4                 50.00     Sequence
DRB1_1501  146  AAPDGFDVVASSAGA  DGFDVVASS         0.2934       2091.3                 50.00     Sequence
DRB1_1501  402  PGPGLGIRIVGEVTA  GIRIVGEVT         0.2931       2098.0                 50.00     Sequence
DRB1_1501  235  VDSAVAAALVQRAIG  AVAAALVQR         0.2927       2106.4                 50.00     Sequence
DRB1_1501  171  RLAGVQYHPEVMHTP  GVQYHPEVM         0.2925       2110.8                 50.00     Sequence
DRB1_1501  207  PANIANALIEQVRTQ  ALIEQVRTQ         0.2916       2132.8                 50.00     Sequence
DRB1_1501  427  SIVREELTAAGLDNQ  IVREELTAA         0.2906       2155.7                 50.00     Sequence
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DRB1_1501  426  DSIVREELTAAGLDN  IVREELTAA         0.2895       2180.7                 50.00     Sequence
DRB1_1501  428  IVREELTAAGLDNQI  IVREELTAA         0.2878       2220.1                 50.00     Sequence
DRB1_1501   43  IPHTASIEEIRARQP  SIEEIRARQ         0.2877       2222.6                 50.00     Sequence
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DRB1_1501  134  QPVWMSHGDAVTAAP  VWMSHGDAV         0.2851       2286.0                 50.00     Sequence
DRB1_1501  424  HADSIVREELTAAGL  IVREELTAA         0.2843       2307.2                 50.00     Sequence
DRB1_1501  222  IGDGHAICGLSGGVD  AICGLSGGV         0.2827       2348.2                 50.00     Sequence
DRB1_1501  425  ADSIVREELTAAGLD  IVREELTAA         0.2822       2360.6                 50.00     Sequence
DRB1_1501  313  IRAFEGAVRDVLDGK  IRAFEGAVR         0.2819       2368.6                 50.00     Sequence
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DRB1_1501  264  AGERAQVQRDFVAAT  QVQRDFVAA         0.2799       2420.2                 50.00     Sequence
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DRB1_1501  247  AIGDRLTCVFVDHGL  AIGDRLTCV         0.2766       2507.4                 50.00     Sequence
DRB1_1501  248  IGDRLTCVFVDHGLL  RLTCVFVDH         0.2759       2526.5                 50.00     Sequence
DRB1_1501  459  QGDGRTYGHPIVLRP  RTYGHPIVL         0.2729       2609.7                 50.00     Sequence
DRB1_1501  390  GLPEEIVARQPFPGP  IVARQPFPG         0.2725       2620.3                 50.00     Sequence
DRB1_1501  422  LRHADSIVREELTAA  IVREELTAA         0.2710       2664.7                 50.00     Sequence
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DRB1_1501   10  ETPARPVLVVDFGAQ  VLVVDFGAQ         0.2661       2808.5                 50.00     Sequence
DRB1_1501  501  NEVAEVNRVVLDITS  EVNRVVLDI         0.2651       2841.1                 50.00     Sequence
DRB1_1501  384  AVGRELGLPEEIVAR  AVGRELGLP         0.2649       2846.4                 50.00     Sequence
DRB1_1501  135  PVWMSHGDAVTAAPD  VWMSHGDAV         0.2648       2849.6                 50.00     Sequence
DRB1_1501  105  IVAHTGTREYGRTEL  IVAHTGTRE         0.2641       2870.5                 50.00     Sequence
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DRB1_1501  458  VQGDGRTYGHPIVLR  RTYGHPIVL         0.2633       2894.5                 50.00     Sequence
DRB1_1501  423  RHADSIVREELTAAG  IVREELTAA         0.2621       2932.6                 50.00     Sequence
DRB1_1501  500  TNEVAEVNRVVLDIT  EVNRVVLDI         0.2608       2975.4                 50.00     Sequence
DRB1_1501  361  GLPDDLKFTLVEPLR  KFTLVEPLR         0.2603       2990.6                 50.00     Sequence
DRB1_1501  457  GVQGDGRTYGHPIVL  GVQGDGRTY         0.2599       3003.6                 50.00     Sequence
DRB1_1501  478  DAMTADWTRVPYEVL  AMTADWTRV         0.2590       3034.0                 50.00     Sequence
DRB1_1501  377  LFKDEVRAVGRELGL  EVRAVGREL         0.2587       3042.8                 50.00     Sequence
DRB1_1501  200  GLGAQWTPANIANAL  GLGAQWTPA         0.2578       3074.1                 50.00     Sequence
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DRB1_1501  401  FPGPGLGIRIVGEVT  GIRIVGEVT         0.2563       3123.8                 50.00     Sequence
DRB1_1501  470  VLRPVSSEDAMTADW  VLRPVSSED         0.2560       3135.1                 50.00     Sequence
DRB1_1501  376  LLFKDEVRAVGRELG  LLFKDEVRA         0.2547       3178.4                 50.00     Sequence
DRB1_1501  181  VMHTPHGQQVLSRFL  GQQVLSRFL         0.2533       3226.9                 50.00     Sequence
DRB1_1501  452  DVRSVGVQGDGRTYG  DVRSVGVQG         0.2524       3258.0                 50.00     Sequence
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DRB1_1501	499	ITNEVAEVNRVVLDI	EVNRVVLDI	0.2496	3356.7	50.00	Sequence
DRB1_1501	271	QRDFVAATGANLVTV	DFVAATGAN	0.2491	3374.9	50.00	Sequence
DRB1_1501	172	LAGVQYHPEVMHTPH	AGVQYHPEV	0.2488	3388.5	50.00	Sequence
DRB1_1501	272	RDFVAATGANLVTVD	DFVAATGAN	0.2479	3421.2	50.00	Sequence
DRB1_1501	456	VGVQGDGRTYGHPIV	GVQGDGRTY	0.2478	3423.3	50.00	Sequence
DRB1_1501	120	KVLGGKLHSDLPEVQ	KVLGGKLHS	0.2475	3435.8	50.00	Sequence
DRB1_1501	156	SSAGAPVAAFEAFDR	PVAAFEAFD	0.2465	3473.1	50.00	Sequence
DRB1_1501	477	EDAMTADWTRVPYEV	AMTADWTRV	0.2454	3515.9	50.00	Sequence
DRB1_1501	476	SEDAMTADWTRVPYE	AMTADWTRV	0.2417	3656.0	50.00	Sequence
DRB1_1501	436	AGLDNQIWQCPVVLL	NQIWQCPVV	0.2417	3659.8	50.00	Sequence
DRB1_1501	217	QVRTQIGDGHAICGL	QIGDGHAIC	0.2395	3745.5	50.00	Sequence
DRB1_1501	389	LGLPEEIVARQPFPG	IVARQPFPG	0.2388	3772.5	50.00	Sequence
DRB1_1501	219	RTQIGDGHAICGLSG	QIGDGHAIC	0.2386	3783.7	50.00	Sequence
DRB1_1501	437	GLDNQIWQCPVVLLA	NQIWQCPVV	0.2372	3840.5	50.00	Sequence
DRB1_1501	331	FLVQGTLYPDVVESG	FLVQGTLYP	0.2367	3862.7	50.00	Sequence
DRB1_1501	455	SVGVQGDGRTYGHPI	GVQGDGRTY	0.2329	4021.9	50.00	Sequence
DRB1_1501	396	VARQPFPGPGLGIRI	ARQPFPGPG	0.2325	4040.8	50.00	Sequence
DRB1_1501	173	AGVQYHPEVMHTPHG	AGVQYHPEV	0.2323	4051.2	50.00	Sequence
DRB1_1501	151	FDVVASSAGAPVAAF	VVASSAGAP	0.2317	4075.9	50.00	Sequence
DRB1_1501	493	ERISTRITNEVAEVN	ISTRITNEV	0.2315	4085.8	50.00	Sequence
DRB1_1501	475	SSEDAMTADWTRVPY	AMTADWTRV	0.2308	4115.2	50.00	Sequence
DRB1_1501	234	GVDSAVAAALVQRAI	AVAAALVQR	0.2289	4203.1	50.00	Sequence
DRB1_1501	435	AAGLDNQIWQCPVVL	NQIWQCPVV	0.2256	4351.9	50.00	Sequence
DRB1_1501	216	EQVRTQIGDGHAICG	QIGDGHAIC	0.2250	4382.5	50.00	Sequence
DRB1_1501	421	TLRHADSIVREELTA	TLRHADSIV	0.2246	4401.9	50.00	Sequence
DRB1_1501	136	VWMSHGDAVTAAPDG	VWMSHGDAV	0.2241	4422.9	50.00	Sequence
DRB1_1501	273	DFVAATGANLVTVDA	DFVAATGAN	0.2226	4495.5	50.00	Sequence
DRB1_1501	479	AMTADWTRVPYEVLE	AMTADWTRV	0.2200	4628.3	50.00	Sequence
DRB1_1501	111	TREYGRTELKVLGGK	EYGRTELKV	0.2188	4687.5	50.00	Sequence
DRB1_1501	494	RISTRITNEVAEVNR	ISTRITNEV	0.2179	4731.1	50.00	Sequence
DRB1_1501	299	SAPEGKRKIIGRQFI	KRKIIGRQF	0.2154	4861.9	50.00	Sequence
DRB1_1501	319	AVRDVLDGKTAEFLV	VLDGKTAEF	0.2145	4911.6	50.00	Sequence
DRB1_1501	438	LDNQIWQCPVVLLAD	NQIWQCPVV	0.2143	4920.5	50.00	Sequence
DRB1_1501	110	GTREYGRTELKVLGG	EYGRTELKV	0.2128	5002.0	50.00	Sequence
DRB1_1501	454	RSVGVQGDGRTYGHP	GVQGDGRTY	0.2127	5006.5	50.00	Sequence
DRB1_1501	434	TAAGLDNQIWQCPVV	TAAGLDNQI	0.2116	5067.6	50.00	Sequence
DRB1_1501	144	VTAAPDGFDVVASSA	DGFDVVASS	0.2111	5091.9	50.00	Sequence
DRB1_1501	439	DNQIWQCPVVLLADV	NQIWQCPVV	0.2089	5213.8	50.00	Sequence
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DRB1_1501	474	VSSEDAMTADWTRVP	AMTADWTRV	0.2087	5225.7	50.00	Sequence
DRB1_1501	321	RDVLDGKTAEFLVQG	VLDGKTAEF	0.2070	5322.7	50.00	Sequence
DRB1_1501	473	PVSSEDAMTADWTRV	AMTADWTRV	0.2060	5382.9	50.00	Sequence
DRB1_1501	320	VRDVLDGKTAEFLVQ	VLDGKTAEF	0.2056	5403.1	50.00	Sequence
DRB1_1501	218	VRTQIGDGHAICGLS	QIGDGHAIC	0.2051	5436.8	50.00	Sequence
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DRB1_1501	109	TGTREYGRTELKVLG	REYGRTELK	0.2006	5707.3	50.00	Sequence
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DRB1_1501	453	VRSVGVQGDGRTYGH	GVQGDGRTY	0.1996	5768.2	50.00	Sequence
DRB1_1501	322	DVLDGKTAEFLVQGT	DVLDGKTAE	0.1992	5794.4	50.00	Sequence
DRB1_1501	339	PDVVESGGGSGTANI	VVESGGGSG	0.1979	5878.4	50.00	Sequence
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DRB1_1501	323	VLDGKTAEFLVQGTL	VLDGKTAEF	0.1927	6216.9	50.00	Sequence
DRB1_1501	64	GGPASVYADGAPKLD	SVYADGAPK	0.1919	6271.6	50.00	Sequence
DRB1_1501	180	EVMHTPHGQQVLSRF	HTPHGQQVL	0.1914	6301.0	50.00	Sequence
DRB1_1501	108	HTGTREYGRTELKVL	EYGRTELKV	0.1912	6318.0	50.00	Sequence
DRB1_1501	67	ASVYADGAPKLDPAL	SVYADGAPK	0.1903	6377.9	50.00	Sequence
DRB1_1501	262	LRAGERAQVQRDFVA	RAQVQRDFV	0.1896	6428.7	50.00	Sequence
DRB1_1501	294	ALSGVSAPEGKRKII	ALSGVSAPE	0.1891	6464.7	50.00	Sequence

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DRB1_1501  338  YPDVVESGGGSGTAN  VVESGGGSG         0.1887       6490.7                  50.00      Sequence
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DRB1_1501  298  VSAPEGKRKIIGRQF  KRKIIGRQF         0.1862       6668.2                  50.00      Sequence
DRB1_1501  432  ELTAAGLDNQIWQCP  TAAGLDNQI         0.1849       6764.7                  50.00      Sequence
DRB1_1501   63  SGGPASVYADGAPKL  SVYADGAPK         0.1846       6781.8                  50.00      Sequence
DRB1_1501  431  EELTAAGLDNQIWQC  TAAGLDNQI         0.1838       6847.3                  50.00      Sequence
DRB1_1501  233  GGVDSAVAAALVQRA  AVAAALVQR         0.1834       6874.3                  50.00      Sequence
DRB1_1501  344  SGGGSGTANIKSHHN  GTANIKSHH         0.1799       7140.6                  50.00      Sequence
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DRB1_1501  495  ISTRITNEVAEVNRV  ISTRITNEV         0.1766       7398.0                  50.00      Sequence
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DRB1_1501  232  SGGVDSAVAAALVQR  AVAAALVQR         0.1748       7545.1                  50.00      Sequence
DRB1_1501  497  TRITNEVAEVNRVVL  RITNEVAEV         0.1747       7553.6                  50.00      Sequence
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DRB1_1501  314  RAFEGAVRDVLDGKT  AVRDVLDGK         0.1599       8863.8                  50.00      Sequence
DRB1_1501  360  GGLPDDLKFTLVEPL  DLKFTLVEP         0.1597       8882.0                  50.00      Sequence
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DRB1_1501  107  AHTGTREYGRTELKV  EYGRTELKV         0.1561       9232.5                  50.00      Sequence
DRB1_1501  275  VAATGANLVTVDAAE  NLVTVDAAE         0.1561       9236.7                  50.00      Sequence
DRB1_1501  343  ESGGGSGTANIKSHH  ESGGGSGTA         0.1558       9262.6                  50.00      Sequence
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DRB1_1501  316  FEGAVRDVLDGKTAE  AVRDVLDGK         0.1527       9583.1                  50.00      Sequence
DRB1_1501  483  DWTRVPYEVLERIST  RVPYEVLER         0.1522       9633.1                  50.00      Sequence
DRB1_1501  280  ANLVTVDAAETFLEA  NLVTVDAAE         0.1521       9642.1                  50.00      Sequence
DRB1_1501  125  KLHSDLPEVQPVWMS  KLHSDLPEV         0.1519       9665.4                  50.00      Sequence
DRB1_1501  231  LSGGVDSAVAAALVQ  GVDSAVAAA         0.1506       9797.0                  50.00      Sequence
DRB1_1501  230  GLSGGVDSAVAAALV  GVDSAVAAA         0.1503       9834.4                  50.00      Sequence
DRB1_1501   73  GAPKLDPALLDLGVP  KLDPALLDL         0.1501       9855.1                  50.00      Sequence
DRB1_1501   61  VLSGGPASVYADGAP  VLSGGPASV         0.1491       9958.0                  50.00      Sequence
DRB1_1501  332  LVQGTLYPDVVESGG  LVQGTLYPD         0.1490       9976.9                  50.00      Sequence
DRB1_1501  229  CGLSGGVDSAVAAAL  LSGGVDSAV         0.1477      10114.4                  50.00      Sequence
DRB1_1501  386  GRELGLPEEIVARQP  GLPEEIVAR         0.1453      10377.7                  50.00      Sequence
DRB1_1501  155  ASSAGAPVAAFEAFD  PVAAFEAFD         0.1444      10477.9                  50.00      Sequence
DRB1_1501  282  LVTVDAAETFLEALS  AAETFLEAL         0.1439      10541.2                  50.00      Sequence
DRB1_1501  296  SGVSAPEGKRKIIGR  EGKRKIIGR         0.1421      10745.3                  50.00      Sequence
DRB1_1501  335  GTLYPDVVESGGGSG  VVESGGGSG         0.1419      10765.8                  50.00      Sequence
DRB1_1501  179  PEVMHTPHGQQVLSR  HTPHGQQVL         0.1416      10799.3                  50.00      Sequence
DRB1_1501  342  VESGGGSGTANIKSH  ESGGGSGTA         0.1406      10925.8                  50.00      Sequence
DRB1_1501  281  NLVTVDAAETFLEAL  NLVTVDAAE         0.1401      10985.2                  50.00      Sequence
DRB1_1501  276  AATGANLVTVDAAET  NLVTVDAAE         0.1381      11220.3                  50.00      Sequence
DRB1_1501  178  HPEVMHTPHGQQVLS  VMHTPHGQQ         0.1379      11246.3                  50.00      Sequence
DRB1_1501  472  RPVSSEDAMTADWTR  PVSSEDAMT         0.1377      11270.6                  50.00      Sequence
DRB1_1501  297  GVSAPEGKRKIIGRQ  EGKRKIIGR         0.1376      11281.3                  50.00      Sequence
DRB1_1501  137  WMSHGDAVTAAPDGF  WMSHGDAVT         0.1354      11556.0                  50.00      Sequence
DRB1_1501    9  PETPARPVLVVDFGA  RPVLVVDFG         0.1335      11792.6                  50.00      Sequence
DRB1_1501  496  STRITNEVAEVNRVV  RITNEVAEV         0.1318      12011.5                  50.00      Sequence
DRB1_1501   62  LSGGPASVYADGAPK  SVYADGAPK         0.1306      12166.9                  50.00      Sequence
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   DRB1_1501  510  VLDITSKPPATIEWE  VLDITSKPP        0.1305      12182.6               50.00     Sequence
   DRB1_1501  175  VQYHPEVMHTPHGQQ  HPEVMHTPH        0.1287      12422.1               50.00     Sequence
   DRB1_1501  481  TADWTRVPYEVLERI  RVPYEVLER        0.1281      12506.9               50.00     Sequence
   DRB1_1501  154  VASSAGAPVAAFEAF  VASSAGAPV        0.1278      12545.2               50.00     Sequence
   DRB1_1501  143  AVTAAPDGFDVVASS  DGFDVVASS        0.1268      12684.1               50.00     Sequence
   DRB1_1501  177  YHPEVMHTPHGQQVL  HPEVMHTPH        0.1263      12751.6               50.00     Sequence
   DRB1_1501  124  GKLHSDLPEVQPVWM  KLHSDLPEV        0.1259      12804.0               50.00     Sequence
   DRB1_1501  122  LGGKLHSDLPEVQPV  LGGKLHSDL        0.1242      13039.7               50.00     Sequence
   DRB1_1501  333  VQGTLYPDVVESGGG  VQGTLYPDV        0.1232      13178.0               50.00     Sequence
   DRB1_1501  480  MTADWTRVPYEVLER  RVPYEVLER        0.1228      13238.8               50.00     Sequence
   DRB1_1501  295  LSGVSAPEGKRKIIG  GVSAPEGKR        0.1226      13273.3               50.00     Sequence
   DRB1_1501  123  GGKLHSDLPEVQPVW  KLHSDLPEV        0.1204      13595.0               50.00     Sequence
   DRB1_1501  359  VGGLPDDLKFTLVEP  DLKFTLVEP        0.1172      14068.4               50.00     Sequence
   DRB1_1501  482  ADWTRVPYEVLERIS  RVPYEVLER        0.1170      14094.5               50.00     Sequence
   DRB1_1501  353  IKSHHNVGGLPDDLK  IKSHHNVGG        0.1149      14426.5               50.00     Sequence
   DRB1_1501  334  QGTLYPDVVESGGGS  TLYPDVVES        0.1146      14468.3               50.00     Sequence
   DRB1_1501  206  TPANIANALIEQVRT  NALIEQVRT        0.1145      14486.6               50.00     Sequence
   DRB1_1501  176  QYHPEVMHTPHGQQV  HPEVMHTPH        0.1121      14867.2               50.00     Sequence
   DRB1_1501    6  IDVPETPARPVLVVD  IDVPETPAR        0.1093      15322.0               50.00     Sequence
   DRB1_1501   69  VYADGAPKLDPALLD  VYADGAPKL        0.1082      15511.0               50.00     Sequence
   DRB1_1501   72  DGAPKLDPALLDLGV  KLDPALLDL        0.1067      15763.4               50.00     Sequence
   DRB1_1501  354  KSHHNVGGLPDDLKF  NVGGLPDDL        0.1061      15856.8               50.00     Sequence
   DRB1_1501   71  ADGAPKLDPALLDLG  KLDPALLDL        0.1030      16409.4               50.00     Sequence
   DRB1_1501  356  HHNVGGLPDDLKFTL  NVGGLPDDL        0.0994      17049.2               50.00     Sequence
   DRB1_1501    8  VPETPARPVLVVDFG  RPVLVVDFG        0.0992      17092.6               50.00     Sequence
   DRB1_1501  201  LGAQWTPANIANALI  LGAQWTPAN        0.0988      17170.8               50.00     Sequence
   DRB1_1501  355  SHHNVGGLPDDLKFT  NVGGLPDDL        0.0984      17249.1               50.00     Sequence
   DRB1_1501  357  HNVGGLPDDLKFTLV  NVGGLPDDL        0.0975      17408.8               50.00     Sequence
   DRB1_1501   70  YADGAPKLDPALLDL  APKLDPALL        0.0975      17418.0               50.00     Sequence
   DRB1_1501    7  DVPETPARPVLVVDF  PARPVLVVD        0.0946      17969.1               50.00     Sequence
   DRB1_1501  358  NVGGLPDDLKFTLVE  DDLKFTLVE        0.0888      19135.8               50.00     Sequence
   DRB1_1501    4  ADIDVPETPARPVLV  IDVPETPAR        0.0862      19684.3               50.00     Sequence
   DRB1_1501    5  DIDVPETPARPVLVV  IDVPETPAR        0.0860      19714.8               50.00     Sequence
   DRB1_1501  142  DAVTAAPDGFDVVAS  AAPDGFDVV        0.0811      20785.5               50.00     Sequence
   DRB1_1501  202  GAQWTPANIANALIE  GAQWTPANI        0.0810      20817.0               50.00     Sequence
   DRB1_1501    0  VVQPADIDVPETPAR  IDVPETPAR        0.0793      21206.9               50.00     Sequence
   DRB1_1501    3  PADIDVPETPARPVL  IDVPETPAR        0.0785      21382.3               50.00     Sequence
   DRB1_1501  138  MSHGDAVTAAPDGFD  MSHGDAVTA        0.0740      22443.8               50.00     Sequence
   DRB1_1501  205  WTPANIANALIEQVR  IANALIEQV        0.0718      22999.6               50.00     Sequence
   DRB1_1501    2  QPADIDVPETPARPV  IDVPETPAR        0.0708      23246.8               50.00     Sequence
   DRB1_1501  140  HGDAVTAAPDGFDVV  HGDAVTAAP        0.0678      24015.3               50.00     Sequence
   DRB1_1501  141  GDAVTAAPDGFDVVA  AAPDGFDVV        0.0663      24397.1               50.00     Sequence
   DRB1_1501  204  QWTPANIANALIEQV  IANALIEQV        0.0655      24602.6               50.00     Sequence
   DRB1_1501    1  VQPADIDVPETPARP  DIDVPETPA        0.0640      25027.9               50.00     Sequence
   DRB1_1501  203  AQWTPANIANALIEQ  TPANIANAL        0.0629      25316.8               50.00     Sequence
   DRB1_1501  139  SHGDAVTAAPDGFDV  HGDAVTAAP        0.0530      28190.5               50.00     Sequence
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Allele: DRB1_1501. Number of high binders 19. Number of weak binders 131. Number of peptides 511

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB3_0101  188  QQVLSRFLHDFAGLG  FLHDFAGLG        0.6593         39.9          SB     0.80     Sequence
   DRB3_0101  189  QVLSRFLHDFAGLGA  FLHDFAGLG        0.6387         49.9          SB     0.80     Sequence
   DRB3_0101  190  VLSRFLHDFAGLGAQ  FLHDFAGLG        0.6108         67.5          WB     1.00     Sequence
   DRB3_0101   15  PVLVVDFGAQYAQLI  FGAQYAQLI        0.6078         69.7          WB     1.00     Sequence
   DRB3_0101   16  VLVVDFGAQYAQLIA  FGAQYAQLI        0.5913         83.2          WB     2.00     Sequence
   DRB3_0101  191  LSRFLHDFAGLGAQW  FLHDFAGLG        0.5765         97.8          WB     2.00     Sequence
   DRB3_0101   17  LVVDFGAQYAQLIAR  FGAQYAQLI        0.5655        110.0          WB     2.00     Sequence
   DRB3_0101  306  KIIGRQFIRAFEGAV  FIRAFEGAV        0.5464        135.4          WB     2.00     Sequence
   DRB3_0101  192  SRFLHDFAGLGAQWT  FLHDFAGLG        0.5405        144.3          WB     2.00     Sequence
   DRB3_0101   11  TPARPVLVVDFGAQY  LVVDFGAQY        0.5342        154.5          WB     2.00     Sequence
   DRB3_0101   12  PARPVLVVDFGAQYA  LVVDFGAQY        0.5255        169.8          WB     4.00     Sequence
   DRB3_0101  372  EPLRLLFKDEVRAVG  LFKDEVRAV        0.5219        176.4          WB     4.00     Sequence
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DRB3_0101  371  VEPLRLLFKDEVRAV  LFKDEVRAV        0.5210        178.2          WB     4.00      Sequence
DRB3_0101  193  RFLHDFAGLGAQWTP  FLHDFAGLG        0.5162        187.7          WB     4.00      Sequence
DRB3_0101  307  IIGRQFIRAFEGAVR  FIRAFEGAV        0.5153        189.4          WB     4.00      Sequence
DRB3_0101  373  PLRLLFKDEVRAVGR  LFKDEVRAV        0.5040        214.1          WB     4.00      Sequence
DRB3_0101   13  ARPVLVVDFGAQYAQ  LVVDFGAQY        0.5024        217.8          WB     4.00      Sequence
DRB3_0101   14  RPVLVVDFGAQYAQL  LVVDFGAQY        0.5007        221.9          WB     4.00      Sequence
DRB3_0101  279  GANLVTVDAAETFLE  VTVDAAETF        0.4885        253.3          WB     4.00      Sequence
DRB3_0101  308  IGRQFIRAFEGAVRD  FIRAFEGAV        0.4859        260.3          WB     4.00      Sequence
DRB3_0101  278  TGANLVTVDAAETFL  VTVDAAETF        0.4844        264.6          WB     4.00      Sequence
DRB3_0101  374  LRLLFKDEVRAVGRE  LFKDEVRAV        0.4811        274.4          WB     4.00      Sequence
DRB3_0101  277  ATGANLVTVDAAETF  VTVDAAETF        0.4741        295.8          WB     4.00      Sequence
DRB3_0101  280  ANLVTVDAAETFLEA  VTVDAAETF        0.4714        304.9          WB     4.00      Sequence
DRB3_0101  375  RLLFKDEVRAVGREL  LFKDEVRAV        0.4674        318.4          WB     4.00      Sequence
DRB3_0101  194  FLHDFAGLGAQWTPA  FLHDFAGLG        0.4665        321.4          WB     4.00      Sequence
DRB3_0101   18  VVDFGAQYAQLIARR  FGAQYAQLI        0.4649        326.9          WB     4.00      Sequence
DRB3_0101  309  GRQFIRAFEGAVRDV  FIRAFEGAV        0.4565        358.2          WB     8.00      Sequence
DRB3_0101  281  NLVTVDAAETFLEAL  VTVDAAETF        0.4519        376.4          WB     8.00      Sequence
DRB3_0101  310  RQFIRAFEGAVRDVL  FIRAFEGAV        0.4446        407.2          WB     8.00      Sequence
DRB3_0101   19  VDFGAQYAQLIARRV  FGAQYAQLI        0.4372        441.1          WB     8.00      Sequence
DRB3_0101  282  LVTVDAAETFLEALS  VTVDAAETF        0.4370        442.2          WB     8.00      Sequence
DRB3_0101  376  LLFKDEVRAVGRELG  LFKDEVRAV        0.4322        465.6          WB     8.00      Sequence
DRB3_0101  311  QFIRAFEGAVRDVLD  FIRAFEGAV        0.4229        515.1                 8.00      Sequence
DRB3_0101   20  DFGAQYAQLIARRVR  FGAQYAQLI        0.4105        589.1                 8.00      Sequence
DRB3_0101  283  VTVDAAETFLEALSG  VTVDAAETF        0.4099        592.4                 8.00      Sequence
DRB3_0101  312  FIRAFEGAVRDVLDG  FIRAFEGAV        0.4088        600.0                 8.00      Sequence
DRB3_0101  264  AGERAQVQRDFVAAT  VQRDFVAAT        0.4051        624.1                 8.00      Sequence
DRB3_0101  377  LFKDEVRAVGRELGL  LFKDEVRAV        0.4017        647.4                 8.00      Sequence
DRB3_0101  265  GERAQVQRDFVAATG  VQRDFVAAT        0.3867        761.6                 8.00      Sequence
DRB3_0101  266  ERAQVQRDFVAATGA  VQRDFVAAT        0.3681        931.7                16.00      Sequence
DRB3_0101   21  FGAQYAQLIARRVRE  FGAQYAQLI        0.3615       1000.7                16.00      Sequence
DRB3_0101  363  PDDLKFTLVEPLRLL  TLVEPLRLL        0.3487       1149.5                16.00      Sequence
DRB3_0101  267  RAQVQRDFVAATGAN  VQRDFVAAT        0.3481       1156.3                16.00      Sequence
DRB3_0101  268  AQVQRDFVAATGANL  VQRDFVAAT        0.3321       1374.8                16.00      Sequence
DRB3_0101  364  DDLKFTLVEPLRLLF  TLVEPLRLL        0.3305       1398.8                16.00      Sequence
DRB3_0101  269  QVQRDFVAATGANLV  VQRDFVAAT        0.3287       1427.6                16.00      Sequence
DRB3_0101  443  WQCPVVLLADVRSVG  VLLADVRSV        0.3192       1580.9                16.00      Sequence
DRB3_0101  437  GLDNQIWQCPVVLLA  IWQCPVVLL        0.3117       1714.3                16.00      Sequence
DRB3_0101  270  VQRDFVAATGANLVT  VQRDFVAAT        0.3067       1810.8                16.00      Sequence
DRB3_0101  249  GDRLTCVFVDHGLLR  VFVDHGLLR        0.3037       1870.8                16.00      Sequence
DRB3_0101  436  AGLDNQIWQCPVVLL  IWQCPVVLL        0.3024       1895.8                16.00      Sequence
DRB3_0101  444  QCPVVLLADVRSVGV  LLADVRSVG        0.3010       1924.8                16.00      Sequence
DRB3_0101  442  IWQCPVVLLADVRSV  VLLADVRSV        0.2958       2036.2                16.00      Sequence
DRB3_0101  365  DLKFTLVEPLRLLFK  TLVEPLRLL        0.2950       2053.9                16.00      Sequence
DRB3_0101  250  DRLTCVFVDHGLLRA  VFVDHGLLR        0.2932       2094.8                32.00      Sequence
DRB3_0101   74  APKLDPALLDLGVPV  ALLDLGVPV        0.2930       2099.2                32.00      Sequence
DRB3_0101  438  LDNQIWQCPVVLLAD  IWQCPVVLL        0.2924       2113.0                32.00      Sequence
DRB3_0101  313  IRAFEGAVRDVLDGK  FEGAVRDVL        0.2880       2216.3                32.00      Sequence
DRB3_0101  130  LPEVQPVWMSHGDAV  VWMSHGDAV        0.2878       2222.3                32.00      Sequence
DRB3_0101   33  VREARVFSEVIPHTA  FSEVIPHTA        0.2863       2257.5                32.00      Sequence
DRB3_0101   75  PKLDPALLDLGVPVL  ALLDLGVPV        0.2857       2271.9                32.00      Sequence
DRB3_0101   56  QPVALVLSGGPASVY  LSGGPASVY        0.2791       2439.4                32.00      Sequence
DRB3_0101  242  ALVQRAIGDRLTCVF  AIGDRLTCV        0.2784       2458.8                32.00      Sequence
DRB3_0101  131  PEVQPVWMSHGDAVT  VWMSHGDAV        0.2769       2498.3                32.00      Sequence
DRB3_0101  445  CPVVLLADVRSVGVQ  LLADVRSVG        0.2760       2524.2                32.00      Sequence
DRB3_0101   57  PVALVLSGGPASVYA  LSGGPASVY        0.2759       2526.8                32.00      Sequence
DRB3_0101   58  VALVLSGGPASVYAD  LSGGPASVY        0.2752       2546.3                32.00      Sequence
DRB3_0101  314  RAFEGAVRDVLDGKT  FEGAVRDVL        0.2734       2596.9                32.00      Sequence
DRB3_0101  243  LVQRAIGDRLTCVFV  AIGDRLTCV        0.2704       2680.8                32.00      Sequence
DRB3_0101  362  LPDDLKFTLVEPLRL  FTLVEPLRL        0.2692       2716.3                32.00      Sequence
DRB3_0101  251  RLTCVFVDHGLLRAG  VFVDHGLLR        0.2691       2720.5                32.00      Sequence
DRB3_0101   34  REARVFSEVIPHTAS  FSEVIPHTA        0.2672       2776.6                32.00      Sequence
DRB3_0101  366  LKFTLVEPLRLLFKD  TLVEPLRLL        0.2654       2831.3                32.00      Sequence
DRB3_0101  244  VQRAIGDRLTCVFVD  AIGDRLTCV        0.2647       2853.0                32.00      Sequence
DRB3_0101  132  EVQPVWMSHGDAVTA  VWMSHGDAV        0.2631       2900.4                32.00      Sequence
DRB3_0101   59  ALVLSGGPASVYADG  LSGGPASVY        0.2612       2962.8                32.00      Sequence
DRB3_0101  315  AFEGAVRDVLDGKTA  FEGAVRDVL        0.2608       2976.2                32.00      Sequence
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DRB3_0101	285	VDAAETFLEALSGVS	FLEALSGVS	0.2587	3043.8	32.00	Sequence
DRB3_0101	368	FTLVEPLRLLFKDEV	TLVEPLRLL	0.2568	3107.7	32.00	Sequence
DRB3_0101	439	DNQIWQCPVVLLADV	IWQCPVVLL	0.2566	3113.1	32.00	Sequence
DRB3_0101	133	VQPVWMSHGDAVTAA	VWMSHGDAV	0.2562	3128.1	32.00	Sequence
DRB3_0101	76	KLDPALLDLGVPVLG	ALLDLGVPV	0.2547	3178.6	32.00	Sequence
DRB3_0101	187	GQQVLSRFLHDFAGL	VLSRFLHDF	0.2529	3240.0	32.00	Sequence
DRB3_0101	446	PVVLLADVRSVGVQG	LLADVRSVG	0.2510	3309.0	32.00	Sequence
DRB3_0101	35	EARVFSEVIPHTASI	FSEVIPHTA	0.2504	3329.7	32.00	Sequence
DRB3_0101	60	LVLSGGPASVYADGA	LSGGPASVY	0.2464	3476.2	32.00	Sequence
DRB3_0101	367	KFTLVEPLRLLFKDE	TLVEPLRLL	0.2464	3476.9	32.00	Sequence
DRB3_0101	252	LTCVFVDHGLLRAGE	VFVDHGLLR	0.2464	3477.3	32.00	Sequence
DRB3_0101	440	NQIWQCPVVLLADVR	IWQCPVVLL	0.2451	3525.3	32.00	Sequence
DRB3_0101	503	VAEVNRVVLDITSKP	VVLDITSKP	0.2448	3536.2	32.00	Sequence
DRB3_0101	369	TLVEPLRLLFKDEVR	TLVEPLRLL	0.2420	3644.4	32.00	Sequence
DRB3_0101	245	QRAIGDRLTCVFVDH	AIGDRLTCV	0.2417	3658.7	32.00	Sequence
DRB3_0101	69	VYADGAPKLDPALLD	VYADGAPKL	0.2416	3662.5	32.00	Sequence
DRB3_0101	241	AALVQRAIGDRLTCV	AIGDRLTCV	0.2409	3687.8	32.00	Sequence
DRB3_0101	246	RAIGDRLTCVFVDHG	AIGDRLTCV	0.2392	3758.7	32.00	Sequence
DRB3_0101	134	QPVWMSHGDAVTAAP	VWMSHGDAV	0.2386	3783.1	32.00	Sequence
DRB3_0101	61	VLSGGPASVYADGAP	LSGGPASVY	0.2368	3855.9	32.00	Sequence
DRB3_0101	184	TPHGQQVLSRFLHDF	VLSRFLHDF	0.2355	3912.8	32.00	Sequence
DRB3_0101	185	PHGQQVLSRFLHDFA	VLSRFLHDF	0.2354	3915.9	32.00	Sequence
DRB3_0101	62	LSGGPASVYADGAPK	LSGGPASVY	0.2346	3948.3	32.00	Sequence
DRB3_0101	316	FEGAVRDVLDGKTAE	FEGAVRDVL	0.2341	3971.4	32.00	Sequence
DRB3_0101	441	QIWQCPVVLLADVRS	IWQCPVVLL	0.2339	3979.1	32.00	Sequence
DRB3_0101	77	LDPALLDLGVPVLGI	ALLDLGVPV	0.2333	4004.4	32.00	Sequence
DRB3_0101	447	VVLLADVRSVGVQGD	LLADVRSVG	0.2316	4082.4	32.00	Sequence
DRB3_0101	135	PVWMSHGDAVTAAPD	VWMSHGDAV	0.2315	4085.3	32.00	Sequence
DRB3_0101	286	DAAETFLEALSGVSA	FLEALSGVS	0.2312	4100.1	32.00	Sequence
DRB3_0101	504	AEVNRVVLDITSKPP	VVLDITSKP	0.2303	4135.9	32.00	Sequence
DRB3_0101	36	ARVFSEVIPHTASIE	FSEVIPHTA	0.2252	4372.7	32.00	Sequence
DRB3_0101	186	HGQQVLSRFLHDFAG	VLSRFLHDF	0.2239	4436.8	32.00	Sequence
DRB3_0101	145	TAAPDGFDVVASSAG	FDVVASSAG	0.2224	4509.3	32.00	Sequence
DRB3_0101	247	AIGDRLTCVFVDHGL	AIGDRLTCV	0.2221	4523.5	32.00	Sequence
DRB3_0101	253	TCVFVDHGLLRAGER	VFVDHGLLR	0.2195	4649.1	32.00	Sequence
DRB3_0101	64	GGPASVYADGAPKLD	VYADGAPKL	0.2188	4686.7	32.00	Sequence
DRB3_0101	448	VLLADVRSVGVQGDG	LLADVRSVG	0.2157	4845.6	32.00	Sequence
DRB3_0101	136	VWMSHGDAVTAAPDG	VWMSHGDAV	0.2151	4875.2	32.00	Sequence
DRB3_0101	214	LIEQVRTQIGDGHAI	TQIGDGHAI	0.2148	4895.1	32.00	Sequence
DRB3_0101	37	RVFSEVIPHTASIEE	FSEVIPHTA	0.2116	5064.4	32.00	Sequence
DRB3_0101	505	EVNRVVLDITSKPPA	VVLDITSKP	0.2102	5145.9	32.00	Sequence
DRB3_0101	65	GPASVYADGAPKLDP	VYADGAPKL	0.2099	5161.0	32.00	Sequence
DRB3_0101	331	FLVQGTLYPDVVESG	LYPDVVESG	0.2084	5244.4	32.00	Sequence
DRB3_0101	400	PFPGPGLGIRIVGEV	LGIRIVGEV	0.2075	5293.0	32.00	Sequence
DRB3_0101	302	EGKRKIIGRQFIRAF	IGRQFIRAF	0.2074	5302.2	32.00	Sequence
DRB3_0101	146	AAPDGFDVVASSAGA	FDVVASSAG	0.2061	5376.5	50.00	Sequence
DRB3_0101	171	RLAGVQYHPEVMHTP	YHPEVMHTP	0.2051	5434.6	50.00	Sequence
DRB3_0101	227	AICGLSGGVDSAVAA	GGVDSAVAA	0.2037	5516.9	50.00	Sequence
DRB3_0101	248	IGDRLTCVFVDHGLL	IGDRLTCVF	0.2033	5542.5	50.00	Sequence
DRB3_0101	287	AAETFLEALSGVSAP	FLEALSGVS	0.2027	5576.1	50.00	Sequence
DRB3_0101	215	IEQVRTQIGDGHAIC	TQIGDGHAI	0.2023	5604.4	50.00	Sequence
DRB3_0101	360	GGLPDDLKFTLVEPL	LKFTLVEPL	0.2007	5700.5	50.00	Sequence
DRB3_0101	305	RKIIGRQFIRAFEGA	IGRQFIRAF	0.2001	5737.4	50.00	Sequence
DRB3_0101	38	VFSEVIPHTASIEEI	FSEVIPHTA	0.1987	5824.8	50.00	Sequence
DRB3_0101	71	ADGAPKLDPALLDLG	PKLDPALLD	0.1986	5830.5	50.00	Sequence
DRB3_0101	108	HTGTREYGRTELKVL	YGRTELKVL	0.1985	5837.8	50.00	Sequence
DRB3_0101	303	GKRKIIGRQFIRAFE	IGRQFIRAF	0.1981	5862.8	50.00	Sequence
DRB3_0101	254	CVFVDHGLLRAGERA	VFVDHGLLR	0.1980	5871.5	50.00	Sequence
DRB3_0101	78	DPALLDLGVPVLGIC	ALLDLGVPV	0.1965	5966.3	50.00	Sequence
DRB3_0101	401	FPGPGLGIRIVGEVT	LGIRIVGEV	0.1964	5968.8	50.00	Sequence
DRB3_0101	370	LVEPLRLLFKDEVRA	LRLLFKDEV	0.1960	6000.4	50.00	Sequence
DRB3_0101	63	SGGPASVYADGAPKL	VYADGAPKL	0.1959	6007.1	50.00	Sequence
DRB3_0101	507	NRVVLDITSKPPATI	VVLDITSKP	0.1958	6010.8	50.00	Sequence
DRB3_0101	66	PASVYADGAPKLDPA	VYADGAPKL	0.1950	6065.6	50.00	Sequence
DRB3_0101	474	VSSEDAMTADWTRVP	MTADWTRVP	0.1947	6085.0	50.00	Sequence
DRB3_0101	332	LVQGTLYPDVVESGG	LYPDVVESG	0.1942	6115.6	50.00	Sequence

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DRB3_0101  172  LAGVQYHPEVMHTPH  YHPEVMHTP        0.1942       6118.5                 50.00     Sequence
DRB3_0101  361  GLPDDLKFTLVEPLR  LKFTLVEPL        0.1911       6321.0                 50.00     Sequence
DRB3_0101  506  VNRVVLDITSKPPAT  VVLDITSKP        0.1910       6327.8                 50.00     Sequence
DRB3_0101  356  HHNVGGLPDDLKFTL  GLPDDLKFT        0.1904       6372.0                 50.00     Sequence
DRB3_0101  228  ICGLSGGVDSAVAAA  GGVDSAVAA        0.1900       6398.7                 50.00     Sequence
DRB3_0101  216  EQVRTQIGDGHAICG  TQIGDGHAI        0.1886       6494.9                 50.00     Sequence
DRB3_0101  229  CGLSGGVDSAVAAAL  GGVDSAVAA        0.1886       6498.9                 50.00     Sequence
DRB3_0101  357  HNVGGLPDDLKFTLV  GLPDDLKFT        0.1880       6537.9                 50.00     Sequence
DRB3_0101  271  QRDFVAATGANLVTV  VAATGANLV        0.1874       6581.9                 50.00     Sequence
DRB3_0101   72  DGAPKLDPALLDLGV  PKLDPALLD        0.1872       6599.9                 50.00     Sequence
DRB3_0101  508  RVVLDITSKPPATIE  VVLDITSKP        0.1871       6606.0                 50.00     Sequence
DRB3_0101  304  KRKIIGRQFIRAFEG  IGRQFIRAF        0.1862       6671.9                 50.00     Sequence
DRB3_0101  217  QVRTQIGDGHAICGL  TQIGDGHAI        0.1859       6690.1                 50.00     Sequence
DRB3_0101   67  ASVYADGAPKLDPAL  VYADGAPKL        0.1844       6798.1                 50.00     Sequence
DRB3_0101   73  GAPKLDPALLDLGVP  PKLDPALLD        0.1839       6838.9                 50.00     Sequence
DRB3_0101  358  NVGGLPDDLKFTLVE  GLPDDLKFT        0.1834       6870.9                 50.00     Sequence
DRB3_0101  402  PGPGLGIRIVGEVTA  LGIRIVGEV        0.1831       6895.0                 50.00     Sequence
DRB3_0101  173  AGVQYHPEVMHTPHG  VQYHPEVMH        0.1829       6914.0                 50.00     Sequence
DRB3_0101   79  PALLDLGVPVLGICY  ALLDLGVPV        0.1815       7016.6                 50.00     Sequence
DRB3_0101  109  TGTREYGRTELKVLG  YGRTELKVL        0.1805       7093.4                 50.00     Sequence
DRB3_0101   92  CYGFQAMAQALGGIV  MAQALGGIV        0.1803       7104.4                 50.00     Sequence
DRB3_0101   39  FSEVIPHTASIEEIR  FSEVIPHTA        0.1797       7157.6                 50.00     Sequence
DRB3_0101  272  RDFVAATGANLVTVD  VAATGANLV        0.1794       7177.1                 50.00     Sequence
DRB3_0101  333  VQGTLYPDVVESGGG  LYPDVVESG        0.1792       7189.7                 50.00     Sequence
DRB3_0101  230  GLSGGVDSAVAAALV  GGVDSAVAA        0.1787       7228.7                 50.00     Sequence
DRB3_0101  218  VRTQIGDGHAICGLS  TQIGDGHAI        0.1782       7273.1                 50.00     Sequence
DRB3_0101  475  SSEDAMTADWTRVPY  MTADWTRVP        0.1775       7324.1                 50.00     Sequence
DRB3_0101  477  EDAMTADWTRVPYEV  MTADWTRVP        0.1775       7324.7                 50.00     Sequence
DRB3_0101  435  AAGLDNQIWQCPVVL  QIWQCPVVL        0.1771       7355.0                 50.00     Sequence
DRB3_0101  204  QWTPANIANALIEQV  IANALIEQV        0.1769       7378.1                 50.00     Sequence
DRB3_0101   68  SVYADGAPKLDPALL  VYADGAPKL        0.1763       7422.4                 50.00     Sequence
DRB3_0101  120  KVLGGKLHSDLPEVQ  LHSDLPEVQ        0.1755       7487.4                 50.00     Sequence
DRB3_0101   70  YADGAPKLDPALLDL  PKLDPALLD        0.1751       7519.5                 50.00     Sequence
DRB3_0101  359  VGGLPDDLKFTLVEP  GLPDDLKFT        0.1747       7550.2                 50.00     Sequence
DRB3_0101  422  LRHADSIVREELTAA  IVREELTAA        0.1741       7600.7                 50.00     Sequence
DRB3_0101  288  AETFLEALSGVSAPE  FLEALSGVS        0.1738       7623.1                 50.00     Sequence
DRB3_0101  147  APDGFDVVASSAGAP  FDVVASSAG        0.1737       7635.2                 50.00     Sequence
DRB3_0101  255  VFVDHGLLRAGERAQ  VFVDHGLLR        0.1734       7657.0                 50.00     Sequence
DRB3_0101  231  LSGGVDSAVAAALVQ  GGVDSAVAA        0.1726       7723.6                 50.00     Sequence
DRB3_0101  489  YEVLERISTRITNEV  ISTRITNEV        0.1723       7752.1                 50.00     Sequence
DRB3_0101  176  QYHPEVMHTPHGQQV  MHTPHGQQV        0.1720       7774.7                 50.00     Sequence
DRB3_0101   80  ALLDLGVPVLGICYG  ALLDLGVPV        0.1709       7866.0                 50.00     Sequence
DRB3_0101  208  ANIANALIEQVRTQI  IANALIEQV        0.1706       7892.5                 50.00     Sequence
DRB3_0101  273  DFVAATGANLVTVDA  VAATGANLV        0.1702       7927.4                 50.00     Sequence
DRB3_0101  205  WTPANIANALIEQVR  IANALIEQV        0.1695       7988.0                 50.00     Sequence
DRB3_0101   93  YGFQAMAQALGGIVA  MAQALGGIV        0.1691       8019.9                 50.00     Sequence
DRB3_0101  180  EVMHTPHGQQVLSRF  HGQQVLSRF        0.1686       8064.3                 50.00     Sequence
DRB3_0101  181  VMHTPHGQQVLSRFL  HGQQVLSRF        0.1676       8153.5                 50.00     Sequence
DRB3_0101  174  GVQYHPEVMHTPHGQ  VQYHPEVMH        0.1671       8195.2                 50.00     Sequence
DRB3_0101  403  GPGLGIRIVGEVTAK  LGIRIVGEV        0.1665       8250.8                 50.00     Sequence
DRB3_0101  404  PGLGIRIVGEVTAKR  LGIRIVGEV        0.1665       8251.1                 50.00     Sequence
DRB3_0101  478  DAMTADWTRVPYEVL  MTADWTRVP        0.1658       8317.3                 50.00     Sequence
DRB3_0101  219  RTQIGDGHAICGLSG  TQIGDGHAI        0.1652       8367.6                 50.00     Sequence
DRB3_0101  121  VLGGKLHSDLPEVQP  LHSDLPEVQ        0.1650       8392.0                 50.00     Sequence
DRB3_0101  417  KRLDTLRHADSIVRE  LRHADSIVR        0.1647       8414.6                 50.00     Sequence
DRB3_0101   83  DLGVPVLGICYGFQA  LGICYGFQA        0.1646       8427.9                 50.00     Sequence
DRB3_0101  122  LGGKLHSDLPEVQPV  LHSDLPEVQ        0.1645       8437.1                 50.00     Sequence
DRB3_0101  492  LERISTRITNEVAEV  ISTRITNEV        0.1639       8484.1                 50.00     Sequence
DRB3_0101  500  TNEVAEVNRVVLDIT  VNRVVLDIT        0.1639       8491.6                 50.00     Sequence
DRB3_0101  148  PDGFDVVASSAGAPV  FDVVASSAG        0.1638       8495.7                 50.00     Sequence
DRB3_0101  177  YHPEVMHTPHGQQVL  MHTPHGQQV        0.1638       8501.0                 50.00     Sequence
DRB3_0101  182  MHTPHGQQVLSRFLH  HGQQVLSRF        0.1637       8506.0                 50.00     Sequence
DRB3_0101  416  AKRLDTLRHADSIVR  LRHADSIVR        0.1633       8542.4                 50.00     Sequence
DRB3_0101  476  SEDAMTADWTRVPYE  MTADWTRVP        0.1629       8576.7                 50.00     Sequence
DRB3_0101  209  NIANALIEQVRTQIG  IANALIEQV        0.1628       8593.2                 50.00     Sequence
DRB3_0101  206  TPANIANALIEQVRT  IANALIEQV        0.1623       8640.3                 50.00     Sequence
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DRB3_0101	140	HGDAVTAAPDGFDVV	AAPDGFDVV	0.1615	8715.5	50.00	Sequence
DRB3_0101	197	DFAGLGAQWTPANIA	AQWTPANIA	0.1610	8755.1	50.00	Sequence
DRB3_0101	110	GTREYGRTELKVLGG	YGRTELKVL	0.1610	8758.2	50.00	Sequence
DRB3_0101	334	QGTLYPDVVESGGGS	LYPDVVESG	0.1607	8787.8	50.00	Sequence
DRB3_0101	170	RRLAGVQYHPEVMHT	VQYHPEVMH	0.1600	8856.1	50.00	Sequence
DRB3_0101	405	GLGIRIVGEVTAKRL	LGIRIVGEV	0.1599	8865.0	50.00	Sequence
DRB3_0101	479	AMTADWTRVPYEVLE	MTADWTRVP	0.1598	8876.8	50.00	Sequence
DRB3_0101	123	GGKLHSDLPEVQPVW	LHSDLPEVQ	0.1589	8964.0	50.00	Sequence
DRB3_0101	493	ERISTRITNEVAEVN	ISTRITNEV	0.1577	9074.8	50.00	Sequence
DRB3_0101	149	DGFDVVASSAGAPVA	FDVVASSAG	0.1573	9117.9	50.00	Sequence
DRB3_0101	94	GFQAMAQALGGIVAH	MAQALGGIV	0.1568	9162.8	50.00	Sequence
DRB3_0101	220	TQIGDGHAICGLSGG	TQIGDGHAI	0.1568	9163.4	50.00	Sequence
DRB3_0101	509	VVLDITSKPPATIEW	VVLDITSKP	0.1568	9166.1	50.00	Sequence
DRB3_0101	169	DRRLAGVQYHPEVMH	VQYHPEVMH	0.1564	9206.2	50.00	Sequence
DRB3_0101	289	ETFLEALSGVSAPEG	FLEALSGVS	0.1562	9223.0	50.00	Sequence
DRB3_0101	327	KTAEFLVQGTLYPDV	VQGTLYPDV	0.1561	9233.5	50.00	Sequence
DRB3_0101	418	RLDTLRHADSIVREE	LRHADSIVR	0.1557	9276.5	50.00	Sequence
DRB3_0101	502	EVAEVNRVVLDITSK	VNRVVLDIT	0.1556	9281.9	50.00	Sequence
DRB3_0101	274	FVAATGANLVTVDAA	VAATGANLV	0.1556	9282.5	50.00	Sequence
DRB3_0101	151	FDVVASSAGAPVAAF	FDVVASSAG	0.1554	9304.2	50.00	Sequence
DRB3_0101	84	LGVPVLGICYGFQAM	LGICYGFQA	0.1550	9350.5	50.00	Sequence
DRB3_0101	490	EVLERISTRITNEVA	ISTRITNEV	0.1545	9396.4	50.00	Sequence
DRB3_0101	141	GDAVTAAPDGFDVVA	AAPDGFDVV	0.1544	9405.0	50.00	Sequence
DRB3_0101	501	NEVAEVNRVVLDITS	VNRVVLDIT	0.1542	9429.7	50.00	Sequence
DRB3_0101	225	GHAICGLSGGVDSAV	LSGGVDSAV	0.1539	9455.6	50.00	Sequence
DRB3_0101	495	ISTRITNEVAEVNRV	ISTRITNEV	0.1533	9519.2	50.00	Sequence
DRB3_0101	419	LDTLRHADSIVREEL	LRHADSIVR	0.1530	9553.5	50.00	Sequence
DRB3_0101	87	PVLGICYGFQAMAQA	YGFQAMAQA	0.1528	9570.0	50.00	Sequence
DRB3_0101	498	RITNEVAEVNRVVLD	NEVAEVNRV	0.1523	9626.7	50.00	Sequence
DRB3_0101	210	IANALIEQVRTQIGD	IANALIEQV	0.1523	9627.4	50.00	Sequence
DRB3_0101	125	KLHSDLPEVQPVWMS	LHSDLPEVQ	0.1522	9630.7	50.00	Sequence
DRB3_0101	494	RISTRITNEVAEVNR	ISTRITNEV	0.1521	9647.3	50.00	Sequence
DRB3_0101	335	GTLYPDVVESGGGSG	LYPDVVESG	0.1518	9673.7	50.00	Sequence
DRB3_0101	406	LGIRIVGEVTAKRLD	LGIRIVGEV	0.1518	9678.1	50.00	Sequence
DRB3_0101	207	PANIANALIEQVRTQ	IANALIEQV	0.1513	9729.9	50.00	Sequence
DRB3_0101	449	LLADVRSVGVQGDGR	LLADVRSVG	0.1511	9753.9	50.00	Sequence
DRB3_0101	318	GAVRDVLDGKTAEFL	VLDGKTAEF	0.1498	9887.2	50.00	Sequence
DRB3_0101	81	LLDLGVPVLGICYGF	PVLGICYGF	0.1494	9931.1	50.00	Sequence
DRB3_0101	226	HAICGLSGGVDSAVA	LSGGVDSAV	0.1492	9946.3	50.00	Sequence
DRB3_0101	150	GFDVVASSAGAPVAA	FDVVASSAG	0.1484	10038.8	50.00	Sequence
DRB3_0101	491	VLERISTRITNEVAE	ISTRITNEV	0.1481	10073.9	50.00	Sequence
DRB3_0101	232	SGGVDSAVAAALVQR	GGVDSAVAA	0.1472	10174.2	50.00	Sequence
DRB3_0101	420	DTLRHADSIVREELT	LRHADSIVR	0.1470	10192.4	50.00	Sequence
DRB3_0101	198	FAGLGAQWTPANIAN	AQWTPANIA	0.1470	10193.9	50.00	Sequence
DRB3_0101	175	VQYHPEVMHTPHGQQ	VQYHPEVMH	0.1469	10200.0	50.00	Sequence
DRB3_0101	336	TLYPDVVESGGGSGT	LYPDVVESG	0.1463	10272.6	50.00	Sequence
DRB3_0101	328	TAEFLVQGTLYPDVV	VQGTLYPDV	0.1461	10289.5	50.00	Sequence
DRB3_0101	284	TVDAAETFLEALSGV	TFLEALSGV	0.1455	10357.6	50.00	Sequence
DRB3_0101	195	LHDFAGLGAQWTPAN	FAGLGAQWT	0.1441	10516.2	50.00	Sequence
DRB3_0101	138	MSHGDAVTAAPDGFD	AVTAAPDGF	0.1438	10550.9	50.00	Sequence
DRB3_0101	85	GVPVLGICYGFQAMA	LGICYGFQA	0.1434	10591.8	50.00	Sequence
DRB3_0101	95	FQAMAQALGGIVAHT	MAQALGGIV	0.1430	10639.8	50.00	Sequence
DRB3_0101	499	ITNEVAEVNRVVLDI	NEVAEVNRV	0.1427	10680.0	50.00	Sequence
DRB3_0101	142	DAVTAAPDGFDVVAS	AVTAAPDGF	0.1425	10700.2	50.00	Sequence
DRB3_0101	496	STRITNEVAEVNRVV	RITNEVAEV	0.1421	10742.3	50.00	Sequence
DRB3_0101	139	SHGDAVTAAPDGFDV	AVTAAPDGF	0.1417	10793.2	50.00	Sequence
DRB3_0101	423	RHADSIVREELTAAG	IVREELTAA	0.1417	10795.5	50.00	Sequence
DRB3_0101	96	QAMAQALGGIVAHTG	MAQALGGIV	0.1407	10911.8	50.00	Sequence
DRB3_0101	290	TFLEALSGVSAPEGK	FLEALSGVS	0.1405	10935.8	50.00	Sequence
DRB3_0101	421	TLRHADSIVREELTA	LRHADSIVR	0.1402	10966.1	50.00	Sequence
DRB3_0101	143	AVTAAPDGFDVVASS	AVTAAPDGF	0.1400	10997.2	50.00	Sequence
DRB3_0101	137	WMSHGDAVTAAPDGF	AVTAAPDGF	0.1395	11048.3	50.00	Sequence
DRB3_0101	497	TRITNEVAEVNRVVL	RITNEVAEV	0.1382	11207.2	50.00	Sequence
DRB3_0101	275	VAATGANLVTVDAAE	VAATGANLV	0.1381	11221.6	50.00	Sequence
DRB3_0101	111	TREYGRTELKVLGGK	YGRTELKVL	0.1374	11301.5	50.00	Sequence
DRB3_0101	196	HDFAGLGAQWTPANI	FAGLGAQWT	0.1369	11364.3	50.00	Sequence

DRB3_0101	480	MTADWTRVPYEVLER	MTADWTRVP	0.1369	11368.8	50.00	Sequence
DRB3_0101	82	LDLGVPVLGICYGFQ	LDLGVPVLG	0.1364	11429.1	50.00	Sequence
DRB3_0101	178	HPEVMHTPHGQQVLS	MHTPHGQQV	0.1362	11454.3	50.00	Sequence
DRB3_0101	25	YAQLIARRVREARVF	RRVREARVF	0.1362	11458.2	50.00	Sequence
DRB3_0101	124	GKLHSDLPEVQPVWM	LHSDLPEVQ	0.1361	11462.9	50.00	Sequence
DRB3_0101	233	GGVDSAVAAALVQRA	GGVDSAVAA	0.1354	11553.5	50.00	Sequence
DRB3_0101	424	HADSIVREELTAAGL	IVREELTAA	0.1351	11592.7	50.00	Sequence
DRB3_0101	317	EGAVRDVLDGKTAEF	VLDGKTAEF	0.1348	11628.9	50.00	Sequence
DRB3_0101	97	AMAQALGGIVAHTGT	MAQALGGIV	0.1345	11672.5	50.00	Sequence
DRB3_0101	425	ADSIVREELTAAGLD	IVREELTAA	0.1336	11774.9	50.00	Sequence
DRB3_0101	326	GKTAEFLVQGTLYPD	FLVQGTLYP	0.1328	11887.0	50.00	Sequence
DRB3_0101	47	ASIEEIRARQPVALV	IRARQPVAL	0.1326	11909.3	50.00	Sequence
DRB3_0101	162	VAAFEAFDRRLAGVQ	FDRRLAGVQ	0.1315	12047.1	50.00	Sequence
DRB3_0101	86	VPVLGICYGFQAMAQ	LGICYGFQA	0.1310	12120.8	50.00	Sequence
DRB3_0101	119	LKVLGGKLHSDLPEV	KLHSDLPEV	0.1309	12127.2	50.00	Sequence
DRB3_0101	483	DWTRVPYEVLERIST	YEVLERIST	0.1306	12171.9	50.00	Sequence
DRB3_0101	200	GLGAQWTPANIANAL	AQWTPANIA	0.1306	12175.6	50.00	Sequence
DRB3_0101	201	LGAQWTPANIANALI	AQWTPANIA	0.1298	12280.1	50.00	Sequence
DRB3_0101	325	DGKTAEFLVQGTLYP	FLVQGTLYP	0.1293	12343.6	50.00	Sequence
DRB3_0101	428	IVREELTAAGLDNQI	IVREELTAA	0.1290	12377.9	50.00	Sequence
DRB3_0101	112	REYGRTELKVLGGKL	YGRTELKVL	0.1290	12379.3	50.00	Sequence
DRB3_0101	88	VLGICYGFQAMAQAL	YGFQAMAQA	0.1266	12707.3	50.00	Sequence
DRB3_0101	179	PEVMHTPHGQQVLSR	MHTPHGQQV	0.1265	12723.4	50.00	Sequence
DRB3_0101	426	DSIVREELTAAGLDN	IVREELTAA	0.1264	12731.2	50.00	Sequence
DRB3_0101	355	SHHNVGGLPDDLKFT	GLPDDLKFT	0.1263	12755.8	50.00	Sequence
DRB3_0101	337	LYPDVVESGGGSGTA	LYPDVVESG	0.1260	12788.4	50.00	Sequence
DRB3_0101	329	AEFLVQGTLYPDVVE	VQGTLYPDV	0.1260	12796.7	50.00	Sequence
DRB3_0101	48	SIEEIRARQPVALVL	RARQPVALV	0.1252	12904.0	50.00	Sequence
DRB3_0101	199	AGLGAQWTPANIANA	AQWTPANIA	0.1247	12979.1	50.00	Sequence
DRB3_0101	330	EFLVQGTLYPDVVES	VQGTLYPDV	0.1243	13022.9	50.00	Sequence
DRB3_0101	431	EELTAAGLDNQIWQC	TAAGLDNQI	0.1241	13051.0	50.00	Sequence
DRB3_0101	319	AVRDVLDGKTAEFLV	VLDGKTAEF	0.1236	13123.0	50.00	Sequence
DRB3_0101	415	TAKRLDTLRHADSIV	TLRHADSIV	0.1233	13163.5	50.00	Sequence
DRB3_0101	98	MAQALGGIVAHTGTR	MAQALGGIV	0.1224	13292.9	50.00	Sequence
DRB3_0101	113	EYGRTELKVLGGKLH	YGRTELKVL	0.1224	13300.8	50.00	Sequence
DRB3_0101	202	GAQWTPANIANALIE	AQWTPANIA	0.1217	13404.1	50.00	Sequence
DRB3_0101	26	AQLIARRVREARVFS	RRVREARVF	0.1211	13490.6	50.00	Sequence
DRB3_0101	163	AAFEAFDRRLAGVQY	FDRRLAGVQ	0.1208	13537.6	50.00	Sequence
DRB3_0101	434	TAAGLDNQIWQCPVV	TAAGLDNQI	0.1207	13551.8	50.00	Sequence
DRB3_0101	28	LIARRVREARVFSEV	RRVREARVF	0.1200	13644.0	50.00	Sequence
DRB3_0101	27	QLIARRVREARVFSE	RRVREARVF	0.1200	13651.7	50.00	Sequence
DRB3_0101	432	ELTAAGLDNQIWQCP	TAAGLDNQI	0.1193	13745.4	50.00	Sequence
DRB3_0101	183	HTPHGQQVLSRFLHD	HGQQVLSRF	0.1192	13762.4	50.00	Sequence
DRB3_0101	484	WTRVPYEVLERISTR	YEVLERIST	0.1190	13798.7	50.00	Sequence
DRB3_0101	485	TRVPYEVLERISTRI	YEVLERIST	0.1189	13814.1	50.00	Sequence
DRB3_0101	427	SIVREELTAAGLDNQ	IVREELTAA	0.1175	14026.5	50.00	Sequence
DRB3_0101	10	ETPARPVLVVDFGAQ	ARPVLVVDF	0.1175	14029.2	50.00	Sequence
DRB3_0101	320	VRDVLDGKTAEFLVQ	VLDGKTAEF	0.1174	14035.9	50.00	Sequence
DRB3_0101	89	LGICYGFQAMAQALG	YGFQAMAQA	0.1167	14148.1	50.00	Sequence
DRB3_0101	114	YGRTELKVLGGKLHS	YGRTELKVL	0.1159	14274.5	50.00	Sequence
DRB3_0101	433	LTAAGLDNQIWQCPV	TAAGLDNQI	0.1156	14312.6	50.00	Sequence
DRB3_0101	49	IEEIRARQPVALVLS	RARQPVALV	0.1151	14388.8	50.00	Sequence
DRB3_0101	203	AQWTPANIANALIEQ	AQWTPANIA	0.1148	14439.5	50.00	Sequence
DRB3_0101	321	RDVLDGKTAEFLVQG	VLDGKTAEF	0.1146	14470.8	50.00	Sequence
DRB3_0101	144	VTAAPDGFDVVASSA	AAPDGFDVV	0.1142	14533.4	50.00	Sequence
DRB3_0101	291	FLEALSGVSAPEGKR	FLEALSGVS	0.1141	14545.0	50.00	Sequence
DRB3_0101	55	RQPVALVLSGGPASV	VLSGGPASV	0.1137	14609.0	50.00	Sequence
DRB3_0101	29	IARRVREARVFSEVI	RRVREARVF	0.1134	14656.2	50.00	Sequence
DRB3_0101	469	IVLRPVSSEDAMTAD	VSSEDAMTA	0.1132	14687.5	50.00	Sequence
DRB3_0101	486	RVPYEVLERISTRIT	YEVLERIST	0.1129	14733.0	50.00	Sequence
DRB3_0101	46	TASIEEIRARQPVAL	IRARQPVAL	0.1104	15143.7	50.00	Sequence
DRB3_0101	262	LRAGERAQVQRDFVA	LRAGERAQV	0.1104	15145.7	50.00	Sequence
DRB3_0101	322	DVLDGKTAEFLVQGT	VLDGKTAEF	0.1103	15161.2	50.00	Sequence
DRB3_0101	378	FKDEVRAVGRELGLP	FKDEVRAVG	0.1103	15163.9	50.00	Sequence
DRB3_0101	161	PVAAFEAFDRRLAGV	FEAFDRRLA	0.1101	15184.6	50.00	Sequence
DRB3_0101	238	AVAAALVQRAIGDRL	VQRAIGDRL	0.1099	15227.5	50.00	Sequence

DRB3_0101	126	LHSDLPEVQPVWMSH	LHSDLPEVQ	0.1089	15385.8	50.00	Sequence
DRB3_0101	470	VLRPVSSEDAMTADW	VSSEDAMTA	0.1085	15454.6	50.00	Sequence
DRB3_0101	323	VLDGKTAEFLVQGTL	VLDGKTAEF	0.1079	15560.6	50.00	Sequence
DRB3_0101	30	ARRVREARVFSEVIP	RRVREARVF	0.1076	15600.7	50.00	Sequence
DRB3_0101	164	AFEAFDRRLAGVQYH	FDRRLAGVQ	0.1071	15695.4	50.00	Sequence
DRB3_0101	256	FVDHGLLRAGERAQV	LRAGERAQV	0.1070	15717.3	50.00	Sequence
DRB3_0101	100	QALGGIVAHTGTREY	VAHTGTREY	0.1063	15821.7	50.00	Sequence
DRB3_0101	487	VPYEVLERISTRITN	YEVLERIST	0.1063	15832.7	50.00	Sequence
DRB3_0101	239	VAAALVQRAIGDRLT	VQRAIGDRL	0.1059	15901.3	50.00	Sequence
DRB3_0101	101	ALGGIVAHTGTREYG	VAHTGTREY	0.1054	15984.3	50.00	Sequence
DRB3_0101	31	RRVREARVFSEVIPH	RRVREARVF	0.1044	16150.2	50.00	Sequence
DRB3_0101	160	APVAAFEAFDRRLAG	FEAFDRRLA	0.1041	16212.5	50.00	Sequence
DRB3_0101	4	ADIDVPETPARPVLV	ETPARPVLV	0.1039	16248.5	50.00	Sequence
DRB3_0101	159	GAPVAAFEAFDRRLA	FEAFDRRLA	0.1036	16292.8	50.00	Sequence
DRB3_0101	0	VVQPADIDVPETPAR	IDVPETPAR	0.1035	16315.6	50.00	Sequence
DRB3_0101	240	AAALVQRAIGDRLTC	VQRAIGDRL	0.1034	16331.1	50.00	Sequence
DRB3_0101	102	LGGIVAHTGTREYGR	VAHTGTREY	0.1034	16336.4	50.00	Sequence
DRB3_0101	468	PIVLRPVSSEDAMTA	VSSEDAMTA	0.1031	16395.4	50.00	Sequence
DRB3_0101	104	GIVAHTGTREYGRTE	VAHTGTREY	0.1025	16497.2	50.00	Sequence
DRB3_0101	8	VPETPARPVLVVDFG	ARPVLVVDF	0.1023	16535.1	50.00	Sequence
DRB3_0101	430	REELTAAGLDNQIWQ	TAAGLDNQI	0.1021	16573.6	50.00	Sequence
DRB3_0101	257	VDHGLLRAGERAQVQ	LRAGERAQV	0.1012	16734.3	50.00	Sequence
DRB3_0101	457	GVQGDGRTYGHPIVL	VQGDGRTYG	0.1011	16753.7	50.00	Sequence
DRB3_0101	458	VQGDGRTYGHPIVLR	TYGHPIVLR	0.1008	16802.2	50.00	Sequence
DRB3_0101	50	EEIRARQPVALVLSG	IRARQPVAL	0.1002	16900.8	50.00	Sequence
DRB3_0101	9	PETPARPVLVVDFGA	ARPVLVVDF	0.0996	17016.2	50.00	Sequence
DRB3_0101	473	PVSSEDAMTADWTRV	VSSEDAMTA	0.0995	17037.8	50.00	Sequence
DRB3_0101	22	GAQYAQLIARRVREA	YAQLIARRV	0.0995	17045.5	50.00	Sequence
DRB3_0101	165	FEAFDRRLAGVQYHP	FDRRLAGVQ	0.0989	17155.2	50.00	Sequence
DRB3_0101	471	LRPVSSEDAMTADWT	VSSEDAMTA	0.0983	17266.2	50.00	Sequence
DRB3_0101	261	LLRAGERAQVQRDFV	LRAGERAQV	0.0978	17354.3	50.00	Sequence
DRB3_0101	105	IVAHTGTREYGRTEL	VAHTGTREY	0.0975	17415.6	50.00	Sequence
DRB3_0101	263	RAGERAQVQRDFVAA	AQVQRDFVA	0.0971	17493.8	50.00	Sequence
DRB3_0101	51	EIRARQPVALVLSGG	RARQPVALV	0.0965	17602.6	50.00	Sequence
DRB3_0101	103	GGIVAHTGTREYGRT	VAHTGTREY	0.0958	17738.5	50.00	Sequence
DRB3_0101	452	DVRSVGVQGDGRTYG	VQGDGRTYG	0.0957	17761.0	50.00	Sequence
DRB3_0101	152	DVVASSAGAPVAAFE	SAGAPVAAF	0.0956	17768.5	50.00	Sequence
DRB3_0101	52	IRARQPVALVLSGGP	RARQPVALV	0.0954	17820.4	50.00	Sequence
DRB3_0101	211	ANALIEQVRTQIGDG	LIEQVRTQI	0.0952	17845.7	50.00	Sequence
DRB3_0101	260	GLLRAGERAQVQRDF	LRAGERAQV	0.0948	17925.5	50.00	Sequence
DRB3_0101	481	TADWTRVPYEVLERI	DWTRVPYEV	0.0947	17952.0	50.00	Sequence
DRB3_0101	324	LDGKTAEFLVQGTLY	LDGKTAEFL	0.0942	18041.6	50.00	Sequence
DRB3_0101	429	VREELTAAGLDNQIW	TAAGLDNQI	0.0939	18094.8	50.00	Sequence
DRB3_0101	23	AQYAQLIARRVREAR	YAQLIARRV	0.0938	18125.7	50.00	Sequence
DRB3_0101	106	VAHTGTREYGRTELK	VAHTGTREY	0.0936	18159.3	50.00	Sequence
DRB3_0101	455	SVGVQGDGRTYGHPI	VQGDGRTYG	0.0935	18183.9	50.00	Sequence
DRB3_0101	6	IDVPETPARPVLVVD	ETPARPVLV	0.0933	18225.3	50.00	Sequence
DRB3_0101	453	VRSVGVQGDGRTYGH	VQGDGRTYG	0.0932	18233.3	50.00	Sequence
DRB3_0101	24	QYAQLIARRVREARV	YAQLIARRV	0.0931	18263.8	50.00	Sequence
DRB3_0101	472	RPVSSEDAMTADWTR	VSSEDAMTA	0.0928	18316.2	50.00	Sequence
DRB3_0101	7	DVPETPARPVLVVDF	ARPVLVVDF	0.0926	18364.6	50.00	Sequence
DRB3_0101	53	RARQPVALVLSGGPA	RARQPVALV	0.0912	18638.5	50.00	Sequence
DRB3_0101	488	PYEVLERISTRITNE	YEVLERIST	0.0900	18880.0	50.00	Sequence
DRB3_0101	259	HGLLRAGERAQVQRD	LRAGERAQV	0.0899	18897.2	50.00	Sequence
DRB3_0101	258	DHGLLRAGERAQVQR	LRAGERAQV	0.0896	18964.5	50.00	Sequence
DRB3_0101	91	ICYGFQAMAQALGGI	YGFQAMAQA	0.0893	19028.5	50.00	Sequence
DRB3_0101	482	ADWTRVPYEVLERIS	DWTRVPYEV	0.0891	19064.9	50.00	Sequence
DRB3_0101	90	GICYGFQAMAQALGG	YGFQAMAQA	0.0888	19123.2	50.00	Sequence
DRB3_0101	212	NALIEQVRTQIGDGH	LIEQVRTQI	0.0887	19141.8	50.00	Sequence
DRB3_0101	167	AFDRRLAGVQYHPEV	FDRRLAGVQ	0.0880	19297.2	50.00	Sequence
DRB3_0101	168	FDRRLAGVQYHPEVM	FDRRLAGVQ	0.0872	19464.1	50.00	Sequence
DRB3_0101	510	VLDITSKPPATIEWE	ITSKPPATI	0.0872	19472.5	50.00	Sequence
DRB3_0101	5	DIDVPETPARPVLVV	ETPARPVLV	0.0866	19581.7	50.00	Sequence
DRB3_0101	1	VQPADIDVPETPARP	IDVPETPAR	0.0865	19609.1	50.00	Sequence
DRB3_0101	117	TELKVLGGKLHSDLP	LGGKLHSDL	0.0864	19641.6	50.00	Sequence
DRB3_0101	454	RSVGVQGDGRTYGHP	VQGDGRTYG	0.0860	19714.6	50.00	Sequence

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DRB3_0101  463  RTYGHPIVLRPVSSE  IVLRPVSSE        0.0856      19811.7                 50.00     Sequence
DRB3_0101  127  HSDLPEVQPVWMSHG  SDLPEVQPV        0.0853      19875.9                 50.00     Sequence
DRB3_0101  118  ELKVLGGKLHSDLPE  LGGKLHSDL        0.0852      19886.9                 50.00     Sequence
DRB3_0101  223  GDGHAICGLSGGVDS  AICGLSGGV        0.0851      19910.3                 50.00     Sequence
DRB3_0101  153  VVASSAGAPVAAFEA  SAGAPVAAF        0.0841      20128.2                 50.00     Sequence
DRB3_0101  456  VGVQGDGRTYGHPIV  VQGDGRTYG        0.0839      20161.1                 50.00     Sequence
DRB3_0101  459  QGDGRTYGHPIVLRP  TYGHPIVLR        0.0837      20223.8                 50.00     Sequence
DRB3_0101  213  ALIEQVRTQIGDGHA  LIEQVRTQI        0.0831      20356.4                 50.00     Sequence
DRB3_0101  276  AATGANLVTVDAAET  LVTVDAAET        0.0828      20405.8                 50.00     Sequence
DRB3_0101  464  TYGHPIVLRPVSSED  TYGHPIVLR        0.0822      20545.4                 50.00     Sequence
DRB3_0101  460  GDGRTYGHPIVLRPV  TYGHPIVLR        0.0822      20553.4                 50.00     Sequence
DRB3_0101  116  RTELKVLGGKLHSDL  LGGKLHSDL        0.0818      20631.2                 50.00     Sequence
DRB3_0101  154  VASSAGAPVAAFEAF  SAGAPVAAF        0.0817      20655.1                 50.00     Sequence
DRB3_0101  354  KSHHNVGGLPDDLKF  GGLPDDLKF        0.0814      20726.0                 50.00     Sequence
DRB3_0101  128  SDLPEVQPVWMSHGD  SDLPEVQPV        0.0808      20855.8                 50.00     Sequence
DRB3_0101  156  SSAGAPVAAFEAFDR  SAGAPVAAF        0.0807      20878.2                 50.00     Sequence
DRB3_0101   54  ARQPVALVLSGGPAS  LVLSGGPAS        0.0806      20899.4                 50.00     Sequence
DRB3_0101  387  RELGLPEEIVARQPF  LGLPEEIVA        0.0800      21046.5                 50.00     Sequence
DRB3_0101  155  ASSAGAPVAAFEAFD  SAGAPVAAF        0.0797      21107.1                 50.00     Sequence
DRB3_0101  224  DGHAICGLSGGVDSA  AICGLSGGV        0.0794      21176.9                 50.00     Sequence
DRB3_0101  383  RAVGRELGLPEEIVA  LGLPEEIVA        0.0793      21196.6                 50.00     Sequence
DRB3_0101  157  SAGAPVAAFEAFDRR  SAGAPVAAF        0.0781      21472.2                 50.00     Sequence
DRB3_0101    2  QPADIDVPETPARPV  IDVPETPAR        0.0776      21598.7                 50.00     Sequence
DRB3_0101  235  VDSAVAAALVQRAIG  VDSAVAAAL        0.0773      21659.1                 50.00     Sequence
DRB3_0101  461  DGRTYGHPIVLRPVS  TYGHPIVLR        0.0767      21814.4                 50.00     Sequence
DRB3_0101  384  AVGRELGLPEEIVAR  LGLPEEIVA        0.0765      21857.1                 50.00     Sequence
DRB3_0101   32  RVREARVFSEVIPHT  RVFSEVIPH        0.0763      21900.9                 50.00     Sequence
DRB3_0101  412  GEVTAKRLDTLRHAD  KRLDTLRHA        0.0763      21902.6                 50.00     Sequence
DRB3_0101  408  IRIVGEVTAKRLDTL  IVGEVTAKR        0.0759      21989.2                 50.00     Sequence
DRB3_0101  411  VGEVTAKRLDTLRHA  KRLDTLRHA        0.0752      22162.6                 50.00     Sequence
DRB3_0101  466  GHPIVLRPVSSEDAM  IVLRPVSSE        0.0750      22205.4                 50.00     Sequence
DRB3_0101  115  GRTELKVLGGKLHSD  VLGGKLHSD        0.0749      22240.0                 50.00     Sequence
DRB3_0101    3  PADIDVPETPARPVL  IDVPETPAR        0.0744      22346.6                 50.00     Sequence
DRB3_0101  414  VTAKRLDTLRHADSI  KRLDTLRHA        0.0742      22407.6                 50.00     Sequence
DRB3_0101  381  EVRAVGRELGLPEEI  RELGLPEEI        0.0736      22548.9                 50.00     Sequence
DRB3_0101  234  GVDSAVAAALVQRAI  VDSAVAAAL        0.0736      22557.5                 50.00     Sequence
DRB3_0101  222  IGDGHAICGLSGGVD  AICGLSGGV        0.0729      22715.9                 50.00     Sequence
DRB3_0101  221  QIGDGHAICGLSGGV  AICGLSGGV        0.0729      22717.6                 50.00     Sequence
DRB3_0101  465  YGHPIVLRPVSSEDA  IVLRPVSSE        0.0728      22746.9                 50.00     Sequence
DRB3_0101  129  DLPEVQPVWMSHGDA  PEVQPVWMS        0.0724      22831.3                 50.00     Sequence
DRB3_0101  467  HPIVLRPVSSEDAMT  IVLRPVSSE        0.0724      22850.3                 50.00     Sequence
DRB3_0101  407  GIRIVGEVTAKRLDT  IVGEVTAKR        0.0723      22857.7                 50.00     Sequence
DRB3_0101  166  EAFDRRLAGVQYHPE  FDRRLAGVQ        0.0722      22890.6                 50.00     Sequence
DRB3_0101  353  IKSHHNVGGLPDDLK  NVGGLPDDL        0.0716      23029.7                 50.00     Sequence
DRB3_0101  385  VGRELGLPEEIVARQ  LGLPEEIVA        0.0708      23253.3                 50.00     Sequence
DRB3_0101  462  GRTYGHPIVLRPVSS  TYGHPIVLR        0.0707      23274.7                 50.00     Sequence
DRB3_0101  413  EVTAKRLDTLRHADS  KRLDTLRHA        0.0706      23292.4                 50.00     Sequence
DRB3_0101  388  ELGLPEEIVARQPFP  LGLPEEIVA        0.0706      23298.9                 50.00     Sequence
DRB3_0101  382  VRAVGRELGLPEEIV  RELGLPEEI        0.0705      23317.6                 50.00     Sequence
DRB3_0101  409  RIVGEVTAKRLDTLR  IVGEVTAKR        0.0702      23391.4                 50.00     Sequence
DRB3_0101  410  IVGEVTAKRLDTLRH  IVGEVTAKR        0.0692      23647.6                 50.00     Sequence
DRB3_0101  237  SAVAAALVQRAIGDR  VAAALVQRA        0.0680      23964.7                 50.00     Sequence
DRB3_0101  352  NIKSHHNVGGLPDDL  NVGGLPDDL        0.0676      24056.1                 50.00     Sequence
DRB3_0101  389  LGLPEEIVARQPFPG  LGLPEEIVA        0.0663      24395.3                 50.00     Sequence
DRB3_0101  299  SAPEGKRKIIGRQFI  RKIIGRQFI        0.0653      24677.0                 50.00     Sequence
DRB3_0101  386  GRELGLPEEIVARQP  LGLPEEIVA        0.0648      24814.0                 50.00     Sequence
DRB3_0101   41  EVIPHTASIEEIRAR  ASIEEIRAR        0.0624      25440.1                 50.00     Sequence
DRB3_0101   99  AQALGGIVAHTGTRE  GIVAHTGTR        0.0586      26531.1                 50.00     Sequence
DRB3_0101  300  APEGKRKIIGRQFIR  RKIIGRQFI        0.0581      26672.2                 50.00     Sequence
DRB3_0101  390  GLPEEIVARQPFPGP  IVARQPFPG        0.0579      26712.3                 50.00     Sequence
DRB3_0101  451  ADVRSVGVQGDGRTY  GVQGDGRTY        0.0574      26857.2                 50.00     Sequence
DRB3_0101   40  SEVIPHTASIEEIRA  HTASIEEIR        0.0566      27095.1                 50.00     Sequence
DRB3_0101  301  PEGKRKIIGRQFIRA  RKIIGRQFI        0.0562      27227.9                 50.00     Sequence
DRB3_0101  236  DSAVAAALVQRAIGD  VAAALVQRA        0.0542      27830.5                 50.00     Sequence
DRB3_0101  450  LADVRSVGVQGDGRT  LADVRSVGV        0.0517      28585.5                 50.00     Sequence
DRB3_0101   44  PHTASIEEIRARQPV  ASIEEIRAR        0.0507      28882.7                 50.00     Sequence
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   DRB3_0101   42  VIPHTASIEEIRARQ  ASIEEIRAR        0.0489      29465.7                 50.00     Sequence
   DRB3_0101  393  EEIVARQPFPGPGLG  IVARQPFPG        0.0484      29622.0                 50.00     Sequence
   DRB3_0101  379  KDEVRAVGRELGLPE  EVRAVGREL        0.0479      29781.8                 50.00     Sequence
   DRB3_0101  107  AHTGTREYGRTELKV  HTGTREYGR        0.0479      29782.4                 50.00     Sequence
   DRB3_0101  391  LPEEIVARQPFPGPG  IVARQPFPG        0.0479      29783.4                 50.00     Sequence
   DRB3_0101  392  PEEIVARQPFPGPGL  IVARQPFPG        0.0478      29818.8                 50.00     Sequence
   DRB3_0101  351  ANIKSHHNVGGLPDD  HNVGGLPDD        0.0463      30292.3                 50.00     Sequence
   DRB3_0101  380  DEVRAVGRELGLPEE  EVRAVGREL        0.0459      30421.7                 50.00     Sequence
   DRB3_0101  158  AGAPVAAFEAFDRRL  VAAFEAFDR        0.0459      30436.6                 50.00     Sequence
   DRB3_0101   43  IPHTASIEEIRARQP  ASIEEIRAR        0.0453      30618.9                 50.00     Sequence
   DRB3_0101  345  GGGSGTANIKSHHNV  ANIKSHHNV        0.0440      31071.1                 50.00     Sequence
   DRB3_0101  395  IVARQPFPGPGLGIR  IVARQPFPG        0.0432      31342.6                 50.00     Sequence
   DRB3_0101   45  HTASIEEIRARQPVA  ASIEEIRAR        0.0430      31411.5                 50.00     Sequence
   DRB3_0101  298  VSAPEGKRKIIGRQF  KRKIIGRQF        0.0425      31559.7                 50.00     Sequence
   DRB3_0101  348  SGTANIKSHHNVGGL  ANIKSHHNV        0.0421      31696.2                 50.00     Sequence
   DRB3_0101  347  GSGTANIKSHHNVGG  IKSHHNVGG        0.0420      31738.7                 50.00     Sequence
   DRB3_0101  349  GTANIKSHHNVGGLP  ANIKSHHNV        0.0415      31909.9                 50.00     Sequence
   DRB3_0101  350  TANIKSHHNVGGLPD  ANIKSHHNV        0.0413      31966.2                 50.00     Sequence
   DRB3_0101  346  GGSGTANIKSHHNVG  ANIKSHHNV        0.0404      32311.9                 50.00     Sequence
   DRB3_0101  394  EIVARQPFPGPGLGI  IVARQPFPG        0.0397      32550.1                 50.00     Sequence
   DRB3_0101  396  VARQPFPGPGLGIRI  FPGPGLGIR        0.0375      33337.8                 50.00     Sequence
   DRB3_0101  295  LSGVSAPEGKRKIIG  GVSAPEGKR        0.0358      33952.3                 50.00     Sequence
   DRB3_0101  294  ALSGVSAPEGKRKII  GVSAPEGKR        0.0354      34078.5                 50.00     Sequence
   DRB3_0101  397  ARQPFPGPGLGIRIV  FPGPGLGIR        0.0353      34144.2                 50.00     Sequence
   DRB3_0101  398  RQPFPGPGLGIRIVG  FPGPGLGIR        0.0351      34214.5                 50.00     Sequence
   DRB3_0101  296  SGVSAPEGKRKIIGR  GVSAPEGKR        0.0335      34798.4                 50.00     Sequence
   DRB3_0101  293  EALSGVSAPEGKRKI  SAPEGKRKI        0.0331      34945.9                 50.00     Sequence
   DRB3_0101  297  GVSAPEGKRKIIGRQ  GVSAPEGKR        0.0316      35527.7                 50.00     Sequence
   DRB3_0101  339  PDVVESGGGSGTANI  GGGSGTANI        0.0310      35741.7                 50.00     Sequence
   DRB3_0101  399  QPFPGPGLGIRIVGE  FPGPGLGIR        0.0290      36541.3                 50.00     Sequence
   DRB3_0101  292  LEALSGVSAPEGKRK  GVSAPEGKR        0.0273      37222.5                 50.00     Sequence
   DRB3_0101  344  SGGGSGTANIKSHHN  TANIKSHHN        0.0271      37304.3                 50.00     Sequence
   DRB3_0101  340  DVVESGGGSGTANIK  GGGSGTANI        0.0266      37480.3                 50.00     Sequence
   DRB3_0101  343  ESGGGSGTANIKSHH  GGGSGTANI        0.0254      37990.7                 50.00     Sequence
   DRB3_0101  338  YPDVVESGGGSGTAN  VVESGGGSG        0.0251      38109.7                 50.00     Sequence
   DRB3_0101  342  VESGGGSGTANIKSH  GGGSGTANI        0.0242      38480.9                 50.00     Sequence
   DRB3_0101  341  VVESGGGSGTANIKS  GGGSGTANI        0.0241      38533.0                 50.00     Sequence
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Allele: DRB3_0101. Number of high binders 2. Number of weak binders 31. Number of peptides 511

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB4_0101  304  KRKIIGRQFIRAFEG  RKIIGRQFI        0.6944         27.3          SB     2.00     Sequence
   DRB4_0101  303  GKRKIIGRQFIRAFE  RKIIGRQFI        0.6842         30.5          SB     2.00     Sequence
   DRB4_0101  305  RKIIGRQFIRAFEGA  RKIIGRQFI        0.6710         35.2          SB     4.00     Sequence
   DRB4_0101  302  EGKRKIIGRQFIRAF  RKIIGRQFI        0.6693         35.8          SB     4.00     Sequence
   DRB4_0101  368  FTLVEPLRLLFKDEV  PLRLLFKDE        0.6660         37.1          SB     4.00     Sequence
   DRB4_0101  466  GHPIVLRPVSSEDAM  HPIVLRPVS        0.6616         38.9          SB     4.00     Sequence
   DRB4_0101  465  YGHPIVLRPVSSEDA  HPIVLRPVS        0.6581         40.4          SB     4.00     Sequence
   DRB4_0101  301  PEGKRKIIGRQFIRA  RKIIGRQFI        0.6455         46.3          SB     4.00     Sequence
   DRB4_0101  369  TLVEPLRLLFKDEVR  LRLLFKDEV        0.6378         50.4          WB     4.00     Sequence
   DRB4_0101   13  ARPVLVVDFGAQYAQ  ARPVLVVDF        0.6318         53.7          WB     4.00     Sequence
   DRB4_0101  467  HPIVLRPVSSEDAMT  LRPVSSEDA        0.6311         54.1          WB     4.00     Sequence
   DRB4_0101   12  PARPVLVVDFGAQYA  ARPVLVVDF        0.6274         56.3          WB     8.00     Sequence
   DRB4_0101  367  KFTLVEPLRLLFKDE  FTLVEPLRL        0.6178         62.5          WB     8.00     Sequence
   DRB4_0101  187  GQQVLSRFLHDFAGL  QQVLSRFLH        0.6168         63.2          WB     8.00     Sequence
   DRB4_0101  370  LVEPLRLLFKDEVRA  LRLLFKDEV        0.6166         63.3          WB     8.00     Sequence
   DRB4_0101  170  RRLAGVQYHPEVMHT  RRLAGVQYH        0.6160         63.7          WB     8.00     Sequence
   DRB4_0101   11  TPARPVLVVDFGAQY  ARPVLVVDF        0.6089         68.8          WB     8.00     Sequence
   DRB4_0101  169  DRRLAGVQYHPEVMH  RRLAGVQYH        0.6057         71.2          WB     8.00     Sequence
   DRB4_0101  366  LKFTLVEPLRLLFKD  LKFTLVEPL        0.6034         73.1          WB     8.00     Sequence
   DRB4_0101  372  EPLRLLFKDEVRAVG  LRLLFKDEV        0.6027         73.6          WB     8.00     Sequence
   DRB4_0101  186  HGQQVLSRFLHDFAG  QQVLSRFLH        0.6021         74.1          WB     8.00     Sequence
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DRB4_0101  300  APEGKRKIIGRQFIR  RKIIGRQFI        0.5989         76.7           WB     8.00      Sequence
DRB4_0101  371  VEPLRLLFKDEVRAV  LRLLFKDEV        0.5981         77.4           WB     8.00      Sequence
DRB4_0101  185  PHGQQVLSRFLHDFA  QQVLSRFLH        0.5946         80.3           WB     8.00      Sequence
DRB4_0101  365  DLKFTLVEPLRLLFK  LKFTLVEPL        0.5852         88.9           WB     8.00      Sequence
DRB4_0101  188  QQVLSRFLHDFAGLG  QQVLSRFLH        0.5849         89.2           WB     8.00      Sequence
DRB4_0101  364  DDLKFTLVEPLRLLF  LKFTLVEPL        0.5792         94.9           WB     8.00      Sequence
DRB4_0101   50  EEIRARQPVALVLSG  EIRARQPVA        0.5791         95.1           WB     8.00      Sequence
DRB4_0101   49  IEEIRARQPVALVLS  EIRARQPVA        0.5757         98.6           WB     8.00      Sequence
DRB4_0101  362  LPDDLKFTLVEPLRL  LKFTLVEPL        0.5717        102.9           WB     8.00      Sequence
DRB4_0101   87  PVLGICYGFQAMAQA  YGFQAMAQA        0.5714        103.3           WB     8.00      Sequence
DRB4_0101  404  PGLGIRIVGEVTAKR  IRIVGEVTA        0.5709        103.9           WB     8.00      Sequence
DRB4_0101  168  FDRRLAGVQYHPEVM  RRLAGVQYH        0.5707        104.0           WB     8.00      Sequence
DRB4_0101  464  TYGHPIVLRPVSSED  HPIVLRPVS        0.5700        104.8           WB     8.00      Sequence
DRB4_0101   48  SIEEIRARQPVALVL  EEIRARQPV        0.5670        108.3           WB    16.00      Sequence
DRB4_0101  118  ELKVLGGKLHSDLPE  LKVLGGKLH        0.5622        114.1           WB    16.00      Sequence
DRB4_0101   10  ETPARPVLVVDFGAQ  ARPVLVVDF        0.5602        116.6           WB    16.00      Sequence
DRB4_0101   14  RPVLVVDFGAQYAQL  RPVLVVDFG        0.5589        118.3           WB    16.00      Sequence
DRB4_0101  213  ALIEQVRTQIGDGHA  IEQVRTQIG        0.5557        122.5           WB    16.00      Sequence
DRB4_0101  413  EVTAKRLDTLRHADS  LDTLRHADS        0.5553        123.0           WB    16.00      Sequence
DRB4_0101  117  TELKVLGGKLHSDLP  LKVLGGKLH        0.5551        123.2           WB    16.00      Sequence
DRB4_0101  403  GPGLGIRIVGEVTAK  IRIVGEVTA        0.5551        123.2           WB    16.00      Sequence
DRB4_0101  361  GLPDDLKFTLVEPLR  LKFTLVEPL        0.5548        123.6           WB    16.00      Sequence
DRB4_0101  363  PDDLKFTLVEPLRLL  LKFTLVEPL        0.5546        123.9           WB    16.00      Sequence
DRB4_0101  406  LGIRIVGEVTAKRLD  IRIVGEVTA        0.5541        124.5           WB    16.00      Sequence
DRB4_0101  407  GIRIVGEVTAKRLDT  IRIVGEVTA        0.5527        126.4           WB    16.00      Sequence
DRB4_0101  463  RTYGHPIVLRPVSSE  HPIVLRPVS        0.5520        127.4           WB    16.00      Sequence
DRB4_0101  212  NALIEQVRTQIGDGH  IEQVRTQIG        0.5492        131.3           WB    16.00      Sequence
DRB4_0101  462  GRTYGHPIVLRPVSS  HPIVLRPVS        0.5491        131.4           WB    16.00      Sequence
DRB4_0101  189  QVLSRFLHDFAGLGA  LSRFLHDFA        0.5483        132.6           WB    16.00      Sequence
DRB4_0101  414  VTAKRLDTLRHADSI  LDTLRHADS        0.5471        134.3           WB    16.00      Sequence
DRB4_0101   85  GVPVLGICYGFQAMA  VPVLGICYG        0.5461        135.8           WB    16.00      Sequence
DRB4_0101  116  RTELKVLGGKLHSDL  LKVLGGKLH        0.5461        135.8           WB    16.00      Sequence
DRB4_0101  408  IRIVGEVTAKRLDTL  IRIVGEVTA        0.5461        135.8           WB    16.00      Sequence
DRB4_0101  416  AKRLDTLRHADSIVR  LDTLRHADS        0.5453        137.0           WB    16.00      Sequence
DRB4_0101   47  ASIEEIRARQPVALV  EEIRARQPV        0.5439        139.0           WB    16.00      Sequence
DRB4_0101   88  VLGICYGFQAMAQAL  YGFQAMAQA        0.5424        141.4           WB    16.00      Sequence
DRB4_0101  415  TAKRLDTLRHADSIV  LDTLRHADS        0.5423        141.4           WB    16.00      Sequence
DRB4_0101  119  LKVLGGKLHSDLPEV  LKVLGGKLH        0.5403        144.7           WB    16.00      Sequence
DRB4_0101    9  PETPARPVLVVDFGA  ARPVLVVDF        0.5397        145.6           WB    16.00      Sequence
DRB4_0101  405  GLGIRIVGEVTAKRL  IRIVGEVTA        0.5382        147.8           WB    16.00      Sequence
DRB4_0101  402  PGPGLGIRIVGEVTA  IRIVGEVTA        0.5376        148.9           WB    16.00      Sequence
DRB4_0101   86  VPVLGICYGFQAMAQ  VPVLGICYG        0.5364        150.7           WB    16.00      Sequence
DRB4_0101  306  KIIGRQFIRAFEGAV  KIIGRQFIR        0.5360        151.5           WB    16.00      Sequence
DRB4_0101  167  AFDRRLAGVQYHPEV  RRLAGVQYH        0.5358        151.7           WB    16.00      Sequence
DRB4_0101   89  LGICYGFQAMAQALG  YGFQAMAQA        0.5358        151.8           WB    16.00      Sequence
DRB4_0101  360  GGLPDDLKFTLVEPL  LKFTLVEPL        0.5358        151.8           WB    16.00      Sequence
DRB4_0101  468  PIVLRPVSSEDAMTA  LRPVSSEDA        0.5354        152.4           WB    16.00      Sequence
DRB4_0101  214  LIEQVRTQIGDGHAI  LIEQVRTQI        0.5332        156.1           WB    16.00      Sequence
DRB4_0101  115  GRTELKVLGGKLHSD  LKVLGGKLH        0.5321        158.0           WB    16.00      Sequence
DRB4_0101   90  GICYGFQAMAQALGG  YGFQAMAQA        0.5316        158.9           WB    16.00      Sequence
DRB4_0101  417  KRLDTLRHADSIVRE  LDTLRHADS        0.5300        161.6           WB    16.00      Sequence
DRB4_0101   51  EIRARQPVALVLSGG  EIRARQPVA        0.5294        162.8           WB    16.00      Sequence
DRB4_0101  166  EAFDRRLAGVQYHPE  RRLAGVQYH        0.5235        173.5           WB    16.00      Sequence
DRB4_0101  114  YGRTELKVLGGKLHS  LKVLGGKLH        0.5228        174.7           WB    16.00      Sequence
DRB4_0101   84  LGVPVLGICYGFQAM  VPVLGICYG        0.5202        179.7           WB    16.00      Sequence
DRB4_0101  503  VAEVNRVVLDITSKP  VNRVVLDIT        0.5189        182.3           WB    16.00      Sequence
DRB4_0101  392  PEEIVARQPFPGPGL  EEIVARQPF        0.5185        183.0           WB    16.00      Sequence
DRB4_0101   46  TASIEEIRARQPVAL  EEIRARQPV        0.5184        183.3           WB    16.00      Sequence
DRB4_0101  165  FEAFDRRLAGVQYHP  RRLAGVQYH        0.5175        185.0           WB    16.00      Sequence
DRB4_0101  502  EVAEVNRVVLDITSK  VNRVVLDIT        0.5175        185.1           WB    16.00      Sequence
DRB4_0101  470  VLRPVSSEDAMTADW  LRPVSSEDA        0.5171        185.8           WB    16.00      Sequence
DRB4_0101  439  DNQIWQCPVVLLADV  CPVVLLADV        0.5134        193.4           WB    16.00      Sequence
DRB4_0101  501  NEVAEVNRVVLDITS  VNRVVLDIT        0.5120        196.4           WB    16.00      Sequence
DRB4_0101   15  PVLVVDFGAQYAQLI  FGAQYAQLI        0.5111        198.3           WB    16.00      Sequence
DRB4_0101  391  LPEEIVARQPFPGPG  EEIVARQPF        0.5036        215.2           WB    16.00      Sequence
DRB4_0101  500  TNEVAEVNRVVLDIT  EVNRVVLDI        0.5034        215.5           WB    16.00      Sequence
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DRB4_0101  440  NQIWQCPVVLLADVR  CPVVLLADV         0.5030          216.5          WB    16.00      Sequence
DRB4_0101   52  IRARQPVALVLSGGP  QPVALVLSG         0.5027          217.3          WB    16.00      Sequence
DRB4_0101  441  QIWQCPVVLLADVRS  CPVVLLADV         0.5011          220.9          WB    16.00      Sequence
DRB4_0101   82  LDLGVPVLGICYGFQ  LDLGVPVLG         0.4998          224.0          WB    16.00      Sequence
DRB4_0101  469  IVLRPVSSEDAMTAD  LRPVSSEDA         0.4995          224.9          WB    16.00      Sequence
DRB4_0101  307  IIGRQFIRAFEGAVR  RQFIRAFEG         0.4964          232.6          WB    32.00      Sequence
DRB4_0101  444  QCPVVLLADVRSVGV  CPVVLLADV         0.4962          232.9          WB    32.00      Sequence
DRB4_0101  418  RLDTLRHADSIVREE  LDTLRHADS         0.4952          235.6          WB    32.00      Sequence
DRB4_0101  184  TPHGQQVLSRFLHDF  QQVLSRFLH         0.4941          238.4          WB    32.00      Sequence
DRB4_0101  211  ANALIEQVRTQIGDG  IEQVRTQIG         0.4935          239.8          WB    32.00      Sequence
DRB4_0101  505  EVNRVVLDITSKPPA  VNRVVLDIT         0.4935          240.0          WB    32.00      Sequence
DRB4_0101  445  CPVVLLADVRSVGVQ  CPVVLLADV         0.4926          242.4          WB    32.00      Sequence
DRB4_0101  504  AEVNRVVLDITSKPP  VNRVVLDIT         0.4921          243.6          WB    32.00      Sequence
DRB4_0101  461  DGRTYGHPIVLRPVS  HPIVLRPVS         0.4904          248.0          WB    32.00      Sequence
DRB4_0101  210  IANALIEQVRTQIGD  IEQVRTQIG         0.4902          248.7          WB    32.00      Sequence
DRB4_0101  393  EEIVARQPFPGPGLG  EEIVARQPF         0.4872          257.0          WB    32.00      Sequence
DRB4_0101  443  WQCPVVLLADVRSVG  CPVVLLADV         0.4856          261.3          WB    32.00      Sequence
DRB4_0101  390  GLPEEIVARQPFPGP  EEIVARQPF         0.4839          266.3          WB    32.00      Sequence
DRB4_0101  299  SAPEGKRKIIGRQFI  RKIIGRQFI         0.4822          271.0          WB    32.00      Sequence
DRB4_0101  308  IGRQFIRAFEGAVRD  RQFIRAFEG         0.4792          280.0          WB    32.00      Sequence
DRB4_0101  425  ADSIVREELTAAGLD  DSIVREELT         0.4772          286.3          WB    32.00      Sequence
DRB4_0101   81  LLDLGVPVLGICYGF  PVLGICYGF         0.4764          288.8          WB    32.00      Sequence
DRB4_0101  373  PLRLLFKDEVRAVGR  LRLLFKDEV         0.4759          290.2          WB    32.00      Sequence
DRB4_0101   83  DLGVPVLGICYGFQA  VPVLGICYG         0.4752          292.5          WB    32.00      Sequence
DRB4_0101  442  IWQCPVVLLADVRSV  CPVVLLADV         0.4720          302.8          WB    32.00      Sequence
DRB4_0101  389  LGLPEEIVARQPFPG  EEIVARQPF         0.4711          305.8          WB    32.00      Sequence
DRB4_0101   91  ICYGFQAMAQALGGI  YGFQAMAQA         0.4690          312.7          WB    32.00      Sequence
DRB4_0101  178  HPEVMHTPHGQQVLS  HPEVMHTPH         0.4684          314.9          WB    32.00      Sequence
DRB4_0101  412  GEVTAKRLDTLRHAD  AKRLDTLRH         0.4666          321.0          WB    32.00      Sequence
DRB4_0101  309  GRQFIRAFEGAVRDV  RQFIRAFEG         0.4628          334.3          WB    32.00      Sequence
DRB4_0101  177  YHPEVMHTPHGQQVL  HPEVMHTPH         0.4618          338.0          WB    32.00      Sequence
DRB4_0101  190  VLSRFLHDFAGLGAQ  LSRFLHDFA         0.4617          338.4          WB    32.00      Sequence
DRB4_0101  424  HADSIVREELTAAGL  DSIVREELT         0.4615          339.0          WB    32.00      Sequence
DRB4_0101  419  LDTLRHADSIVREEL  LDTLRHADS         0.4604          343.1          WB    32.00      Sequence
DRB4_0101  451  ADVRSVGVQGDGRTY  VRSVGVQGD         0.4600          344.7          WB    32.00      Sequence
DRB4_0101  209  NIANALIEQVRTQIG  IEQVRTQIG         0.4599          345.0          WB    32.00      Sequence
DRB4_0101  471  LRPVSSEDAMTADWT  LRPVSSEDA         0.4597          345.8          WB    32.00      Sequence
DRB4_0101  164  AFEAFDRRLAGVQYH  RRLAGVQYH         0.4597          345.9          WB    32.00      Sequence
DRB4_0101   53  RARQPVALVLSGGPA  QPVALVLSG         0.4589          349.0          WB    32.00      Sequence
DRB4_0101  450  LADVRSVGVQGDGRT  VRSVGVQGD         0.4575          354.0          WB    32.00      Sequence
DRB4_0101  183  HTPHGQQVLSRFLHD  QQVLSRFLH         0.4553          362.7          WB    32.00      Sequence
DRB4_0101  452  DVRSVGVQGDGRTYG  VRSVGVQGD         0.4539          368.0          WB    32.00      Sequence
DRB4_0101  411  VGEVTAKRLDTLRHA  KRLDTLRHA         0.4537          369.0          WB    32.00      Sequence
DRB4_0101  113  EYGRTELKVLGGKLH  LKVLGGKLH         0.4520          375.9          WB    32.00      Sequence
DRB4_0101  248  IGDRLTCVFVDHGLL  CVFVDHGLL         0.4511          379.6          WB    32.00      Sequence
DRB4_0101  487  VPYEVLERISTRITN  VPYEVLERI         0.4508          380.7          WB    32.00      Sequence
DRB4_0101  388  ELGLPEEIVARQPFP  EEIVARQPF         0.4508          380.9          WB    32.00      Sequence
DRB4_0101  215  IEQVRTQIGDGHAIC  IEQVRTQIG         0.4495          386.0          WB    32.00      Sequence
DRB4_0101  176  QYHPEVMHTPHGQQV  HPEVMHTPH         0.4471          396.3          WB    32.00      Sequence
DRB4_0101  486  RVPYEVLERISTRIT  VPYEVLERI         0.4470          396.7          WB    32.00      Sequence
DRB4_0101  423  RHADSIVREELTAAG  DSIVREELT         0.4442          408.8          WB    32.00      Sequence
DRB4_0101  506  VNRVVLDITSKPPAT  VNRVVLDIT         0.4431          414.1          WB    32.00      Sequence
DRB4_0101  171  RLAGVQYHPEVMHTP  RLAGVQYHP         0.4429          414.8          WB    32.00      Sequence
DRB4_0101  175  VQYHPEVMHTPHGQQ  HPEVMHTPH         0.4419          419.3          WB    32.00      Sequence
DRB4_0101    8  VPETPARPVLVVDFG  ARPVLVVDF         0.4401          427.7          WB    32.00      Sequence
DRB4_0101  422  LRHADSIVREELTAA  DSIVREELT         0.4394          430.8          WB    32.00      Sequence
DRB4_0101  485  TRVPYEVLERISTRI  VPYEVLERI         0.4347          453.1          WB    32.00      Sequence
DRB4_0101  182  MHTPHGQQVLSRFLH  QQVLSRFLH         0.4342          455.9          WB    32.00      Sequence
DRB4_0101  174  GVQYHPEVMHTPHGQ  HPEVMHTPH         0.4339          457.2          WB    32.00      Sequence
DRB4_0101   26  AQLIARRVREARVFS  ARRVREARV         0.4333          460.1          WB    32.00      Sequence
DRB4_0101   54  ARQPVALVLSGGPAS  QPVALVLSG         0.4325          463.9          WB    32.00      Sequence
DRB4_0101  249  GDRLTCVFVDHGLLR  CVFVDHGLL         0.4321          466.0          WB    32.00      Sequence
DRB4_0101   16  VLVVDFGAQYAQLIA  LVVDFGAQY         0.4307          473.2          WB    32.00      Sequence
DRB4_0101  310  RQFIRAFEGAVRDVL  RQFIRAFEG         0.4290          482.1          WB    32.00      Sequence
DRB4_0101  120  KVLGGKLHSDLPEVQ  KVLGGKLHS         0.4285          484.7          WB    32.00      Sequence
DRB4_0101  484  WTRVPYEVLERISTR  VPYEVLERI         0.4259          498.7          WB    32.00      Sequence
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DRB4_0101  173  AGVQYHPEVMHTPHG  HPEVMHTPH         0.4256         500.2              32.00      Sequence
DRB4_0101   17  LVVDFGAQYAQLIAR  LVVDFGAQY         0.4238         509.9              32.00      Sequence
DRB4_0101  246  RAIGDRLTCVFVDHG  IGDRLTCVF         0.4238         510.0              32.00      Sequence
DRB4_0101  250  DRLTCVFVDHGLLRA  CVFVDHGLL         0.4236         511.3              32.00      Sequence
DRB4_0101   45  HTASIEEIRARQPVA  EEIRARQPV         0.4223         518.1              32.00      Sequence
DRB4_0101  239  VAAALVQRAIGDRLT  VAAALVQRA         0.4218         521.1              32.00      Sequence
DRB4_0101  247  AIGDRLTCVFVDHGL  IGDRLTCVF         0.4214         523.6              32.00      Sequence
DRB4_0101  381  EVRAVGRELGLPEEI  VRAVGRELG         0.4197         533.1              32.00      Sequence
DRB4_0101   55  RQPVALVLSGGPASV  QPVALVLSG         0.4197         533.4              32.00      Sequence
DRB4_0101   35  EARVFSEVIPHTASI  FSEVIPHTA         0.4194         534.8              32.00      Sequence
DRB4_0101   92  CYGFQAMAQALGGIV  YGFQAMAQA         0.4176         545.5              32.00      Sequence
DRB4_0101  483  DWTRVPYEVLERIST  VPYEVLERI         0.4159         555.6              32.00      Sequence
DRB4_0101  387  RELGLPEEIVARQPF  EEIVARQPF         0.4158         556.1              32.00      Sequence
DRB4_0101   25  YAQLIARRVREARVF  ARRVREARV         0.4149         561.2              32.00      Sequence
DRB4_0101  421  TLRHADSIVREELTA  DSIVREELT         0.4146         563.3              32.00      Sequence
DRB4_0101  410  IVGEVTAKRLDTLRH  VGEVTAKRL         0.4142         565.6              32.00      Sequence
DRB4_0101  401  FPGPGLGIRIVGEVT  LGIRIVGEV         0.4137         568.7              32.00      Sequence
DRB4_0101  238  AVAAALVQRAIGDRL  VAAALVQRA         0.4125         576.3              32.00      Sequence
DRB4_0101  426  DSIVREELTAAGLDN  DSIVREELT         0.4123         577.8              32.00      Sequence
DRB4_0101  453  VRSVGVQGDGRTYGH  VRSVGVQGD         0.4094         595.7              32.00      Sequence
DRB4_0101  191  LSRFLHDFAGLGAQW  LSRFLHDFA         0.4084         602.4              32.00      Sequence
DRB4_0101  380  DEVRAVGRELGLPEE  VRAVGRELG         0.4078         606.1              32.00      Sequence
DRB4_0101   36  ARVFSEVIPHTASIE  FSEVIPHTA         0.4059         618.9              32.00      Sequence
DRB4_0101   80  ALLDLGVPVLGICYG  LDLGVPVLG         0.4049         625.5              32.00      Sequence
DRB4_0101   56  QPVALVLSGGPASVY  QPVALVLSG         0.4027         640.8              32.00      Sequence
DRB4_0101  400  PFPGPGLGIRIVGEV  LGIRIVGEV         0.4024         642.8              32.00      Sequence
DRB4_0101  482  ADWTRVPYEVLERIS  VPYEVLERI         0.4022         644.3              32.00      Sequence
DRB4_0101  245  QRAIGDRLTCVFVDH  IGDRLTCVF         0.4015         649.0              50.00      Sequence
DRB4_0101  240  AAALVQRAIGDRLTC  AALVQRAIG         0.3979         675.0              50.00      Sequence
DRB4_0101  172  LAGVQYHPEVMHTPH  HPEVMHTPH         0.3973         679.1              50.00      Sequence
DRB4_0101  449  LLADVRSVGVQGDGR  VRSVGVQGD         0.3956         691.8              50.00      Sequence
DRB4_0101  420  DTLRHADSIVREELT  DTLRHADSI         0.3950         696.2              50.00      Sequence
DRB4_0101   34  REARVFSEVIPHTAS  FSEVIPHTA         0.3938         705.4              50.00      Sequence
DRB4_0101  448  VLLADVRSVGVQGDG  VRSVGVQGD         0.3887         745.4              50.00      Sequence
DRB4_0101  126  LHSDLPEVQPVWMSH  LPEVQPVWM         0.3878         752.5              50.00      Sequence
DRB4_0101   33  VREARVFSEVIPHTA  FSEVIPHTA         0.3876         754.1              50.00      Sequence
DRB4_0101  379  KDEVRAVGRELGLPE  VRAVGRELG         0.3865         763.4              50.00      Sequence
DRB4_0101   27  QLIARRVREARVFSE  RRVREARVF         0.3864         764.6              50.00      Sequence
DRB4_0101   28  LIARRVREARVFSEV  RRVREARVF         0.3851         775.3              50.00      Sequence
DRB4_0101  374  LRLLFKDEVRAVGRE  LRLLFKDEV         0.3846         779.4              50.00      Sequence
DRB4_0101   93  YGFQAMAQALGGIVA  YGFQAMAQA         0.3840         784.2              50.00      Sequence
DRB4_0101  125  KLHSDLPEVQPVWMS  LPEVQPVWM         0.3823         798.8              50.00      Sequence
DRB4_0101  507  NRVVLDITSKPPATI  VLDITSKPP         0.3822         800.2              50.00      Sequence
DRB4_0101  100  QALGGIVAHTGTREY  GGIVAHTGT         0.3817         804.2              50.00      Sequence
DRB4_0101  244  VQRAIGDRLTCVFVD  VQRAIGDRL         0.3813         807.4              50.00      Sequence
DRB4_0101  409  RIVGEVTAKRLDTLR  VGEVTAKRL         0.3812         808.6              50.00      Sequence
DRB4_0101   29  IARRVREARVFSEVI  RRVREARVF         0.3805         814.9              50.00      Sequence
DRB4_0101  490  EVLERISTRITNEVA  LERISTRIT         0.3793         825.4              50.00      Sequence
DRB4_0101  491  VLERISTRITNEVAE  LERISTRIT         0.3791         827.6              50.00      Sequence
DRB4_0101  237  SAVAAALVQRAIGDR  VAAALVQRA         0.3787         830.9              50.00      Sequence
DRB4_0101  481  TADWTRVPYEVLERI  VPYEVLERI         0.3775         841.4              50.00      Sequence
DRB4_0101  499  ITNEVAEVNRVVLDI  EVNRVVLDI         0.3773         843.0              50.00      Sequence
DRB4_0101  359  VGGLPDDLKFTLVEP  VGGLPDDLK         0.3767         848.7              50.00      Sequence
DRB4_0101   24  QYAQLIARRVREARV  ARRVREARV         0.3763         852.5              50.00      Sequence
DRB4_0101  181  VMHTPHGQQVLSRFL  MHTPHGQQV         0.3759         856.5              50.00      Sequence
DRB4_0101  447  VVLLADVRSVGVQGD  VRSVGVQGD         0.3757         857.7              50.00      Sequence
DRB4_0101   18  VVDFGAQYAQLIARR  FGAQYAQLI         0.3722         891.4              50.00      Sequence
DRB4_0101   37  RVFSEVIPHTASIEE  FSEVIPHTA         0.3718         895.6              50.00      Sequence
DRB4_0101  378  FKDEVRAVGRELGLP  VRAVGRELG         0.3717         896.2              50.00      Sequence
DRB4_0101   99  AQALGGIVAHTGTRE  LGGIVAHTG         0.3709         903.6              50.00      Sequence
DRB4_0101  508  RVVLDITSKPPATIE  VLDITSKPP         0.3707         905.6              50.00      Sequence
DRB4_0101  489  YEVLERISTRITNEV  LERISTRIT         0.3702         910.7              50.00      Sequence
DRB4_0101  488  PYEVLERISTRITNE  LERISTRIT         0.3694         919.0              50.00      Sequence
DRB4_0101  382  VRAVGRELGLPEEIV  VRAVGRELG         0.3687         925.6              50.00      Sequence
DRB4_0101  266  ERAQVQRDFVAATGA  ERAQVQRDF         0.3667         946.2              50.00      Sequence
DRB4_0101  328  TAEFLVQGTLYPDVV  EFLVQGTLY         0.3655         957.8              50.00      Sequence
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DRB4_0101   98  MAQALGGIVAHTGTR  LGGIVAHTG         0.3653        959.9                 50.00      Sequence
DRB4_0101  130  LPEVQPVWMSHGDAV  LPEVQPVWM         0.3651        962.2                 50.00      Sequence
DRB4_0101  377  LFKDEVRAVGRELGL  VRAVGRELG         0.3647        967.0                 50.00      Sequence
DRB4_0101  124  GKLHSDLPEVQPVWM  LPEVQPVWM         0.3640        973.6                 50.00      Sequence
DRB4_0101  128  SDLPEVQPVWMSHGD  LPEVQPVWM         0.3632        982.1                 50.00      Sequence
DRB4_0101   30  ARRVREARVFSEVIP  ARRVREARV         0.3628        986.4                 50.00      Sequence
DRB4_0101  241  AALVQRAIGDRLTCV  AALVQRAIG         0.3626        989.1                 50.00      Sequence
DRB4_0101  236  DSAVAAALVQRAIGD  VAAALVQRA         0.3623        992.0                 50.00      Sequence
DRB4_0101   72  DGAPKLDPALLDLGV  APKLDPALL         0.3603       1013.4                 50.00      Sequence
DRB4_0101  208  ANIANALIEQVRTQI  LIEQVRTQI         0.3603       1014.2                 50.00      Sequence
DRB4_0101   73  GAPKLDPALLDLGVP  APKLDPALL         0.3572       1048.7                 50.00      Sequence
DRB4_0101  129  DLPEVQPVWMSHGDA  LPEVQPVWM         0.3530       1096.9                 50.00      Sequence
DRB4_0101  251  RLTCVFVDHGLLRAG  CVFVDHGLL         0.3530       1096.9                 50.00      Sequence
DRB4_0101   71  ADGAPKLDPALLDLG  APKLDPALL         0.3527       1100.1                 50.00      Sequence
DRB4_0101   74  APKLDPALLDLGVPV  APKLDPALL         0.3525       1102.6                 50.00      Sequence
DRB4_0101  261  LLRAGERAQVQRDFV  ERAQVQRDF         0.3466       1176.1                 50.00      Sequence
DRB4_0101  329  AEFLVQGTLYPDVVE  AEFLVQGTL         0.3453       1193.0                 50.00      Sequence
DRB4_0101   31  RRVREARVFSEVIPH  RRVREARVF         0.3444       1203.4                 50.00      Sequence
DRB4_0101  327  KTAEFLVQGTLYPDV  AEFLVQGTL         0.3427       1226.2                 50.00      Sequence
DRB4_0101  265  GERAQVQRDFVAATG  ERAQVQRDF         0.3425       1228.7                 50.00      Sequence
DRB4_0101   76  KLDPALLDLGVPVLG  LDLGVPVLG         0.3420       1235.8                 50.00      Sequence
DRB4_0101   79  PALLDLGVPVLGICY  LDLGVPVLG         0.3415       1241.9                 50.00      Sequence
DRB4_0101  101  ALGGIVAHTGTREYG  GGIVAHTGT         0.3415       1241.9                 50.00      Sequence
DRB4_0101  122  LGGKLHSDLPEVQPV  LGGKLHSDL         0.3409       1250.1                 50.00      Sequence
DRB4_0101  311  QFIRAFEGAVRDVLD  QFIRAFEGA         0.3403       1258.4                 50.00      Sequence
DRB4_0101   77  LDPALLDLGVPVLGI  LDLGVPVLG         0.3391       1274.6                 50.00      Sequence
DRB4_0101  179  PEVMHTPHGQQVLSR  MHTPHGQQV         0.3384       1284.3                 50.00      Sequence
DRB4_0101  376  LLFKDEVRAVGRELG  VRAVGRELG         0.3384       1284.9                 50.00      Sequence
DRB4_0101  278  TGANLVTVDAAETFL  ANLVTVDAA         0.3378       1293.5                 50.00      Sequence
DRB4_0101  127  HSDLPEVQPVWMSHG  LPEVQPVWM         0.3374       1298.8                 50.00      Sequence
DRB4_0101   38  VFSEVIPHTASIEEI  FSEVIPHTA         0.3366       1310.3                 50.00      Sequence
DRB4_0101   97  AMAQALGGIVAHTGT  GGIVAHTGT         0.3362       1315.1                 50.00      Sequence
DRB4_0101  262  LRAGERAQVQRDFVA  ERAQVQRDF         0.3361       1317.7                 50.00      Sequence
DRB4_0101  216  EQVRTQIGDGHAICG  VRTQIGDGH         0.3359       1320.2                 50.00      Sequence
DRB4_0101  427  SIVREELTAAGLDNQ  SIVREELTA         0.3347       1337.7                 50.00      Sequence
DRB4_0101   78  DPALLDLGVPVLGIC  LDLGVPVLG         0.3339       1349.0                 50.00      Sequence
DRB4_0101  446  PVVLLADVRSVGVQG  VVLLADVRS         0.3332       1359.3                 50.00      Sequence
DRB4_0101  460  GDGRTYGHPIVLRPV  GHPIVLRPV         0.3328       1365.5                 50.00      Sequence
DRB4_0101  435  AAGLDNQIWQCPVVL  AAGLDNQIW         0.3317       1382.1                 50.00      Sequence
DRB4_0101  437  GLDNQIWQCPVVLLA  NQIWQCPVV         0.3313       1387.5                 50.00      Sequence
DRB4_0101  193  RFLHDFAGLGAQWTP  RFLHDFAGL         0.3295       1414.8                 50.00      Sequence
DRB4_0101  277  ATGANLVTVDAAETF  ANLVTVDAA         0.3284       1430.8                 50.00      Sequence
DRB4_0101  326  GKTAEFLVQGTLYPD  EFLVQGTLY         0.3283       1432.7                 50.00      Sequence
DRB4_0101  436  AGLDNQIWQCPVVLL  NQIWQCPVV         0.3277       1442.8                 50.00      Sequence
DRB4_0101   39  FSEVIPHTASIEEIR  FSEVIPHTA         0.3266       1459.7                 50.00      Sequence
DRB4_0101  235  VDSAVAAALVQRAIG  VAAALVQRA         0.3250       1485.9                 50.00      Sequence
DRB4_0101  263  RAGERAQVQRDFVAA  ERAQVQRDF         0.3246       1490.9                 50.00      Sequence
DRB4_0101  279  GANLVTVDAAETFLE  ANLVTVDAA         0.3246       1492.4                 50.00      Sequence
DRB4_0101  264  AGERAQVQRDFVAAT  ERAQVQRDF         0.3243       1496.8                 50.00      Sequence
DRB4_0101  242  ALVQRAIGDRLTCVF  IGDRLTCVF         0.3236       1508.4                 50.00      Sequence
DRB4_0101  121  VLGGKLHSDLPEVQP  LGGKLHSDL         0.3233       1513.4                 50.00      Sequence
DRB4_0101    7  DVPETPARPVLVVDF  ARPVLVVDF         0.3223       1529.0                 50.00      Sequence
DRB4_0101   58  VALVLSGGPASVYAD  VALVLSGGP         0.3216       1541.6                 50.00      Sequence
DRB4_0101   75  PKLDPALLDLGVPVL  LLDLGVPVL         0.3210       1550.9                 50.00      Sequence
DRB4_0101   57  PVALVLSGGPASVYA  VALVLSGGP         0.3207       1556.8                 50.00      Sequence
DRB4_0101   44  PHTASIEEIRARQPV  EEIRARQPV         0.3203       1562.1                 50.00      Sequence
DRB4_0101  509  VVLDITSKPPATIEW  VLDITSKPP         0.3202       1565.0                 50.00      Sequence
DRB4_0101  102  LGGIVAHTGTREYGR  GGIVAHTGT         0.3197       1573.5                 50.00      Sequence
DRB4_0101  492  LERISTRITNEVAEV  LERISTRIT         0.3195       1576.6                 50.00      Sequence
DRB4_0101  318  GAVRDVLDGKTAEFL  VRDVLDGKT         0.3187       1590.5                 50.00      Sequence
DRB4_0101  325  DGKTAEFLVQGTLYP  EFLVQGTLY         0.3166       1626.2                 50.00      Sequence
DRB4_0101  180  EVMHTPHGQQVLSRF  MHTPHGQQV         0.3164       1630.2                 50.00      Sequence
DRB4_0101   21  FGAQYAQLIARRVRE  FGAQYAQLI         0.3154       1647.8                 50.00      Sequence
DRB4_0101   19  VDFGAQYAQLIARRV  VDFGAQYAQ         0.3145       1664.2                 50.00      Sequence
DRB4_0101   94  GFQAMAQALGGIVAH  GFQAMAQAL         0.3137       1678.5                 50.00      Sequence
DRB4_0101   20  DFGAQYAQLIARRVR  FGAQYAQLI         0.3137       1679.1                 50.00      Sequence
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DRB4_0101	510	VLDITSKPPATIEWE	LDITSKPPA	0.3134	1683.3	50.00	Sequence
DRB4_0101	276	AATGANLVTVDAAET	ANLVTVDAA	0.3126	1698.2	50.00	Sequence
DRB4_0101	32	RVREARVFSEVIPHT	ARVFSEVIP	0.3126	1699.1	50.00	Sequence
DRB4_0101	123	GGKLHSDLPEVQPVW	LHSDLPEVQ	0.3114	1720.2	50.00	Sequence
DRB4_0101	275	VAATGANLVTVDAAE	ANLVTVDAA	0.3092	1762.7	50.00	Sequence
DRB4_0101	194	FLHDFAGLGAQWTPA	LHDFAGLGA	0.3092	1763.1	50.00	Sequence
DRB4_0101	357	HNVGGLPDDLKFTLV	VGGLPDDLK	0.3084	1777.5	50.00	Sequence
DRB4_0101	386	GRELGLPEEIVARQP	RELGLPEEI	0.3075	1795.6	50.00	Sequence
DRB4_0101	195	LHDFAGLGAQWTPAN	AGLGAQWTP	0.3069	1806.1	50.00	Sequence
DRB4_0101	192	SRFLHDFAGLGAQWT	LHDFAGLGA	0.3065	1813.4	50.00	Sequence
DRB4_0101	163	AAFEAFDRRLAGVQY	DRRLAGVQY	0.3061	1821.5	50.00	Sequence
DRB4_0101	23	AQYAQLIARRVREAR	AQLIARRVR	0.3045	1854.0	50.00	Sequence
DRB4_0101	267	RAQVQRDFVAATGAN	RAQVQRDFV	0.3028	1888.7	50.00	Sequence
DRB4_0101	280	ANLVTVDAAETFLEA	ANLVTVDAA	0.3027	1890.4	50.00	Sequence
DRB4_0101	243	LVQRAIGDRLTCVFV	RAIGDRLTC	0.3012	1922.0	50.00	Sequence
DRB4_0101	253	TCVFVDHGLLRAGER	CVFVDHGLL	0.3006	1934.6	50.00	Sequence
DRB4_0101	438	LDNQIWQCPVVLLAD	NQIWQCPVV	0.2988	1972.5	50.00	Sequence
DRB4_0101	199	AGLGAQWTPANIANA	AGLGAQWTP	0.2987	1975.2	50.00	Sequence
DRB4_0101	252	LTCVFVDHGLLRAGE	CVFVDHGLL	0.2979	1992.4	50.00	Sequence
DRB4_0101	234	GVDSAVAAALVQRAI	VAAALVQRA	0.2949	2056.0	50.00	Sequence
DRB4_0101	217	QVRTQIGDGHAICGL	VRTQIGDGH	0.2947	2060.6	50.00	Sequence
DRB4_0101	330	EFLVQGTLYPDVVES	EFLVQGTLY	0.2945	2066.5	50.00	Sequence
DRB4_0101	431	EELTAAGLDNQIWQC	GLDNQIWQC	0.2945	2066.8	50.00	Sequence
DRB4_0101	356	HHNVGGLPDDLKFTL	HNVGGLPDD	0.2934	2089.7	50.00	Sequence
DRB4_0101	103	GGIVAHTGTREYGRT	GGIVAHTGT	0.2933	2092.4	50.00	Sequence
DRB4_0101	324	LDGKTAEFLVQGTLY	AEFLVQGTL	0.2927	2106.3	50.00	Sequence
DRB4_0101	312	FIRAFEGAVRDVLDG	IRAFEGAVR	0.2924	2113.7	50.00	Sequence
DRB4_0101	260	GLLRAGERAQVQRDF	ERAQVQRDF	0.2918	2126.6	50.00	Sequence
DRB4_0101	96	QAMAQALGGIVAHTG	LGGIVAHTG	0.2918	2126.8	50.00	Sequence
DRB4_0101	198	FAGLGAQWTPANIAN	AGLGAQWTP	0.2918	2127.0	50.00	Sequence
DRB4_0101	131	PEVQPVWMSHGDAVT	EVQPVWMSH	0.2915	2134.7	50.00	Sequence
DRB4_0101	274	FVAATGANLVTVDAA	ANLVTVDAA	0.2875	2228.2	50.00	Sequence
DRB4_0101	434	TAAGLDNQIWQCPVV	NQIWQCPVV	0.2875	2228.4	50.00	Sequence
DRB4_0101	317	EGAVRDVLDGKTAEF	VRDVLDGKT	0.2873	2233.4	50.00	Sequence
DRB4_0101	254	CVFVDHGLLRAGERA	CVFVDHGLL	0.2861	2262.5	50.00	Sequence
DRB4_0101	70	YADGAPKLDPALLDL	APKLDPALL	0.2858	2270.6	50.00	Sequence
DRB4_0101	433	LTAAGLDNQIWQCPV	GLDNQIWQC	0.2830	2338.8	50.00	Sequence
DRB4_0101	132	EVQPVWMSHGDAVTA	VQPVWMSHG	0.2815	2378.8	50.00	Sequence
DRB4_0101	197	DFAGLGAQWTPANIA	AGLGAQWTP	0.2809	2392.3	50.00	Sequence
DRB4_0101	358	NVGGLPDDLKFTLVE	LPDDLKFTL	0.2799	2418.8	50.00	Sequence
DRB4_0101	207	PANIANALIEQVRTQ	IANALIEQV	0.2786	2454.3	50.00	Sequence
DRB4_0101	394	EIVARQPFPGPGLGI	EIVARQPFP	0.2778	2474.8	50.00	Sequence
DRB4_0101	399	QPFPGPGLGIRIVGE	GPGLGIRIV	0.2766	2507.2	50.00	Sequence
DRB4_0101	95	FQAMAQALGGIVAHT	FQAMAQALG	0.2752	2546.5	50.00	Sequence
DRB4_0101	196	HDFAGLGAQWTPANI	AGLGAQWTP	0.2745	2565.1	50.00	Sequence
DRB4_0101	383	RAVGRELGLPEEIVA	RAVGRELGL	0.2745	2565.5	50.00	Sequence
DRB4_0101	22	GAQYAQLIARRVREA	AQLIARRVR	0.2743	2570.5	50.00	Sequence
DRB4_0101	289	ETFLEALSGVSAPEG	LEALSGVSA	0.2741	2575.8	50.00	Sequence
DRB4_0101	316	FEGAVRDVLDGKTAE	VRDVLDGKT	0.2730	2606.5	50.00	Sequence
DRB4_0101	218	VRTQIGDGHAICGLS	VRTQIGDGH	0.2723	2626.7	50.00	Sequence
DRB4_0101	498	RITNEVAEVNRVVLD	VAEVNRVVL	0.2716	2645.8	50.00	Sequence
DRB4_0101	315	AFEGAVRDVLDGKTA	VRDVLDGKT	0.2716	2647.5	50.00	Sequence
DRB4_0101	454	RSVGVQGDGRTYGHP	RSVGVQGDG	0.2713	2656.7	50.00	Sequence
DRB4_0101	320	VRDVLDGKTAEFLVQ	VRDVLDGKT	0.2691	2720.6	50.00	Sequence
DRB4_0101	290	TFLEALSGVSAPEGK	LEALSGVSA	0.2672	2775.1	50.00	Sequence
DRB4_0101	288	AETFLEALSGVSAPE	TFLEALSGV	0.2661	2807.6	50.00	Sequence
DRB4_0101	323	VLDGKTAEFLVQGTL	AEFLVQGTL	0.2659	2813.9	50.00	Sequence
DRB4_0101	314	RAFEGAVRDVLDGKT	VRDVLDGKT	0.2650	2842.5	50.00	Sequence
DRB4_0101	268	AQVQRDFVAATGANL	RDFVAATGA	0.2647	2851.9	50.00	Sequence
DRB4_0101	146	AAPDGFDVVASSAGA	FDVVASSAG	0.2637	2883.1	50.00	Sequence
DRB4_0101	432	ELTAAGLDNQIWQCP	GLDNQIWQC	0.2615	2952.8	50.00	Sequence
DRB4_0101	233	GGVDSAVAAALVQRA	VAAALVQRA	0.2597	3010.4	50.00	Sequence
DRB4_0101	319	AVRDVLDGKTAEFLV	VRDVLDGKT	0.2591	3031.0	50.00	Sequence
DRB4_0101	147	APDGFDVVASSAGAP	FDVVASSAG	0.2578	3073.4	50.00	Sequence
DRB4_0101	162	VAAFEAFDRRLAGVQ	FEAFDRRLA	0.2565	3117.3	50.00	Sequence
DRB4_0101	354	KSHHNVGGLPDDLKF	VGGLPDDLK	0.2558	3141.6	50.00	Sequence

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DRB4_0101  298  VSAPEGKRKIIGRQF  KRKIIGRQF        0.2525        3254.9                 50.00     Sequence
DRB4_0101  161  PVAAFEAFDRRLAGV  FEAFDRRLA        0.2521        3268.7                 50.00     Sequence
DRB4_0101  287  AAETFLEALSGVSAP  LEALSGVSA        0.2518        3279.8                 50.00     Sequence
DRB4_0101  148  PDGFDVVASSAGAPV  FDVVASSAG        0.2509        3311.6                 50.00     Sequence
DRB4_0101  160  APVAAFEAFDRRLAG  APVAAFEAF        0.2504        3328.4                 50.00     Sequence
DRB4_0101  493  ERISTRITNEVAEVN  ERISTRITN        0.2504        3328.6                 50.00     Sequence
DRB4_0101  149  DGFDVVASSAGAPVA  GFDVVASSA        0.2501        3340.8                 50.00     Sequence
DRB4_0101  159  GAPVAAFEAFDRRLA  APVAAFEAF        0.2499        3348.3                 50.00     Sequence
DRB4_0101  355  SHHNVGGLPDDLKFT  HNVGGLPDD        0.2496        3356.5                 50.00     Sequence
DRB4_0101   40  SEVIPHTASIEEIRA  EVIPHTASI        0.2483        3404.0                 50.00     Sequence
DRB4_0101  349  GTANIKSHHNVGGLP  ANIKSHHNV        0.2477        3426.7                 50.00     Sequence
DRB4_0101  375  RLLFKDEVRAVGREL  LLFKDEVRA        0.2474        3437.7                 50.00     Sequence
DRB4_0101  497  TRITNEVAEVNRVVL  VAEVNRVVL        0.2460        3490.5                 50.00     Sequence
DRB4_0101  428  IVREELTAAGLDNQI  VREELTAAG        0.2460        3492.2                 50.00     Sequence
DRB4_0101  145  TAAPDGFDVVASSAG  FDVVASSAG        0.2452        3522.5                 50.00     Sequence
DRB4_0101  133  VQPVWMSHGDAVTAA  QPVWMSHGD        0.2438        3577.6                 50.00     Sequence
DRB4_0101  331  FLVQGTLYPDVVESG  FLVQGTLYP        0.2435        3586.3                 50.00     Sequence
DRB4_0101  429  VREELTAAGLDNQIW  AAGLDNQIW        0.2428        3614.1                 50.00     Sequence
DRB4_0101  353  IKSHHNVGGLPDDLK  VGGLPDDLK        0.2414        3670.3                 50.00     Sequence
DRB4_0101  385  VGRELGLPEEIVARQ  RELGLPEEI        0.2410        3684.8                 50.00     Sequence
DRB4_0101  286  DAAETFLEALSGVSA  LEALSGVSA        0.2406        3699.8                 50.00     Sequence
DRB4_0101  259  HGLLRAGERAQVQRD  LLRAGERAQ        0.2401        3720.1                 50.00     Sequence
DRB4_0101  258  DHGLLRAGERAQVQR  LLRAGERAQ        0.2400        3725.8                 50.00     Sequence
DRB4_0101  206  TPANIANALIEQVRT  IANALIEQV        0.2400        3726.5                 50.00     Sequence
DRB4_0101  351  ANIKSHHNVGGLPDD  ANIKSHHNV        0.2399        3730.6                 50.00     Sequence
DRB4_0101  430  REELTAAGLDNQIWQ  AAGLDNQIW        0.2398        3735.4                 50.00     Sequence
DRB4_0101  257  VDHGLLRAGERAQVQ  LLRAGERAQ        0.2394        3751.9                 50.00     Sequence
DRB4_0101  348  SGTANIKSHHNVGGL  ANIKSHHNV        0.2382        3801.1                 50.00     Sequence
DRB4_0101  150  GFDVVASSAGAPVAA  GFDVVASSA        0.2373        3837.5                 50.00     Sequence
DRB4_0101  291  FLEALSGVSAPEGKR  LEALSGVSA        0.2355        3913.4                 50.00     Sequence
DRB4_0101  456  VGVQGDGRTYGHPIV  GRTYGHPIV        0.2354        3917.1                 50.00     Sequence
DRB4_0101  459  QGDGRTYGHPIVLRP  RTYGHPIVL        0.2346        3947.9                 50.00     Sequence
DRB4_0101  398  RQPFPGPGLGIRIVG  GPGLGIRIV        0.2341        3972.9                 50.00     Sequence
DRB4_0101  158  AGAPVAAFEAFDRRL  AAFEAFDRR        0.2333        4006.2                 50.00     Sequence
DRB4_0101  205  WTPANIANALIEQVR  IANALIEQV        0.2332        4010.9                 50.00     Sequence
DRB4_0101   41  EVIPHTASIEEIRAR  EVIPHTASI        0.2315        4086.6                 50.00     Sequence
DRB4_0101  350  TANIKSHHNVGGLPD  ANIKSHHNV        0.2313        4093.2                 50.00     Sequence
DRB4_0101  313  IRAFEGAVRDVLDGK  IRAFEGAVR        0.2311        4104.2                 50.00     Sequence
DRB4_0101  347  GSGTANIKSHHNVGG  ANIKSHHNV        0.2308        4113.8                 50.00     Sequence
DRB4_0101  225  GHAICGLSGGVDSAV  GHAICGLSG        0.2307        4119.7                 50.00     Sequence
DRB4_0101  384  AVGRELGLPEEIVAR  RELGLPEEI        0.2305        4127.1                 50.00     Sequence
DRB4_0101  480  MTADWTRVPYEVLER  WTRVPYEVL        0.2305        4128.8                 50.00     Sequence
DRB4_0101  271  QRDFVAATGANLVTV  RDFVAATGA        0.2298        4158.5                 50.00     Sequence
DRB4_0101  112  REYGRTELKVLGGKL  REYGRTELK        0.2278        4250.2                 50.00     Sequence
DRB4_0101  472  RPVSSEDAMTADWTR  RPVSSEDAM        0.2272        4277.1                 50.00     Sequence
DRB4_0101  269  QVQRDFVAATGANLV  RDFVAATGA        0.2264        4315.9                 50.00     Sequence
DRB4_0101  346  GGSGTANIKSHHNVG  ANIKSHHNV        0.2260        4336.3                 50.00     Sequence
DRB4_0101  256  FVDHGLLRAGERAQV  LLRAGERAQ        0.2260        4336.8                 50.00     Sequence
DRB4_0101  204  QWTPANIANALIEQV  IANALIEQV        0.2235        4454.0                 50.00     Sequence
DRB4_0101  457  GVQGDGRTYGHPIVL  RTYGHPIVL        0.2232        4468.7                 50.00     Sequence
DRB4_0101   59  ALVLSGGPASVYADG  ALVLSGGPA        0.2228        4490.0                 50.00     Sequence
DRB4_0101  270  VQRDFVAATGANLVT  RDFVAATGA        0.2227        4492.8                 50.00     Sequence
DRB4_0101  224  DGHAICGLSGGVDSA  GHAICGLSG        0.2210        4576.0                 50.00     Sequence
DRB4_0101  458  VQGDGRTYGHPIVLR  RTYGHPIVL        0.2198        4634.3                 50.00     Sequence
DRB4_0101   43  IPHTASIEEIRARQP  IEEIRARQP        0.2192        4665.5                 50.00     Sequence
DRB4_0101  134  QPVWMSHGDAVTAAP  QPVWMSHGD        0.2190        4675.8                 50.00     Sequence
DRB4_0101  494  RISTRITNEVAEVNR  ISTRITNEV        0.2178        4736.9                 50.00     Sequence
DRB4_0101  223  GDGHAICGLSGGVDS  GHAICGLSG        0.2120        5046.1                 50.00     Sequence
DRB4_0101  255  VFVDHGLLRAGERAQ  GLLRAGERA        0.2108        5111.0                 50.00     Sequence
DRB4_0101  322  DVLDGKTAEFLVQGT  LDGKTAEFL        0.2103        5138.2                 50.00     Sequence
DRB4_0101  345  GGGSGTANIKSHHNV  ANIKSHHNV        0.2098        5166.4                 50.00     Sequence
DRB4_0101  281  NLVTVDAAETFLEAL  NLVTVDAAE        0.2095        5183.6                 50.00     Sequence
DRB4_0101  272  RDFVAATGANLVTVD  RDFVAATGA        0.2094        5185.8                 50.00     Sequence
DRB4_0101  292  LEALSGVSAPEGKRK  LEALSGVSA        0.2080        5266.1                 50.00     Sequence
DRB4_0101  495  ISTRITNEVAEVNRV  ISTRITNEV        0.2072        5313.8                 50.00     Sequence
DRB4_0101  479  AMTADWTRVPYEVLE  WTRVPYEVL        0.2071        5319.0                 50.00     Sequence
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DRB4_0101	157	SAGAPVAAFEAFDRR	APVAAFEAF	0.2069	5332.2	50.00	Sequence
DRB4_0101	478	DAMTADWTRVPYEVL	WTRVPYEVL	0.2058	5392.7	50.00	Sequence
DRB4_0101	69	VYADGAPKLDPALLD	APKLDPALL	0.2028	5569.1	50.00	Sequence
DRB4_0101	60	LVLSGGPASVYADGA	LVLSGGPAS	0.1978	5885.0	50.00	Sequence
DRB4_0101	229	CGLSGGVDSAVAAAL	CGLSGGVDS	0.1976	5896.5	50.00	Sequence
DRB4_0101	111	TREYGRTELKVLGGK	REYGRTELK	0.1967	5955.0	50.00	Sequence
DRB4_0101	221	QIGDGHAICGLSGGV	GHAICGLSG	0.1960	5998.5	50.00	Sequence
DRB4_0101	321	RDVLDGKTAEFLVQG	LDGKTAEFL	0.1943	6111.6	50.00	Sequence
DRB4_0101	200	GLGAQWTPANIANAL	GAQWTPANI	0.1942	6118.8	50.00	Sequence
DRB4_0101	352	NIKSHHNVGGLPDDL	HHNVGGLPD	0.1916	6291.4	50.00	Sequence
DRB4_0101	110	GTREYGRTELKVLGG	REYGRTELK	0.1903	6376.2	50.00	Sequence
DRB4_0101	222	IGDGHAICGLSGGVD	GHAICGLSG	0.1900	6397.2	50.00	Sequence
DRB4_0101	201	LGAQWTPANIANALI	GAQWTPANI	0.1898	6411.1	50.00	Sequence
DRB4_0101	151	FDVVASSAGAPVAAF	FDVVASSAG	0.1897	6422.0	50.00	Sequence
DRB4_0101	226	HAICGLSGGVDSAVA	CGLSGGVDS	0.1851	6746.7	50.00	Sequence
DRB4_0101	220	TQIGDGHAICGLSGG	GHAICGLSG	0.1842	6814.4	50.00	Sequence
DRB4_0101	230	GLSGGVDSAVAAALV	LSGGVDSAV	0.1830	6906.1	50.00	Sequence
DRB4_0101	285	VDAAETFLEALSGVS	TFLEALSGV	0.1819	6987.2	50.00	Sequence
DRB4_0101	109	TGTREYGRTELKVLG	REYGRTELK	0.1807	7075.1	50.00	Sequence
DRB4_0101	455	SVGVQGDGRTYGHPI	VGVQGDGRT	0.1800	7127.5	50.00	Sequence
DRB4_0101	202	GAQWTPANIANALIE	GAQWTPANI	0.1794	7174.3	50.00	Sequence
DRB4_0101	231	LSGGVDSAVAAALVQ	LSGGVDSAV	0.1784	7254.3	50.00	Sequence
DRB4_0101	219	RTQIGDGHAICGLSG	GHAICGLSG	0.1780	7286.2	50.00	Sequence
DRB4_0101	68	SVYADGAPKLDPALL	APKLDPALL	0.1773	7344.1	50.00	Sequence
DRB4_0101	106	VAHTGTREYGRTELK	REYGRTELK	0.1771	7359.9	50.00	Sequence
DRB4_0101	232	SGGVDSAVAAALVQR	DSAVAAALV	0.1770	7370.0	50.00	Sequence
DRB4_0101	228	ICGLSGGVDSAVAAA	CGLSGGVDS	0.1745	7568.6	50.00	Sequence
DRB4_0101	227	AICGLSGGVDSAVAA	CGLSGGVDS	0.1729	7699.0	50.00	Sequence
DRB4_0101	496	STRITNEVAEVNRVV	STRITNEVA	0.1725	7735.9	50.00	Sequence
DRB4_0101	108	HTGTREYGRTELKVL	REYGRTELK	0.1717	7798.8	50.00	Sequence
DRB4_0101	333	VQGTLYPDVVESGGG	VQGTLYPDV	0.1710	7864.1	50.00	Sequence
DRB4_0101	144	VTAAPDGFDVVASSA	DGFDVVASS	0.1706	7891.7	50.00	Sequence
DRB4_0101	332	LVQGTLYPDVVESGG	VQGTLYPDV	0.1706	7898.0	50.00	Sequence
DRB4_0101	107	AHTGTREYGRTELKV	REYGRTELK	0.1697	7968.1	50.00	Sequence
DRB4_0101	293	EALSGVSAPEGKRKI	LSGVSAPEG	0.1687	8057.7	50.00	Sequence
DRB4_0101	473	PVSSEDAMTADWTRV	VSSEDAMTA	0.1666	8246.9	50.00	Sequence
DRB4_0101	203	AQWTPANIANALIEQ	PANIANALI	0.1616	8700.3	50.00	Sequence
DRB4_0101	273	DFVAATGANLVTVDA	VAATGANLV	0.1584	9005.9	50.00	Sequence
DRB4_0101	104	GIVAHTGTREYGRTE	VAHTGTREY	0.1561	9235.1	50.00	Sequence
DRB4_0101	6	IDVPETPARPVLVVD	VPETPARPV	0.1559	9260.0	50.00	Sequence
DRB4_0101	4	ADIDVPETPARPVLV	ADIDVPETP	0.1546	9389.9	50.00	Sequence
DRB4_0101	61	VLSGGPASVYADGAP	LSGGPASVY	0.1543	9417.7	50.00	Sequence
DRB4_0101	397	ARQPFPGPGLGIRIV	GPGLGIRIV	0.1523	9623.7	50.00	Sequence
DRB4_0101	294	ALSGVSAPEGKRKII	LSGVSAPEG	0.1509	9767.7	50.00	Sequence
DRB4_0101	476	SEDAMTADWTRVPYE	TADWTRVPY	0.1508	9785.6	50.00	Sequence
DRB4_0101	477	EDAMTADWTRVPYEV	TADWTRVPY	0.1483	10054.1	50.00	Sequence
DRB4_0101	475	SSEDAMTADWTRVPY	TADWTRVPY	0.1479	10092.5	50.00	Sequence
DRB4_0101	474	VSSEDAMTADWTRVP	VSSEDAMTA	0.1471	10182.0	50.00	Sequence
DRB4_0101	283	VTVDAAETFLEALSG	VTVDAAETF	0.1467	10226.6	50.00	Sequence
DRB4_0101	42	VIPHTASIEEIRARQ	PHTASIEEI	0.1467	10229.8	50.00	Sequence
DRB4_0101	282	LVTVDAAETFLEALS	VTVDAAETF	0.1456	10343.1	50.00	Sequence
DRB4_0101	284	TVDAAETFLEALSGV	ETFLEALSG	0.1454	10371.2	50.00	Sequence
DRB4_0101	334	QGTLYPDVVESGGGS	QGTLYPDVV	0.1430	10637.7	50.00	Sequence
DRB4_0101	143	AVTAAPDGFDVVASS	DGFDVVASS	0.1429	10658.3	50.00	Sequence
DRB4_0101	5	DIDVPETPARPVLVV	VPETPARPV	0.1419	10765.5	50.00	Sequence
DRB4_0101	0	VVQPADIDVPETPAR	ADIDVPETP	0.1407	10915.2	50.00	Sequence
DRB4_0101	3	PADIDVPETPARPVL	ADIDVPETP	0.1363	11446.4	50.00	Sequence
DRB4_0101	62	LSGGPASVYADGAPK	LSGGPASVY	0.1339	11745.3	50.00	Sequence
DRB4_0101	156	SSAGAPVAAFEAFDR	APVAAFEAF	0.1339	11745.8	50.00	Sequence
DRB4_0101	135	PVWMSHGDAVTAAPD	PVWMSHGDA	0.1331	11843.4	50.00	Sequence
DRB4_0101	105	IVAHTGTREYGRTEL	TREYGRTEL	0.1318	12019.2	50.00	Sequence
DRB4_0101	295	LSGVSAPEGKRKIIG	LSGVSAPEG	0.1307	12160.1	50.00	Sequence
DRB4_0101	2	QPADIDVPETPARPV	ADIDVPETP	0.1303	12206.0	50.00	Sequence
DRB4_0101	1	VQPADIDVPETPARP	ADIDVPETP	0.1273	12611.5	50.00	Sequence
DRB4_0101	152	DVVASSAGAPVAAFE	DVVASSAGA	0.1198	13679.4	50.00	Sequence
DRB4_0101	142	DAVTAAPDGFDVVAS	DAVTAAPDG	0.1196	13710.6	50.00	Sequence

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    DRB4_0101  336  TLYPDVVESGGGSGT  YPDVVESGG        0.1186      13858.3                  50.00     Sequence
    DRB4_0101  335  GTLYPDVVESGGGSG  YPDVVESGG        0.1175      14021.3                  50.00     Sequence
    DRB4_0101  155  ASSAGAPVAAFEAFD  APVAAFEAF        0.1145      14481.7                  50.00     Sequence
    DRB4_0101  141  GDAVTAAPDGFDVVA  GDAVTAAPD        0.1145      14488.3                  50.00     Sequence
    DRB4_0101  140  HGDAVTAAPDGFDVV  GDAVTAAPD        0.1117      14930.6                  50.00     Sequence
    DRB4_0101  138  MSHGDAVTAAPDGFD  MSHGDAVTA        0.1088      15415.3                  50.00     Sequence
    DRB4_0101  344  SGGGSGTANIKSHHN  SGTANIKSH        0.1082      15499.6                  50.00     Sequence
    DRB4_0101  296  SGVSAPEGKRKIIGR  SGVSAPEGK        0.1080      15542.9                  50.00     Sequence
    DRB4_0101  337  LYPDVVESGGGSGTA  YPDVVESGG        0.1074      15650.4                  50.00     Sequence
    DRB4_0101  137  WMSHGDAVTAAPDGF  GDAVTAAPD        0.1071      15700.5                  50.00     Sequence
    DRB4_0101  136  VWMSHGDAVTAAPDG  VWMSHGDAV        0.1070      15703.9                  50.00     Sequence
    DRB4_0101  395  IVARQPFPGPGLGIR  IVARQPFPG        0.1066      15784.4                  50.00     Sequence
    DRB4_0101  297  GVSAPEGKRKIIGRQ  EGKRKIIGR        0.1040      16232.3                  50.00     Sequence
    DRB4_0101  154  VASSAGAPVAAFEAF  APVAAFEAF        0.1027      16466.9                  50.00     Sequence
    DRB4_0101   67  ASVYADGAPKLDPAL  ADGAPKLDP        0.0986      17198.9                  50.00     Sequence
    DRB4_0101  139  SHGDAVTAAPDGFDV  GDAVTAAPD        0.0973      17456.7                  50.00     Sequence
    DRB4_0101  338  YPDVVESGGGSGTAN  YPDVVESGG        0.0935      18181.3                  50.00     Sequence
    DRB4_0101  396  VARQPFPGPGLGIRI  RQPFPGPGL        0.0910      18679.6                  50.00     Sequence
    DRB4_0101   65  GPASVYADGAPKLDP  SVYADGAPK        0.0881      19268.2                  50.00     Sequence
    DRB4_0101  343  ESGGGSGTANIKSHH  SGTANIKSH        0.0843      20076.2                  50.00     Sequence
    DRB4_0101   64  GGPASVYADGAPKLD  PASVYADGA        0.0836      20244.4                  50.00     Sequence
    DRB4_0101   63  SGGPASVYADGAPKL  ASVYADGAP        0.0828      20402.1                  50.00     Sequence
    DRB4_0101   66  PASVYADGAPKLDPA  ASVYADGAP        0.0812      20771.8                  50.00     Sequence
    DRB4_0101  153  VVASSAGAPVAAFEA  VASSAGAPV        0.0782      21459.5                  50.00     Sequence
    DRB4_0101  339  PDVVESGGGSGTANI  VESGGGSGT        0.0677      24025.7                  50.00     Sequence
    DRB4_0101  342  VESGGGSGTANIKSH  SGTANIKSH        0.0635      25154.6                  50.00     Sequence
    DRB4_0101  340  DVVESGGGSGTANIK  VESGGGSGT        0.0587      26486.7                  50.00     Sequence
    DRB4_0101  341  VVESGGGSGTANIKS  VESGGGSGT        0.0557      27362.0                  50.00     Sequence
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Allele: DRB4_0101. Number of high binders 8. Number of weak binders 145. Number of peptides 511

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       Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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    DRB5_0101  366  LKFTLVEPLRLLFKD  FTLVEPLRL        0.8011          8.6          SB     0.80     Sequence
    DRB5_0101  365  DLKFTLVEPLRLLFK  FTLVEPLRL        0.7963          9.1          SB     0.80     Sequence
    DRB5_0101  364  DDLKFTLVEPLRLLF  FTLVEPLRL        0.7937          9.3          SB     0.80     Sequence
    DRB5_0101  310  RQFIRAFEGAVRDVL  IRAFEGAVR        0.7882          9.9          SB     0.80     Sequence
    DRB5_0101  367  KFTLVEPLRLLFKDE  FTLVEPLRL        0.7822         10.6          SB     0.80     Sequence
    DRB5_0101  363  PDDLKFTLVEPLRLL  FTLVEPLRL        0.7807         10.7          SB     0.80     Sequence
    DRB5_0101  309  GRQFIRAFEGAVRDV  IRAFEGAVR        0.7800         10.8          SB     0.80     Sequence
    DRB5_0101  311  QFIRAFEGAVRDVLD  IRAFEGAVR        0.7599         13.4          SB     2.00     Sequence
    DRB5_0101  308  IGRQFIRAFEGAVRD  IRAFEGAVR        0.7579         13.7          SB     2.00     Sequence
    DRB5_0101  362  LPDDLKFTLVEPLRL  FTLVEPLRL        0.7494         15.0          SB     2.00     Sequence
    DRB5_0101  312  FIRAFEGAVRDVLDG  IRAFEGAVR        0.7166         21.5          SB     4.00     Sequence
    DRB5_0101   21  FGAQYAQLIARRVRE  YAQLIARRV        0.7153         21.8          SB     4.00     Sequence
    DRB5_0101  408  IRIVGEVTAKRLDTL  IVGEVTAKR        0.7090         23.3          SB     4.00     Sequence
    DRB5_0101  407  GIRIVGEVTAKRLDT  IVGEVTAKR        0.7056         24.2          SB     4.00     Sequence
    DRB5_0101   20  DFGAQYAQLIARRVR  YAQLIARRV        0.7040         24.6          SB     4.00     Sequence
    DRB5_0101   22  GAQYAQLIARRVREA  YAQLIARRV        0.7011         25.4          SB     4.00     Sequence
    DRB5_0101  307  IIGRQFIRAFEGAVR  IRAFEGAVR        0.6936         27.5          SB     4.00     Sequence
    DRB5_0101  406  LGIRIVGEVTAKRLD  IVGEVTAKR        0.6834         30.7          SB     4.00     Sequence
    DRB5_0101  409  RIVGEVTAKRLDTLR  IVGEVTAKR        0.6826         31.0          SB     4.00     Sequence
    DRB5_0101   23  AQYAQLIARRVREAR  YAQLIARRV        0.6788         32.3          SB     4.00     Sequence
    DRB5_0101  287  AAETFLEALSGVSAP  FLEALSGVS        0.6732         34.3          SB     4.00     Sequence
    DRB5_0101  368  FTLVEPLRLLFKDEV  FTLVEPLRL        0.6729         34.5          SB     4.00     Sequence
    DRB5_0101  288  AETFLEALSGVSAPE  FLEALSGVS        0.6719         34.8          SB     4.00     Sequence
    DRB5_0101  417  KRLDTLRHADSIVRE  LRHADSIVR        0.6705         35.3          SB     4.00     Sequence
    DRB5_0101  416  AKRLDTLRHADSIVR  LRHADSIVR        0.6631         38.3          SB     8.00     Sequence
    DRB5_0101  286  DAAETFLEALSGVSA  FLEALSGVS        0.6566         41.1          SB     8.00     Sequence
    DRB5_0101  405  GLGIRIVGEVTAKRL  IVGEVTAKR        0.6548         41.9          SB     8.00     Sequence
    DRB5_0101  289  ETFLEALSGVSAPEG  FLEALSGVS        0.6530         42.7          SB     8.00     Sequence
    DRB5_0101   19  VDFGAQYAQLIARRV  YAQLIARRV        0.6505         43.9          SB     8.00     Sequence
    DRB5_0101  410  IVGEVTAKRLDTLRH  IVGEVTAKR        0.6444         46.9          SB     8.00     Sequence
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DRB5_0101   24  QYAQLIARRVREARV  YAQLIARRV        0.6286          55.6          WB     8.00      Sequence
DRB5_0101  285  VDAAETFLEALSGVS  FLEALSGVS        0.6168          63.2          WB     8.00      Sequence
DRB5_0101  418  RLDTLRHADSIVREE  LRHADSIVR        0.6133          65.6          WB     8.00      Sequence
DRB5_0101  419  LDTLRHADSIVREEL  LRHADSIVR        0.6067          70.5          WB     8.00      Sequence
DRB5_0101  420  DTLRHADSIVREELT  LRHADSIVR        0.5970          78.3          WB    16.00      Sequence
DRB5_0101  313  IRAFEGAVRDVLDGK  IRAFEGAVR        0.5911          83.5          WB    16.00      Sequence
DRB5_0101   25  YAQLIARRVREARVF  YAQLIARRV        0.5902          84.3          WB    16.00      Sequence
DRB5_0101   37  RVFSEVIPHTASIEE  RVFSEVIPH        0.5752          99.1          WB    16.00      Sequence
DRB5_0101  421  TLRHADSIVREELTA  LRHADSIVR        0.5725         102.1          WB    16.00      Sequence
DRB5_0101  290  TFLEALSGVSAPEGK  FLEALSGVS        0.5707         104.1          WB    16.00      Sequence
DRB5_0101   36  ARVFSEVIPHTASIE  RVFSEVIPH        0.5693         105.6          WB    16.00      Sequence
DRB5_0101   28  LIARRVREARVFSEV  RRVREARVF        0.5670         108.3          WB    16.00      Sequence
DRB5_0101   29  IARRVREARVFSEVI  RRVREARVF        0.5658         109.8          WB    16.00      Sequence
DRB5_0101  422  LRHADSIVREELTAA  LRHADSIVR        0.5650         110.7          WB    16.00      Sequence
DRB5_0101  271  QRDFVAATGANLVTV  FVAATGANL        0.5643         111.6          WB    16.00      Sequence
DRB5_0101  404  PGLGIRIVGEVTAKR  IVGEVTAKR        0.5638         112.1          WB    16.00      Sequence
DRB5_0101   27  QLIARRVREARVFSE  RRVREARVF        0.5630         113.1          WB    16.00      Sequence
DRB5_0101   26  AQLIARRVREARVFS  RRVREARVF        0.5626         113.6          WB    16.00      Sequence
DRB5_0101  272  RDFVAATGANLVTVD  FVAATGANL        0.5548         123.6          WB    16.00      Sequence
DRB5_0101   35  EARVFSEVIPHTASI  RVFSEVIPH        0.5536         125.2          WB    16.00      Sequence
DRB5_0101  270  VQRDFVAATGANLVT  FVAATGANL        0.5535         125.4          WB    16.00      Sequence
DRB5_0101  306  KIIGRQFIRAFEGAV  FIRAFEGAV        0.5514         128.2          WB    16.00      Sequence
DRB5_0101   18  VVDFGAQYAQLIARR  AQYAQLIAR        0.5510         128.8          WB    16.00      Sequence
DRB5_0101   92  CYGFQAMAQALGGIV  FQAMAQALG        0.5467         134.9          WB    16.00      Sequence
DRB5_0101   30  ARRVREARVFSEVIP  RRVREARVF        0.5426         141.0          WB    16.00      Sequence
DRB5_0101   91  ICYGFQAMAQALGGI  GFQAMAQAL        0.5418         142.3          WB    16.00      Sequence
DRB5_0101   93  YGFQAMAQALGGIVA  FQAMAQALG        0.5399         145.3          WB    16.00      Sequence
DRB5_0101   89  LGICYGFQAMAQALG  GFQAMAQAL        0.5360         151.4          WB    16.00      Sequence
DRB5_0101   90  GICYGFQAMAQALGG  GFQAMAQAL        0.5326         157.1          WB    16.00      Sequence
DRB5_0101  486  RVPYEVLERISTRIT  VLERISTRI        0.5323         157.7          WB    16.00      Sequence
DRB5_0101  269  QVQRDFVAATGANLV  FVAATGANL        0.5298         161.9          WB    16.00      Sequence
DRB5_0101   34  REARVFSEVIPHTAS  RVFSEVIPH        0.5275         166.0          WB    16.00      Sequence
DRB5_0101   31  RRVREARVFSEVIPH  RRVREARVF        0.5205         179.1          WB    32.00      Sequence
DRB5_0101  255  VFVDHGLLRAGERAQ  HGLLRAGER        0.5199         180.4          WB    32.00      Sequence
DRB5_0101  100  QALGGIVAHTGTREY  GIVAHTGTR        0.5171         185.8          WB    32.00      Sequence
DRB5_0101  485  TRVPYEVLERISTRI  VLERISTRI        0.5167         186.6          WB    32.00      Sequence
DRB5_0101  487  VPYEVLERISTRITN  VLERISTRI        0.5134         193.4          WB    32.00      Sequence
DRB5_0101  256  FVDHGLLRAGERAQV  HGLLRAGER        0.5105         199.7          WB    32.00      Sequence
DRB5_0101  101  ALGGIVAHTGTREYG  GIVAHTGTR        0.5089         203.0          WB    32.00      Sequence
DRB5_0101  273  DFVAATGANLVTVDA  FVAATGANL        0.5041         214.0          WB    32.00      Sequence
DRB5_0101  254  CVFVDHGLLRAGERA  VFVDHGLLR        0.4972         230.4          WB    32.00      Sequence
DRB5_0101   88  VLGICYGFQAMAQAL  GFQAMAQAL        0.4960         233.5          WB    32.00      Sequence
DRB5_0101  488  PYEVLERISTRITNE  VLERISTRI        0.4958         234.1          WB    32.00      Sequence
DRB5_0101  192  SRFLHDFAGLGAQWT  FLHDFAGLG        0.4926         242.2          WB    32.00      Sequence
DRB5_0101  268  AQVQRDFVAATGANL  FVAATGANL        0.4897         250.1          WB    32.00      Sequence
DRB5_0101  370  LVEPLRLLFKDEVRA  VEPLRLLFK        0.4883         253.8          WB    32.00      Sequence
DRB5_0101  102  LGGIVAHTGTREYGR  GIVAHTGTR        0.4876         255.7          WB    32.00      Sequence
DRB5_0101  257  VDHGLLRAGERAQVQ  HGLLRAGER        0.4863         259.2          WB    32.00      Sequence
DRB5_0101   33  VREARVFSEVIPHTA  RVFSEVIPH        0.4857         261.0          WB    32.00      Sequence
DRB5_0101  489  YEVLERISTRITNEV  VLERISTRI        0.4832         268.1          WB    32.00      Sequence
DRB5_0101  191  LSRFLHDFAGLGAQW  FLHDFAGLG        0.4829         268.9          WB    32.00      Sequence
DRB5_0101  193  RFLHDFAGLGAQWTP  FLHDFAGLG        0.4786         281.8          WB    32.00      Sequence
DRB5_0101   17  LVVDFGAQYAQLIAR  FGAQYAQLI        0.4783         282.8          WB    32.00      Sequence
DRB5_0101  103  GGIVAHTGTREYGRT  GIVAHTGTR        0.4782         283.1          WB    32.00      Sequence
DRB5_0101   99  AQALGGIVAHTGTRE  GIVAHTGTR        0.4771         286.6          WB    32.00      Sequence
DRB5_0101  253  TCVFVDHGLLRAGER  VFVDHGLLR        0.4768         287.3          WB    32.00      Sequence
DRB5_0101  371  VEPLRLLFKDEVRAV  LRLLFKDEV        0.4737         297.3          WB    32.00      Sequence
DRB5_0101  258  DHGLLRAGERAQVQR  HGLLRAGER        0.4730         299.4          WB    32.00      Sequence
DRB5_0101  291  FLEALSGVSAPEGKR  FLEALSGVS        0.4689         313.2          WB    32.00      Sequence
DRB5_0101  462  GRTYGHPIVLRPVSS  YGHPIVLRP        0.4657         324.1          WB    32.00      Sequence
DRB5_0101  113  EYGRTELKVLGGKLH  LKVLGGKLH        0.4655         324.7          WB    32.00      Sequence
DRB5_0101  114  YGRTELKVLGGKLHS  LKVLGGKLH        0.4639         330.5          WB    32.00      Sequence
DRB5_0101  190  VLSRFLHDFAGLGAQ  FLHDFAGLG        0.4610         341.1          WB    32.00      Sequence
DRB5_0101  104  GIVAHTGTREYGRTE  GIVAHTGTR        0.4605         342.9          WB    32.00      Sequence
DRB5_0101   32  RVREARVFSEVIPHT  RVREARVFS        0.4601         344.4          WB    32.00      Sequence
DRB5_0101  484  WTRVPYEVLERISTR  RVPYEVLER        0.4601         344.4          WB    32.00      Sequence
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DRB5_0101  238  AVAAALVQRAIGDRL  AVAAALVQR       0.4591       348.0       WB   32.00     Sequence
DRB5_0101  463  RTYGHPIVLRPVSSE  YGHPIVLRP       0.4588       349.2       WB   32.00     Sequence
DRB5_0101  464  TYGHPIVLRPVSSED  PIVLRPVSS       0.4586       349.9       WB   32.00     Sequence
DRB5_0101   94  GFQAMAQALGGIVAH  GFQAMAQAL       0.4579       352.5       WB   32.00     Sequence
DRB5_0101  259  HGLLRAGERAQVQRD  LLRAGERAQ       0.4548       364.8       WB   32.00     Sequence
DRB5_0101  251  RLTCVFVDHGLLRAG  VFVDHGLLR       0.4521       375.6       WB   32.00     Sequence
DRB5_0101  189  QVLSRFLHDFAGLGA  FLHDFAGLG       0.4498       384.9       WB   32.00     Sequence
DRB5_0101  369  TLVEPLRLLFKDEVR  VEPLRLLFK       0.4488       388.9       WB   32.00     Sequence
DRB5_0101  115  GRTELKVLGGKLHSD  LKVLGGKLH       0.4483       391.2       WB   32.00     Sequence
DRB5_0101   47  ASIEEIRARQPVALV  IRARQPVAL       0.4439       410.4       WB   32.00     Sequence
DRB5_0101  250  DRLTCVFVDHGLLRA  VFVDHGLLR       0.4405       425.5       WB   32.00     Sequence
DRB5_0101   98  MAQALGGIVAHTGTR  GIVAHTGTR       0.4392       431.7       WB   32.00     Sequence
DRB5_0101  237  SAVAAALVQRAIGDR  AVAAALVQR       0.4377       438.9       WB   32.00     Sequence
DRB5_0101   46  TASIEEIRARQPVAL  IRARQPVAL       0.4369       442.6       WB   32.00     Sequence
DRB5_0101  252  LTCVFVDHGLLRAGE  VFVDHGLLR       0.4361       446.3       WB   32.00     Sequence
DRB5_0101  372  EPLRLLFKDEVRAVG  LLFKDEVRA       0.4347       453.5       WB   32.00     Sequence
DRB5_0101  304  KRKIIGRQFIRAFEG  IIGRQFIRA       0.4334       459.8       WB   32.00     Sequence
DRB5_0101  465  YGHPIVLRPVSSEDA  PIVLRPVSS       0.4315       469.3       WB   32.00     Sequence
DRB5_0101  508  RVVLDITSKPPATIE  ITSKPPATI       0.4311       471.2       WB   32.00     Sequence
DRB5_0101  507  NRVVLDITSKPPATI  RVVLDITSK       0.4300       477.0       WB   32.00     Sequence
DRB5_0101  116  RTELKVLGGKLHSDL  LKVLGGKLH       0.4291       481.8       WB   32.00     Sequence
DRB5_0101   48  SIEEIRARQPVALVL  IRARQPVAL       0.4278       488.3       WB   32.00     Sequence
DRB5_0101  236  DSAVAAALVQRAIGD  AVAAALVQR       0.4276       489.4       WB   32.00     Sequence
DRB5_0101  305  RKIIGRQFIRAFEGA  KIIGRQFIR       0.4259       498.7       WB   32.00     Sequence
DRB5_0101   38  VFSEVIPHTASIEEI  FSEVIPHTA       0.4253       501.8            32.00     Sequence
DRB5_0101  194  FLHDFAGLGAQWTPA  FLHDFAGLG       0.4247       505.1            32.00     Sequence
DRB5_0101  162  VAAFEAFDRRLAGVQ  VAAFEAFDR       0.4222       518.9            32.00     Sequence
DRB5_0101  483  DWTRVPYEVLERIST  RVPYEVLER       0.4217       521.5            32.00     Sequence
DRB5_0101   49  IEEIRARQPVALVLS  IRARQPVAL       0.4206       527.8            32.00     Sequence
DRB5_0101   87  PVLGICYGFQAMAQA  YGFQAMAQA       0.4199       532.1            32.00     Sequence
DRB5_0101  164  AFEAFDRRLAGVQYH  RRLAGVQYH       0.4194       534.9            32.00     Sequence
DRB5_0101  303  GKRKIIGRQFIRAFE  IIGRQFIRA       0.4185       540.4            32.00     Sequence
DRB5_0101  490  EVLERISTRITNEVA  VLERISTRI       0.4179       543.6            32.00     Sequence
DRB5_0101  117  TELKVLGGKLHSDLP  LKVLGGKLH       0.4179       543.7            32.00     Sequence
DRB5_0101  235  VDSAVAAALVQRAIG  AVAAALVQR       0.4173       546.9            32.00     Sequence
DRB5_0101  184  TPHGQQVLSRFLHDF  GQQVLSRFL       0.4162       553.8            32.00     Sequence
DRB5_0101  461  DGRTYGHPIVLRPVS  YGHPIVLRP       0.4149       561.2            32.00     Sequence
DRB5_0101   50  EEIRARQPVALVLSG  IRARQPVAL       0.4128       574.5            32.00     Sequence
DRB5_0101  185  PHGQQVLSRFLHDFA  QVLSRFLHD       0.4126       575.6            32.00     Sequence
DRB5_0101  373  PLRLLFKDEVRAVGR  LLFKDEVRA       0.4119       579.8            50.00     Sequence
DRB5_0101  239  VAAALVQRAIGDRLT  ALVQRAIGD       0.4117       581.6            50.00     Sequence
DRB5_0101  294  ALSGVSAPEGKRKII  GVSAPEGKR       0.4088       599.9            50.00     Sequence
DRB5_0101  284  TVDAAETFLEALSGV  ETFLEALSG       0.4076       607.9            50.00     Sequence
DRB5_0101  415  TAKRLDTLRHADSIV  AKRLDTLRH       0.4072       610.5            50.00     Sequence
DRB5_0101  167  AFDRRLAGVQYHPEV  RRLAGVQYH       0.4045       628.2            50.00     Sequence
DRB5_0101  161  PVAAFEAFDRRLAGV  VAAFEAFDR       0.4031       638.1            50.00     Sequence
DRB5_0101  118  ELKVLGGKLHSDLPE  LKVLGGKLH       0.4004       656.7            50.00     Sequence
DRB5_0101  165  FEAFDRRLAGVQYHP  RRLAGVQYH       0.4003       657.8            50.00     Sequence
DRB5_0101  445  CPVVLLADVRSVGVQ  PVVLLADVR       0.3998       660.9            50.00     Sequence
DRB5_0101  444  QCPVVLLADVRSVGV  PVVLLADVR       0.3996       662.3            50.00     Sequence
DRB5_0101  411  VGEVTAKRLDTLRHA  VGEVTAKRL       0.3993       664.7            50.00     Sequence
DRB5_0101  295  LSGVSAPEGKRKIIG  GVSAPEGKR       0.3988       668.4            50.00     Sequence
DRB5_0101  302  EGKRKIIGRQFIRAF  IIGRQFIRA       0.3986       670.2            50.00     Sequence
DRB5_0101  188  QQVLSRFLHDFAGLG  FLHDFAGLG       0.3985       670.3            50.00     Sequence
DRB5_0101  293  EALSGVSAPEGKRKI  GVSAPEGKR       0.3984       671.2            50.00     Sequence
DRB5_0101  374  LRLLFKDEVRAVGRE  LLFKDEVRA       0.3983       671.7            50.00     Sequence
DRB5_0101  183  HTPHGQQVLSRFLHD  QVLSRFLHD       0.3983       672.1            50.00     Sequence
DRB5_0101  160  APVAAFEAFDRRLAG  VAAFEAFDR       0.3968       683.2            50.00     Sequence
DRB5_0101  166  EAFDRRLAGVQYHPE  RRLAGVQYH       0.3966       684.8            50.00     Sequence
DRB5_0101   51  EIRARQPVALVLSGG  IRARQPVAL       0.3943       701.9            50.00     Sequence
DRB5_0101   16  VLVVDFGAQYAQLIA  FGAQYAQLI       0.3924       716.2            50.00     Sequence
DRB5_0101  446  PVVLLADVRSVGVQG  PVVLLADVR       0.3917       721.9            50.00     Sequence
DRB5_0101  159  GAPVAAFEAFDRRLA  VAAFEAFDR       0.3889       744.1            50.00     Sequence
DRB5_0101  414  VTAKRLDTLRHADSI  AKRLDTLRH       0.3878       752.9            50.00     Sequence
DRB5_0101  240  AAALVQRAIGDRLTC  ALVQRAIGD       0.3856       771.3            50.00     Sequence
DRB5_0101  112  REYGRTELKVLGGKL  GRTELKVLG       0.3851       775.3            50.00     Sequence
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DRB5_0101  460  GDGRTYGHPIVLRPV  YGHPIVLRP        0.3842        782.6                 50.00     Sequence
DRB5_0101  234  GVDSAVAAALVQRAI  AVAAALVQR        0.3833        790.0                 50.00     Sequence
DRB5_0101  482  ADWTRVPYEVLERIS  RVPYEVLER        0.3818        803.5                 50.00     Sequence
DRB5_0101  506  VNRVVLDITSKPPAT  RVVLDITSK        0.3812        808.5                 50.00     Sequence
DRB5_0101  375  RLLFKDEVRAVGREL  LLFKDEVRA        0.3805        814.6                 50.00     Sequence
DRB5_0101   95  FQAMAQALGGIVAHT  FQAMAQALG        0.3805        814.8                 50.00     Sequence
DRB5_0101  466  GHPIVLRPVSSEDAM  PIVLRPVSS        0.3790        827.9                 50.00     Sequence
DRB5_0101  163  AAFEAFDRRLAGVQY  AFEAFDRRL        0.3775        841.9                 50.00     Sequence
DRB5_0101   86  VPVLGICYGFQAMAQ  CYGFQAMAQ        0.3761        854.7                 50.00     Sequence
DRB5_0101  413  EVTAKRLDTLRHADS  AKRLDTLRH        0.3759        856.1                 50.00     Sequence
DRB5_0101  443  WQCPVVLLADVRSVG  VVLLADVRS        0.3758        857.2                 50.00     Sequence
DRB5_0101  168  FDRRLAGVQYHPEVM  RRLAGVQYH        0.3751        863.7                 50.00     Sequence
DRB5_0101  182  MHTPHGQQVLSRFLH  PHGQQVLSR        0.3742        872.4                 50.00     Sequence
DRB5_0101   85  GVPVLGICYGFQAMA  LGICYGFQA        0.3741        873.4                 50.00     Sequence
DRB5_0101  241  AALVQRAIGDRLTCV  VQRAIGDRL        0.3736        878.1                 50.00     Sequence
DRB5_0101  292  LEALSGVSAPEGKRK  GVSAPEGKR        0.3686        926.3                 50.00     Sequence
DRB5_0101  249  GDRLTCVFVDHGLLR  VFVDHGLLR        0.3684        929.1                 50.00     Sequence
DRB5_0101  301  PEGKRKIIGRQFIRA  KIIGRQFIR        0.3667        946.1                 50.00     Sequence
DRB5_0101  412  GEVTAKRLDTLRHAD  AKRLDTLRH        0.3657        955.8                 50.00     Sequence
DRB5_0101  390  GLPEEIVARQPFPGP  GLPEEIVAR        0.3633        981.4                 50.00     Sequence
DRB5_0101  186  HGQQVLSRFLHDFAG  GQQVLSRFL        0.3617        998.3                 50.00     Sequence
DRB5_0101  505  EVNRVVLDITSKPPA  RVVLDITSK        0.3612       1003.8                 50.00     Sequence
DRB5_0101  467  HPIVLRPVSSEDAMT  PIVLRPVSS        0.3610       1006.5                 50.00     Sequence
DRB5_0101  447  VVLLADVRSVGVQGD  LADVRSVGV        0.3609       1006.9                 50.00     Sequence
DRB5_0101  181  VMHTPHGQQVLSRFL  PHGQQVLSR        0.3608       1008.3                 50.00     Sequence
DRB5_0101   56  QPVALVLSGGPASVY  VALVLSGGP        0.3582       1036.8                 50.00     Sequence
DRB5_0101  327  KTAEFLVQGTLYPDV  FLVQGTLYP        0.3575       1044.5                 50.00     Sequence
DRB5_0101  296  SGVSAPEGKRKIIGR  GVSAPEGKR        0.3572       1048.8                 50.00     Sequence
DRB5_0101  328  TAEFLVQGTLYPDVV  FLVQGTLYP        0.3570       1050.7                 50.00     Sequence
DRB5_0101  233  GGVDSAVAAALVQRA  AVAAALVQR        0.3562       1059.9                 50.00     Sequence
DRB5_0101  150  GFDVVASSAGAPVAA  FDVVASSAG        0.3561       1061.2                 50.00     Sequence
DRB5_0101  149  DGFDVVASSAGAPVA  FDVVASSAG        0.3551       1072.9                 50.00     Sequence
DRB5_0101  481  TADWTRVPYEVLERI  RVPYEVLER        0.3528       1098.9                 50.00     Sequence
DRB5_0101  491  VLERISTRITNEVAE  VLERISTRI        0.3528       1099.0                 50.00     Sequence
DRB5_0101   15  PVLVVDFGAQYAQLI  FGAQYAQLI        0.3525       1102.9                 50.00     Sequence
DRB5_0101  209  NIANALIEQVRTQIG  NALIEQVRT        0.3523       1105.0                 50.00     Sequence
DRB5_0101  326  GKTAEFLVQGTLYPD  FLVQGTLYP        0.3516       1114.2                 50.00     Sequence
DRB5_0101  158  AGAPVAAFEAFDRRL  VAAFEAFDR        0.3514       1116.0                 50.00     Sequence
DRB5_0101   45  HTASIEEIRARQPVA  ASIEEIRAR        0.3514       1116.3                 50.00     Sequence
DRB5_0101  361  GLPDDLKFTLVEPLR  LKFTLVEPL        0.3510       1121.4                 50.00     Sequence
DRB5_0101  468  PIVLRPVSSEDAMTA  PIVLRPVSS        0.3505       1127.7                 50.00     Sequence
DRB5_0101   58  VALVLSGGPASVYAD  VALVLSGGP        0.3501       1131.5                 50.00     Sequence
DRB5_0101  314  RAFEGAVRDVLDGKT  RAFEGAVRD        0.3500       1133.3                 50.00     Sequence
DRB5_0101  389  LGLPEEIVARQPFPG  GLPEEIVAR        0.3488       1148.3                 50.00     Sequence
DRB5_0101  509  VVLDITSKPPATIEW  ITSKPPATI        0.3486       1150.2                 50.00     Sequence
DRB5_0101  187  GQQVLSRFLHDFAGL  GQQVLSRFL        0.3469       1171.9                 50.00     Sequence
DRB5_0101   57  PVALVLSGGPASVYA  VALVLSGGP        0.3466       1176.0                 50.00     Sequence
DRB5_0101   84  LGVPVLGICYGFQAM  LGICYGFQA        0.3452       1194.0                 50.00     Sequence
DRB5_0101  210  IANALIEQVRTQIGD  NALIEQVRT        0.3449       1198.0                 50.00     Sequence
DRB5_0101  448  VLLADVRSVGVQGDG  LADVRSVGV        0.3441       1208.0                 50.00     Sequence
DRB5_0101  442  IWQCPVVLLADVRSV  VVLLADVRS        0.3433       1218.1                 50.00     Sequence
DRB5_0101  459  QGDGRTYGHPIVLRP  YGHPIVLRP        0.3431       1221.5                 50.00     Sequence
DRB5_0101  376  LLFKDEVRAVGRELG  LLFKDEVRA        0.3429       1224.0                 50.00     Sequence
DRB5_0101  148  PDGFDVVASSAGAPV  FDVVASSAG        0.3428       1224.8                 50.00     Sequence
DRB5_0101   55  RQPVALVLSGGPASV  VALVLSGGP        0.3390       1277.0                 50.00     Sequence
DRB5_0101  260  GLLRAGERAQVQRDF  LLRAGERAQ        0.3389       1277.2                 50.00     Sequence
DRB5_0101   39  FSEVIPHTASIEEIR  FSEVIPHTA        0.3379       1292.2                 50.00     Sequence
DRB5_0101  329  AEFLVQGTLYPDVVE  FLVQGTLYP        0.3379       1292.3                 50.00     Sequence
DRB5_0101  274  FVAATGANLVTVDAA  FVAATGANL        0.3366       1310.5                 50.00     Sequence
DRB5_0101  449  LLADVRSVGVQGDGR  LADVRSVGV        0.3364       1312.3                 50.00     Sequence
DRB5_0101  111  TREYGRTELKVLGGK  GRTELKVLG        0.3332       1359.0                 50.00     Sequence
DRB5_0101  297  GVSAPEGKRKIIGRQ  GVSAPEGKR        0.3332       1359.5                 50.00     Sequence
DRB5_0101   43  IPHTASIEEIRARQP  ASIEEIRAR        0.3329       1363.1                 50.00     Sequence
DRB5_0101  169  DRRLAGVQYHPEVMH  RRLAGVQYH        0.3313       1387.1                 50.00     Sequence
DRB5_0101  208  ANIANALIEQVRTQI  ALIEQVRTQ        0.3311       1390.5                 50.00     Sequence
DRB5_0101  441  QIWQCPVVLLADVRS  PVVLLADVR        0.3307       1397.1                 50.00     Sequence
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DRB5_0101  325  DGKTAEFLVQGTLYP  FLVQGTLYP        0.3292        1419.8                 50.00      Sequence
DRB5_0101  119  LKVLGGKLHSDLPEV  LKVLGGKLH        0.3290        1422.6                 50.00      Sequence
DRB5_0101  170  RRLAGVQYHPEVMHT  RRLAGVQYH        0.3279        1438.7                 50.00      Sequence
DRB5_0101  232  SGGVDSAVAAALVQR  AVAAALVQR        0.3260        1469.9                 50.00      Sequence
DRB5_0101   44  PHTASIEEIRARQPV  ASIEEIRAR        0.3254        1478.7                 50.00      Sequence
DRB5_0101  211  ANALIEQVRTQIGDG  LIEQVRTQI        0.3242        1498.2                 50.00      Sequence
DRB5_0101   52  IRARQPVALVLSGGP  IRARQPVAL        0.3240        1501.3                 50.00      Sequence
DRB5_0101  450  LADVRSVGVQGDGRT  LADVRSVGV        0.3226        1524.0                 50.00      Sequence
DRB5_0101   42  VIPHTASIEEIRARQ  IPHTASIEE        0.3208        1554.1                 50.00      Sequence
DRB5_0101  242  ALVQRAIGDRLTCVF  VQRAIGDRL        0.3207        1556.6                 50.00      Sequence
DRB5_0101  180  EVMHTPHGQQVLSRF  PHGQQVLSR        0.3186        1592.2                 50.00      Sequence
DRB5_0101  440  NQIWQCPVVLLADVR  PVVLLADVR        0.3185        1594.1                 50.00      Sequence
DRB5_0101  330  EFLVQGTLYPDVVES  FLVQGTLYP        0.3163        1631.2                 50.00      Sequence
DRB5_0101  510  VLDITSKPPATIEWE  ITSKPPATI        0.3144        1665.9                 50.00      Sequence
DRB5_0101    4  ADIDVPETPARPVLV  IDVPETPAR        0.3118        1713.3                 50.00      Sequence
DRB5_0101  176  QYHPEVMHTPHGQQV  QYHPEVMHT        0.3110        1727.7                 50.00      Sequence
DRB5_0101  110  GTREYGRTELKVLGG  GRTELKVLG        0.3104        1739.4                 50.00      Sequence
DRB5_0101    5  DIDVPETPARPVLVV  IDVPETPAR        0.3102        1742.9                 50.00      Sequence
DRB5_0101  175  VQYHPEVMHTPHGQQ  YHPEVMHTP        0.3092        1763.0                 50.00      Sequence
DRB5_0101  504  AEVNRVVLDITSKPP  RVVLDITSK        0.3076        1792.1                 50.00      Sequence
DRB5_0101  452  DVRSVGVQGDGRTYG  VRSVGVQGD        0.3068        1809.1                 50.00      Sequence
DRB5_0101   96  QAMAQALGGIVAHTG  QAMAQALGG        0.3048        1847.5                 50.00      Sequence
DRB5_0101  391  LPEEIVARQPFPGPG  IVARQPFPG        0.3041        1862.0                 50.00      Sequence
DRB5_0101   83  DLGVPVLGICYGFQA  GVPVLGICY        0.3028        1889.3                 50.00      Sequence
DRB5_0101   54  ARQPVALVLSGGPAS  VALVLSGGP        0.3025        1893.8                 50.00      Sequence
DRB5_0101  151  FDVVASSAGAPVAAF  FDVVASSAG        0.3016        1913.6                 50.00      Sequence
DRB5_0101  157  SAGAPVAAFEAFDRR  VAAFEAFDR        0.3003        1940.0                 50.00      Sequence
DRB5_0101  403  GPGLGIRIVGEVTAK  IRIVGEVTA        0.2990        1968.6                 50.00      Sequence
DRB5_0101    6  IDVPETPARPVLVVD  IDVPETPAR        0.2988        1972.3                 50.00      Sequence
DRB5_0101  147  APDGFDVVASSAGAP  FDVVASSAG        0.2987        1973.7                 50.00      Sequence
DRB5_0101  320  VRDVLDGKTAEFLVQ  LDGKTAEFL        0.2982        1983.9                 50.00      Sequence
DRB5_0101  392  PEEIVARQPFPGPGL  IVARQPFPG        0.2979        1992.3                 50.00      Sequence
DRB5_0101  379  KDEVRAVGRELGLPE  KDEVRAVGR        0.2975        2000.5                 50.00      Sequence
DRB5_0101  393  EEIVARQPFPGPGLG  IVARQPFPG        0.2974        2002.3                 50.00      Sequence
DRB5_0101  105  IVAHTGTREYGRTEL  VAHTGTREY        0.2971        2008.5                 50.00      Sequence
DRB5_0101    3  PADIDVPETPARPVL  IDVPETPAR        0.2959        2034.8                 50.00      Sequence
DRB5_0101   41  EVIPHTASIEEIRAR  IPHTASIEE        0.2949        2056.7                 50.00      Sequence
DRB5_0101  451  ADVRSVGVQGDGRTY  VRSVGVQGD        0.2941        2074.0                 50.00      Sequence
DRB5_0101  212  NALIEQVRTQIGDGH  NALIEQVRT        0.2927        2105.9                 50.00      Sequence
DRB5_0101  195  LHDFAGLGAQWTPAN  FAGLGAQWT        0.2919        2124.8                 50.00      Sequence
DRB5_0101  174  GVQYHPEVMHTPHGQ  QYHPEVMHT        0.2918        2126.2                 50.00      Sequence
DRB5_0101  243  LVQRAIGDRLTCVFV  VQRAIGDRL        0.2918        2128.1                 50.00      Sequence
DRB5_0101  179  PEVMHTPHGQQVLSR  PHGQQVLSR        0.2886        2202.7                 50.00      Sequence
DRB5_0101  207  PANIANALIEQVRTQ  ALIEQVRTQ        0.2861        2263.0                 50.00      Sequence
DRB5_0101  350  TANIKSHHNVGGLPD  IKSHHNVGG        0.2838        2318.5                 50.00      Sequence
DRB5_0101  349  GTANIKSHHNVGGLP  IKSHHNVGG        0.2826        2350.6                 50.00      Sequence
DRB5_0101  177  YHPEVMHTPHGQQVL  EVMHTPHGQ        0.2807        2398.4                 50.00      Sequence
DRB5_0101  378  FKDEVRAVGRELGLP  KDEVRAVGR        0.2803        2410.0                 50.00      Sequence
DRB5_0101  133  VQPVWMSHGDAVTAA  WMSHGDAVT        0.2802        2410.9                 50.00      Sequence
DRB5_0101  387  RELGLPEEIVARQPF  GLPEEIVAR        0.2801        2414.3                 50.00      Sequence
DRB5_0101  125  KLHSDLPEVQPVWMS  LPEVQPVWM        0.2791        2441.5                 50.00      Sequence
DRB5_0101  109  TGTREYGRTELKVLG  YGRTELKVL        0.2785        2456.9                 50.00      Sequence
DRB5_0101  351  ANIKSHHNVGGLPDD  IKSHHNVGG        0.2783        2462.5                 50.00      Sequence
DRB5_0101  300  APEGKRKIIGRQFIR  KIIGRQFIR        0.2774        2484.9                 50.00      Sequence
DRB5_0101  225  GHAICGLSGGVDSAV  AICGLSGGV        0.2760        2522.7                 50.00      Sequence
DRB5_0101  224  DGHAICGLSGGVDSA  AICGLSGGV        0.2759        2526.0                 50.00      Sequence
DRB5_0101  394  EIVARQPFPGPGLGI  IVARQPFPG        0.2759        2526.1                 50.00      Sequence
DRB5_0101  126  LHSDLPEVQPVWMSH  LPEVQPVWM        0.2754        2540.4                 50.00      Sequence
DRB5_0101  388  ELGLPEEIVARQPFP  GLPEEIVAR        0.2751        2549.4                 50.00      Sequence
DRB5_0101  173  AGVQYHPEVMHTPHG  QYHPEVMHT        0.2744        2567.0                 50.00      Sequence
DRB5_0101   14  RPVLVVDFGAQYAQL  LVVDFGAQY        0.2743        2570.1                 50.00      Sequence
DRB5_0101   97  AMAQALGGIVAHTGT  ALGGIVAHT        0.2732        2601.2                 50.00      Sequence
DRB5_0101  196  HDFAGLGAQWTPANI  FAGLGAQWT        0.2728        2611.5                 50.00      Sequence
DRB5_0101  348  SGTANIKSHHNVGGL  IKSHHNVGG        0.2726        2617.0                 50.00      Sequence
DRB5_0101  331  FLVQGTLYPDVVESG  FLVQGTLYP        0.2725        2622.5                 50.00      Sequence
DRB5_0101  426  DSIVREELTAAGLDN  VREELTAAG        0.2711        2660.4                 50.00      Sequence
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DRB5_0101	283	VTVDAAETFLEALSG	ETFLEALSG	0.2709	2667.3	50.00	Sequence
DRB5_0101	347	GSGTANIKSHHNVGG	GSGTANIKS	0.2698	2698.2	50.00	Sequence
DRB5_0101	380	DEVRAVGRELGLPEE	EVRAVGREL	0.2690	2721.2	50.00	Sequence
DRB5_0101	480	MTADWTRVPYEVLER	RVPYEVLER	0.2689	2724.7	50.00	Sequence
DRB5_0101	469	IVLRPVSSEDAMTAD	VSSEDAMTA	0.2687	2731.6	50.00	Sequence
DRB5_0101	377	LFKDEVRAVGRELGL	KDEVRAVGR	0.2685	2738.4	50.00	Sequence
DRB5_0101	53	RARQPVALVLSGGPA	VALVLSGGP	0.2683	2743.3	50.00	Sequence
DRB5_0101	223	GDGHAICGLSGGVDS	AICGLSGGV	0.2681	2750.5	50.00	Sequence
DRB5_0101	319	AVRDVLDGKTAEFLV	VRDVLDGKT	0.2677	2762.2	50.00	Sequence
DRB5_0101	132	EVQPVWMSHGDAVTA	WMSHGDAVT	0.2676	2764.0	50.00	Sequence
DRB5_0101	453	VRSVGVQGDGRTYGH	VGVQGDGRT	0.2655	2827.0	50.00	Sequence
DRB5_0101	261	LLRAGERAQVQRDFV	LLRAGERAQ	0.2647	2851.9	50.00	Sequence
DRB5_0101	203	AQWTPANIANALIEQ	WTPANIANA	0.2638	2878.7	50.00	Sequence
DRB5_0101	497	TRITNEVAEVNRVVL	NEVAEVNRV	0.2637	2882.7	50.00	Sequence
DRB5_0101	427	SIVREELTAAGLDNQ	IVREELTAA	0.2624	2922.8	50.00	Sequence
DRB5_0101	352	NIKSHHNVGGLPDDL	IKSHHNVGG	0.2619	2938.3	50.00	Sequence
DRB5_0101	172	LAGVQYHPEVMHTPH	QYHPEVMHT	0.2619	2940.9	50.00	Sequence
DRB5_0101	437	GLDNQIWQCPVVLLA	QIWQCPVVL	0.2605	2984.5	50.00	Sequence
DRB5_0101	124	GKLHSDLPEVQPVWM	LPEVQPVWM	0.2604	2986.5	50.00	Sequence
DRB5_0101	503	VAEVNRVVLDITSKP	RVVLDITSK	0.2600	3001.3	50.00	Sequence
DRB5_0101	496	STRITNEVAEVNRVV	ITNEVAEVN	0.2597	3011.7	50.00	Sequence
DRB5_0101	146	AAPDGFDVVASSAGA	FDVVASSAG	0.2593	3022.3	50.00	Sequence
DRB5_0101	127	HSDLPEVQPVWMSHG	LPEVQPVWM	0.2589	3035.9	50.00	Sequence
DRB5_0101	279	GANLVTVDAAETFLE	LVTVDAAET	0.2585	3049.6	50.00	Sequence
DRB5_0101	321	RDVLDGKTAEFLVQG	LDGKTAEFL	0.2582	3060.3	50.00	Sequence
DRB5_0101	438	LDNQIWQCPVVLLAD	QIWQCPVVL	0.2578	3072.3	50.00	Sequence
DRB5_0101	134	QPVWMSHGDAVTAAP	WMSHGDAVT	0.2576	3078.2	50.00	Sequence
DRB5_0101	384	AVGRELGLPEEIVAR	GLPEEIVAR	0.2571	3094.8	50.00	Sequence
DRB5_0101	439	DNQIWQCPVVLLADV	QIWQCPVVL	0.2563	3122.5	50.00	Sequence
DRB5_0101	280	ANLVTVDAAETFLEA	LVTVDAAET	0.2562	3126.9	50.00	Sequence
DRB5_0101	205	WTPANIANALIEQVR	WTPANIANA	0.2555	3150.8	50.00	Sequence
DRB5_0101	385	VGRELGLPEEIVARQ	GLPEEIVAR	0.2555	3151.5	50.00	Sequence
DRB5_0101	495	ISTRITNEVAEVNRV	ITNEVAEVN	0.2547	3179.4	50.00	Sequence
DRB5_0101	381	EVRAVGRELGLPEEI	EVRAVGREL	0.2545	3185.6	50.00	Sequence
DRB5_0101	318	GAVRDVLDGKTAEFL	VRDVLDGKT	0.2538	3209.3	50.00	Sequence
DRB5_0101	2	QPADIDVPETPARPV	IDVPETPAR	0.2530	3236.7	50.00	Sequence
DRB5_0101	204	QWTPANIANALIEQV	WTPANIANA	0.2523	3261.0	50.00	Sequence
DRB5_0101	425	ADSIVREELTAAGLD	IVREELTAA	0.2521	3268.2	50.00	Sequence
DRB5_0101	470	VLRPVSSEDAMTADW	VSSEDAMTA	0.2519	3274.9	50.00	Sequence
DRB5_0101	178	HPEVMHTPHGQQVLS	VMHTPHGQQ	0.2516	3284.6	50.00	Sequence
DRB5_0101	386	GRELGLPEEIVARQP	GLPEEIVAR	0.2513	3295.5	50.00	Sequence
DRB5_0101	202	GAQWTPANIANALIE	WTPANIANA	0.2509	3310.8	50.00	Sequence
DRB5_0101	201	LGAQWTPANIANALI	WTPANIANA	0.2487	3389.6	50.00	Sequence
DRB5_0101	222	IGDGHAICGLSGGVD	ICGLSGGVD	0.2479	3420.5	50.00	Sequence
DRB5_0101	395	IVARQPFPGPGLGIR	IVARQPFPG	0.2476	3430.3	50.00	Sequence
DRB5_0101	128	SDLPEVQPVWMSHGD	LPEVQPVWM	0.2474	3438.2	50.00	Sequence
DRB5_0101	13	ARPVLVVDFGAQYAQ	LVVDFGAQY	0.2462	3483.7	50.00	Sequence
DRB5_0101	200	GLGAQWTPANIANAL	WTPANIANA	0.2455	3511.7	50.00	Sequence
DRB5_0101	281	NLVTVDAAETFLEAL	LVTVDAAET	0.2452	3521.7	50.00	Sequence
DRB5_0101	82	LDLGVPVLGICYGFQ	GVPVLGICY	0.2429	3611.4	50.00	Sequence
DRB5_0101	424	HADSIVREELTAAGL	IVREELTAA	0.2426	3621.6	50.00	Sequence
DRB5_0101	59	ALVLSGGPASVYADG	LVLSGGPAS	0.2426	3621.7	50.00	Sequence
DRB5_0101	197	DFAGLGAQWTPANIA	FAGLGAQWT	0.2423	3635.2	50.00	Sequence
DRB5_0101	498	RITNEVAEVNRVVLD	NEVAEVNRV	0.2421	3643.5	50.00	Sequence
DRB5_0101	171	RLAGVQYHPEVMHTP	QYHPEVMHT	0.2413	3673.5	50.00	Sequence
DRB5_0101	267	RAQVQRDFVAATGAN	DFVAATGAN	0.2412	3677.7	50.00	Sequence
DRB5_0101	478	DAMTADWTRVPYEVL	AMTADWTRV	0.2398	3731.9	50.00	Sequence
DRB5_0101	206	TPANIANALIEQVRT	ANIANALIE	0.2393	3753.8	50.00	Sequence
DRB5_0101	493	ERISTRITNEVAEVN	ERISTRITN	0.2364	3872.7	50.00	Sequence
DRB5_0101	346	GGSGTANIKSHHNVG	GSGTANIKS	0.2359	3893.2	50.00	Sequence
DRB5_0101	40	SEVIPHTASIEEIRA	IPHTASIEE	0.2359	3895.3	50.00	Sequence
DRB5_0101	298	VSAPEGKRKIIGRQF	VSAPEGKRK	0.2357	3903.0	50.00	Sequence
DRB5_0101	476	SEDAMTADWTRVPYE	AMTADWTRV	0.2348	3941.4	50.00	Sequence
DRB5_0101	323	VLDGKTAEFLVQGTL	LDGKTAEFL	0.2345	3954.1	50.00	Sequence
DRB5_0101	156	SSAGAPVAAFEAFDR	VAAFEAFDR	0.2345	3954.9	50.00	Sequence
DRB5_0101	231	LSGGVDSAVAAALVQ	SAVAAALVQ	0.2342	3966.6	50.00	Sequence

DRB5_0101	454	RSVGVQGDGRTYGHP	SVGVQGDGR	0.2336	3992.1	50.00	Sequence
DRB5_0101	135	PVWMSHGDAVTAAPD	WMSHGDAVT	0.2325	4040.3	50.00	Sequence
DRB5_0101	282	LVTVDAAETFLEALS	LVTVDAAET	0.2319	4067.3	50.00	Sequence
DRB5_0101	278	TGANLVTVDAAETFL	LVTVDAAET	0.2317	4077.7	50.00	Sequence
DRB5_0101	322	DVLDGKTAEFLVQGT	LDGKTAEFL	0.2310	4108.0	50.00	Sequence
DRB5_0101	213	ALIEQVRTQIGDGHA	ALIEQVRTQ	0.2302	4143.7	50.00	Sequence
DRB5_0101	428	IVREELTAAGLDNQI	IVREELTAA	0.2301	4147.4	50.00	Sequence
DRB5_0101	477	EDAMTADWTRVPYEV	AMTADWTRV	0.2300	4150.4	50.00	Sequence
DRB5_0101	106	VAHTGTREYGRTELK	VAHTGTREY	0.2297	4166.6	50.00	Sequence
DRB5_0101	129	DLPEVQPVWMSHGDA	LPEVQPVWM	0.2266	4309.2	50.00	Sequence
DRB5_0101	494	RISTRITNEVAEVNR	RITNEVAEV	0.2261	4330.7	50.00	Sequence
DRB5_0101	199	AGLGAQWTPANIANA	WTPANIANA	0.2236	4449.6	50.00	Sequence
DRB5_0101	401	FPGPGLGIRIVGEVT	FPGPGLGIR	0.2233	4464.4	50.00	Sequence
DRB5_0101	131	PEVQPVWMSHGDAVT	WMSHGDAVT	0.2229	4481.2	50.00	Sequence
DRB5_0101	474	VSSEDAMTADWTRVP	AMTADWTRV	0.2219	4531.9	50.00	Sequence
DRB5_0101	226	HAICGLSGGVDSAVA	AICGLSGGV	0.2218	4538.2	50.00	Sequence
DRB5_0101	12	PARPVLVVDFGAQYA	LVVDFGAQY	0.2212	4567.7	50.00	Sequence
DRB5_0101	130	LPEVQPVWMSHGDAV	LPEVQPVWM	0.2211	4569.1	50.00	Sequence
DRB5_0101	423	RHADSIVREELTAAG	IVREELTAA	0.2210	4573.7	50.00	Sequence
DRB5_0101	198	FAGLGAQWTPANIAN	FAGLGAQWT	0.2209	4579.6	50.00	Sequence
DRB5_0101	475	SSEDAMTADWTRVPY	AMTADWTRV	0.2200	4624.3	50.00	Sequence
DRB5_0101	324	LDGKTAEFLVQGTLY	EFLVQGTLY	0.2199	4628.5	50.00	Sequence
DRB5_0101	402	PGPGLGIRIVGEVTA	IRIVGEVTA	0.2199	4628.9	50.00	Sequence
DRB5_0101	492	LERISTRITNEVAEV	ERISTRITN	0.2199	4630.8	50.00	Sequence
DRB5_0101	473	PVSSEDAMTADWTRV	AMTADWTRV	0.2196	4645.9	50.00	Sequence
DRB5_0101	317	EGAVRDVLDGKTAEF	VRDVLDGKT	0.2179	4729.8	50.00	Sequence
DRB5_0101	108	HTGTREYGRTELKVL	YGRTELKVL	0.2161	4825.0	50.00	Sequence
DRB5_0101	382	VRAVGRELGLPEEIV	VGRELGLPE	0.2159	4834.3	50.00	Sequence
DRB5_0101	80	ALLDLGVPVLGICYG	GVPVLGICY	0.2152	4872.8	50.00	Sequence
DRB5_0101	221	QIGDGHAICGLSGGV	GHAICGLSG	0.2152	4874.8	50.00	Sequence
DRB5_0101	244	VQRAIGDRLTCVFVD	VQRAIGDRL	0.2125	5019.3	50.00	Sequence
DRB5_0101	499	ITNEVAEVNRVVLDI	NEVAEVNRV	0.2103	5139.7	50.00	Sequence
DRB5_0101	400	PFPGPGLGIRIVGEV	FPGPGLGIR	0.2101	5149.5	50.00	Sequence
DRB5_0101	81	LLDLGVPVLGICYGF	GVPVLGICY	0.2101	5150.8	50.00	Sequence
DRB5_0101	145	TAAPDGFDVVASSAG	FDVVASSAG	0.2097	5170.6	50.00	Sequence
DRB5_0101	248	IGDRLTCVFVDHGLL	RLTCVFVDH	0.2096	5177.4	50.00	Sequence
DRB5_0101	353	IKSHHNVGGLPDDLK	IKSHHNVGG	0.2082	5256.8	50.00	Sequence
DRB5_0101	136	VWMSHGDAVTAAPDG	WMSHGDAVT	0.2064	5359.9	50.00	Sequence
DRB5_0101	7	DVPETPARPVLVVDF	DVPETPARP	0.2060	5385.3	50.00	Sequence
DRB5_0101	458	VQGDGRTYGHPIVLR	RTYGHPIVL	0.2058	5395.2	50.00	Sequence
DRB5_0101	67	ASVYADGAPKLDPAL	SVYADGAPK	0.2057	5399.2	50.00	Sequence
DRB5_0101	66	PASVYADGAPKLDPA	SVYADGAPK	0.2040	5501.6	50.00	Sequence
DRB5_0101	277	ATGANLVTVDAAETF	LVTVDAAET	0.2027	5580.8	50.00	Sequence
DRB5_0101	472	RPVSSEDAMTADWTR	VSSEDAMTA	0.2020	5622.2	50.00	Sequence
DRB5_0101	479	AMTADWTRVPYEVLE	AMTADWTRV	0.2011	5678.5	50.00	Sequence
DRB5_0101	455	SVGVQGDGRTYGHPI	SVGVQGDGR	0.2009	5688.8	50.00	Sequence
DRB5_0101	60	LVLSGGPASVYADGA	LVLSGGPAS	0.2005	5714.3	50.00	Sequence
DRB5_0101	456	VGVQGDGRTYGHPIV	VGVQGDGRT	0.1995	5772.8	50.00	Sequence
DRB5_0101	120	KVLGGKLHSDLPEVQ	KVLGGKLHS	0.1994	5780.6	50.00	Sequence
DRB5_0101	436	AGLDNQIWQCPVVLL	QIWQCPVVL	0.1972	5917.1	50.00	Sequence
DRB5_0101	79	PALLDLGVPVLGICY	GVPVLGICY	0.1968	5948.4	50.00	Sequence
DRB5_0101	383	RAVGRELGLPEEIVA	VGRELGLPE	0.1965	5967.0	50.00	Sequence
DRB5_0101	65	GPASVYADGAPKLDP	SVYADGAPK	0.1957	6019.2	50.00	Sequence
DRB5_0101	502	EVAEVNRVVLDITSK	RVVLDITSK	0.1952	6051.1	50.00	Sequence
DRB5_0101	345	GGGSGTANIKSHHNV	GSGTANIKS	0.1947	6079.8	50.00	Sequence
DRB5_0101	68	SVYADGAPKLDPALL	SVYADGAPK	0.1946	6090.4	50.00	Sequence
DRB5_0101	471	LRPVSSEDAMTADWT	VSSEDAMTA	0.1930	6198.7	50.00	Sequence
DRB5_0101	399	QPFPGPGLGIRIVGE	FPGPGLGIR	0.1926	6222.4	50.00	Sequence
DRB5_0101	262	LRAGERAQVQRDFVA	GERAQVQRD	0.1918	6274.3	50.00	Sequence
DRB5_0101	1	VQPADIDVPETPARP	IDVPETPAR	0.1898	6411.4	50.00	Sequence
DRB5_0101	299	SAPEGKRKIIGRQFI	GKRKIIGRQ	0.1892	6452.6	50.00	Sequence
DRB5_0101	500	TNEVAEVNRVVLDIT	NEVAEVNRV	0.1891	6465.1	50.00	Sequence
DRB5_0101	398	RQPFPGPGLGIRIVG	FPGPGLGIR	0.1880	6537.2	50.00	Sequence
DRB5_0101	137	WMSHGDAVTAAPDGF	WMSHGDAVT	0.1838	6841.2	50.00	Sequence
DRB5_0101	263	RAGERAQVQRDFVAA	GERAQVQRD	0.1837	6847.6	50.00	Sequence
DRB5_0101	11	TPARPVLVVDFGAQY	LVVDFGAQY	0.1822	6965.6	50.00	Sequence

DRB5_0101	435	AAGLDNQIWQCPVVL	QIWQCPVVL	0.1820	6980.8	50.00	Sequence
DRB5_0101	397	ARQPFPGPGLGIRIV	FPGPGLGIR	0.1819	6982.4	50.00	Sequence
DRB5_0101	247	AIGDRLTCVFVDHGL	RLTCVFVDH	0.1790	7209.0	50.00	Sequence
DRB5_0101	344	SGGGSGTANIKSHHN	GSGTANIKS	0.1784	7255.4	50.00	Sequence
DRB5_0101	501	NEVAEVNRVVLDITS	EVAEVNRVV	0.1780	7284.9	50.00	Sequence
DRB5_0101	276	AATGANLVTVDAAET	LVTVDAAET	0.1744	7577.1	50.00	Sequence
DRB5_0101	429	VREELTAAGLDNQIW	VREELTAAG	0.1735	7648.9	50.00	Sequence
DRB5_0101	64	GGPASVYADGAPKLD	SVYADGAPK	0.1733	7665.6	50.00	Sequence
DRB5_0101	396	VARQPFPGPGLGIRI	FPGPGLGIR	0.1722	7760.9	50.00	Sequence
DRB5_0101	354	KSHHNVGGLPDDLKF	HHNVGGLPD	0.1720	7779.0	50.00	Sequence
DRB5_0101	123	GGKLHSDLPEVQPVW	LHSDLPEVQ	0.1719	7781.3	50.00	Sequence
DRB5_0101	315	AFEGAVRDVLDGKTA	VRDVLDGKT	0.1708	7879.5	50.00	Sequence
DRB5_0101	227	AICGLSGGVDSAVAA	AICGLSGGV	0.1693	8007.8	50.00	Sequence
DRB5_0101	230	GLSGGVDSAVAAALV	VDSAVAAAL	0.1670	8210.2	50.00	Sequence
DRB5_0101	107	AHTGTREYGRTELKV	HTGTREYGR	0.1662	8277.7	50.00	Sequence
DRB5_0101	152	DVVASSAGAPVAAFE	DVVASSAGA	0.1661	8284.7	50.00	Sequence
DRB5_0101	316	FEGAVRDVLDGKTAE	VRDVLDGKT	0.1638	8493.1	50.00	Sequence
DRB5_0101	264	AGERAQVQRDFVAAT	GERAQVQRD	0.1628	8593.0	50.00	Sequence
DRB5_0101	246	RAIGDRLTCVFVDHG	RLTCVFVDH	0.1620	8668.3	50.00	Sequence
DRB5_0101	214	LIEQVRTQIGDGHAI	LIEQVRTQI	0.1609	8770.7	50.00	Sequence
DRB5_0101	220	TQIGDGHAICGLSGG	GHAICGLSG	0.1596	8895.1	50.00	Sequence
DRB5_0101	265	GERAQVQRDFVAATG	GERAQVQRD	0.1594	8907.0	50.00	Sequence
DRB5_0101	457	GVQGDGRTYGHPIVL	RTYGHPIVL	0.1557	9272.1	50.00	Sequence
DRB5_0101	245	QRAIGDRLTCVFVDH	GDRLTCVFV	0.1517	9686.6	50.00	Sequence
DRB5_0101	63	SGGPASVYADGAPKL	SVYADGAPK	0.1459	10308.8	50.00	Sequence
DRB5_0101	138	MSHGDAVTAAPDGFD	AVTAAPDGF	0.1450	10418.6	50.00	Sequence
DRB5_0101	122	LGGKLHSDLPEVQPV	LHSDLPEVQ	0.1448	10432.4	50.00	Sequence
DRB5_0101	355	SHHNVGGLPDDLKFT	HHNVGGLPD	0.1436	10573.9	50.00	Sequence
DRB5_0101	360	GGLPDDLKFTLVEPL	LKFTLVEPL	0.1430	10645.3	50.00	Sequence
DRB5_0101	153	VVASSAGAPVAAFEA	VVASSAGAP	0.1429	10652.7	50.00	Sequence
DRB5_0101	266	ERAQVQRDFVAATGA	RDFVAATGA	0.1410	10877.8	50.00	Sequence
DRB5_0101	140	HGDAVTAAPDGFDVV	AVTAAPDGF	0.1400	10988.2	50.00	Sequence
DRB5_0101	343	ESGGGSGTANIKSHH	GSGTANIKS	0.1400	10992.8	50.00	Sequence
DRB5_0101	219	RTQIGDGHAICGLSG	GHAICGLSG	0.1362	11451.2	50.00	Sequence
DRB5_0101	229	CGLSGGVDSAVAAAL	VDSAVAAAL	0.1339	11741.3	50.00	Sequence
DRB5_0101	139	SHGDAVTAAPDGFDV	AVTAAPDGF	0.1332	11832.1	50.00	Sequence
DRB5_0101	141	GDAVTAAPDGFDVVA	AVTAAPDGF	0.1323	11941.6	50.00	Sequence
DRB5_0101	356	HHNVGGLPDDLKFTL	HHNVGGLPD	0.1308	12147.2	50.00	Sequence
DRB5_0101	121	VLGGKLHSDLPEVQP	LHSDLPEVQ	0.1278	12550.8	50.00	Sequence
DRB5_0101	78	DPALLDLGVPVLGIC	ALLDLGVPV	0.1258	12815.2	50.00	Sequence
DRB5_0101	154	VASSAGAPVAAFEAF	VASSAGAPV	0.1248	12963.8	50.00	Sequence
DRB5_0101	0	VVQPADIDVPETPAR	IDVPETPAR	0.1225	13280.4	50.00	Sequence
DRB5_0101	77	LDPALLDLGVPVLGI	ALLDLGVPV	0.1220	13351.8	50.00	Sequence
DRB5_0101	69	VYADGAPKLDPALLD	VYADGAPKL	0.1217	13397.7	50.00	Sequence
DRB5_0101	8	VPETPARPVLVVDFG	VPETPARPV	0.1216	13419.9	50.00	Sequence
DRB5_0101	228	ICGLSGGVDSAVAAA	ICGLSGGVD	0.1212	13479.0	50.00	Sequence
DRB5_0101	61	VLSGGPASVYADGAP	VLSGGPASV	0.1211	13491.8	50.00	Sequence
DRB5_0101	430	REELTAAGLDNQIWQ	ELTAAGLDN	0.1207	13542.3	50.00	Sequence
DRB5_0101	10	ETPARPVLVVDFGAQ	ETPARPVLV	0.1172	14071.9	50.00	Sequence
DRB5_0101	142	DAVTAAPDGFDVVAS	AVTAAPDGF	0.1167	14139.9	50.00	Sequence
DRB5_0101	155	ASSAGAPVAAFEAFD	GAPVAAFEA	0.1166	14161.5	50.00	Sequence
DRB5_0101	342	VESGGGSGTANIKSH	GSGTANIKS	0.1159	14264.3	50.00	Sequence
DRB5_0101	215	IEQVRTQIGDGHAIC	VRTQIGDGH	0.1147	14455.4	50.00	Sequence
DRB5_0101	217	QVRTQIGDGHAICGL	VRTQIGDGH	0.1146	14476.6	50.00	Sequence
DRB5_0101	332	LVQGTLYPDVVESGG	LVQGTLYPD	0.1137	14614.7	50.00	Sequence
DRB5_0101	336	TLYPDVVESGGGSGT	YPDVVESGG	0.1094	15300.2	50.00	Sequence
DRB5_0101	144	VTAAPDGFDVVASSA	GFDVVASSA	0.1063	15821.0	50.00	Sequence
DRB5_0101	341	VVESGGGSGTANIKS	VVESGGGSG	0.1055	15973.4	50.00	Sequence
DRB5_0101	335	GTLYPDVVESGGGSG	YPDVVESGG	0.1043	16168.9	50.00	Sequence
DRB5_0101	338	YPDVVESGGGSGTAN	DVVESGGGS	0.1041	16217.2	50.00	Sequence
DRB5_0101	432	ELTAAGLDNQIWQCP	ELTAAGLDN	0.1034	16329.7	50.00	Sequence
DRB5_0101	337	LYPDVVESGGGSGTA	DVVESGGGS	0.1034	16336.6	50.00	Sequence
DRB5_0101	216	EQVRTQIGDGHAICG	VRTQIGDGH	0.1020	16584.4	50.00	Sequence
DRB5_0101	431	EELTAAGLDNQIWQC	ELTAAGLDN	0.1015	16674.9	50.00	Sequence
DRB5_0101	62	LSGGPASVYADGAPK	SVYADGAPK	0.0977	17364.8	50.00	Sequence
DRB5_0101	275	VAATGANLVTVDAAE	ATGANLVTV	0.0962	17666.1	50.00	Sequence

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   DRB5_0101   76  KLDPALLDLGVPVLG  ALLDLGVPV        0.0961      17680.1                50.00     Sequence
   DRB5_0101  339  PDVVESGGGSGTANI  DVVESGGGS        0.0940      18083.2                50.00     Sequence
   DRB5_0101  434  TAAGLDNQIWQCPVV  GLDNQIWQC        0.0937      18135.2                50.00     Sequence
   DRB5_0101  143  AVTAAPDGFDVVASS  AVTAAPDGF        0.0930      18276.6                50.00     Sequence
   DRB5_0101  340  DVVESGGGSGTANIK  DVVESGGGS        0.0915      18576.4                50.00     Sequence
   DRB5_0101  218  VRTQIGDGHAICGLS  VRTQIGDGH        0.0910      18673.4                50.00     Sequence
   DRB5_0101  334  QGTLYPDVVESGGGS  YPDVVESGG        0.0908      18714.8                50.00     Sequence
   DRB5_0101    9  PETPARPVLVVDFGA  ETPARPVLV        0.0882      19250.2                50.00     Sequence
   DRB5_0101  333  VQGTLYPDVVESGGG  TLYPDVVES        0.0882      19251.7                50.00     Sequence
   DRB5_0101   75  PKLDPALLDLGVPVL  ALLDLGVPV        0.0842      20105.6                50.00     Sequence
   DRB5_0101  433  LTAAGLDNQIWQCPV  LTAAGLDNQ        0.0826      20460.0                50.00     Sequence
   DRB5_0101   74  APKLDPALLDLGVPV  ALLDLGVPV        0.0714      23095.8                50.00     Sequence
   DRB5_0101  359  VGGLPDDLKFTLVEP  GLPDDLKFT        0.0664      24363.1                50.00     Sequence
   DRB5_0101  357  HNVGGLPDDLKFTLV  HNVGGLPDD        0.0660      24480.4                50.00     Sequence
   DRB5_0101   70  YADGAPKLDPALLDL  YADGAPKLD        0.0617      25658.2                50.00     Sequence
   DRB5_0101  358  NVGGLPDDLKFTLVE  GLPDDLKFT        0.0599      26159.7                50.00     Sequence
   DRB5_0101   73  GAPKLDPALLDLGVP  LDPALLDLG        0.0476      29864.7                50.00     Sequence
   DRB5_0101   72  DGAPKLDPALLDLGV  LDPALLDLG        0.0476      29867.9                50.00     Sequence
   DRB5_0101   71  ADGAPKLDPALLDLG  PKLDPALLD        0.0439      31098.0                50.00     Sequence
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Allele: DRB5_0101. Number of high binders 30. Number of weak binders 90. Number of peptides 511

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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         IAb  153  VVASSAGAPVAAFEA  SSAGAPVAA        0.6889         29.0          SB     0.40     Sequence
         IAb  154  VASSAGAPVAAFEAF  SSAGAPVAA        0.6728         34.5          SB     0.80     Sequence
         IAb  155  ASSAGAPVAAFEAFD  SSAGAPVAA        0.6639         38.0          SB     0.80     Sequence
         IAb  152  DVVASSAGAPVAAFE  SSAGAPVAA        0.6600         39.6          SB     0.80     Sequence
         IAb  151  FDVVASSAGAPVAAF  VVASSAGAP        0.6334         52.8          WB     1.00     Sequence
         IAb  461  DGRTYGHPIVLRPVS  RTYGHPIVL        0.6298         54.9          WB     1.00     Sequence
         IAb  462  GRTYGHPIVLRPVSS  RTYGHPIVL        0.6270         56.6          WB     2.00     Sequence
         IAb  460  GDGRTYGHPIVLRPV  RTYGHPIVL        0.6269         56.6          WB     2.00     Sequence
         IAb  201  LGAQWTPANIANALI  AQWTPANIA        0.6252         57.7          WB     2.00     Sequence
         IAb   59  ALVLSGGPASVYADG  LVLSGGPAS        0.6215         60.1          WB     2.00     Sequence
         IAb   58  VALVLSGGPASVYAD  LVLSGGPAS        0.6183         62.2          WB     2.00     Sequence
         IAb  200  GLGAQWTPANIANAL  AQWTPANIA        0.6164         63.5          WB     2.00     Sequence
         IAb  199  AGLGAQWTPANIANA  AQWTPANIA        0.6047         72.0          WB     2.00     Sequence
         IAb  150  GFDVVASSAGAPVAA  VVASSAGAP        0.6044         72.2          WB     2.00     Sequence
         IAb  459  QGDGRTYGHPIVLRP  RTYGHPIVL        0.5991         76.5          WB     2.00     Sequence
         IAb   57  PVALVLSGGPASVYA  LVLSGGPAS        0.5969         78.4          WB     2.00     Sequence
         IAb  198  FAGLGAQWTPANIAN  AQWTPANIA        0.5941         80.8          WB     2.00     Sequence
         IAb  202  GAQWTPANIANALIE  AQWTPANIA        0.5855         88.7          WB     2.00     Sequence
         IAb  197  DFAGLGAQWTPANIA  AQWTPANIA        0.5673        107.9          WB     4.00     Sequence
         IAb  156  SSAGAPVAAFEAFDR  SSAGAPVAA        0.5622        114.1          WB     4.00     Sequence
         IAb   56  QPVALVLSGGPASVY  LVLSGGPAS        0.5593        117.7          WB     4.00     Sequence
         IAb   60  LVLSGGPASVYADGA  LVLSGGPAS        0.5573        120.3          WB     4.00     Sequence
         IAb  196  HDFAGLGAQWTPANI  HDFAGLGAQ        0.5530        126.1          WB     4.00     Sequence
         IAb   90  GICYGFQAMAQALGG  YGFQAMAQA        0.5422        141.6          WB     4.00     Sequence
         IAb   91  ICYGFQAMAQALGGI  YGFQAMAQA        0.5419        142.1          WB     4.00     Sequence
         IAb  271  QRDFVAATGANLVTV  DFVAATGAN        0.5411        143.3          WB     4.00     Sequence
         IAb  272  RDFVAATGANLVTVD  DFVAATGAN        0.5399        145.3          WB     4.00     Sequence
         IAb   92  CYGFQAMAQALGGIV  YGFQAMAQA        0.5398        145.4          WB     4.00     Sequence
         IAb   67  ASVYADGAPKLDPAL  YADGAPKLD        0.5361        151.2          WB     4.00     Sequence
         IAb   89  LGICYGFQAMAQALG  YGFQAMAQA        0.5320        158.1          WB     4.00     Sequence
         IAb  203  AQWTPANIANALIEQ  AQWTPANIA        0.5261        168.5          WB     4.00     Sequence
         IAb  149  DGFDVVASSAGAPVA  VVASSAGAP        0.5261        168.6          WB     4.00     Sequence
         IAb  463  RTYGHPIVLRPVSSE  RTYGHPIVL        0.5241        172.2          WB     4.00     Sequence
         IAb  270  VQRDFVAATGANLVT  DFVAATGAN        0.5222        175.8          WB     4.00     Sequence
         IAb   66  PASVYADGAPKLDPA  YADGAPKLD        0.5104        199.8          WB     8.00     Sequence
         IAb  273  DFVAATGANLVTVDA  DFVAATGAN        0.5078        205.6          WB     8.00     Sequence
         IAb   55  RQPVALVLSGGPASV  LVLSGGPAS        0.5053        211.2          WB     8.00     Sequence
         IAb   93  YGFQAMAQALGGIVA  YGFQAMAQA        0.5042        213.6          WB     8.00     Sequence
         IAb   88  VLGICYGFQAMAQAL  YGFQAMAQA        0.5040        214.2          WB     8.00     Sequence
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IAb  458  VQGDGRTYGHPIVLR  RTYGHPIVL         0.5015          220.0          WB    8.00       Sequence
IAb   36  ARVFSEVIPHTASIE  RVFSEVIPH         0.4981          228.3          WB    8.00       Sequence
IAb  195  LHDFAGLGAQWTPAN  HDFAGLGAQ         0.4960          233.5          WB    8.00       Sequence
IAb  269  QVQRDFVAATGANLV  RDFVAATGA         0.4941          238.3          WB    8.00       Sequence
IAb   68  SVYADGAPKLDPALL  SVYADGAPK         0.4819          271.9          WB    8.00       Sequence
IAb  194  FLHDFAGLGAQWTPA  HDFAGLGAQ         0.4798          278.3          WB    8.00       Sequence
IAb  193  RFLHDFAGLGAQWTP  HDFAGLGAQ         0.4718          303.5          WB    8.00       Sequence
IAb   65  GPASVYADGAPKLDP  SVYADGAPK         0.4714          304.9          WB    8.00       Sequence
IAb   37  RVFSEVIPHTASIEE  RVFSEVIPH         0.4703          308.3          WB    8.00       Sequence
IAb  311  QFIRAFEGAVRDVLD  FIRAFEGAV         0.4672          318.7          WB    8.00       Sequence
IAb  312  FIRAFEGAVRDVLDG  RAFEGAVRD         0.4651          326.2          WB    8.00       Sequence
IAb   35  EARVFSEVIPHTASI  FSEVIPHTA         0.4617          338.6          WB    8.00       Sequence
IAb  310  RQFIRAFEGAVRDVL  FIRAFEGAV         0.4602          344.1          WB    8.00       Sequence
IAb  457  GVQGDGRTYGHPIVL  RTYGHPIVL         0.4600          344.7          WB    8.00       Sequence
IAb   50  EEIRARQPVALVLSG  IRARQPVAL         0.4549          364.4          WB    8.00       Sequence
IAb   51  EIRARQPVALVLSGG  IRARQPVAL         0.4528          372.6          WB    8.00       Sequence
IAb   49  IEEIRARQPVALVLS  IRARQPVAL         0.4528          372.6          WB    8.00       Sequence
IAb  268  AQVQRDFVAATGANL  FVAATGANL         0.4497          385.3          WB    8.00       Sequence
IAb   87  PVLGICYGFQAMAQA  YGFQAMAQA         0.4473          395.4          WB    8.00       Sequence
IAb   21  FGAQYAQLIARRVRE  AQYAQLIAR         0.4462          400.1          WB    8.00       Sequence
IAb  192  SRFLHDFAGLGAQWT  HDFAGLGAQ         0.4454          403.8          WB    8.00       Sequence
IAb   19  VDFGAQYAQLIARRV  FGAQYAQLI         0.4452          404.6          WB    8.00       Sequence
IAb   20  DFGAQYAQLIARRVR  AQYAQLIAR         0.4398          429.0          WB    8.00       Sequence
IAb   34  REARVFSEVIPHTAS  RVFSEVIPH         0.4395          430.4          WB    8.00       Sequence
IAb  234  GVDSAVAAALVQRAI  SAVAAALVQ         0.4391          432.1          WB    8.00       Sequence
IAb  233  GGVDSAVAAALVQRA  GGVDSAVAA         0.4384          435.3          WB    8.00       Sequence
IAb  510  VLDITSKPPATIEWE  ITSKPPATI         0.4351          451.4          WB    8.00       Sequence
IAb  395  IVARQPFPGPGLGIR  IVARQPFPG         0.4343          455.0          WB   16.00       Sequence
IAb   64  GGPASVYADGAPKLD  SVYADGAPK         0.4299          477.6          WB   16.00       Sequence
IAb  235  VDSAVAAALVQRAIG  SAVAAALVQ         0.4260          498.1          WB   16.00       Sequence
IAb  148  PDGFDVVASSAGAPV  VVASSAGAP         0.4257          499.5          WB   16.00       Sequence
IAb  309  GRQFIRAFEGAVRDV  FIRAFEGAV         0.4244          506.6               16.00       Sequence
IAb  236  DSAVAAALVQRAIGD  SAVAAALVQ         0.4239          509.4               16.00       Sequence
IAb   22  GAQYAQLIARRVREA  AQYAQLIAR         0.4226          516.8               16.00       Sequence
IAb   48  SIEEIRARQPVALVL  IRARQPVAL         0.4204          529.0               16.00       Sequence
IAb  232  SGGVDSAVAAALVQR  VDSAVAAAL         0.4185          539.8               16.00       Sequence
IAb  509  VVLDITSKPPATIEW  ITSKPPATI         0.4180          543.0               16.00       Sequence
IAb  172  LAGVQYHPEVMHTPH  GVQYHPEVM         0.4168          550.2               16.00       Sequence
IAb   39  FSEVIPHTASIEEIR  FSEVIPHTA         0.4168          550.4               16.00       Sequence
IAb   38  VFSEVIPHTASIEEI  FSEVIPHTA         0.4152          559.9               16.00       Sequence
IAb  237  SAVAAALVQRAIGDR  SAVAAALVQ         0.4151          560.1               16.00       Sequence
IAb   61  VLSGGPASVYADGAP  VLSGGPASV         0.4147          562.9               16.00       Sequence
IAb  440  NQIWQCPVVLLADVR  QIWQCPVVL         0.4142          566.0               16.00       Sequence
IAb   52  IRARQPVALVLSGGP  IRARQPVAL         0.4140          566.8               16.00       Sequence
IAb  173  AGVQYHPEVMHTPHG  GVQYHPEVM         0.4112          584.4               16.00       Sequence
IAb  231  LSGGVDSAVAAALVQ  VDSAVAAAL         0.4110          585.6               16.00       Sequence
IAb  394  EIVARQPFPGPGLGI  IVARQPFPG         0.4103          590.3               16.00       Sequence
IAb  171  RLAGVQYHPEVMHTP  GVQYHPEVM         0.4101          591.4               16.00       Sequence
IAb  274  FVAATGANLVTVDAA  FVAATGANL         0.4096          594.9               16.00       Sequence
IAb  439  DNQIWQCPVVLLADV  QIWQCPVVL         0.4080          605.2               16.00       Sequence
IAb   33  VREARVFSEVIPHTA  FSEVIPHTA         0.4046          627.4               16.00       Sequence
IAb   18  VVDFGAQYAQLIARR  FGAQYAQLI         0.4020          645.6               16.00       Sequence
IAb  438  LDNQIWQCPVVLLAD  QIWQCPVVL         0.4012          651.4               16.00       Sequence
IAb   69  VYADGAPKLDPALLD  YADGAPKLD         0.3928          712.8               16.00       Sequence
IAb  174  GVQYHPEVMHTPHGQ  GVQYHPEVM         0.3902          733.7               16.00       Sequence
IAb  308  IGRQFIRAFEGAVRD  FIRAFEGAV         0.3862          766.1               16.00       Sequence
IAb  204  QWTPANIANALIEQV  WTPANIANA         0.3854          772.4               16.00       Sequence
IAb  205  WTPANIANALIEQVR  WTPANIANA         0.3824          798.5               16.00       Sequence
IAb  230  GLSGGVDSAVAAALV  GGVDSAVAA         0.3819          802.5               16.00       Sequence
IAb  365  DLKFTLVEPLRLLFK  FTLVEPLRL         0.3782          835.2               16.00       Sequence
IAb  191  LSRFLHDFAGLGAQW  HDFAGLGAQ         0.3774          842.7               16.00       Sequence
IAb  508  RVVLDITSKPPATIE  ITSKPPATI         0.3772          844.4               16.00       Sequence
IAb  441  QIWQCPVVLLADVRS  QIWQCPVVL         0.3759          855.9               16.00       Sequence
IAb  366  LKFTLVEPLRLLFKD  FTLVEPLRL         0.3752          862.8               16.00       Sequence
IAb   17  LVVDFGAQYAQLIAR  FGAQYAQLI         0.3749          865.4               16.00       Sequence
IAb  364  DDLKFTLVEPLRLLF  FTLVEPLRL         0.3749          865.5               16.00       Sequence
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IAb	94	GFQAMAQALGGIVAH	FQAMAQALG	0.3749	865.9	16.00	Sequence
IAb	437	GLDNQIWQCPVVLLA	QIWQCPVVL	0.3735	878.8	16.00	Sequence
IAb	393	EEIVARQPFPGPGLG	IVARQPFPG	0.3724	889.4	16.00	Sequence
IAb	54	ARQPVALVLSGGPAS	LVLSGGPAS	0.3690	923.1	16.00	Sequence
IAb	147	APDGFDVVASSAGAP	VVASSAGAP	0.3679	933.5	16.00	Sequence
IAb	396	VARQPFPGPGLGIRI	QPFPGPGLG	0.3668	945.1	16.00	Sequence
IAb	47	ASIEEIRARQPVALV	IRARQPVAL	0.3638	976.0	16.00	Sequence
IAb	95	FQAMAQALGGIVAHT	FQAMAQALG	0.3618	997.1	16.00	Sequence
IAb	97	AMAQALGGIVAHTGT	QALGGIVAH	0.3618	997.4	16.00	Sequence
IAb	363	PDDLKFTLVEPLRLL	FTLVEPLRL	0.3603	1014.3	16.00	Sequence
IAb	98	MAQALGGIVAHTGTR	QALGGIVAH	0.3583	1035.7	16.00	Sequence
IAb	313	IRAFEGAVRDVLDGK	RAFEGAVRD	0.3581	1038.6	16.00	Sequence
IAb	170	RRLAGVQYHPEVMHT	GVQYHPEVM	0.3562	1060.3	16.00	Sequence
IAb	397	ARQPFPGPGLGIRIV	QPFPGPGLG	0.3555	1067.6	16.00	Sequence
IAb	398	RQPFPGPGLGIRIVG	RQPFPGPGL	0.3529	1098.0	16.00	Sequence
IAb	190	VLSRFLHDFAGLGAQ	HDFAGLGAQ	0.3470	1171.0	16.00	Sequence
IAb	392	PEEIVARQPFPGPGL	IVARQPFPG	0.3451	1195.1	32.00	Sequence
IAb	291	FLEALSGVSAPEGKR	LEALSGVSA	0.3450	1196.8	32.00	Sequence
IAb	96	QAMAQALGGIVAHTG	AQALGGIVA	0.3448	1198.9	32.00	Sequence
IAb	507	NRVVLDITSKPPATI	ITSKPPATI	0.3442	1206.3	32.00	Sequence
IAb	229	CGLSGGVDSAVAAAL	GGVDSAVAA	0.3439	1210.9	32.00	Sequence
IAb	99	AQALGGIVAHTGTRE	QALGGIVAH	0.3408	1252.1	32.00	Sequence
IAb	307	IIGRQFIRAFEGAVR	FIRAFEGAV	0.3405	1255.9	32.00	Sequence
IAb	157	SAGAPVAAFEAFDRR	GAPVAAFEA	0.3397	1267.3	32.00	Sequence
IAb	70	YADGAPKLDPALLDL	YADGAPKLD	0.3381	1288.6	32.00	Sequence
IAb	40	SEVIPHTASIEEIRA	VIPHTASIE	0.3369	1305.4	32.00	Sequence
IAb	63	SGGPASVYADGAPKL	SVYADGAPK	0.3361	1316.5	32.00	Sequence
IAb	16	VLVVDFGAQYAQLIA	FGAQYAQLI	0.3343	1343.3	32.00	Sequence
IAb	292	LEALSGVSAPEGKRK	LEALSGVSA	0.3339	1349.6	32.00	Sequence
IAb	267	RAQVQRDFVAATGAN	RDFVAATGA	0.3328	1365.4	32.00	Sequence
IAb	23	AQYAQLIARRVREAR	AQYAQLIAR	0.3302	1404.0	32.00	Sequence
IAb	290	TFLEALSGVSAPEGK	LEALSGVSA	0.3299	1408.5	32.00	Sequence
IAb	367	KFTLVEPLRLLFKDE	FTLVEPLRL	0.3287	1426.4	32.00	Sequence
IAb	362	LPDDLKFTLVEPLRL	FTLVEPLRL	0.3269	1454.6	32.00	Sequence
IAb	134	QPVWMSHGDAVTAAP	PVWMSHGDA	0.3248	1487.8	32.00	Sequence
IAb	7	DVPETPARPVLVVDF	ETPARPVLV	0.3238	1505.4	32.00	Sequence
IAb	6	IDVPETPARPVLVVD	ETPARPVLV	0.3232	1513.9	32.00	Sequence
IAb	275	VAATGANLVTVDAAE	VAATGANLV	0.3204	1560.7	32.00	Sequence
IAb	5	DIDVPETPARPVLVV	ETPARPVLV	0.3193	1579.4	32.00	Sequence
IAb	135	PVWMSHGDAVTAAPD	PVWMSHGDA	0.3183	1597.6	32.00	Sequence
IAb	289	ETFLEALSGVSAPEG	LEALSGVSA	0.3152	1651.8	32.00	Sequence
IAb	41	EVIPHTASIEEIRAR	VIPHTASIE	0.3130	1691.6	32.00	Sequence
IAb	8	VPETPARPVLVVDFG	ETPARPVLV	0.3115	1718.7	32.00	Sequence
IAb	288	AETFLEALSGVSAPE	LEALSGVSA	0.3114	1721.4	32.00	Sequence
IAb	42	VIPHTASIEEIRARQ	VIPHTASIE	0.3096	1754.9	32.00	Sequence
IAb	468	PIVLRPVSSEDAMTA	IVLRPVSSE	0.3094	1758.1	32.00	Sequence
IAb	62	LSGGPASVYADGAPK	SVYADGAPK	0.3060	1825.1	32.00	Sequence
IAb	46	TASIEEIRARQPVAL	IRARQPVAL	0.3056	1832.1	32.00	Sequence
IAb	169	DRRLAGVQYHPEVMH	GVQYHPEVM	0.3033	1879.0	32.00	Sequence
IAb	137	WMSHGDAVTAAPDGF	GDAVTAAPD	0.3014	1918.1	32.00	Sequence
IAb	293	EALSGVSAPEGKRKI	EALSGVSAP	0.3003	1940.3	32.00	Sequence
IAb	133	VQPVWMSHGDAVTAA	PVWMSHGDA	0.2959	2036.0	32.00	Sequence
IAb	4	ADIDVPETPARPVLV	ETPARPVLV	0.2951	2053.2	32.00	Sequence
IAb	287	AAETFLEALSGVSAP	LEALSGVSA	0.2917	2129.9	32.00	Sequence
IAb	158	AGAPVAAFEAFDRRL	GAPVAAFEA	0.2916	2132.2	32.00	Sequence
IAb	159	GAPVAAFEAFDRRLA	GAPVAAFEA	0.2892	2187.7	32.00	Sequence
IAb	465	YGHPIVLRPVSSEDA	PIVLRPVSS	0.2882	2212.2	32.00	Sequence
IAb	136	VWMSHGDAVTAAPDG	WMSHGDAVT	0.2877	2222.6	32.00	Sequence
IAb	53	RARQPVALVLSGGPA	ALVLSGGPA	0.2853	2281.2	32.00	Sequence
IAb	119	LKVLGGKLHSDLPEV	LKVLGGKLH	0.2853	2283.4	32.00	Sequence
IAb	86	VPVLGICYGFQAMAQ	ICYGFQAMA	0.2850	2289.1	32.00	Sequence
IAb	100	QALGGIVAHTGTREY	QALGGIVAH	0.2844	2305.7	32.00	Sequence
IAb	384	AVGRELGLPEEIVAR	RELGLPEEI	0.2775	2482.5	32.00	Sequence
IAb	168	FDRRLAGVQYHPEVM	GVQYHPEVM	0.2767	2504.0	32.00	Sequence
IAb	467	HPIVLRPVSSEDAMT	PIVLRPVSS	0.2762	2518.2	32.00	Sequence
IAb	9	PETPARPVLVVDFGA	ETPARPVLV	0.2752	2546.9	32.00	Sequence

IAb	206	TPANIANALIEQVRT	ANIANALIE	0.2719	2639.6	32.00	Sequence
IAb	464	TYGHPIVLRPVSSED	PIVLRPVSS	0.2718	2641.0	32.00	Sequence
IAb	175	VQYHPEVMHTPHGQQ	VQYHPEVMH	0.2702	2688.1	32.00	Sequence
IAb	466	GHPIVLRPVSSEDAM	IVLRPVSSE	0.2664	2799.0	32.00	Sequence
IAb	385	VGRELGLPEEIVARQ	RELGLPEEI	0.2654	2829.2	32.00	Sequence
IAb	118	ELKVLGGKLHSDLPE	LKVLGGKLH	0.2646	2855.1	32.00	Sequence
IAb	306	KIIGRQFIRAFEGAV	FIRAFEGAV	0.2637	2883.1	32.00	Sequence
IAb	228	ICGLSGGVDSAVAAA	GGVDSAVAA	0.2634	2893.2	32.00	Sequence
IAb	32	RVREARVFSEVIPHT	RVFSEVIPH	0.2620	2938.0	32.00	Sequence
IAb	138	MSHGDAVTAAPDGFD	GDAVTAAPD	0.2616	2949.6	32.00	Sequence
IAb	15	PVLVVDFGAQYAQLI	FGAQYAQLI	0.2585	3051.5	32.00	Sequence
IAb	368	FTLVEPLRLLFKDEV	FTLVEPLRL	0.2584	3053.4	32.00	Sequence
IAb	117	TELKVLGGKLHSDLP	LKVLGGKLH	0.2576	3081.1	32.00	Sequence
IAb	286	DAAETFLEALSGVSA	FLEALSGVS	0.2562	3125.3	32.00	Sequence
IAb	132	EVQPVWMSHGDAVTA	MSHGDAVTA	0.2560	3132.2	32.00	Sequence
IAb	383	RAVGRELGLPEEIVA	RELGLPEEI	0.2559	3136.1	32.00	Sequence
IAb	266	ERAQVQRDFVAATGA	RDFVAATGA	0.2550	3168.4	32.00	Sequence
IAb	10	ETPARPVLVVDFGAQ	ETPARPVLV	0.2535	3220.5	32.00	Sequence
IAb	294	ALSGVSAPEGKRKII	SGVSAPEGK	0.2524	3257.0	32.00	Sequence
IAb	140	HGDAVTAAPDGFDVV	GDAVTAAPD	0.2516	3285.3	32.00	Sequence
IAb	139	SHGDAVTAAPDGFDV	GDAVTAAPD	0.2496	3359.8	32.00	Sequence
IAb	177	YHPEVMHTPHGQQVL	EVMHTPHGQ	0.2491	3376.1	32.00	Sequence
IAb	382	VRAVGRELGLPEEIV	RELGLPEEI	0.2486	3393.8	32.00	Sequence
IAb	436	AGLDNQIWQCPVVLL	QIWQCPVVL	0.2480	3415.8	32.00	Sequence
IAb	469	IVLRPVSSEDAMTAD	IVLRPVSSE	0.2442	3558.8	32.00	Sequence
IAb	295	LSGVSAPEGKRKIIG	SGVSAPEGK	0.2415	3667.6	50.00	Sequence
IAb	116	RTELKVLGGKLHSDL	LKVLGGKLH	0.2409	3688.5	50.00	Sequence
IAb	259	HGLLRAGERAQVQRD	LLRAGERAQ	0.2407	3699.3	50.00	Sequence
IAb	179	PEVMHTPHGQQVLSR	EVMHTPHGQ	0.2393	3756.1	50.00	Sequence
IAb	207	PANIANALIEQVRTQ	ANIANALIE	0.2385	3788.3	50.00	Sequence
IAb	131	PEVQPVWMSHGDAVT	PVWMSHGDA	0.2380	3807.8	50.00	Sequence
IAb	260	GLLRAGERAQVQRDF	GLLRAGERA	0.2378	3815.0	50.00	Sequence
IAb	189	QVLSRFLHDFAGLGA	SRFLHDFAG	0.2372	3841.3	50.00	Sequence
IAb	146	AAPDGFDVVASSAGA	FDVVASSAG	0.2364	3874.8	50.00	Sequence
IAb	141	GDAVTAAPDGFDVVA	GDAVTAAPD	0.2360	3891.0	50.00	Sequence
IAb	391	LPEEIVARQPFPGPG	IVARQPFPG	0.2347	3947.8	50.00	Sequence
IAb	176	QYHPEVMHTPHGQQV	EVMHTPHGQ	0.2341	3969.7	50.00	Sequence
IAb	399	QPFPGPGLGIRIVGE	QPFPGPGLG	0.2327	4030.3	50.00	Sequence
IAb	258	DHGLLRAGERAQVQR	LLRAGERAQ	0.2308	4113.7	50.00	Sequence
IAb	381	EVRAVGRELGLPEEI	RELGLPEEI	0.2301	4144.8	50.00	Sequence
IAb	178	HPEVMHTPHGQQVLS	EVMHTPHGQ	0.2295	4172.3	50.00	Sequence
IAb	285	VDAAETFLEALSGVS	AETFLEALS	0.2266	4308.9	50.00	Sequence
IAb	85	GVPVLGICYGFQAMA	ICYGFQAMA	0.2262	4323.9	50.00	Sequence
IAb	342	VESGGGSGTANIKSH	SGGGSGTAN	0.2246	4402.8	50.00	Sequence
IAb	160	APVAAFEAFDRRLAG	APVAAFEAF	0.2244	4412.9	50.00	Sequence
IAb	180	EVMHTPHGQQVLSRF	HTPHGQQVL	0.2236	4448.2	50.00	Sequence
IAb	238	AVAAALVQRAIGDRL	VAAALVQRA	0.2226	4498.5	50.00	Sequence
IAb	208	ANIANALIEQVRTQI	ANIANALIE	0.2222	4517.2	50.00	Sequence
IAb	314	RAFEGAVRDVLDGKT	RAFEGAVRD	0.2219	4532.8	50.00	Sequence
IAb	328	TAEFLVQGTLYPDVV	FLVQGTLYP	0.2216	4544.3	50.00	Sequence
IAb	103	GGIVAHTGTREYGRT	VAHTGTREY	0.2162	4821.5	50.00	Sequence
IAb	331	FLVQGTLYPDVVESG	FLVQGTLYP	0.2160	4831.1	50.00	Sequence
IAb	343	ESGGGSGTANIKSHH	SGGGSGTAN	0.2144	4917.2	50.00	Sequence
IAb	3	PADIDVPETPARPVL	DVPETPARP	0.2141	4933.4	50.00	Sequence
IAb	257	VDHGLLRAGERAQVQ	GLLRAGERA	0.2140	4935.3	50.00	Sequence
IAb	24	QYAQLIARRVREARV	YAQLIARRV	0.2140	4938.4	50.00	Sequence
IAb	329	AEFLVQGTLYPDVVE	FLVQGTLYP	0.2129	4994.8	50.00	Sequence
IAb	341	VVESGGGSGTANIKS	SGGGSGTAN	0.2124	5022.8	50.00	Sequence
IAb	276	AATGANLVTVDAAET	AATGANLVT	0.2113	5080.1	50.00	Sequence
IAb	386	GRELGLPEEIVARQP	RELGLPEEI	0.2108	5111.7	50.00	Sequence
IAb	72	DGAPKLDPALLDLGV	PKLDPALLD	0.2100	5156.8	50.00	Sequence
IAb	102	LGGIVAHTGTREYGR	GIVAHTGTR	0.2099	5161.0	50.00	Sequence
IAb	115	GRTELKVLGGKLHSD	LKVLGGKLH	0.2095	5181.0	50.00	Sequence
IAb	31	RRVREARVFSEVIPH	RVFSEVIPH	0.2094	5185.9	50.00	Sequence
IAb	73	GAPKLDPALLDLGVP	PKLDPALLD	0.2087	5225.6	50.00	Sequence
IAb	25	YAQLIARRVREARVF	YAQLIARRV	0.2080	5268.3	50.00	Sequence

IAb	506	VNRVVLDITSKPPAT	DITSKPPAT	0.2077	5281.9	50.00	Sequence
IAb	344	SGGGSGTANIKSHHN	SGGGSGTAN	0.2077	5282.4	50.00	Sequence
IAb	390	GLPEEIVARQPFPGP	IVARQPFPG	0.2075	5298.6	50.00	Sequence
IAb	471	LRPVSSEDAMTADWT	LRPVSSEDA	0.2067	5339.6	50.00	Sequence
IAb	104	GIVAHTGTREYGRTE	GIVAHTGTR	0.2063	5364.2	50.00	Sequence
IAb	435	AAGLDNQIWQCPVVL	QIWQCPVVL	0.2061	5378.5	50.00	Sequence
IAb	470	VLRPVSSEDAMTADW	LRPVSSEDA	0.2060	5384.4	50.00	Sequence
IAb	227	AICGLSGGVDSAVAA	GGVDSAVAA	0.2047	5458.0	50.00	Sequence
IAb	71	ADGAPKLDPALLDLG	APKLDPALL	0.2041	5494.9	50.00	Sequence
IAb	327	KTAEFLVQGTLYPDV	FLVQGTLYP	0.2035	5528.3	50.00	Sequence
IAb	167	AFDRRLAGVQYHPEV	RRLAGVQYH	0.2030	5560.8	50.00	Sequence
IAb	256	FVDHGLLRAGERAQV	GLLRAGERA	0.2029	5567.7	50.00	Sequence
IAb	165	FEAFDRRLAGVQYHP	FEAFDRRLA	0.2028	5574.7	50.00	Sequence
IAb	340	DVVESGGGSGTANIK	SGGGSGTAN	0.2022	5609.5	50.00	Sequence
IAb	130	LPEVQPVWMSHGDAV	VQPVWMSHG	0.2014	5659.9	50.00	Sequence
IAb	101	ALGGIVAHTGTREYG	GIVAHTGTR	0.2004	5719.6	50.00	Sequence
IAb	188	QQVLSRFLHDFAGLG	FLHDFAGLG	0.2002	5728.2	50.00	Sequence
IAb	456	VGVQGDGRTYGHPIV	GRTYGHPIV	0.1998	5756.1	50.00	Sequence
IAb	120	KVLGGKLHSDLPEVQ	KVLGGKLHS	0.1998	5756.2	50.00	Sequence
IAb	326	GKTAEFLVQGTLYPD	FLVQGTLYP	0.1997	5762.2	50.00	Sequence
IAb	330	EFLVQGTLYPDVVES	FLVQGTLYP	0.1977	5891.3	50.00	Sequence
IAb	161	PVAAFEAFDRRLAGV	AAFEAFDRR	0.1967	5953.9	50.00	Sequence
IAb	442	IWQCPVVLLADVRSV	VVLLADVRS	0.1964	5974.4	50.00	Sequence
IAb	162	VAAFEAFDRRLAGVQ	FEAFDRRLA	0.1905	6362.0	50.00	Sequence
IAb	145	TAAPDGFDVVASSAG	FDVVASSAG	0.1900	6402.6	50.00	Sequence
IAb	430	REELTAAGLDNQIWQ	ELTAAGLDN	0.1899	6409.9	50.00	Sequence
IAb	239	VAAALVQRAIGDRLT	VAAALVQRA	0.1889	6477.1	50.00	Sequence
IAb	123	GGKLHSDLPEVQPVW	GKLHSDLPE	0.1880	6538.0	50.00	Sequence
IAb	164	AFEAFDRRLAGVQYH	FEAFDRRLA	0.1877	6559.6	50.00	Sequence
IAb	296	SGVSAPEGKRKIIGR	SGVSAPEGK	0.1876	6567.8	50.00	Sequence
IAb	163	AAFEAFDRRLAGVQY	FEAFDRRLA	0.1853	6730.8	50.00	Sequence
IAb	181	VMHTPHGQQVLSRFL	HTPHGQQVL	0.1853	6732.1	50.00	Sequence
IAb	406	LGIRIVGEVTAKRLD	IRIVGEVTA	0.1853	6736.9	50.00	Sequence
IAb	79	PALLDLGVPVLGICY	LDLGVPVLG	0.1843	6805.7	50.00	Sequence
IAb	407	GIRIVGEVTAKRLDT	IRIVGEVTA	0.1838	6841.1	50.00	Sequence
IAb	129	DLPEVQPVWMSHGDA	PEVQPVWMS	0.1833	6884.2	50.00	Sequence
IAb	325	DGKTAEFLVQGTLYP	AEFLVQGTL	0.1831	6897.6	50.00	Sequence
IAb	282	LVTVDAAETFLEALS	VTVDAAETF	0.1815	7014.7	50.00	Sequence
IAb	339	PDVVESGGGSGTANI	SGGGSGTAN	0.1815	7015.3	50.00	Sequence
IAb	261	LLRAGERAQVQRDFV	LLRAGERAQ	0.1807	7077.7	50.00	Sequence
IAb	429	VREELTAAGLDNQIW	ELTAAGLDN	0.1804	7100.2	50.00	Sequence
IAb	2	QPADIDVPETPARPV	DVPETPARP	0.1802	7114.4	50.00	Sequence
IAb	105	IVAHTGTREYGRTEL	IVAHTGTRE	0.1798	7148.9	50.00	Sequence
IAb	14	RPVLVVDFGAQYAQL	VVDFGAQYA	0.1795	7171.2	50.00	Sequence
IAb	143	AVTAAPDGFDVVASS	AVTAAPDGF	0.1788	7221.5	50.00	Sequence
IAb	361	GLPDDLKFTLVEPLR	LKFTLVEPL	0.1782	7272.6	50.00	Sequence
IAb	405	GLGIRIVGEVTAKRL	IRIVGEVTA	0.1781	7282.3	50.00	Sequence
IAb	124	GKLHSDLPEVQPVWM	GKLHSDLPE	0.1780	7283.3	50.00	Sequence
IAb	431	EELTAAGLDNQIWQC	ELTAAGLDN	0.1780	7287.9	50.00	Sequence
IAb	387	RELGLPEEIVARQPF	RELGLPEEI	0.1776	7317.1	50.00	Sequence
IAb	142	DAVTAAPDGFDVVAS	AVTAAPDGF	0.1771	7356.9	50.00	Sequence
IAb	122	LGGKLHSDLPEVQPV	GKLHSDLPE	0.1770	7363.6	50.00	Sequence
IAb	74	APKLDPALLDLGVPV	PKLDPALLD	0.1769	7372.4	50.00	Sequence
IAb	80	ALLDLGVPVLGICYG	LDLGVPVLG	0.1769	7377.4	50.00	Sequence
IAb	408	IRIVGEVTAKRLDTL	IRIVGEVTA	0.1768	7381.5	50.00	Sequence
IAb	428	IVREELTAAGLDNQI	ELTAAGLDN	0.1756	7478.7	50.00	Sequence
IAb	389	LGLPEEIVARQPFPG	IVARQPFPG	0.1756	7478.7	50.00	Sequence
IAb	280	ANLVTVDAAETFLEA	LVTVDAAET	0.1723	7753.0	50.00	Sequence
IAb	182	MHTPHGQQVLSRFLH	HTPHGQQVL	0.1706	7895.4	50.00	Sequence
IAb	443	WQCPVVLLADVRSVG	VVLLADVRS	0.1698	7966.2	50.00	Sequence
IAb	332	LVQGTLYPDVVESGG	QGTLYPDVV	0.1692	8015.9	50.00	Sequence
IAb	279	GANLVTVDAAETFLE	ANLVTVDAA	0.1679	8126.9	50.00	Sequence
IAb	114	YGRTELKVLGGKLHS	LKVLGGKLH	0.1672	8191.7	50.00	Sequence
IAb	278	TGANLVTVDAAETFL	ANLVTVDAA	0.1671	8198.2	50.00	Sequence
IAb	128	SDLPEVQPVWMSHGD	PEVQPVWMS	0.1670	8203.8	50.00	Sequence
IAb	78	DPALLDLGVPVLGIC	LDLGVPVLG	0.1670	8204.6	50.00	Sequence

IAb	255	VFVDHGLLRAGERAQ	LLRAGERAQ	0.1658	8317.9	50.00	Sequence
IAb	277	ATGANLVTVDAAETF	ANLVTVDAA	0.1635	8520.6	50.00	Sequence
IAb	43	IPHTASIEEIRARQP	IPHTASIEE	0.1631	8562.0	50.00	Sequence
IAb	281	NLVTVDAAETFLEAL	LVTVDAAET	0.1629	8582.9	50.00	Sequence
IAb	166	EAFDRRLAGVQYHPE	RRLAGVQYH	0.1629	8584.7	50.00	Sequence
IAb	492	LERISTRITNEVAEV	LERISTRIT	0.1626	8612.1	50.00	Sequence
IAb	125	KLHSDLPEVQPVWMS	LHSDLPEVQ	0.1615	8715.5	50.00	Sequence
IAb	283	VTVDAAETFLEALSG	VTVDAAETF	0.1612	8738.9	50.00	Sequence
IAb	489	YEVLERISTRITNEV	LERISTRIT	0.1578	9068.9	50.00	Sequence
IAb	333	VQGTLYPDVVESGGG	QGTLYPDVV	0.1577	9076.8	50.00	Sequence
IAb	491	VLERISTRITNEVAE	LERISTRIT	0.1572	9130.8	50.00	Sequence
IAb	77	LDPALLDLGVPVLGI	LDLGVPVLG	0.1569	9153.6	50.00	Sequence
IAb	305	RKIIGRQFIRAFEGA	RQFIRAFEG	0.1564	9206.7	50.00	Sequence
IAb	121	VLGGKLHSDLPEVQP	GKLHSDLPE	0.1561	9236.2	50.00	Sequence
IAb	81	LLDLGVPVLGICYGF	LDLGVPVLG	0.1560	9250.2	50.00	Sequence
IAb	496	STRITNEVAEVNRVV	STRITNEVA	0.1546	9385.5	50.00	Sequence
IAb	490	EVLERISTRITNEVA	LERISTRIT	0.1546	9391.3	50.00	Sequence
IAb	334	QGTLYPDVVESGGGS	QGTLYPDVV	0.1537	9475.4	50.00	Sequence
IAb	404	PGLGIRIVGEVTAKR	GIRIVGEVT	0.1536	9488.4	50.00	Sequence
IAb	495	ISTRITNEVAEVNRV	STRITNEVA	0.1534	9511.0	50.00	Sequence
IAb	486	RVPYEVLERISTRIT	RVPYEVLER	0.1529	9557.9	50.00	Sequence
IAb	13	ARPVLVVDFGAQYAQ	VVDFGAQYA	0.1526	9590.5	50.00	Sequence
IAb	284	TVDAAETFLEALSGV	VDAAETFLE	0.1524	9608.5	50.00	Sequence
IAb	380	DEVRAVGRELGLPEE	EVRAVGREL	0.1513	9732.1	50.00	Sequence
IAb	427	SIVREELTAAGLDNQ	IVREELTAA	0.1505	9810.8	50.00	Sequence
IAb	338	YPDVVESGGGSGTAN	SGGGSGTAN	0.1504	9827.3	50.00	Sequence
IAb	1	VQPADIDVPETPARP	DVPETPARP	0.1502	9842.2	50.00	Sequence
IAb	420	DTLRHADSIVREELT	LRHADSIVR	0.1496	9907.1	50.00	Sequence
IAb	484	WTRVPYEVLERISTR	WTRVPYEVL	0.1492	9953.7	50.00	Sequence
IAb	353	IKSHHNVGGLPDDLK	HHNVGGLPD	0.1490	9969.6	50.00	Sequence
IAb	126	LHSDLPEVQPVWMSH	LHSDLPEVQ	0.1483	10046.1	50.00	Sequence
IAb	226	HAICGLSGGVDSAVA	GLSGGVDSA	0.1479	10093.0	50.00	Sequence
IAb	30	ARRVREARVFSEVIP	RRVREARVF	0.1479	10096.8	50.00	Sequence
IAb	483	DWTRVPYEVLERIST	WTRVPYEVL	0.1476	10125.5	50.00	Sequence
IAb	432	ELTAAGLDNQIWQCP	ELTAAGLDN	0.1476	10129.5	50.00	Sequence
IAb	419	LDTLRHADSIVREEL	LRHADSIVR	0.1468	10209.3	50.00	Sequence
IAb	127	HSDLPEVQPVWMSHG	PEVQPVWMS	0.1456	10348.7	50.00	Sequence
IAb	482	ADWTRVPYEVLERIS	WTRVPYEVL	0.1453	10376.6	50.00	Sequence
IAb	447	VVLLADVRSVGVQGD	VVLLADVRS	0.1420	10757.6	50.00	Sequence
IAb	488	PYEVLERISTRITNE	LERISTRIT	0.1413	10836.6	50.00	Sequence
IAb	403	GPGLGIRIVGEVTAK	IRIVGEVTA	0.1412	10851.8	50.00	Sequence
IAb	480	MTADWTRVPYEVLER	WTRVPYEVL	0.1406	10916.9	50.00	Sequence
IAb	494	RISTRITNEVAEVNR	STRITNEVA	0.1403	10958.4	50.00	Sequence
IAb	187	GQQVLSRFLHDFAGL	SRFLHDFAG	0.1400	10996.8	50.00	Sequence
IAb	352	NIKSHHNVGGLPDDL	HHNVGGLPD	0.1393	11081.7	50.00	Sequence
IAb	472	RPVSSEDAMTADWTR	RPVSSEDAM	0.1391	11099.8	50.00	Sequence
IAb	110	GTREYGRTELKVLGG	REYGRTELK	0.1390	11106.9	50.00	Sequence
IAb	109	TGTREYGRTELKVLG	GTREYGRTE	0.1373	11324.0	50.00	Sequence
IAb	225	GHAICGLSGGVDSAV	GLSGGVDSA	0.1366	11408.7	50.00	Sequence
IAb	418	RLDTLRHADSIVREE	LRHADSIVR	0.1364	11430.9	50.00	Sequence
IAb	485	TRVPYEVLERISTRI	RVPYEVLER	0.1364	11432.4	50.00	Sequence
IAb	320	VRDVLDGKTAEFLVQ	DVLDGKTAE	0.1361	11462.8	50.00	Sequence
IAb	354	KSHHNVGGLPDDLKF	HHNVGGLPD	0.1361	11469.2	50.00	Sequence
IAb	304	KRKIIGRQFIRAFEG	RQFIRAFEG	0.1359	11492.6	50.00	Sequence
IAb	345	GGGSGTANIKSHHNV	SGTANIKSH	0.1357	11510.9	50.00	Sequence
IAb	493	ERISTRITNEVAEVN	STRITNEVA	0.1350	11606.9	50.00	Sequence
IAb	321	RDVLDGKTAEFLVQG	DVLDGKTAE	0.1347	11638.4	50.00	Sequence
IAb	144	VTAAPDGFDVVASSA	VTAAPDGFD	0.1344	11683.2	50.00	Sequence
IAb	319	AVRDVLDGKTAEFLV	DVLDGKTAE	0.1339	11741.4	50.00	Sequence
IAb	421	TLRHADSIVREELTA	LRHADSIVR	0.1331	11842.5	50.00	Sequence
IAb	76	KLDPALLDLGVPVLG	LDLGVPVLG	0.1330	11863.3	50.00	Sequence
IAb	322	DVLDGKTAEFLVQGT	DVLDGKTAE	0.1326	11913.9	50.00	Sequence
IAb	481	TADWTRVPYEVLERI	WTRVPYEVL	0.1321	11970.4	50.00	Sequence
IAb	26	AQLIARRVREARVFS	LIARRVREA	0.1317	12024.8	50.00	Sequence
IAb	497	TRITNEVAEVNRVVL	TRITNEVAE	0.1313	12076.6	50.00	Sequence
IAb	444	QCPVVLLADVRSVGV	VVLLADVRS	0.1310	12123.6	50.00	Sequence

IAb	209	NIANALIEQVRTQIG	NIANALIEQ	0.1306	12172.6	50.00	Sequence
IAb	451	ADVRSVGVQGDGRTY	ADVRSVGVQ	0.1302	12222.6	50.00	Sequence
IAb	379	KDEVRAVGRELGLPE	EVRAVGREL	0.1300	12250.8	50.00	Sequence
IAb	108	HTGTREYGRTELKVL	GTREYGRTE	0.1288	12414.8	50.00	Sequence
IAb	183	HTPHGQQVLSRFLHD	HTPHGQQVL	0.1287	12422.7	50.00	Sequence
IAb	75	PKLDPALLDLGVPVL	PKLDPALLD	0.1283	12476.2	50.00	Sequence
IAb	422	LRHADSIVREELTAA	LRHADSIVR	0.1280	12523.6	50.00	Sequence
IAb	45	HTASIEEIRARQPVA	EIRARQPVA	0.1275	12585.5	50.00	Sequence
IAb	478	DAMTADWTRVPYEVL	DAMTADWTR	0.1273	12614.1	50.00	Sequence
IAb	360	GGLPDDLKFTLVEPL	LKFTLVEPL	0.1270	12649.7	50.00	Sequence
IAb	84	LGVPVLGICYGFQAM	GICYGFQAM	0.1260	12797.4	50.00	Sequence
IAb	473	PVSSEDAMTADWTRV	VSSEDAMTA	0.1247	12965.3	50.00	Sequence
IAb	337	LYPDVVESGGGSGTA	DVVESGGGS	0.1245	12997.1	50.00	Sequence
IAb	474	VSSEDAMTADWTRVP	VSSEDAMTA	0.1244	13010.6	50.00	Sequence
IAb	450	LADVRSVGVQGDGRT	VRSVGVQGD	0.1238	13096.0	50.00	Sequence
IAb	426	DSIVREELTAAGLDN	IVREELTAA	0.1237	13111.5	50.00	Sequence
IAb	446	PVVLLADVRSVGVQG	VVLLADVRS	0.1236	13122.7	50.00	Sequence
IAb	318	GAVRDVLDGKTAEFL	DVLDGKTAE	0.1226	13271.3	50.00	Sequence
IAb	409	RIVGEVTAKRLDTLR	RIVGEVTAK	0.1224	13301.9	50.00	Sequence
IAb	400	PFPGPGLGIRIVGEV	PFPGPGLGI	0.1218	13382.5	50.00	Sequence
IAb	448	VLLADVRSVGVQGDG	VLLADVRSV	0.1217	13403.2	50.00	Sequence
IAb	106	VAHTGTREYGRTELK	VAHTGTREY	0.1213	13455.7	50.00	Sequence
IAb	417	KRLDTLRHADSIVRE	LRHADSIVR	0.1212	13468.2	50.00	Sequence
IAb	82	LDLGVPVLGICYGFQ	LDLGVPVLG	0.1207	13542.6	50.00	Sequence
IAb	355	SHHNVGGLPDDLKFT	HHNVGGLPD	0.1202	13616.9	50.00	Sequence
IAb	12	PARPVLVVDFGAQYA	VVDFGAQYA	0.1198	13676.6	50.00	Sequence
IAb	445	CPVVLLADVRSVGVQ	VVLLADVRS	0.1196	13712.7	50.00	Sequence
IAb	254	CVFVDHGLLRAGERA	FVDHGLLRA	0.1189	13815.3	50.00	Sequence
IAb	487	VPYEVLERISTRITN	LERISTRIT	0.1188	13830.1	50.00	Sequence
IAb	0	VVQPADIDVPETPAR	VQPADIDVP	0.1174	14041.5	50.00	Sequence
IAb	346	GGSGTANIKSHHNVG	SGTANIKSH	0.1170	14097.5	50.00	Sequence
IAb	111	TREYGRTELKVLGGK	REYGRTELK	0.1160	14246.7	50.00	Sequence
IAb	335	GTLYPDVVESGGGSG	GTLYPDVVE	0.1157	14297.2	50.00	Sequence
IAb	348	SGTANIKSHHNVGGL	SGTANIKSH	0.1155	14329.5	50.00	Sequence
IAb	240	AAALVQRAIGDRLTC	AAALVQRAI	0.1152	14370.1	50.00	Sequence
IAb	265	GERAQVQRDFVAATG	VQRDFVAAT	0.1149	14415.6	50.00	Sequence
IAb	113	EYGRTELKVLGGKLH	LKVLGGKLH	0.1144	14506.8	50.00	Sequence
IAb	347	GSGTANIKSHHNVGG	SGTANIKSH	0.1141	14543.8	50.00	Sequence
IAb	477	EDAMTADWTRVPYEV	DAMTADWTR	0.1138	14598.6	50.00	Sequence
IAb	425	ADSIVREELTAAGLD	IVREELTAA	0.1137	14615.2	50.00	Sequence
IAb	186	HGQQVLSRFLHDFAG	QQVLSRFLH	0.1134	14651.8	50.00	Sequence
IAb	224	DGHAICGLSGGVDSA	GLSGGVDSA	0.1122	14855.2	50.00	Sequence
IAb	351	ANIKSHHNVGGLPDD	HHNVGGLPD	0.1121	14865.8	50.00	Sequence
IAb	28	LIARRVREARVFSEV	LIARRVREA	0.1112	15013.3	50.00	Sequence
IAb	453	VRSVGVQGDGRTYGH	VRSVGVQGD	0.1110	15038.7	50.00	Sequence
IAb	402	PGPGLGIRIVGEVTA	IRIVGEVTA	0.1108	15078.1	50.00	Sequence
IAb	375	RLLFKDEVRAVGREL	RLLFKDEVR	0.1108	15079.4	50.00	Sequence
IAb	479	AMTADWTRVPYEVLE	WTRVPYEVL	0.1107	15089.9	50.00	Sequence
IAb	416	AKRLDTLRHADSIVR	LRHADSIVR	0.1106	15114.2	50.00	Sequence
IAb	449	LLADVRSVGVQGDGR	ADVRSVGVQ	0.1106	15117.0	50.00	Sequence
IAb	323	VLDGKTAEFLVQGTL	AEFLVQGTL	0.1102	15176.5	50.00	Sequence
IAb	27	QLIARRVREARVFSE	LIARRVREA	0.1083	15491.9	50.00	Sequence
IAb	324	LDGKTAEFLVQGTLY	AEFLVQGTL	0.1064	15815.0	50.00	Sequence
IAb	452	DVRSVGVQGDGRTYG	VRSVGVQGD	0.1055	15975.5	50.00	Sequence
IAb	219	RTQIGDGHAICGLSG	TQIGDGHAI	0.1054	15990.4	50.00	Sequence
IAb	476	SEDAMTADWTRVPYE	DAMTADWTR	0.1052	16027.1	50.00	Sequence
IAb	505	EVNRVVLDITSKPPA	LDITSKPPA	0.1051	16030.6	50.00	Sequence
IAb	378	FKDEVRAVGRELGLP	EVRAVGREL	0.1051	16034.0	50.00	Sequence
IAb	336	TLYPDVVESGGGSGT	TLYPDVVES	0.1050	16048.8	50.00	Sequence
IAb	303	GKRKIIGRQFIRAFE	IGRQFIRAF	0.1048	16080.1	50.00	Sequence
IAb	29	IARRVREARVFSEVI	RRVREARVF	0.1048	16091.0	50.00	Sequence
IAb	242	ALVQRAIGDRLTCVF	ALVQRAIGD	0.1046	16124.3	50.00	Sequence
IAb	424	HADSIVREELTAAGL	IVREELTAA	0.1040	16221.3	50.00	Sequence
IAb	374	LRLLFKDEVRAVGRE	LLFKDEVRA	0.1039	16248.3	50.00	Sequence
IAb	241	AALVQRAIGDRLTCV	ALVQRAIGD	0.1036	16305.9	50.00	Sequence
IAb	215	IEQVRTQIGDGHAIC	TQIGDGHAI	0.1035	16310.3	50.00	Sequence

IAb	218	VRTQIGDGHAICGLS	TQIGDGHAI	0.1035	16312.1	50.00	Sequence
IAb	11	TPARPVLVVDFGAQY	TPARPVLVV	0.1026	16479.9	50.00	Sequence
IAb	107	AHTGTREYGRTELKV	GTREYGRTE	0.1017	16632.5	50.00	Sequence
IAb	185	PHGQQVLSRFLHDFA	QQVLSRFLH	0.1017	16643.1	50.00	Sequence
IAb	356	HHNVGGLPDDLKFTL	HHNVGGLPD	0.1017	16644.0	50.00	Sequence
IAb	388	ELGLPEEIVARQPFP	EEIVARQPF	0.1013	16703.0	50.00	Sequence
IAb	498	RITNEVAEVNRVVLD	RITNEVAEV	0.1009	16784.4	50.00	Sequence
IAb	253	TCVFVDHGLLRAGER	FVDHGLLRA	0.0987	17182.6	50.00	Sequence
IAb	373	PLRLLFKDEVRAVGR	LLFKDEVRA	0.0987	17190.2	50.00	Sequence
IAb	220	TQIGDGHAICGLSGG	TQIGDGHAI	0.0984	17248.7	50.00	Sequence
IAb	214	LIEQVRTQIGDGHAI	TQIGDGHAI	0.0980	17310.9	50.00	Sequence
IAb	217	QVRTQIGDGHAICGL	TQIGDGHAI	0.0969	17519.9	50.00	Sequence
IAb	377	LFKDEVRAVGRELGL	EVRAVGREL	0.0969	17526.5	50.00	Sequence
IAb	44	PHTASIEEIRARQPV	PHTASIEEI	0.0963	17646.2	50.00	Sequence
IAb	415	TAKRLDTLRHADSIV	AKRLDTLRH	0.0956	17778.7	50.00	Sequence
IAb	262	LRAGERAQVQRDFVA	RAGERAQVQ	0.0952	17849.2	50.00	Sequence
IAb	372	EPLRLLFKDEVRAVG	RLLFKDEVR	0.0933	18224.9	50.00	Sequence
IAb	475	SSEDAMTADWTRVPY	DAMTADWTR	0.0926	18351.1	50.00	Sequence
IAb	210	IANALIEQVRTQIGD	IANALIEQV	0.0926	18363.0	50.00	Sequence
IAb	252	LTCVFVDHGLLRAGE	FVDHGLLRA	0.0919	18506.2	50.00	Sequence
IAb	376	LLFKDEVRAVGRELG	EVRAVGREL	0.0913	18611.4	50.00	Sequence
IAb	434	TAAGLDNQIWQCPVV	NQIWQCPVV	0.0903	18822.3	50.00	Sequence
IAb	423	RHADSIVREELTAAG	IVREELTAA	0.0900	18889.6	50.00	Sequence
IAb	350	TANIKSHHNVGGLPD	SHHNVGGLP	0.0897	18935.6	50.00	Sequence
IAb	251	RLTCVFVDHGLLRAG	FVDHGLLRA	0.0896	18956.5	50.00	Sequence
IAb	371	VEPLRLLFKDEVRAV	LFKDEVRAV	0.0892	19052.6	50.00	Sequence
IAb	250	DRLTCVFVDHGLLRA	FVDHGLLRA	0.0889	19116.4	50.00	Sequence
IAb	263	RAGERAQVQRDFVAA	RAGERAQVQ	0.0881	19269.0	50.00	Sequence
IAb	213	ALIEQVRTQIGDGHA	ALIEQVRTQ	0.0876	19381.3	50.00	Sequence
IAb	216	EQVRTQIGDGHAICG	RTQIGDGHA	0.0871	19491.7	50.00	Sequence
IAb	410	IVGEVTAKRLDTLRH	VGEVTAKRL	0.0856	19808.0	50.00	Sequence
IAb	317	EGAVRDVLDGKTAEF	RDVLDGKTA	0.0850	19942.0	50.00	Sequence
IAb	455	SVGVQGDGRTYGHPI	VGVQGDGRT	0.0844	20053.0	50.00	Sequence
IAb	433	LTAAGLDNQIWQCPV	LTAAGLDNQ	0.0842	20111.5	50.00	Sequence
IAb	112	REYGRTELKVLGGKL	REYGRTELK	0.0839	20162.2	50.00	Sequence
IAb	401	FPGPGLGIRIVGEVT	GIRIVGEVT	0.0829	20382.7	50.00	Sequence
IAb	83	DLGVPVLGICYGFQA	DLGVPVLGI	0.0825	20478.2	50.00	Sequence
IAb	223	GDGHAICGLSGGVDS	GHAICGLSG	0.0824	20495.0	50.00	Sequence
IAb	302	EGKRKIIGRQFIRAF	RKIIGRQFI	0.0822	20537.4	50.00	Sequence
IAb	499	ITNEVAEVNRVVLDI	NEVAEVNRV	0.0815	20706.3	50.00	Sequence
IAb	504	AEVNRVVLDITSKPP	RVVLDITSK	0.0809	20837.1	50.00	Sequence
IAb	349	GTANIKSHHNVGGLP	GTANIKSHH	0.0808	20859.2	50.00	Sequence
IAb	243	LVQRAIGDRLTCVFV	QRAIGDRLT	0.0808	20869.8	50.00	Sequence
IAb	411	VGEVTAKRLDTLRHA	VGEVTAKRL	0.0807	20886.8	50.00	Sequence
IAb	244	VQRAIGDRLTCVFVD	QRAIGDRLT	0.0807	20887.0	50.00	Sequence
IAb	212	NALIEQVRTQIGDGH	ALIEQVRTQ	0.0793	21209.5	50.00	Sequence
IAb	264	AGERAQVQRDFVAAT	VQRDFVAAT	0.0787	21348.8	50.00	Sequence
IAb	222	IGDGHAICGLSGGVD	GHAICGLSG	0.0783	21420.7	50.00	Sequence
IAb	297	GVSAPEGKRKIIGRQ	GVSAPEGKR	0.0775	21608.3	50.00	Sequence
IAb	315	AFEGAVRDVLDGKTA	RDVLDGKTA	0.0766	21821.0	50.00	Sequence
IAb	221	QIGDGHAICGLSGGV	GHAICGLSG	0.0757	22041.6	50.00	Sequence
IAb	245	QRAIGDRLTCVFVDH	QRAIGDRLT	0.0757	22054.0	50.00	Sequence
IAb	369	TLVEPLRLLFKDEVR	TLVEPLRLL	0.0749	22233.3	50.00	Sequence
IAb	414	VTAKRLDTLRHADSI	AKRLDTLRH	0.0732	22649.4	50.00	Sequence
IAb	211	ANALIEQVRTQIGDG	ALIEQVRTQ	0.0717	23012.3	50.00	Sequence
IAb	184	TPHGQQVLSRFLHDF	QQVLSRFLH	0.0705	23317.8	50.00	Sequence
IAb	370	LVEPLRLLFKDEVRA	RLLFKDEVR	0.0688	23763.5	50.00	Sequence
IAb	501	NEVAEVNRVVLDITS	EVAEVNRVV	0.0678	24018.4	50.00	Sequence
IAb	503	VAEVNRVVLDITSKP	RVVLDITSK	0.0655	24601.2	50.00	Sequence
IAb	412	GEVTAKRLDTLRHAD	VTAKRLDTL	0.0646	24842.0	50.00	Sequence
IAb	454	RSVGVQGDGRTYGHP	VGVQGDGRT	0.0629	25320.4	50.00	Sequence
IAb	316	FEGAVRDVLDGKTAE	DVLDGKTAE	0.0627	25375.3	50.00	Sequence
IAb	357	HNVGGLPDDLKFTLV	HNVGGLPDD	0.0622	25508.2	50.00	Sequence
IAb	358	NVGGLPDDLKFTLVE	DDLKFTLVE	0.0619	25579.2	50.00	Sequence
IAb	500	TNEVAEVNRVVLDIT	EVAEVNRVV	0.0617	25636.6	50.00	Sequence
IAb	502	EVAEVNRVVLDITSK	EVAEVNRVV	0.0617	25652.4	50.00	Sequence

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         IAb  413  EVTAKRLDTLRHADS  AKRLDTLRH        0.0612      25791.0                    50.00     Sequence
         IAb  298  VSAPEGKRKIIGRQF  SAPEGKRKI        0.0542      27820.2                    50.00     Sequence
         IAb  301  PEGKRKIIGRQFIRA  RKIIGRQFI        0.0535      28015.1                    50.00     Sequence
         IAb  359  VGGLPDDLKFTLVEP  DDLKFTLVE        0.0510      28794.4                    50.00     Sequence
         IAb  246  RAIGDRLTCVFVDHG  AIGDRLTCV        0.0479      29773.1                    50.00     Sequence
         IAb  299  SAPEGKRKIIGRQFI  SAPEGKRKI        0.0466      30185.7                    50.00     Sequence
         IAb  249  GDRLTCVFVDHGLLR  CVFVDHGLL        0.0455      30573.2                    50.00     Sequence
         IAb  247  AIGDRLTCVFVDHGL  AIGDRLTCV        0.0416      31877.1                    50.00     Sequence
         IAb  300  APEGKRKIIGRQFIR  RKIIGRQFI        0.0409      32134.7                    50.00     Sequence
         IAb  248  IGDRLTCVFVDHGLL  DRLTCVFVD        0.0394      32645.0                    50.00     Sequence
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Allele: IAb. Number of high binders 4. Number of weak binders 66. Number of peptides 511

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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         IAd  234  GVDSAVAAALVQRAI  VAAALVQRA        0.4864        259.0        WB      0.80     Sequence
         IAd  233  GGVDSAVAAALVQRA  VAAALVQRA        0.4771        286.6        WB      0.80     Sequence
         IAd  235  VDSAVAAALVQRAIG  VAAALVQRA        0.4580        352.2        WB      1.00     Sequence
         IAd  236  DSAVAAALVQRAIGD  VAAALVQRA        0.4540        367.9        WB      1.00     Sequence
         IAd  237  SAVAAALVQRAIGDR  VAAALVQRA        0.4539        368.3        WB      1.00     Sequence
         IAd  238  AVAAALVQRAIGDRL  VAAALVQRA        0.4369        442.5        WB      2.00     Sequence
         IAd  474  VSSEDAMTADWTRVP  VSSEDAMTA        0.4350        451.9        WB      2.00     Sequence
         IAd  473  PVSSEDAMTADWTRV  VSSEDAMTA        0.4346        453.6        WB      2.00     Sequence
         IAd  239  VAAALVQRAIGDRLT  VAAALVQRA        0.4338        457.8        WB      2.00     Sequence
         IAd  471  LRPVSSEDAMTADWT  VSSEDAMTA        0.4306        473.6        WB      2.00     Sequence
         IAd   22  GAQYAQLIARRVREA  YAQLIARRV        0.4226        516.9                  2.00     Sequence
         IAd   23  AQYAQLIARRVREAR  YAQLIARRV        0.4213        523.9                  2.00     Sequence
         IAd   43  IPHTASIEEIRARQP  TASIEEIRA        0.4191        536.3                  2.00     Sequence
         IAd  472  RPVSSEDAMTADWTR  VSSEDAMTA        0.4155        557.9                  2.00     Sequence
         IAd  469  IVLRPVSSEDAMTAD  VSSEDAMTA        0.4120        579.4                  2.00     Sequence
         IAd  470  VLRPVSSEDAMTADW  VSSEDAMTA        0.4098        593.5                  2.00     Sequence
         IAd  468  PIVLRPVSSEDAMTA  VSSEDAMTA        0.4053        622.7                  2.00     Sequence
         IAd   21  FGAQYAQLIARRVRE  YAQLIARRV        0.4035        635.0                  2.00     Sequence
         IAd   20  DFGAQYAQLIARRVR  YAQLIARRV        0.3946        699.6                  4.00     Sequence
         IAd   44  PHTASIEEIRARQPV  TASIEEIRA        0.3854        772.5                  4.00     Sequence
         IAd   42  VIPHTASIEEIRARQ  TASIEEIRA        0.3732        881.2                  4.00     Sequence
         IAd  287  AAETFLEALSGVSAP  LEALSGVSA        0.3712        900.6                  4.00     Sequence
         IAd   19  VDFGAQYAQLIARRV  YAQLIARRV        0.3688        925.1                  4.00     Sequence
         IAd  277  ATGANLVTVDAAETF  ANLVTVDAA        0.3677        935.8                  4.00     Sequence
         IAd  265  GERAQVQRDFVAATG  AQVQRDFVA        0.3669        943.5                  4.00     Sequence
         IAd   41  EVIPHTASIEEIRAR  ASIEEIRAR        0.3561       1060.5                  4.00     Sequence
         IAd  185  PHGQQVLSRFLHDFA  PHGQQVLSR        0.3559       1062.7                  4.00     Sequence
         IAd  276  AATGANLVTVDAAET  ANLVTVDAA        0.3551       1072.1                  4.00     Sequence
         IAd  184  TPHGQQVLSRFLHDF  HGQQVLSRF        0.3530       1096.7                  8.00     Sequence
         IAd   24  QYAQLIARRVREARV  YAQLIARRV        0.3520       1108.8                  8.00     Sequence
         IAd  286  DAAETFLEALSGVSA  LEALSGVSA        0.3513       1117.4                  8.00     Sequence
         IAd   28  LIARRVREARVFSEV  VREARVFSE        0.3477       1162.3                  8.00     Sequence
         IAd  266  ERAQVQRDFVAATGA  AQVQRDFVA        0.3454       1191.4                  8.00     Sequence
         IAd  405  GLGIRIVGEVTAKRL  IRIVGEVTA        0.3439       1210.2                  8.00     Sequence
         IAd  183  HTPHGQQVLSRFLHD  HGQQVLSRF        0.3424       1230.2                  8.00     Sequence
         IAd   30  ARRVREARVFSEVIP  VREARVFSE        0.3404       1256.7                  8.00     Sequence
         IAd   29  IARRVREARVFSEVI  VREARVFSE        0.3391       1274.6                  8.00     Sequence
         IAd  466  GHPIVLRPVSSEDAM  GHPIVLRPV        0.3378       1293.5                  8.00     Sequence
         IAd   25  YAQLIARRVREARVF  YAQLIARRV        0.3363       1314.2                  8.00     Sequence
         IAd   96  QAMAQALGGIVAHTG  AQALGGIVA        0.3357       1323.1                  8.00     Sequence
         IAd  406  LGIRIVGEVTAKRLD  IRIVGEVTA        0.3331       1361.4                  8.00     Sequence
         IAd   94  GFQAMAQALGGIVAH  AQALGGIVA        0.3316       1383.5                  8.00     Sequence
         IAd  264  AGERAQVQRDFVAAT  AQVQRDFVA        0.3299       1408.5                  8.00     Sequence
         IAd   93  YGFQAMAQALGGIVA  YGFQAMAQA        0.3279       1439.0                  8.00     Sequence
         IAd  182  MHTPHGQQVLSRFLH  PHGQQVLSR        0.3269       1454.3                  8.00     Sequence
         IAd   50  EEIRARQPVALVLSG  ARQPVALVL        0.3252       1481.6                  8.00     Sequence
         IAd  289  ETFLEALSGVSAPEG  LEALSGVSA        0.3250       1485.5                  8.00     Sequence
         IAd  278  TGANLVTVDAAETFL  ANLVTVDAA        0.3240       1501.4                  8.00     Sequence
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IAd	46	TASIEEIRARQPVAL	ASIEEIRAR	0.3239	1503.8	8.00	Sequence
IAd	95	FQAMAQALGGIVAHT	AMAQALGGI	0.3227	1523.2	8.00	Sequence
IAd	411	VGEVTAKRLDTLRHA	AKRLDTLRH	0.3214	1544.8	8.00	Sequence
IAd	279	GANLVTVDAAETFLE	ANLVTVDAA	0.3212	1548.4	8.00	Sequence
IAd	290	TFLEALSGVSAPEGK	LEALSGVSA	0.3178	1605.1	8.00	Sequence
IAd	263	RAGERAQVQRDFVAA	AQVQRDFVA	0.3172	1615.3	8.00	Sequence
IAd	267	RAQVQRDFVAATGAN	AQVQRDFVA	0.3154	1648.5	8.00	Sequence
IAd	45	HTASIEEIRARQPVA	ASIEEIRAR	0.3152	1651.7	8.00	Sequence
IAd	465	YGHPIVLRPVSSEDA	GHPIVLRPV	0.3148	1659.0	8.00	Sequence
IAd	288	AETFLEALSGVSAPE	LEALSGVSA	0.3147	1660.6	8.00	Sequence
IAd	52	IRARQPVALVLSGGP	RARQPVALV	0.3099	1749.4	8.00	Sequence
IAd	280	ANLVTVDAAETFLEA	ANLVTVDAA	0.3097	1752.9	8.00	Sequence
IAd	416	AKRLDTLRHADSIVR	LRHADSIVR	0.3094	1758.2	8.00	Sequence
IAd	422	LRHADSIVREELTAA	RHADSIVRE	0.3084	1777.7	8.00	Sequence
IAd	51	EIRARQPVALVLSGG	RARQPVALV	0.3069	1805.7	8.00	Sequence
IAd	27	QLIARRVREARVFSE	VREARVFSE	0.3066	1812.1	8.00	Sequence
IAd	97	AMAQALGGIVAHTGT	AQALGGIVA	0.3031	1882.2	8.00	Sequence
IAd	419	LDTLRHADSIVREEL	LRHADSIVR	0.3019	1907.9	8.00	Sequence
IAd	291	FLEALSGVSAPEGKR	LEALSGVSA	0.3013	1920.5	8.00	Sequence
IAd	420	DTLRHADSIVREELT	RHADSIVRE	0.2994	1959.0	16.00	Sequence
IAd	417	KRLDTLRHADSIVRE	LRHADSIVR	0.2991	1965.4	16.00	Sequence
IAd	33	VREARVFSEVIPHTA	VREARVFSE	0.2986	1976.2	16.00	Sequence
IAd	412	GEVTAKRLDTLRHAD	AKRLDTLRH	0.2981	1987.7	16.00	Sequence
IAd	49	IEEIRARQPVALVLS	IRARQPVAL	0.2969	2013.6	16.00	Sequence
IAd	418	RLDTLRHADSIVREE	RHADSIVRE	0.2955	2044.2	16.00	Sequence
IAd	292	LEALSGVSAPEGKRK	LEALSGVSA	0.2947	2061.2	16.00	Sequence
IAd	31	RRVREARVFSEVIPH	VREARVFSE	0.2940	2076.5	16.00	Sequence
IAd	47	ASIEEIRARQPVALV	ASIEEIRAR	0.2934	2090.0	16.00	Sequence
IAd	413	EVTAKRLDTLRHADS	AKRLDTLRH	0.2931	2097.3	16.00	Sequence
IAd	407	GIRIVGEVTAKRLDT	IRIVGEVTA	0.2918	2127.5	16.00	Sequence
IAd	441	QIWQCPVVLLADVRS	CPVVLLADV	0.2917	2129.4	16.00	Sequence
IAd	275	VAATGANLVTVDAAE	ANLVTVDAA	0.2912	2141.2	16.00	Sequence
IAd	421	TLRHADSIVREELTA	RHADSIVRE	0.2901	2165.7	16.00	Sequence
IAd	136	VWMSHGDAVTAAPDG	MSHGDAVTA	0.2887	2200.6	16.00	Sequence
IAd	135	PVWMSHGDAVTAAPD	MSHGDAVTA	0.2869	2244.2	16.00	Sequence
IAd	442	IWQCPVVLLADVRSV	VLLADVRSV	0.2866	2250.0	16.00	Sequence
IAd	240	AAALVQRAIGDRLTC	QRAIGDRLT	0.2862	2259.0	16.00	Sequence
IAd	137	WMSHGDAVTAAPDGF	MSHGDAVTA	0.2862	2259.8	16.00	Sequence
IAd	154	VASSAGAPVAAFEAF	SAGAPVAAF	0.2849	2293.0	16.00	Sequence
IAd	134	QPVWMSHGDAVTAAP	MSHGDAVTA	0.2832	2335.3	16.00	Sequence
IAd	32	RVREARVFSEVIPHT	VREARVFSE	0.2825	2351.4	16.00	Sequence
IAd	114	YGRTELKVLGGKLHS	RTELKVLGG	0.2816	2376.2	16.00	Sequence
IAd	40	SEVIPHTASIEEIRA	TASIEEIRA	0.2808	2396.4	16.00	Sequence
IAd	443	WQCPVVLLADVRSVG	VLLADVRSV	0.2799	2419.0	16.00	Sequence
IAd	138	MSHGDAVTAAPDGFD	MSHGDAVTA	0.2783	2460.5	16.00	Sequence
IAd	404	PGLGIRIVGEVTAKR	IRIVGEVTA	0.2781	2465.9	16.00	Sequence
IAd	414	VTAKRLDTLRHADSI	AKRLDTLRH	0.2752	2547.0	16.00	Sequence
IAd	133	VQPVWMSHGDAVTAA	MSHGDAVTA	0.2738	2584.4	16.00	Sequence
IAd	232	SGGVDSAVAAALVQR	AVAAALVQR	0.2737	2586.7	16.00	Sequence
IAd	53	RARQPVALVLSGGPA	RARQPVALV	0.2736	2589.5	16.00	Sequence
IAd	274	FVAATGANLVTVDAA	ANLVTVDAA	0.2734	2594.5	16.00	Sequence
IAd	268	AQVQRDFVAATGANL	QVQRDFVAA	0.2726	2618.2	16.00	Sequence
IAd	181	VMHTPHGQQVLSRFL	PHGQQVLSR	0.2701	2690.5	16.00	Sequence
IAd	186	HGQQVLSRFLHDFAG	HGQQVLSRF	0.2670	2781.4	16.00	Sequence
IAd	153	VVASSAGAPVAAFEA	SAGAPVAAF	0.2628	2911.3	16.00	Sequence
IAd	475	SSEDAMTADWTRVPY	AMTADWTRV	0.2625	2920.4	16.00	Sequence
IAd	262	LRAGERAQVQRDFVA	AQVQRDFVA	0.2616	2948.8	16.00	Sequence
IAd	113	EYGRTELKVLGGKLH	RTELKVLGG	0.2615	2953.8	16.00	Sequence
IAd	48	SIEEIRARQPVALVL	IRARQPVAL	0.2605	2983.7	16.00	Sequence
IAd	410	IVGEVTAKRLDTLRH	VGEVTAKRL	0.2594	3021.7	16.00	Sequence
IAd	132	EVQPVWMSHGDAVTA	MSHGDAVTA	0.2590	3032.1	16.00	Sequence
IAd	439	DNQIWQCPVVLLADV	WQCPVVLLA	0.2582	3060.0	16.00	Sequence
IAd	440	NQIWQCPVVLLADVR	WQCPVVLLA	0.2582	3061.3	16.00	Sequence
IAd	156	SSAGAPVAAFEAFDR	SAGAPVAAF	0.2576	3080.9	16.00	Sequence
IAd	423	RHADSIVREELTAAG	RHADSIVRE	0.2541	3199.0	16.00	Sequence
IAd	467	HPIVLRPVSSEDAMT	LRPVSSEDA	0.2525	3256.1	16.00	Sequence

IAd	408	IRIVGEVTAKRLDTL	IRIVGEVTA	0.2516	3284.6	16.00	Sequence
IAd	403	GPGLGIRIVGEVTAK	IRIVGEVTA	0.2506	3321.6	16.00	Sequence
IAd	476	SEDAMTADWTRVPYE	AMTADWTRV	0.2501	3341.6	16.00	Sequence
IAd	415	TAKRLDTLRHADSIV	AKRLDTLRH	0.2471	3449.6	16.00	Sequence
IAd	155	ASSAGAPVAAFEAFD	GAPVAAFEA	0.2454	3514.6	16.00	Sequence
IAd	39	FSEVIPHTASIEEIR	FSEVIPHTA	0.2435	3588.3	32.00	Sequence
IAd	92	CYGFQAMAQALGGIV	YGFQAMAQA	0.2428	3614.5	32.00	Sequence
IAd	244	VQRAIGDRLTCVFVD	VQRAIGDRL	0.2425	3625.3	32.00	Sequence
IAd	229	CGLSGGVDSAVAAAL	GGVDSAVAA	0.2420	3645.0	32.00	Sequence
IAd	180	EVMHTPHGQQVLSRF	PHGQQVLSR	0.2392	3758.7	32.00	Sequence
IAd	478	DAMTADWTRVPYEVL	AMTADWTRV	0.2390	3764.7	32.00	Sequence
IAd	112	REYGRTELKVLGGKL	RTELKVLGG	0.2380	3807.0	32.00	Sequence
IAd	157	SAGAPVAAFEAFDRR	GAPVAAFEA	0.2371	3843.3	32.00	Sequence
IAd	444	QCPVVLLADVRSVGV	VVLLADVRS	0.2363	3876.4	32.00	Sequence
IAd	12	PARPVLVVDFGAQYA	ARPVLVVDF	0.2354	3917.0	32.00	Sequence
IAd	231	LSGGVDSAVAAALVQ	GGVDSAVAA	0.2325	4039.8	32.00	Sequence
IAd	245	QRAIGDRLTCVFVDH	QRAIGDRLT	0.2318	4072.0	32.00	Sequence
IAd	477	EDAMTADWTRVPYEV	AMTADWTRV	0.2314	4088.7	32.00	Sequence
IAd	151	FDVVASSAGAPVAAF	VASSAGAPV	0.2300	4152.3	32.00	Sequence
IAd	230	GLSGGVDSAVAAALV	GGVDSAVAA	0.2297	4164.6	32.00	Sequence
IAd	11	TPARPVLVVDFGAQY	ARPVLVVDF	0.2296	4168.2	32.00	Sequence
IAd	504	AEVNRVVLDITSKPP	RVVLDITSK	0.2289	4199.8	32.00	Sequence
IAd	402	PGPGLGIRIVGEVTA	IRIVGEVTA	0.2284	4225.2	32.00	Sequence
IAd	281	NLVTVDAAETFLEAL	LVTVDAAET	0.2278	4252.2	32.00	Sequence
IAd	10	ETPARPVLVVDFGAQ	ARPVLVVDF	0.2270	4290.1	32.00	Sequence
IAd	463	RTYGHPIVLRPVSSE	GHPIVLRPV	0.2254	4364.0	32.00	Sequence
IAd	464	TYGHPIVLRPVSSED	GHPIVLRPV	0.2253	4367.4	32.00	Sequence
IAd	303	GKRKIIGRQFIRAFE	KRKIIGRQF	0.2237	4443.2	32.00	Sequence
IAd	462	GRTYGHPIVLRPVSS	GHPIVLRPV	0.2237	4444.0	32.00	Sequence
IAd	150	GFDVVASSAGAPVAA	ASSAGAPVA	0.2231	4475.7	32.00	Sequence
IAd	241	AALVQRAIGDRLTCV	QRAIGDRLT	0.2212	4568.4	32.00	Sequence
IAd	502	EVAEVNRVVLDITSK	NRVVLDITS	0.2210	4575.7	32.00	Sequence
IAd	302	EGKRKIIGRQFIRAF	KRKIIGRQF	0.2209	4578.9	32.00	Sequence
IAd	424	HADSIVREELTAAGL	REELTAAGL	0.2209	4579.8	32.00	Sequence
IAd	152	DVVASSAGAPVAAFE	VASSAGAPV	0.2196	4648.3	32.00	Sequence
IAd	505	EVNRVVLDITSKPPA	VNRVVLDIT	0.2194	4657.9	32.00	Sequence
IAd	282	LVTVDAAETFLEALS	AAETFLEAL	0.2193	4658.9	32.00	Sequence
IAd	74	APKLDPALLDLGVPV	PALLDLGVP	0.2186	4698.5	32.00	Sequence
IAd	91	ICYGFQAMAQALGGI	YGFQAMAQA	0.2183	4710.7	32.00	Sequence
IAd	503	VAEVNRVVLDITSKP	RVVLDITSK	0.2181	4721.2	32.00	Sequence
IAd	34	REARVFSEVIPHTAS	FSEVIPHTA	0.2177	4744.1	32.00	Sequence
IAd	76	KLDPALLDLGVPVLG	PALLDLGVP	0.2169	4785.2	32.00	Sequence
IAd	246	RAIGDRLTCVFVDHG	GDRLTCVFV	0.2157	4846.0	32.00	Sequence
IAd	26	AQLIARRVREARVFS	ARRVREARV	0.2153	4869.7	32.00	Sequence
IAd	9	PETPARPVLVVDFGA	ARPVLVVDF	0.2148	4892.3	32.00	Sequence
IAd	18	VVDFGAQYAQLIARR	QYAQLIARR	0.2140	4936.3	32.00	Sequence
IAd	77	LDPALLDLGVPVLGI	PALLDLGVP	0.2127	5006.8	32.00	Sequence
IAd	506	VNRVVLDITSKPPAT	VNRVVLDIT	0.2115	5073.2	32.00	Sequence
IAd	75	PKLDPALLDLGVPVL	PALLDLGVP	0.2092	5201.8	32.00	Sequence
IAd	301	PEGKRKIIGRQFIRA	KRKIIGRQF	0.2092	5201.9	32.00	Sequence
IAd	111	TREYGRTELKVLGGK	RTELKVLGG	0.2087	5229.2	32.00	Sequence
IAd	242	ALVQRAIGDRLTCVF	QRAIGDRLT	0.2083	5247.5	32.00	Sequence
IAd	461	DGRTYGHPIVLRPVS	GHPIVLRPV	0.2082	5253.1	32.00	Sequence
IAd	38	VFSEVIPHTASIEEI	FSEVIPHTA	0.2082	5257.2	32.00	Sequence
IAd	445	CPVVLLADVRSVGVQ	VVLLADVRS	0.2074	5304.2	32.00	Sequence
IAd	501	NEVAEVNRVVLDITS	NRVVLDITS	0.2069	5329.4	32.00	Sequence
IAd	438	LDNQIWQCPVVLLAD	WQCPVVLLA	0.2056	5407.3	32.00	Sequence
IAd	447	VVLLADVRSVGVQGD	VVLLADVRS	0.2048	5451.3	32.00	Sequence
IAd	54	ARQPVALVLSGGPAS	ARQPVALVL	0.2041	5495.2	32.00	Sequence
IAd	98	MAQALGGIVAHTGTR	AQALGGIVA	0.2039	5505.0	32.00	Sequence
IAd	224	DGHAICGLSGGVDSA	GHAICGLSG	0.2036	5526.5	32.00	Sequence
IAd	13	ARPVLVVDFGAQYAQ	ARPVLVVDF	0.2031	5553.5	32.00	Sequence
IAd	381	EVRAVGRELGLPEEI	VGRELGLPE	0.2012	5671.1	32.00	Sequence
IAd	380	DEVRAVGRELGLPEE	VGRELGLPE	0.2009	5690.1	32.00	Sequence
IAd	73	GAPKLDPALLDLGVP	APKLDPALL	0.2007	5702.7	32.00	Sequence
IAd	78	DPALLDLGVPVLGIC	PALLDLGVP	0.1994	5779.2	32.00	Sequence

IAd	269	QVQRDFVAATGANLV	QVQRDFVAA	0.1980	5869.0	32.00	Sequence
IAd	315	AFEGAVRDVLDGKTA	RDVLDGKTA	0.1968	5943.7	32.00	Sequence
IAd	481	TADWTRVPYEVLERI	VPYEVLERI	0.1967	5952.7	32.00	Sequence
IAd	110	GTREYGRTELKVLGG	RTELKVLGG	0.1942	6115.5	32.00	Sequence
IAd	221	QIGDGHAICGLSGGV	GHAICGLSG	0.1922	6247.2	32.00	Sequence
IAd	223	GDGHAICGLSGGVDS	GHAICGLSG	0.1914	6302.1	32.00	Sequence
IAd	243	LVQRAIGDRLTCVFV	QRAIGDRLT	0.1908	6341.3	32.00	Sequence
IAd	128	SDLPEVQPVWMSHGD	PEVQPVWMS	0.1905	6364.1	32.00	Sequence
IAd	115	GRTELKVLGGKLHSD	RTELKVLGG	0.1900	6399.3	32.00	Sequence
IAd	383	RAVGRELGLPEEIVA	VGRELGLPE	0.1884	6513.8	32.00	Sequence
IAd	222	IGDGHAICGLSGGVD	GHAICGLSG	0.1883	6519.9	32.00	Sequence
IAd	8	VPETPARPVLVVDFG	ARPVLVVDF	0.1877	6557.6	32.00	Sequence
IAd	479	AMTADWTRVPYEVLE	AMTADWTRV	0.1877	6560.3	32.00	Sequence
IAd	425	ADSIVREELTAAGLD	REELTAAGL	0.1867	6629.6	32.00	Sequence
IAd	382	VRAVGRELGLPEEIV	VGRELGLPE	0.1862	6669.6	32.00	Sequence
IAd	409	RIVGEVTAKRLDTLR	VGEVTAKRL	0.1860	6679.2	32.00	Sequence
IAd	219	RTQIGDGHAICGLSG	GHAICGLSG	0.1851	6751.5	32.00	Sequence
IAd	55	RQPVALVLSGGPASV	RQPVALVLS	0.1849	6763.5	32.00	Sequence
IAd	427	SIVREELTAAGLDNQ	REELTAAGL	0.1847	6777.1	32.00	Sequence
IAd	283	VTVDAAETFLEALSG	AAETFLEAL	0.1845	6793.8	32.00	Sequence
IAd	127	HSDLPEVQPVWMSHG	PEVQPVWMS	0.1841	6824.9	32.00	Sequence
IAd	149	DGFDVVASSAGAPVA	ASSAGAPVA	0.1838	6840.2	32.00	Sequence
IAd	285	VDAAETFLEALSGVS	AAETFLEAL	0.1837	6852.5	32.00	Sequence
IAd	220	TQIGDGHAICGLSGG	GHAICGLSG	0.1836	6855.3	32.00	Sequence
IAd	385	VGRELGLPEEIVARQ	LPEEIVARQ	0.1830	6906.1	32.00	Sequence
IAd	486	RVPYEVLERISTRIT	YEVLERIST	0.1829	6910.4	32.00	Sequence
IAd	300	APEGKRKIIGRQFIR	KRKIIGRQF	0.1827	6923.2	32.00	Sequence
IAd	426	DSIVREELTAAGLDN	REELTAAGL	0.1825	6938.1	32.00	Sequence
IAd	228	ICGLSGGVDSAVAAA	GGVDSAVAA	0.1806	7087.2	32.00	Sequence
IAd	487	VPYEVLERISTRITN	YEVLERIST	0.1805	7094.6	32.00	Sequence
IAd	437	GLDNQIWQCPVVLLA	WQCPVVLLA	0.1798	7149.0	32.00	Sequence
IAd	205	WTPANIANALIEQVR	IANALIEQV	0.1791	7200.4	32.00	Sequence
IAd	460	GDGRTYGHPIVLRPV	GHPIVLRPV	0.1786	7238.5	50.00	Sequence
IAd	428	IVREELTAAGLDNQI	REELTAAGL	0.1784	7256.5	50.00	Sequence
IAd	225	GHAICGLSGGVDSAV	GHAICGLSG	0.1779	7296.7	50.00	Sequence
IAd	384	AVGRELGLPEEIVAR	VGRELGLPE	0.1773	7342.2	50.00	Sequence
IAd	90	GICYGFQAMAQALGG	YGFQAMAQA	0.1772	7352.1	50.00	Sequence
IAd	379	KDEVRAVGRELGLPE	RAVGRELGL	0.1770	7365.6	50.00	Sequence
IAd	158	AGAPVAAFEAFDRRL	GAPVAAFEA	0.1770	7365.8	50.00	Sequence
IAd	159	GAPVAAFEAFDRRLA	GAPVAAFEA	0.1767	7392.0	50.00	Sequence
IAd	37	RVFSEVIPHTASIEE	FSEVIPHTA	0.1749	7533.4	50.00	Sequence
IAd	204	QWTPANIANALIEQV	IANALIEQV	0.1742	7591.5	50.00	Sequence
IAd	482	ADWTRVPYEVLERIS	VPYEVLERI	0.1742	7596.1	50.00	Sequence
IAd	261	LLRAGERAQVQRDFV	GERAQVQRD	0.1732	7674.5	50.00	Sequence
IAd	304	KRKIIGRQFIRAFEG	KRKIIGRQF	0.1730	7690.5	50.00	Sequence
IAd	129	DLPEVQPVWMSHGDA	PEVQPVWMS	0.1728	7704.8	50.00	Sequence
IAd	284	TVDAAETFLEALSGV	AAETFLEAL	0.1726	7725.4	50.00	Sequence
IAd	507	NRVVLDITSKPPATI	RVVLDITSK	0.1717	7803.1	50.00	Sequence
IAd	484	WTRVPYEVLERISTR	YEVLERIST	0.1705	7901.2	50.00	Sequence
IAd	318	GAVRDVLDGKTAEFL	VRDVLDGKT	0.1694	7995.4	50.00	Sequence
IAd	99	AQALGGIVAHTGTRE	AQALGGIVA	0.1684	8087.4	50.00	Sequence
IAd	130	LPEVQPVWMSHGDAV	PEVQPVWMS	0.1660	8295.9	50.00	Sequence
IAd	319	AVRDVLDGKTAEFLV	VRDVLDGKT	0.1660	8301.8	50.00	Sequence
IAd	316	FEGAVRDVLDGKTAE	RDVLDGKTA	0.1659	8303.8	50.00	Sequence
IAd	79	PALLDLGVPVLGICY	PALLDLGVP	0.1656	8331.4	50.00	Sequence
IAd	299	SAPEGKRKIIGRQFI	KRKIIGRQF	0.1652	8371.8	50.00	Sequence
IAd	483	DWTRVPYEVLERIST	YEVLERIST	0.1649	8392.9	50.00	Sequence
IAd	167	AFDRRLAGVQYHPEV	RRLAGVQYH	0.1645	8431.2	50.00	Sequence
IAd	247	AIGDRLTCVFVDHGL	GDRLTCVFV	0.1644	8443.7	50.00	Sequence
IAd	270	VQRDFVAATGANLVT	VQRDFVAAT	0.1642	8459.3	50.00	Sequence
IAd	429	VREELTAAGLDNQIW	REELTAAGL	0.1635	8522.9	50.00	Sequence
IAd	446	PVVLLADVRSVGVQG	VLLADVRSV	0.1634	8537.0	50.00	Sequence
IAd	448	VLLADVRSVGVQGDG	VLLADVRSV	0.1633	8540.3	50.00	Sequence
IAd	72	DGAPKLDPALLDLGV	APKLDPALL	0.1625	8618.6	50.00	Sequence
IAd	116	RTELKVLGGKLHSDL	RTELKVLGG	0.1622	8648.9	50.00	Sequence
IAd	488	PYEVLERISTRITNE	YEVLERIST	0.1607	8786.8	50.00	Sequence

IAd	317	EGAVRDVLDGKTAEF	RDVLDGKTA	0.1599	8864.4	50.00	Sequence
IAd	125	KLHSDLPEVQPVWMS	PEVQPVWMS	0.1597	8884.4	50.00	Sequence
IAd	451	ADVRSVGVQGDGRTY	VRSVGVQGD	0.1595	8899.7	50.00	Sequence
IAd	7	DVPETPARPVLVVDF	ARPVLVVDF	0.1589	8958.3	50.00	Sequence
IAd	387	RELGLPEEIVARQPF	GLPEEIVAR	0.1575	9101.4	50.00	Sequence
IAd	298	VSAPEGKRKIIGRQF	KRKIIGRQF	0.1573	9121.3	50.00	Sequence
IAd	35	EARVFSEVIPHTASI	FSEVIPHTA	0.1572	9128.8	50.00	Sequence
IAd	450	LADVRSVGVQGDGRT	VRSVGVQGD	0.1570	9149.1	50.00	Sequence
IAd	386	GRELGLPEEIVARQP	GLPEEIVAR	0.1570	9149.5	50.00	Sequence
IAd	271	QRDFVAATGANLVTV	RDFVAATGA	0.1569	9152.6	50.00	Sequence
IAd	320	VRDVLDGKTAEFLVQ	RDVLDGKTA	0.1561	9237.7	50.00	Sequence
IAd	213	ALIEQVRTQIGDGHA	RTQIGDGHA	0.1560	9247.9	50.00	Sequence
IAd	260	GLLRAGERAQVQRDF	LRAGERAQV	0.1550	9345.0	50.00	Sequence
IAd	166	EAFDRRLAGVQYHPE	RRLAGVQYH	0.1544	9410.2	50.00	Sequence
IAd	126	LHSDLPEVQPVWMSH	PEVQPVWMS	0.1542	9424.5	50.00	Sequence
IAd	485	TRVPYEVLERISTRI	YEVLERIST	0.1538	9471.7	50.00	Sequence
IAd	227	AICGLSGGVDSAVAA	GGVDSAVAA	0.1534	9509.8	50.00	Sequence
IAd	168	FDRRLAGVQYHPEVM	RRLAGVQYH	0.1529	9558.8	50.00	Sequence
IAd	309	GRQFIRAFEGAVRDV	IRAFEGAVR	0.1513	9727.0	50.00	Sequence
IAd	489	YEVLERISTRITNEV	YEVLERIST	0.1510	9758.8	50.00	Sequence
IAd	500	TNEVAEVNRVVLDIT	NEVAEVNRV	0.1507	9795.8	50.00	Sequence
IAd	131	PEVQPVWMSHGDAVT	PEVQPVWMS	0.1505	9809.2	50.00	Sequence
IAd	2	QPADIDVPETPARPV	PADIDVPET	0.1505	9816.6	50.00	Sequence
IAd	165	FEAFDRRLAGVQYHP	RRLAGVQYH	0.1481	10070.6	50.00	Sequence
IAd	391	LPEEIVARQPFPGPG	EEIVARQPF	0.1472	10170.1	50.00	Sequence
IAd	17	LVVDFGAQYAQLIAR	AQYAQLIAR	0.1469	10203.8	50.00	Sequence
IAd	435	AAGLDNQIWQCPVVL	NQIWQCPVV	0.1468	10210.6	50.00	Sequence
IAd	390	GLPEEIVARQPFPGP	PEEIVARQP	0.1465	10243.8	50.00	Sequence
IAd	214	LIEQVRTQIGDGHAI	IEQVRTQIG	0.1464	10252.0	50.00	Sequence
IAd	71	ADGAPKLDPALLDLG	APKLDPALL	0.1464	10260.9	50.00	Sequence
IAd	308	IGRQFIRAFEGAVRD	IGRQFIRAF	0.1448	10437.5	50.00	Sequence
IAd	160	APVAAFEAFDRRLAG	APVAAFEAF	0.1446	10459.4	50.00	Sequence
IAd	256	FVDHGLLRAGERAQV	FVDHGLLRA	0.1439	10544.0	50.00	Sequence
IAd	310	RQFIRAFEGAVRDVL	AFEGAVRDV	0.1438	10548.4	50.00	Sequence
IAd	248	IGDRLTCVFVDHGLL	GDRLTCVFV	0.1433	10607.1	50.00	Sequence
IAd	449	LLADVRSVGVQGDGR	LADVRSVGV	0.1431	10633.1	50.00	Sequence
IAd	249	GDRLTCVFVDHGLLR	GDRLTCVFV	0.1430	10645.1	50.00	Sequence
IAd	89	LGICYGFQAMAQALG	YGFQAMAQA	0.1429	10653.4	50.00	Sequence
IAd	202	GAQWTPANIANALIE	WTPANIANA	0.1425	10703.3	50.00	Sequence
IAd	56	QPVALVLSGGPASVY	QPVALVLSG	0.1416	10806.4	50.00	Sequence
IAd	389	LGLPEEIVARQPFPG	LPEEIVARQ	0.1410	10870.8	50.00	Sequence
IAd	169	DRRLAGVQYHPEVMH	RRLAGVQYH	0.1409	10891.3	50.00	Sequence
IAd	179	PEVMHTPHGQQVLSR	PHGQQVLSR	0.1408	10899.5	50.00	Sequence
IAd	480	MTADWTRVPYEVLER	RVPYEVLER	0.1405	10932.9	50.00	Sequence
IAd	453	VRSVGVQGDGRTYGH	VRSVGVQGD	0.1404	10951.0	50.00	Sequence
IAd	259	HGLLRAGERAQVQRD	LRAGERAQV	0.1402	10965.3	50.00	Sequence
IAd	257	VDHGLLRAGERAQVQ	LRAGERAQV	0.1399	11010.3	50.00	Sequence
IAd	0	VVQPADIDVPETPAR	PADIDVPET	0.1394	11066.8	50.00	Sequence
IAd	452	DVRSVGVQGDGRTYG	VRSVGVQGD	0.1390	11109.4	50.00	Sequence
IAd	211	ANALIEQVRTQIGDG	IEQVRTQIG	0.1385	11171.4	50.00	Sequence
IAd	250	DRLTCVFVDHGLLRA	FVDHGLLRA	0.1384	11181.3	50.00	Sequence
IAd	273	DFVAATGANLVTVDA	GANLVTVDA	0.1383	11193.4	50.00	Sequence
IAd	212	NALIEQVRTQIGDGH	NALIEQVRT	0.1382	11204.7	50.00	Sequence
IAd	203	AQWTPANIANALIEQ	WTPANIANA	0.1379	11246.8	50.00	Sequence
IAd	388	ELGLPEEIVARQPFP	LPEEIVARQ	0.1377	11268.0	50.00	Sequence
IAd	354	KSHHNVGGLPDDLKF	HHNVGGLPD	0.1375	11290.8	50.00	Sequence
IAd	436	AGLDNQIWQCPVVLL	IWQCPVVLL	0.1372	11335.1	50.00	Sequence
IAd	215	IEQVRTQIGDGHAIC	IEQVRTQIG	0.1359	11485.7	50.00	Sequence
IAd	192	SRFLHDFAGLGAQWT	LHDFAGLGA	0.1336	11778.2	50.00	Sequence
IAd	200	GLGAQWTPANIANAL	WTPANIANA	0.1328	11878.9	50.00	Sequence
IAd	36	ARVFSEVIPHTASIE	FSEVIPHTA	0.1325	11927.1	50.00	Sequence
IAd	321	RDVLDGKTAEFLVQG	RDVLDGKTA	0.1316	12036.8	50.00	Sequence
IAd	148	PDGFDVVASSAGAPV	VASSAGAPV	0.1314	12061.8	50.00	Sequence
IAd	307	IIGRQFIRAFEGAVR	RQFIRAFEG	0.1308	12144.0	50.00	Sequence
IAd	217	QVRTQIGDGHAICGL	RTQIGDGHA	0.1301	12237.2	50.00	Sequence
IAd	392	PEEIVARQPFPGPGL	IVARQPFPG	0.1297	12292.9	50.00	Sequence

IAd	216	EQVRTQIGDGHAICG	RTQIGDGHA	0.1295	12318.9	50.00	Sequence
IAd	498	RITNEVAEVNRVVLD	NEVAEVNRV	0.1294	12323.9	50.00	Sequence
IAd	210	IANALIEQVRTQIGD	IANALIEQV	0.1290	12376.3	50.00	Sequence
IAd	1	VQPADIDVPETPARP	PADIDVPET	0.1287	12419.8	50.00	Sequence
IAd	193	RFLHDFAGLGAQWTP	LHDFAGLGA	0.1284	12466.5	50.00	Sequence
IAd	311	QFIRAFEGAVRDVLD	IRAFEGAVR	0.1282	12492.6	50.00	Sequence
IAd	195	LHDFAGLGAQWTPAN	LHDFAGLGA	0.1274	12594.1	50.00	Sequence
IAd	164	AFEAFDRRLAGVQYH	RRLAGVQYH	0.1273	12613.6	50.00	Sequence
IAd	495	ISTRITNEVAEVNRV	NEVAEVNRV	0.1257	12833.6	50.00	Sequence
IAd	272	RDFVAATGANLVTVD	RDFVAATGA	0.1253	12881.5	50.00	Sequence
IAd	171	RLAGVQYHPEVMHTP	YHPEVMHTP	0.1253	12884.5	50.00	Sequence
IAd	170	RRLAGVQYHPEVMHT	RRLAGVQYH	0.1250	12923.4	50.00	Sequence
IAd	353	IKSHHNVGGLPDDLK	KSHHNVGGL	0.1250	12927.9	50.00	Sequence
IAd	312	FIRAFEGAVRDVLDG	IRAFEGAVR	0.1250	12935.0	50.00	Sequence
IAd	14	RPVLVVDFGAQYAQL	RPVLVVDFG	0.1243	13031.1	50.00	Sequence
IAd	378	FKDEVRAVGRELGLP	VRAVGRELG	0.1242	13047.1	50.00	Sequence
IAd	109	TGTREYGRTELKVLG	GRTELKVLG	0.1242	13048.8	50.00	Sequence
IAd	314	RAFEGAVRDVLDGKT	VRDVLDGKT	0.1238	13092.2	50.00	Sequence
IAd	201	LGAQWTPANIANALI	WTPANIANA	0.1236	13127.6	50.00	Sequence
IAd	124	GKLHSDLPEVQPVWM	KLHSDLPEV	0.1230	13217.1	50.00	Sequence
IAd	194	FLHDFAGLGAQWTPA	LHDFAGLGA	0.1226	13266.6	50.00	Sequence
IAd	496	STRITNEVAEVNRVV	NEVAEVNRV	0.1217	13404.9	50.00	Sequence
IAd	226	HAICGLSGGVDSAVA	HAICGLSGG	0.1216	13419.6	50.00	Sequence
IAd	393	EEIVARQPFPGPGLG	IVARQPFPG	0.1212	13475.5	50.00	Sequence
IAd	430	REELTAAGLDNQIWQ	REELTAAGL	0.1208	13531.7	50.00	Sequence
IAd	352	NIKSHHNVGGLPDDL	KSHHNVGGL	0.1208	13537.4	50.00	Sequence
IAd	499	ITNEVAEVNRVVLDI	NEVAEVNRV	0.1198	13681.7	50.00	Sequence
IAd	209	NIANALIEQVRTQIG	IANALIEQV	0.1196	13700.9	50.00	Sequence
IAd	251	RLTCVFVDHGLLRAG	FVDHGLLRA	0.1192	13774.6	50.00	Sequence
IAd	117	TELKVLGGKLHSDLP	TELKVLGGK	0.1191	13789.2	50.00	Sequence
IAd	199	AGLGAQWTPANIANA	WTPANIANA	0.1176	14010.0	50.00	Sequence
IAd	139	SHGDAVTAAPDGFDV	SHGDAVTAA	0.1172	14074.1	50.00	Sequence
IAd	191	LSRFLHDFAGLGAQW	LHDFAGLGA	0.1154	14340.8	50.00	Sequence
IAd	190	VLSRFLHDFAGLGAQ	LHDFAGLGA	0.1148	14437.0	50.00	Sequence
IAd	258	DHGLLRAGERAQVQR	LRAGERAQV	0.1145	14488.2	50.00	Sequence
IAd	64	GGPASVYADGAPKLD	VYADGAPKL	0.1131	14704.5	50.00	Sequence
IAd	362	LPDDLKFTLVEPLRL	FTLVEPLRL	0.1131	14708.7	50.00	Sequence
IAd	363	PDDLKFTLVEPLRLL	LKFTLVEPL	0.1131	14713.7	50.00	Sequence
IAd	351	ANIKSHHNVGGLPDD	KSHHNVGGL	0.1125	14796.8	50.00	Sequence
IAd	119	LKVLGGKLHSDLPEV	KLHSDLPEV	0.1120	14885.7	50.00	Sequence
IAd	70	YADGAPKLDPALLDL	APKLDPALL	0.1117	14933.6	50.00	Sequence
IAd	118	ELKVLGGKLHSDLPE	ELKVLGGKL	0.1117	14935.9	50.00	Sequence
IAd	497	TRITNEVAEVNRVVL	NEVAEVNRV	0.1116	14939.6	50.00	Sequence
IAd	323	VLDGKTAEFLVQGTL	GKTAEFLVQ	0.1116	14955.1	50.00	Sequence
IAd	161	PVAAFEAFDRRLAGV	VAAFEAFDR	0.1114	14978.5	50.00	Sequence
IAd	254	CVFVDHGLLRAGERA	FVDHGLLRA	0.1105	15126.8	50.00	Sequence
IAd	63	SGGPASVYADGAPKL	VYADGAPKL	0.1104	15147.5	50.00	Sequence
IAd	3	PADIDVPETPARPVL	PADIDVPET	0.1100	15216.0	50.00	Sequence
IAd	306	KIIGRQFIRAFEGAV	RQFIRAFEG	0.1098	15238.2	50.00	Sequence
IAd	376	LLFKDEVRAVGRELG	LLFKDEVRA	0.1096	15268.4	50.00	Sequence
IAd	208	ANIANALIEQVRTQI	IANALIEQV	0.1096	15274.0	50.00	Sequence
IAd	305	RKIIGRQFIRAFEGA	RQFIRAFEG	0.1096	15281.3	50.00	Sequence
IAd	313	IRAFEGAVRDVLDGK	AFEGAVRDV	0.1093	15326.5	50.00	Sequence
IAd	434	TAAGLDNQIWQCPVV	NQIWQCPVV	0.1089	15395.5	50.00	Sequence
IAd	162	VAAFEAFDRRLAGVQ	VAAFEAFDR	0.1086	15447.9	50.00	Sequence
IAd	163	AAFEAFDRRLAGVQY	AAFEAFDRR	0.1085	15455.2	50.00	Sequence
IAd	255	VFVDHGLLRAGERAQ	FVDHGLLRA	0.1076	15613.0	50.00	Sequence
IAd	69	VYADGAPKLDPALLD	VYADGAPKL	0.1065	15800.0	50.00	Sequence
IAd	206	TPANIANALIEQVRT	IANALIEQV	0.1063	15826.5	50.00	Sequence
IAd	65	GPASVYADGAPKLDP	VYADGAPKL	0.1063	15834.4	50.00	Sequence
IAd	364	DDLKFTLVEPLRLLF	FTLVEPLRL	0.1047	16108.8	50.00	Sequence
IAd	454	RSVGVQGDGRTYGHP	RSVGVQGDG	0.1045	16132.7	50.00	Sequence
IAd	322	DVLDGKTAEFLVQGT	GKTAEFLVQ	0.1045	16134.6	50.00	Sequence
IAd	196	HDFAGLGAQWTPANI	FAGLGAQWT	0.1037	16276.6	50.00	Sequence
IAd	88	VLGICYGFQAMAQAL	YGFQAMAQA	0.1029	16422.0	50.00	Sequence
IAd	365	DLKFTLVEPLRLLFK	FTLVEPLRL	0.1029	16423.1	50.00	Sequence

IAd	172	LAGVQYHPEVMHTPH	YHPEVMHTP	0.1028	16433.8	50.00	Sequence
IAd	207	PANIANALIEQVRTQ	IANALIEQV	0.1023	16527.6	50.00	Sequence
IAd	57	PVALVLSGGPASVYA	ALVLSGGPA	0.1013	16701.2	50.00	Sequence
IAd	377	LFKDEVRAVGRELGL	VRAVGRELG	0.1013	16715.0	50.00	Sequence
IAd	490	EVLERISTRITNEVA	LERISTRIT	0.1006	16838.2	50.00	Sequence
IAd	326	GKTAEFLVQGTLYPD	TAEFLVQGT	0.1005	16854.4	50.00	Sequence
IAd	324	LDGKTAEFLVQGTLY	GKTAEFLVQ	0.0990	17130.9	50.00	Sequence
IAd	253	TCVFVDHGLLRAGER	FVDHGLLRA	0.0981	17296.0	50.00	Sequence
IAd	68	SVYADGAPKLDPALL	VYADGAPKL	0.0979	17344.1	50.00	Sequence
IAd	123	GGKLHSDLPEVQPVW	KLHSDLPEV	0.0977	17371.0	50.00	Sequence
IAd	366	LKFTLVEPLRLLFKD	LKFTLVEPL	0.0974	17423.9	50.00	Sequence
IAd	350	TANIKSHHNVGGLPD	KSHHNVGGL	0.0962	17655.4	50.00	Sequence
IAd	433	LTAAGLDNQIWQCPV	AAGLDNQIW	0.0956	17777.1	50.00	Sequence
IAd	293	EALSGVSAPEGKRKI	EALSGVSAP	0.0951	17871.2	50.00	Sequence
IAd	432	ELTAAGLDNQIWQCP	AAGLDNQIW	0.0949	17910.5	50.00	Sequence
IAd	187	GQQVLSRFLHDFAGL	GQQVLSRFL	0.0945	17984.7	50.00	Sequence
IAd	122	LGGKLHSDLPEVQPV	KLHSDLPEV	0.0942	18034.4	50.00	Sequence
IAd	6	IDVPETPARPVLVVD	VPETPARPV	0.0942	18041.6	50.00	Sequence
IAd	508	RVVLDITSKPPATIE	RVVLDITSK	0.0924	18390.3	50.00	Sequence
IAd	375	RLLFKDEVRAVGREL	LLFKDEVRA	0.0924	18406.2	50.00	Sequence
IAd	189	QVLSRFLHDFAGLGA	LHDFAGLGA	0.0917	18545.1	50.00	Sequence
IAd	198	FAGLGAQWTPANIAN	AQWTPANIA	0.0913	18625.0	50.00	Sequence
IAd	492	LERISTRITNEVAEV	LERISTRIT	0.0910	18677.0	50.00	Sequence
IAd	373	PLRLLFKDEVRAVGR	LLFKDEVRA	0.0906	18769.8	50.00	Sequence
IAd	327	KTAEFLVQGTLYPDV	TAEFLVQGT	0.0905	18774.1	50.00	Sequence
IAd	374	LRLLFKDEVRAVGRE	LLFKDEVRA	0.0901	18860.4	50.00	Sequence
IAd	331	FLVQGTLYPDVVESG	FLVQGTLYP	0.0898	18918.8	50.00	Sequence
IAd	145	TAAPDGFDVVASSAG	GFDVVASSA	0.0898	18922.1	50.00	Sequence
IAd	87	PVLGICYGFQAMAQA	YGFQAMAQA	0.0885	19187.2	50.00	Sequence
IAd	328	TAEFLVQGTLYPDVV	TAEFLVQGT	0.0885	19197.2	50.00	Sequence
IAd	147	APDGFDVVASSAGAP	GFDVVASSA	0.0879	19317.8	50.00	Sequence
IAd	197	DFAGLGAQWTPANIA	AQWTPANIA	0.0877	19354.7	50.00	Sequence
IAd	66	PASVYADGAPKLDPA	VYADGAPKL	0.0876	19389.0	50.00	Sequence
IAd	146	AAPDGFDVVASSAGA	GFDVVASSA	0.0873	19444.7	50.00	Sequence
IAd	15	PVLVVDFGAQYAQLI	PVLVVDFGA	0.0872	19466.0	50.00	Sequence
IAd	325	DGKTAEFLVQGTLYP	TAEFLVQGT	0.0865	19621.6	50.00	Sequence
IAd	371	VEPLRLLFKDEVRAV	LLFKDEVRA	0.0862	19675.6	50.00	Sequence
IAd	120	KVLGGKLHSDLPEVQ	KLHSDLPEV	0.0861	19691.6	50.00	Sequence
IAd	67	ASVYADGAPKLDPAL	VYADGAPKL	0.0858	19766.9	50.00	Sequence
IAd	431	EELTAAGLDNQIWQC	EELTAAGLD	0.0852	19892.7	50.00	Sequence
IAd	176	QYHPEVMHTPHGQQV	YHPEVMHTP	0.0851	19909.2	50.00	Sequence
IAd	144	VTAAPDGFDVVASSA	GFDVVASSA	0.0844	20062.6	50.00	Sequence
IAd	252	LTCVFVDHGLLRAGE	FVDHGLLRA	0.0844	20071.5	50.00	Sequence
IAd	121	VLGGKLHSDLPEVQP	KLHSDLPEV	0.0837	20212.2	50.00	Sequence
IAd	173	AGVQYHPEVMHTPHG	YHPEVMHTP	0.0837	20215.1	50.00	Sequence
IAd	101	ALGGIVAHTGTREYG	LGGIVAHTG	0.0822	20541.2	50.00	Sequence
IAd	100	QALGGIVAHTGTREY	QALGGIVAH	0.0815	20697.6	50.00	Sequence
IAd	372	EPLRLLFKDEVRAVG	LLFKDEVRA	0.0792	21232.9	50.00	Sequence
IAd	297	GVSAPEGKRKIIGRQ	GKRKIIGRQ	0.0789	21290.6	50.00	Sequence
IAd	491	VLERISTRITNEVAE	LERISTRIT	0.0789	21300.3	50.00	Sequence
IAd	80	ALLDLGVPVLGICYG	ALLDLGVPV	0.0787	21348.1	50.00	Sequence
IAd	361	GLPDDLKFTLVEPLR	LKFTLVEPL	0.0783	21434.4	50.00	Sequence
IAd	494	RISTRITNEVAEVNR	RITNEVAEV	0.0782	21452.3	50.00	Sequence
IAd	332	LVQGTLYPDVVESGG	LYPDVVESG	0.0776	21602.3	50.00	Sequence
IAd	5	DIDVPETPARPVLVV	VPETPARPV	0.0774	21635.7	50.00	Sequence
IAd	218	VRTQIGDGHAICGLS	RTQIGDGHA	0.0774	21639.0	50.00	Sequence
IAd	329	AEFLVQGTLYPDVVE	FLVQGTLYP	0.0769	21769.5	50.00	Sequence
IAd	348	SGTANIKSHHNVGGL	SGTANIKSH	0.0768	21777.8	50.00	Sequence
IAd	61	VLSGGPASVYADGAP	PASVYADGA	0.0760	21968.8	50.00	Sequence
IAd	175	VQYHPEVMHTPHGQQ	YHPEVMHTP	0.0756	22063.3	50.00	Sequence
IAd	330	EFLVQGTLYPDVVES	LVQGTLYPD	0.0751	22180.4	50.00	Sequence
IAd	62	LSGGPASVYADGAPK	PASVYADGA	0.0749	22241.2	50.00	Sequence
IAd	174	GVQYHPEVMHTPHGQ	YHPEVMHTP	0.0748	22269.8	50.00	Sequence
IAd	394	EIVARQPFPGPGLGI	IVARQPFPG	0.0745	22334.0	50.00	Sequence
IAd	58	VALVLSGGPASVYAD	ALVLSGGPA	0.0745	22336.0	50.00	Sequence
IAd	108	HTGTREYGRTELKVL	YGRTELKVL	0.0741	22429.0	50.00	Sequence

IAd	59	ALVLSGGPASVYADG	ALVLSGGPA	0.0739	22477.1	50.00	Sequence
IAd	493	ERISTRITNEVAEVN	RITNEVAEV	0.0732	22643.3	50.00	Sequence
IAd	4	ADIDVPETPARPVLV	VPETPARPV	0.0732	22654.3	50.00	Sequence
IAd	102	LGGIVAHTGTREYGR	LGGIVAHTG	0.0731	22673.0	50.00	Sequence
IAd	360	GGLPDDLKFTLVEPL	LKFTLVEPL	0.0728	22753.1	50.00	Sequence
IAd	188	QQVLSRFLHDFAGLG	QQVLSRFLH	0.0721	22921.1	50.00	Sequence
IAd	370	LVEPLRLLFKDEVRA	LLFKDEVRA	0.0718	22983.2	50.00	Sequence
IAd	349	GTANIKSHHNVGGLP	KSHHNVGGL	0.0701	23425.3	50.00	Sequence
IAd	355	SHHNVGGLPDDLKFT	HHNVGGLPD	0.0698	23501.2	50.00	Sequence
IAd	177	YHPEVMHTPHGQQVL	YHPEVMHTP	0.0697	23516.5	50.00	Sequence
IAd	60	LVLSGGPASVYADGA	GPASVYADG	0.0693	23616.9	50.00	Sequence
IAd	395	IVARQPFPGPGLGIR	IVARQPFPG	0.0689	23720.1	50.00	Sequence
IAd	333	VQGTLYPDVVESGGG	LYPDVVESG	0.0670	24208.4	50.00	Sequence
IAd	459	QGDGRTYGHPIVLRP	YGHPIVLRP	0.0633	25208.9	50.00	Sequence
IAd	345	GGGSGTANIKSHHNV	GSGTANIKS	0.0629	25319.8	50.00	Sequence
IAd	103	GGIVAHTGTREYGRT	VAHTGTREY	0.0625	25417.3	50.00	Sequence
IAd	401	FPGPGLGIRIVGEVT	LGIRIVGEV	0.0615	25696.0	50.00	Sequence
IAd	455	SVGVQGDGRTYGHPI	VGVQGDGRT	0.0596	26233.1	50.00	Sequence
IAd	16	VLVVDFGAQYAQLIA	GAQYAQLIA	0.0595	26270.9	50.00	Sequence
IAd	347	GSGTANIKSHHNVGG	GSGTANIKS	0.0590	26418.6	50.00	Sequence
IAd	367	KFTLVEPLRLLFKDE	FTLVEPLRL	0.0580	26693.0	50.00	Sequence
IAd	346	GGSGTANIKSHHNVG	GSGTANIKS	0.0577	26791.1	50.00	Sequence
IAd	344	SGGGSGTANIKSHHN	GSGTANIKS	0.0561	27247.4	50.00	Sequence
IAd	368	FTLVEPLRLLFKDEV	FTLVEPLRL	0.0555	27426.0	50.00	Sequence
IAd	104	GIVAHTGTREYGRTE	VAHTGTREY	0.0528	28251.0	50.00	Sequence
IAd	334	QGTLYPDVVESGGGS	LYPDVVESG	0.0520	28490.4	50.00	Sequence
IAd	356	HHNVGGLPDDLKFTL	HHNVGGLPD	0.0519	28520.3	50.00	Sequence
IAd	85	GVPVLGICYGFQAMA	VPVLGICYG	0.0509	28812.2	50.00	Sequence
IAd	510	VLDITSKPPATIEWE	LDITSKPPA	0.0501	29070.8	50.00	Sequence
IAd	140	HGDAVTAAPDGFDVV	HGDAVTAAP	0.0484	29624.6	50.00	Sequence
IAd	335	GTLYPDVVESGGGSG	TLYPDVVES	0.0475	29891.5	50.00	Sequence
IAd	343	ESGGGSGTANIKSHH	SGTANIKSH	0.0475	29897.7	50.00	Sequence
IAd	456	VGVQGDGRTYGHPIV	VGVQGDGRT	0.0467	30160.8	50.00	Sequence
IAd	86	VPVLGICYGFQAMAQ	VPVLGICYG	0.0465	30238.3	50.00	Sequence
IAd	105	IVAHTGTREYGRTEL	VAHTGTREY	0.0462	30328.4	50.00	Sequence
IAd	81	LLDLGVPVLGICYGF	LDLGVPVLG	0.0459	30429.6	50.00	Sequence
IAd	336	TLYPDVVESGGGSGT	LYPDVVESG	0.0458	30457.6	50.00	Sequence
IAd	82	LDLGVPVLGICYGFQ	LDLGVPVLG	0.0454	30601.0	50.00	Sequence
IAd	83	DLGVPVLGICYGFQA	LGVPVLGIC	0.0453	30640.7	50.00	Sequence
IAd	342	VESGGGSGTANIKSH	SGTANIKSH	0.0441	31022.7	50.00	Sequence
IAd	400	PFPGPGLGIRIVGEV	LGIRIVGEV	0.0440	31054.9	50.00	Sequence
IAd	178	HPEVMHTPHGQQVLS	MHTPHGQQV	0.0432	31346.6	50.00	Sequence
IAd	84	LGVPVLGICYGFQAM	VPVLGICYG	0.0430	31392.8	50.00	Sequence
IAd	142	DAVTAAPDGFDVVAS	PDGFDVVAS	0.0418	31813.4	50.00	Sequence
IAd	396	VARQPFPGPGLGIRI	ARQPFPGPG	0.0412	32012.6	50.00	Sequence
IAd	143	AVTAAPDGFDVVASS	PDGFDVVAS	0.0391	32737.3	50.00	Sequence
IAd	458	VQGDGRTYGHPIVLR	TYGHPIVLR	0.0383	33048.4	50.00	Sequence
IAd	509	VVLDITSKPPATIEW	LDITSKPPA	0.0357	33983.2	50.00	Sequence
IAd	106	VAHTGTREYGRTELK	VAHTGTREY	0.0353	34125.0	50.00	Sequence
IAd	457	GVQGDGRTYGHPIVL	GVQGDGRTY	0.0353	34128.0	50.00	Sequence
IAd	296	SGVSAPEGKRKIIGR	VSAPEGKRK	0.0344	34476.5	50.00	Sequence
IAd	357	HNVGGLPDDLKFTLV	HNVGGLPDD	0.0341	34587.1	50.00	Sequence
IAd	397	ARQPFPGPGLGIRIV	ARQPFPGPG	0.0331	34942.5	50.00	Sequence
IAd	337	LYPDVVESGGGSGTA	LYPDVVESG	0.0324	35214.6	50.00	Sequence
IAd	295	LSGVSAPEGKRKIIG	LSGVSAPEG	0.0322	35281.8	50.00	Sequence
IAd	141	GDAVTAAPDGFDVVA	DAVTAAPDG	0.0313	35628.9	50.00	Sequence
IAd	107	AHTGTREYGRTELKV	AHTGTREYG	0.0311	35725.8	50.00	Sequence
IAd	341	VVESGGGSGTANIKS	GSGTANIKS	0.0302	36068.0	50.00	Sequence
IAd	369	TLVEPLRLLFKDEVR	VEPLRLLFK	0.0287	36634.4	50.00	Sequence
IAd	294	ALSGVSAPEGKRKII	LSGVSAPEG	0.0275	37142.0	50.00	Sequence
IAd	358	NVGGLPDDLKFTLVE	PDDLKFTLV	0.0236	38737.8	50.00	Sequence
IAd	359	VGGLPDDLKFTLVEP	PDDLKFTLV	0.0235	38772.2	50.00	Sequence
IAd	398	RQPFPGPGLGIRIVG	PGPGLGIRI	0.0187	40826.7	50.00	Sequence
IAd	338	YPDVVESGGGSGTAN	VESGGGSGT	0.0160	42069.7	50.00	Sequence
IAd	339	PDVVESGGGSGTANI	VESGGGSGT	0.0155	42276.0	50.00	Sequence
IAd	399	QPFPGPGLGIRIVGE	PGPGLGIRI	0.0143	42841.0	50.00	Sequence

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         IAd  340  DVVESGGGSGTANIK  VESGGGSGT        0.0119     43966.6               50.00     Sequence
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Allele: IAd. Number of high binders 0. Number of weak binders 10. Number of peptides 511

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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         IAs    0  VVQPADIDVPETPAR  ADIDVPETP        0.3729       884.9                1.00     Sequence
         IAs    1  VQPADIDVPETPARP  ADIDVPETP        0.3672       940.4                1.00     Sequence
         IAs   25  YAQLIARRVREARVF  RRVREARVF        0.3492      1143.1                2.00     Sequence
         IAs   26  AQLIARRVREARVFS  RRVREARVF        0.3287      1427.4                2.00     Sequence
         IAs   27  QLIARRVREARVFSE  RRVREARVF        0.3115      1719.4                4.00     Sequence
         IAs  381  EVRAVGRELGLPEEI  RELGLPEEI        0.3031      1882.5                4.00     Sequence
         IAs   28  LIARRVREARVFSEV  RRVREARVF        0.2951      2052.8                4.00     Sequence
         IAs   30  ARRVREARVFSEVIP  RRVREARVF        0.2902      2164.1                4.00     Sequence
         IAs    2  QPADIDVPETPARPV  ADIDVPETP        0.2900      2168.3                4.00     Sequence
         IAs  382  VRAVGRELGLPEEIV  RELGLPEEI        0.2880      2216.9                4.00     Sequence
         IAs   31  RRVREARVFSEVIPH  RRVREARVF        0.2847      2296.6                4.00     Sequence
         IAs    3  PADIDVPETPARPVL  ADIDVPETP        0.2830      2340.3                4.00     Sequence
         IAs   29  IARRVREARVFSEVI  RRVREARVF        0.2798      2422.3                4.00     Sequence
         IAs  383  RAVGRELGLPEEIVA  RELGLPEEI        0.2742      2572.7                4.00     Sequence
         IAs  389  LGLPEEIVARQPFPG  EIVARQPFP        0.2702      2686.8                4.00     Sequence
         IAs  384  AVGRELGLPEEIVAR  RELGLPEEI        0.2669      2784.2                4.00     Sequence
         IAs  290  TFLEALSGVSAPEGK  SGVSAPEGK        0.2661      2810.3                4.00     Sequence
         IAs  390  GLPEEIVARQPFPGP  EIVARQPFP        0.2590      3033.5                8.00     Sequence
         IAs  392  PEEIVARQPFPGPGL  EIVARQPFP        0.2585      3048.6                8.00     Sequence
         IAs  388  ELGLPEEIVARQPFP  EIVARQPFP        0.2545      3183.7                8.00     Sequence
         IAs  291  FLEALSGVSAPEGKR  SGVSAPEGK        0.2531      3232.6                8.00     Sequence
         IAs  391  LPEEIVARQPFPGPG  EIVARQPFP        0.2512      3299.3                8.00     Sequence
         IAs  393  EEIVARQPFPGPGLG  EIVARQPFP        0.2468      3462.8                8.00     Sequence
         IAs  137  WMSHGDAVTAAPDGF  AVTAAPDGF        0.2457      3501.6                8.00     Sequence
         IAs  435  AAGLDNQIWQCPVVL  QIWQCPVVL        0.2441      3563.3                8.00     Sequence
         IAs  292  LEALSGVSAPEGKRK  SGVSAPEGK        0.2416      3660.3                8.00     Sequence
         IAs  138  MSHGDAVTAAPDGFD  AVTAAPDGF        0.2383      3793.2                8.00     Sequence
         IAs  466  GHPIVLRPVSSEDAM  RPVSSEDAM        0.2374      3830.5                8.00     Sequence
         IAs  139  SHGDAVTAAPDGFDV  AVTAAPDGF        0.2373      3835.8                8.00     Sequence
         IAs  140  HGDAVTAAPDGFDVV  GDAVTAAPD        0.2357      3903.3                8.00     Sequence
         IAs  440  NQIWQCPVVLLADVR  QIWQCPVVL        0.2351      3929.4                8.00     Sequence
         IAs  386  GRELGLPEEIVARQP  RELGLPEEI        0.2345      3954.6                8.00     Sequence
         IAs  293  EALSGVSAPEGKRKI  SGVSAPEGK        0.2340      3975.6                8.00     Sequence
         IAs  171  RLAGVQYHPEVMHTP  LAGVQYHPE        0.2338      3985.6                8.00     Sequence
         IAs  441  QIWQCPVVLLADVRS  QIWQCPVVL        0.2332      4010.1                8.00     Sequence
         IAs  172  LAGVQYHPEVMHTPH  LAGVQYHPE        0.2328      4025.8                8.00     Sequence
         IAs    4  ADIDVPETPARPVLV  ADIDVPETP        0.2328      4027.9                8.00     Sequence
         IAs  394  EIVARQPFPGPGLGI  EIVARQPFP        0.2284      4222.1                8.00     Sequence
         IAs  436  AGLDNQIWQCPVVLL  QIWQCPVVL        0.2218      4537.8                8.00     Sequence
         IAs  295  LSGVSAPEGKRKIIG  SGVSAPEGK        0.2181      4721.5                8.00     Sequence
         IAs  385  VGRELGLPEEIVARQ  RELGLPEEI        0.2172      4770.6                8.00     Sequence
         IAs  294  ALSGVSAPEGKRKII  SGVSAPEGK        0.2168      4789.5                8.00     Sequence
         IAs  437  GLDNQIWQCPVVLLA  QIWQCPVVL        0.2108      5111.3               16.00     Sequence
         IAs  439  DNQIWQCPVVLLADV  QIWQCPVVL        0.2088      5221.5               16.00     Sequence
         IAs  174  GVQYHPEVMHTPHGQ  EVMHTPHGQ        0.2063      5362.5               16.00     Sequence
         IAs  387  RELGLPEEIVARQPF  RELGLPEEI        0.2044      5479.1               16.00     Sequence
         IAs  438  LDNQIWQCPVVLLAD  QIWQCPVVL        0.2037      5518.8               16.00     Sequence
         IAs  175  VQYHPEVMHTPHGQQ  EVMHTPHGQ        0.2031      5553.3               16.00     Sequence
         IAs  176  QYHPEVMHTPHGQQV  EVMHTPHGQ        0.2019      5626.3               16.00     Sequence
         IAs  177  YHPEVMHTPHGQQVL  YHPEVMHTP        0.2016      5642.4               16.00     Sequence
         IAs    8  VPETPARPVLVVDFG  RPVLVVDFG        0.2013      5663.6               16.00     Sequence
         IAs  277  ATGANLVTVDAAETF  VTVDAAETF        0.1985      5840.1               16.00     Sequence
         IAs  510  VLDITSKPPATIEWE  KPPATIEWE        0.1933      6175.1               16.00     Sequence
         IAs  467  HPIVLRPVSSEDAMT  RPVSSEDAM        0.1913      6313.3               16.00     Sequence
         IAs  136  VWMSHGDAVTAAPDG  GDAVTAAPD        0.1897      6422.3               16.00     Sequence
         IAs  141  GDAVTAAPDGFDVVA  GDAVTAAPD        0.1895      6431.9               16.00     Sequence
         IAs  153  VVASSAGAPVAAFEA  VVASSAGAP        0.1847      6777.3               16.00     Sequence
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IAs	173	AGVQYHPEVMHTPHG	YHPEVMHTP	0.1824	6949.0	16.00	Sequence
IAs	9	PETPARPVLVVDFGA	RPVLVVDFG	0.1805	7093.6	16.00	Sequence
IAs	152	DVVASSAGAPVAAFE	VVASSAGAP	0.1792	7195.6	16.00	Sequence
IAs	68	SVYADGAPKLDPALL	DGAPKLDPA	0.1776	7320.5	16.00	Sequence
IAs	66	PASVYADGAPKLDPA	SVYADGAPK	0.1745	7567.8	16.00	Sequence
IAs	167	AFDRRLAGVQYHPEV	LAGVQYHPE	0.1724	7740.9	16.00	Sequence
IAs	151	FDVVASSAGAPVAAF	VVASSAGAP	0.1715	7814.6	16.00	Sequence
IAs	67	ASVYADGAPKLDPAL	DGAPKLDPA	0.1688	8046.5	16.00	Sequence
IAs	10	ETPARPVLVVDFGAQ	RPVLVVDFG	0.1671	8202.5	16.00	Sequence
IAs	462	GRTYGHPIVLRPVSS	RTYGHPIVL	0.1669	8214.5	16.00	Sequence
IAs	168	FDRRLAGVQYHPEVM	LAGVQYHPE	0.1668	8226.8	16.00	Sequence
IAs	170	RRLAGVQYHPEVMHT	LAGVQYHPE	0.1660	8297.3	16.00	Sequence
IAs	150	GFDVVASSAGAPVAA	VVASSAGAP	0.1658	8312.7	16.00	Sequence
IAs	135	PVWMSHGDAVTAAPD	GDAVTAAPD	0.1657	8327.6	16.00	Sequence
IAs	169	DRRLAGVQYHPEVMH	LAGVQYHPE	0.1631	8565.3	16.00	Sequence
IAs	463	RTYGHPIVLRPVSSE	RTYGHPIVL	0.1621	8655.0	16.00	Sequence
IAs	380	DEVRAVGRELGLPEE	AVGRELGLP	0.1595	8906.7	32.00	Sequence
IAs	257	VDHGLLRAGERAQVQ	RAGERAQVQ	0.1594	8908.9	32.00	Sequence
IAs	200	GLGAQWTPANIANAL	TPANIANAL	0.1582	9028.4	32.00	Sequence
IAs	166	EAFDRRLAGVQYHPE	RRLAGVQYH	0.1569	9152.0	32.00	Sequence
IAs	197	DFAGLGAQWTPANIA	AQWTPANIA	0.1567	9175.4	32.00	Sequence
IAs	460	GDGRTYGHPIVLRPV	RTYGHPIVL	0.1561	9233.6	32.00	Sequence
IAs	461	DGRTYGHPIVLRPVS	RTYGHPIVL	0.1556	9284.3	32.00	Sequence
IAs	149	DGFDVVASSAGAPVA	VVASSAGAP	0.1551	9331.7	32.00	Sequence
IAs	296	SGVSAPEGKRKIIGR	SGVSAPEGK	0.1545	9397.6	32.00	Sequence
IAs	45	HTASIEEIRARQPVA	EEIRARQPV	0.1537	9474.3	32.00	Sequence
IAs	465	YGHPIVLRPVSSEDA	HPIVLRPVS	0.1535	9496.4	32.00	Sequence
IAs	198	FAGLGAQWTPANIAN	AQWTPANIA	0.1528	9573.8	32.00	Sequence
IAs	199	AGLGAQWTPANIANA	AQWTPANIA	0.1514	9714.6	32.00	Sequence
IAs	13	ARPVLVVDFGAQYAQ	RPVLVVDFG	0.1513	9726.5	32.00	Sequence
IAs	471	LRPVSSEDAMTADWT	RPVSSEDAM	0.1509	9774.4	32.00	Sequence
IAs	472	RPVSSEDAMTADWTR	RPVSSEDAM	0.1500	9863.4	32.00	Sequence
IAs	468	PIVLRPVSSEDAMTA	RPVSSEDAM	0.1498	9891.7	32.00	Sequence
IAs	154	VASSAGAPVAAFEAF	APVAAFEAF	0.1493	9944.3	32.00	Sequence
IAs	12	PARPVLVVDFGAQYA	RPVLVVDFG	0.1492	9950.5	32.00	Sequence
IAs	464	TYGHPIVLRPVSSED	HPIVLRPVS	0.1491	9960.5	32.00	Sequence
IAs	278	TGANLVTVDAAETFL	VTVDAAETF	0.1489	9988.4	32.00	Sequence
IAs	328	TAEFLVQGTLYPDVV	QGTLYPDVV	0.1488	9999.2	32.00	Sequence
IAs	444	QCPVVLLADVRSVGV	PVVLLADVR	0.1487	10007.0	32.00	Sequence
IAs	49	IEEIRARQPVALVLS	IEEIRARQP	0.1485	10025.5	32.00	Sequence
IAs	65	GPASVYADGAPKLDP	SVYADGAPK	0.1485	10031.3	32.00	Sequence
IAs	46	TASIEEIRARQPVAL	IEEIRARQP	0.1480	10085.9	32.00	Sequence
IAs	442	IWQCPVVLLADVRSV	PVVLLADVR	0.1478	10107.5	32.00	Sequence
IAs	64	GGPASVYADGAPKLD	SVYADGAPK	0.1476	10124.3	32.00	Sequence
IAs	395	IVARQPFPGPGLGIR	VARQPFPGP	0.1464	10257.8	32.00	Sequence
IAs	300	APEGKRKIIGRQFIR	KIIGRQFIR	0.1460	10306.2	32.00	Sequence
IAs	324	LDGKTAEFLVQGTLY	EFLVQGTLY	0.1452	10396.1	32.00	Sequence
IAs	63	SGGPASVYADGAPKL	SVYADGAPK	0.1450	10410.8	32.00	Sequence
IAs	47	ASIEEIRARQPVALV	IEEIRARQP	0.1449	10424.9	32.00	Sequence
IAs	155	ASSAGAPVAAFEAFD	APVAAFEAF	0.1448	10436.4	32.00	Sequence
IAs	445	CPVVLLADVRSVGVQ	PVVLLADVR	0.1448	10442.0	32.00	Sequence
IAs	14	RPVLVVDFGAQYAQL	RPVLVVDFG	0.1447	10444.7	32.00	Sequence
IAs	443	WQCPVVLLADVRSVG	PVVLLADVR	0.1441	10512.1	32.00	Sequence
IAs	11	TPARPVLVVDFGAQY	RPVLVVDFG	0.1441	10513.0	32.00	Sequence
IAs	329	AEFLVQGTLYPDVVE	QGTLYPDVV	0.1434	10592.1	32.00	Sequence
IAs	32	RVREARVFSEVIPHT	RVFSEVIPH	0.1428	10666.3	32.00	Sequence
IAs	470	VLRPVSSEDAMTADW	RPVSSEDAM	0.1427	10681.4	32.00	Sequence
IAs	148	PDGFDVVASSAGAPV	VVASSAGAP	0.1425	10703.4	32.00	Sequence
IAs	44	PHTASIEEIRARQPV	EEIRARQPV	0.1417	10790.3	32.00	Sequence
IAs	459	QGDGRTYGHPIVLRP	RTYGHPIVL	0.1408	10895.1	32.00	Sequence
IAs	48	SIEEIRARQPVALVL	IRARQPVAL	0.1396	11043.6	32.00	Sequence
IAs	62	LSGGPASVYADGAPK	ASVYADGAP	0.1387	11150.2	32.00	Sequence
IAs	361	GLPDDLKFTLVEPLR	LKFTLVEPL	0.1386	11158.4	32.00	Sequence
IAs	124	GKLHSDLPEVQPVWM	LHSDLPEVQ	0.1385	11178.6	32.00	Sequence
IAs	125	KLHSDLPEVQPVWMS	SDLPEVQPV	0.1384	11184.9	32.00	Sequence
IAs	194	FLHDFAGLGAQWTPA	AGLGAQWTP	0.1379	11246.9	32.00	Sequence

IAs	330	EFLVQGTLYPDVVES	VQGTLYPDV	0.1364	11426.2	32.00	Sequence
IAs	301	PEGKRKIIGRQFIRA	KIIGRQFIR	0.1360	11475.4	32.00	Sequence
IAs	279	GANLVTVDAAETFLE	VTVDAAETF	0.1358	11507.1	32.00	Sequence
IAs	469	IVLRPVSSEDAMTAD	RPVSSEDAM	0.1353	11568.2	32.00	Sequence
IAs	33	VREARVFSEVIPHTA	RVFSEVIPH	0.1351	11590.9	32.00	Sequence
IAs	366	LKFTLVEPLRLLFKD	LKFTLVEPL	0.1351	11596.0	32.00	Sequence
IAs	399	QPFPGPGLGIRIVGE	QPFPGPGLG	0.1340	11732.7	32.00	Sequence
IAs	362	LPDDLKFTLVEPLRL	LKFTLVEPL	0.1338	11752.8	32.00	Sequence
IAs	196	HDFAGLGAQWTPANI	AGLGAQWTP	0.1338	11757.5	32.00	Sequence
IAs	195	LHDFAGLGAQWTPAN	AGLGAQWTP	0.1335	11795.3	32.00	Sequence
IAs	122	LGGKLHSDLPEVQPV	SDLPEVQPV	0.1332	11827.9	32.00	Sequence
IAs	126	LHSDLPEVQPVWMSH	SDLPEVQPV	0.1326	11915.6	32.00	Sequence
IAs	207	PANIANALIEQVRTQ	ALIEQVRTQ	0.1325	11921.8	32.00	Sequence
IAs	205	WTPANIANALIEQVR	WTPANIANA	0.1321	11976.6	32.00	Sequence
IAs	120	KVLGGKLHSDLPEVQ	LHSDLPEVQ	0.1319	11993.8	32.00	Sequence
IAs	69	VYADGAPKLDPALLD	DGAPKLDPA	0.1318	12014.4	32.00	Sequence
IAs	457	GVQGDGRTYGHPIVL	RTYGHPIVL	0.1316	12033.0	32.00	Sequence
IAs	202	GAQWTPANIANALIE	ANIANALIE	0.1316	12044.7	32.00	Sequence
IAs	365	DLKFTLVEPLRLLFK	LKFTLVEPL	0.1314	12069.4	32.00	Sequence
IAs	203	AQWTPANIANALIEQ	WTPANIANA	0.1304	12200.2	32.00	Sequence
IAs	325	DGKTAEFLVQGTLYP	EFLVQGTLY	0.1298	12272.4	32.00	Sequence
IAs	70	YADGAPKLDPALLDL	APKLDPALL	0.1295	12321.9	32.00	Sequence
IAs	363	PDDLKFTLVEPLRLL	LKFTLVEPL	0.1286	12440.2	32.00	Sequence
IAs	458	VQGDGRTYGHPIVLR	RTYGHPIVL	0.1283	12472.0	32.00	Sequence
IAs	302	EGKRKIIGRQFIRAF	KIIGRQFIR	0.1282	12483.5	32.00	Sequence
IAs	397	ARQPFPGPGLGIRIV	QPFPGPGLG	0.1266	12713.0	32.00	Sequence
IAs	364	DDLKFTLVEPLRLLF	LKFTLVEPL	0.1264	12738.9	32.00	Sequence
IAs	71	ADGAPKLDPALLDLG	APKLDPALL	0.1261	12776.2	32.00	Sequence
IAs	121	VLGGKLHSDLPEVQP	LHSDLPEVQ	0.1257	12836.2	32.00	Sequence
IAs	123	GGKLHSDLPEVQPVW	SDLPEVQPV	0.1256	12846.1	32.00	Sequence
IAs	34	REARVFSEVIPHTAS	RVFSEVIPH	0.1247	12973.2	32.00	Sequence
IAs	327	KTAEFLVQGTLYPDV	EFLVQGTLY	0.1245	12994.9	32.00	Sequence
IAs	208	ANIANALIEQVRTQI	ALIEQVRTQ	0.1244	13009.0	32.00	Sequence
IAs	305	RKIIGRQFIRAFEGA	KIIGRQFIR	0.1241	13057.4	32.00	Sequence
IAs	303	GKRKIIGRQFIRAFE	KIIGRQFIR	0.1239	13080.3	32.00	Sequence
IAs	289	ETFLEALSGVSAPEG	EALSGVSAP	0.1234	13158.5	32.00	Sequence
IAs	204	QWTPANIANALIEQV	WTPANIANA	0.1230	13207.1	32.00	Sequence
IAs	275	VAATGANLVTVDAAE	ATGANLVTV	0.1230	13215.9	32.00	Sequence
IAs	274	FVAATGANLVTVDAA	ATGANLVTV	0.1230	13219.7	32.00	Sequence
IAs	326	GKTAEFLVQGTLYPD	EFLVQGTLY	0.1216	13421.6	32.00	Sequence
IAs	331	FLVQGTLYPDVVESG	QGTLYPDVV	0.1214	13444.7	32.00	Sequence
IAs	272	RDFVAATGANLVTVD	TGANLVTVD	0.1211	13481.2	32.00	Sequence
IAs	333	VQGTLYPDVVESGGG	QGTLYPDVV	0.1208	13526.2	32.00	Sequence
IAs	332	LVQGTLYPDVVESGG	QGTLYPDVV	0.1195	13725.8	32.00	Sequence
IAs	273	DFVAATGANLVTVDA	TGANLVTVD	0.1194	13744.7	32.00	Sequence
IAs	280	ANLVTVDAAETFLEA	VTVDAAETF	0.1193	13750.6	32.00	Sequence
IAs	157	SAGAPVAAFEAFDRR	SAGAPVAAF	0.1193	13757.3	32.00	Sequence
IAs	76	KLDPALLDLGVPVLG	LDLGVPVLG	0.1182	13916.0	32.00	Sequence
IAs	72	DGAPKLDPALLDLGV	APKLDPALL	0.1176	14006.2	32.00	Sequence
IAs	396	VARQPFPGPGLGIRI	VARQPFPGP	0.1172	14071.5	32.00	Sequence
IAs	480	MTADWTRVPYEVLER	ADWTRVPYE	0.1161	14239.3	32.00	Sequence
IAs	237	SAVAAALVQRAIGDR	SAVAAALVQ	0.1158	14281.3	32.00	Sequence
IAs	231	LSGGVDSAVAAALVQ	SAVAAALVQ	0.1158	14281.6	32.00	Sequence
IAs	258	DHGLLRAGERAQVQR	RAGERAQVQ	0.1153	14362.0	32.00	Sequence
IAs	80	ALLDLGVPVLGICYG	LLDLGVPVL	0.1147	14448.4	32.00	Sequence
IAs	232	SGGVDSAVAAALVQR	SAVAAALVQ	0.1142	14526.0	32.00	Sequence
IAs	147	APDGFDVVASSAGAP	VVASSAGAP	0.1138	14600.7	32.00	Sequence
IAs	77	LDPALLDLGVPVLGI	LDPALLDLG	0.1137	14610.6	32.00	Sequence
IAs	304	KRKIIGRQFIRAFEG	KIIGRQFIR	0.1134	14658.6	32.00	Sequence
IAs	477	EDAMTADWTRVPYEV	ADWTRVPYE	0.1132	14687.3	32.00	Sequence
IAs	36	ARVFSEVIPHTASIE	RVFSEVIPH	0.1131	14712.9	32.00	Sequence
IAs	506	VNRVVLDITSKPPAT	VLDITSKPP	0.1130	14716.9	32.00	Sequence
IAs	400	PFPGPGLGIRIVGEV	LGIRIVGEV	0.1129	14745.5	32.00	Sequence
IAs	24	QYAQLIARRVREARV	QYAQLIARR	0.1119	14902.3	32.00	Sequence
IAs	236	DSAVAAALVQRAIGD	SAVAAALVQ	0.1119	14905.1	32.00	Sequence
IAs	78	DPALLDLGVPVLGIC	PALLDLGVP	0.1109	15067.5	50.00	Sequence

IAs	403	GPGLGIRIVGEVTAK	RIVGEVTAK	0.1108	15075.0	50.00	Sequence
IAs	53	RARQPVALVLSGGPA	ALVLSGGPA	0.1106	15115.5	50.00	Sequence
IAs	276	AATGANLVTVDAAET	ATGANLVTV	0.1105	15125.8	50.00	Sequence
IAs	398	RQPFPGPGLGIRIVG	QPFPGPGLG	0.1104	15150.6	50.00	Sequence
IAs	156	SSAGAPVAAFEAFDR	APVAAFEAF	0.1100	15202.3	50.00	Sequence
IAs	476	SEDAMTADWTRVPYE	ADWTRVPYE	0.1094	15308.9	50.00	Sequence
IAs	206	TPANIANALIEQVRT	TPANIANAL	0.1093	15326.3	50.00	Sequence
IAs	263	RAGERAQVQRDFVAA	RAGERAQVQ	0.1091	15354.6	50.00	Sequence
IAs	37	RVFSEVIPHTASIEE	RVFSEVIPH	0.1087	15423.2	50.00	Sequence
IAs	210	IANALIEQVRTQIGD	ALIEQVRTQ	0.1087	15428.7	50.00	Sequence
IAs	35	EARVFSEVIPHTASI	RVFSEVIPH	0.1085	15454.9	50.00	Sequence
IAs	401	FPGPGLGIRIVGEVT	LGIRIVGEV	0.1084	15473.5	50.00	Sequence
IAs	82	LDLGVPVLGICYGFQ	VLGICYGFQ	0.1083	15486.4	50.00	Sequence
IAs	262	LRAGERAQVQRDFVA	RAGERAQVQ	0.1077	15597.9	50.00	Sequence
IAs	505	EVNRVVLDITSKPPA	LDITSKPPA	0.1075	15627.1	50.00	Sequence
IAs	209	NIANALIEQVRTQIG	ALIEQVRTQ	0.1068	15752.2	50.00	Sequence
IAs	259	HGLLRAGERAQVQRD	RAGERAQVQ	0.1066	15770.9	50.00	Sequence
IAs	54	ARQPVALVLSGGPAS	ALVLSGGPA	0.1065	15791.1	50.00	Sequence
IAs	79	PALLDLGVPVLGICY	PALLDLGVP	0.1062	15841.9	50.00	Sequence
IAs	235	VDSAVAAALVQRAIG	SAVAAALVQ	0.1062	15849.6	50.00	Sequence
IAs	504	AEVNRVVLDITSKPP	VVLDITSKP	0.1061	15857.2	50.00	Sequence
IAs	360	GGLPDDLKFTLVEPL	LKFTLVEPL	0.1057	15928.7	50.00	Sequence
IAs	478	DAMTADWTRVPYEVL	ADWTRVPYE	0.1052	16026.4	50.00	Sequence
IAs	479	AMTADWTRVPYEVLE	ADWTRVPYE	0.1047	16104.8	50.00	Sequence
IAs	201	LGAQWTPANIANALI	TPANIANAL	0.1045	16147.2	50.00	Sequence
IAs	239	VAAALVQRAIGDRLT	VAAALVQRA	0.1038	16265.9	50.00	Sequence
IAs	508	RVVLDITSKPPATIE	VLDITSKPP	0.1032	16372.7	50.00	Sequence
IAs	282	LVTVDAAETFLEALS	VTVDAAETF	0.1031	16380.7	50.00	Sequence
IAs	128	SDLPEVQPVWMSHGD	SDLPEVQPV	0.1031	16387.4	50.00	Sequence
IAs	509	VVLDITSKPPATIEW	VLDITSKPP	0.1031	16391.0	50.00	Sequence
IAs	165	FEAFDRRLAGVQYHP	RRLAGVQYH	0.1021	16573.6	50.00	Sequence
IAs	43	IPHTASIEEIRARQP	ASIEEIRAR	0.1020	16584.7	50.00	Sequence
IAs	507	NRVVLDITSKPPATI	VLDITSKPP	0.1017	16645.7	50.00	Sequence
IAs	411	VGEVTAKRLDTLRHA	KRLDTLRHA	0.1016	16653.2	50.00	Sequence
IAs	261	LLRAGERAQVQRDFV	RAGERAQVQ	0.1015	16673.1	50.00	Sequence
IAs	81	LLDLGVPVLGICYGF	LGVPVLGIC	0.1012	16734.7	50.00	Sequence
IAs	271	QRDFVAATGANLVTV	VAATGANLV	0.1007	16822.4	50.00	Sequence
IAs	281	NLVTVDAAETFLEAL	VTVDAAETF	0.1006	16828.2	50.00	Sequence
IAs	283	VTVDAAETFLEALSG	VTVDAAETF	0.1003	16895.7	50.00	Sequence
IAs	238	AVAAALVQRAIGDRL	VAAALVQRA	0.1000	16945.5	50.00	Sequence
IAs	404	PGLGIRIVGEVTAKR	RIVGEVTAK	0.0990	17133.0	50.00	Sequence
IAs	55	RQPVALVLSGGPASV	ALVLSGGPA	0.0984	17245.9	50.00	Sequence
IAs	234	GVDSAVAAALVQRAI	SAVAAALVQ	0.0981	17291.7	50.00	Sequence
IAs	74	APKLDPALLDLGVPV	ALLDLGVPV	0.0977	17379.1	50.00	Sequence
IAs	127	HSDLPEVQPVWMSHG	SDLPEVQPV	0.0975	17403.2	50.00	Sequence
IAs	260	GLLRAGERAQVQRDF	RAGERAQVQ	0.0973	17452.5	50.00	Sequence
IAs	405	GLGIRIVGEVTAKRL	RIVGEVTAK	0.0971	17490.0	50.00	Sequence
IAs	288	AETFLEALSGVSAPE	ALSGVSAPE	0.0967	17562.8	50.00	Sequence
IAs	130	LPEVQPVWMSHGDAV	VWMSHGDAV	0.0961	17672.0	50.00	Sequence
IAs	412	GEVTAKRLDTLRHAD	KRLDTLRHA	0.0960	17693.3	50.00	Sequence
IAs	299	SAPEGKRKIIGRQFI	RKIIGRQFI	0.0958	17730.4	50.00	Sequence
IAs	142	DAVTAAPDGFDVVAS	DAVTAAPDG	0.0949	17902.4	50.00	Sequence
IAs	306	KIIGRQFIRAFEGAV	KIIGRQFIR	0.0943	18024.2	50.00	Sequence
IAs	431	EELTAAGLDNQIWQC	EELTAAGLD	0.0939	18105.8	50.00	Sequence
IAs	434	TAAGLDNQIWQCPVV	NQIWQCPVV	0.0938	18123.0	50.00	Sequence
IAs	379	KDEVRAVGRELGLPE	AVGRELGLP	0.0937	18147.5	50.00	Sequence
IAs	164	AFEAFDRRLAGVQYH	RRLAGVQYH	0.0935	18175.4	50.00	Sequence
IAs	402	PGPGLGIRIVGEVTA	LGIRIVGEV	0.0935	18179.4	50.00	Sequence
IAs	133	VQPVWMSHGDAVTAA	PVWMSHGDA	0.0935	18179.6	50.00	Sequence
IAs	425	ADSIVREELTAAGLD	EELTAAGLD	0.0932	18246.4	50.00	Sequence
IAs	233	GGVDSAVAAALVQRA	SAVAAALVQ	0.0930	18280.2	50.00	Sequence
IAs	430	REELTAAGLDNQIWQ	EELTAAGLD	0.0922	18429.9	50.00	Sequence
IAs	450	LADVRSVGVQGDGRT	RSVGVQGDG	0.0922	18439.5	50.00	Sequence
IAs	449	LLADVRSVGVQGDGR	RSVGVQGDG	0.0917	18546.7	50.00	Sequence
IAs	446	PVVLLADVRSVGVQG	PVVLLADVR	0.0916	18558.0	50.00	Sequence
IAs	414	VTAKRLDTLRHADSI	KRLDTLRHA	0.0914	18603.2	50.00	Sequence

IAs	50	EEIRARQPVALVLSG	EEIRARQPV	0.0912	18632.2	50.00	Sequence
IAs	378	FKDEVRAVGRELGLP	AVGRELGLP	0.0912	18634.8	50.00	Sequence
IAs	56	QPVALVLSGGPASVY	ALVLSGGPA	0.0911	18650.6	50.00	Sequence
IAs	92	CYGFQAMAQALGGIV	YGFQAMAQA	0.0911	18657.8	50.00	Sequence
IAs	58	VALVLSGGPASVYAD	ALVLSGGPA	0.0905	18780.8	50.00	Sequence
IAs	91	ICYGFQAMAQALGGI	YGFQAMAQA	0.0903	18822.7	50.00	Sequence
IAs	41	EVIPHTASIEEIRAR	ASIEEIRAR	0.0902	18843.0	50.00	Sequence
IAs	355	SHHNVGGLPDDLKFT	NVGGLPDDL	0.0901	18861.6	50.00	Sequence
IAs	451	ADVRSVGVQGDGRTY	ADVRSVGVQ	0.0901	18871.4	50.00	Sequence
IAs	75	PKLDPALLDLGVPVL	ALLDLGVPV	0.0895	18984.5	50.00	Sequence
IAs	354	KSHHNVGGLPDDLKF	NVGGLPDDL	0.0892	19046.6	50.00	Sequence
IAs	352	NIKSHHNVGGLPDDL	NVGGLPDDL	0.0890	19081.9	50.00	Sequence
IAs	353	IKSHHNVGGLPDDLK	NVGGLPDDL	0.0890	19095.9	50.00	Sequence
IAs	143	AVTAAPDGFDVVASS	AVTAAPDGF	0.0887	19146.8	50.00	Sequence
IAs	413	EVTAKRLDTLRHADS	KRLDTLRHA	0.0886	19163.8	50.00	Sequence
IAs	369	TLVEPLRLLFKDEVR	RLLFKDEVR	0.0880	19290.1	50.00	Sequence
IAs	88	VLGICYGFQAMAQAL	YGFQAMAQA	0.0878	19342.7	50.00	Sequence
IAs	158	AGAPVAAFEAFDRRL	APVAAFEAF	0.0873	19437.6	50.00	Sequence
IAs	84	LGVPVLGICYGFQAM	LGVPVLGIC	0.0872	19454.4	50.00	Sequence
IAs	57	PVALVLSGGPASVYA	ALVLSGGPA	0.0872	19463.9	50.00	Sequence
IAs	448	VLLADVRSVGVQGDG	RSVGVQGDG	0.0869	19527.4	50.00	Sequence
IAs	93	YGFQAMAQALGGIVA	YGFQAMAQA	0.0866	19586.8	50.00	Sequence
IAs	132	EVQPVWMSHGDAVTA	VWMSHGDAV	0.0865	19608.0	50.00	Sequence
IAs	83	DLGVPVLGICYGFQA	LGVPVLGIC	0.0863	19663.3	50.00	Sequence
IAs	87	PVLGICYGFQAMAQA	YGFQAMAQA	0.0862	19670.5	50.00	Sequence
IAs	131	PEVQPVWMSHGDAVT	VWMSHGDAV	0.0862	19676.5	50.00	Sequence
IAs	129	DLPEVQPVWMSHGDA	LPEVQPVWM	0.0861	19698.0	50.00	Sequence
IAs	323	VLDGKTAEFLVQGTL	AEFLVQGTL	0.0860	19724.6	50.00	Sequence
IAs	453	VRSVGVQGDGRTYGH	RSVGVQGDG	0.0849	19962.1	50.00	Sequence
IAs	429	VREELTAAGLDNQIW	EELTAAGLD	0.0847	19994.5	50.00	Sequence
IAs	134	QPVWMSHGDAVTAAP	HGDAVTAAP	0.0845	20033.7	50.00	Sequence
IAs	42	VIPHTASIEEIRARQ	ASIEEIRAR	0.0838	20188.2	50.00	Sequence
IAs	456	VGVQGDGRTYGHPIV	GDGRTYGHP	0.0835	20254.3	50.00	Sequence
IAs	90	GICYGFQAMAQALGG	YGFQAMAQA	0.0833	20310.5	50.00	Sequence
IAs	321	RDVLDGKTAEFLVQG	RDVLDGKTA	0.0824	20490.6	50.00	Sequence
IAs	481	TADWTRVPYEVLERI	ADWTRVPYE	0.0812	20771.6	50.00	Sequence
IAs	345	GGGSGTANIKSHHNV	ANIKSHHNV	0.0806	20909.8	50.00	Sequence
IAs	320	VRDVLDGKTAEFLVQ	RDVLDGKTA	0.0805	20933.1	50.00	Sequence
IAs	334	QGTLYPDVVESGGGS	QGTLYPDVV	0.0802	21005.1	50.00	Sequence
IAs	426	DSIVREELTAAGLDN	EELTAAGLD	0.0801	21022.3	50.00	Sequence
IAs	254	CVFVDHGLLRAGERA	HGLLRAGER	0.0798	21094.8	50.00	Sequence
IAs	452	DVRSVGVQGDGRTYG	RSVGVQGDG	0.0794	21166.1	50.00	Sequence
IAs	119	LKVLGGKLHSDLPEV	LKVLGGKLH	0.0793	21209.2	50.00	Sequence
IAs	475	SSEDAMTADWTRVPY	MTADWTRVP	0.0790	21270.4	50.00	Sequence
IAs	482	ADWTRVPYEVLERIS	ADWTRVPYE	0.0789	21295.7	50.00	Sequence
IAs	433	LTAAGLDNQIWQCPV	AAGLDNQIW	0.0787	21346.9	50.00	Sequence
IAs	315	AFEGAVRDVLDGKTA	RDVLDGKTA	0.0781	21467.1	50.00	Sequence
IAs	370	LVEPLRLLFKDEVRA	RLLFKDEVR	0.0773	21660.5	50.00	Sequence
IAs	423	RHADSIVREELTAAG	RHADSIVRE	0.0772	21681.2	50.00	Sequence
IAs	427	SIVREELTAAGLDNQ	EELTAAGLD	0.0772	21695.3	50.00	Sequence
IAs	159	GAPVAAFEAFDRRLA	APVAAFEAF	0.0771	21716.2	50.00	Sequence
IAs	86	VPVLGICYGFQAMAQ	VPVLGICYG	0.0768	21788.9	50.00	Sequence
IAs	503	VAEVNRVVLDITSKP	RVVLDITSK	0.0766	21826.4	50.00	Sequence
IAs	308	IGRQFIRAFEGAVRD	RAFEGAVRD	0.0764	21881.7	50.00	Sequence
IAs	256	FVDHGLLRAGERAQV	HGLLRAGER	0.0756	22055.7	50.00	Sequence
IAs	255	VFVDHGLLRAGERAQ	HGLLRAGER	0.0751	22177.8	50.00	Sequence
IAs	20	DFGAQYAQLIARRVR	DFGAQYAQL	0.0746	22311.8	50.00	Sequence
IAs	417	KRLDTLRHADSIVRE	KRLDTLRHA	0.0744	22362.6	50.00	Sequence
IAs	253	TCVFVDHGLLRAGER	HGLLRAGER	0.0741	22424.1	50.00	Sequence
IAs	89	LGICYGFQAMAQALG	YGFQAMAQA	0.0741	22437.2	50.00	Sequence
IAs	422	LRHADSIVREELTAA	RHADSIVRE	0.0741	22437.9	50.00	Sequence
IAs	7	DVPETPARPVLVVDF	ARPVLVVDF	0.0739	22470.0	50.00	Sequence
IAs	432	ELTAAGLDNQIWQCP	LTAAGLDNQ	0.0738	22496.0	50.00	Sequence
IAs	428	IVREELTAAGLDNQI	EELTAAGLD	0.0732	22648.0	50.00	Sequence
IAs	316	FEGAVRDVLDGKTAE	FEGAVRDVL	0.0727	22760.0	50.00	Sequence
IAs	73	GAPKLDPALLDLGVP	PALLDLGVP	0.0726	22787.3	50.00	Sequence

IAs	421	TLRHADSIVREELTA	RHADSIVRE	0.0725	22816.4	50.00	Sequence
IAs	269	QVQRDFVAATGANLV	VAATGANLV	0.0719	22979.0	50.00	Sequence
IAs	454	RSVGVQGDGRTYGHP	RSVGVQGDG	0.0717	23011.8	50.00	Sequence
IAs	160	APVAAFEAFDRRLAG	APVAAFEAF	0.0717	23024.5	50.00	Sequence
IAs	18	VVDFGAQYAQLIARR	QYAQLIARR	0.0714	23088.4	50.00	Sequence
IAs	494	RISTRITNEVAEVNR	RITNEVAEV	0.0713	23108.6	50.00	Sequence
IAs	193	RFLHDFAGLGAQWTP	AGLGAQWTP	0.0713	23120.4	50.00	Sequence
IAs	21	FGAQYAQLIARRVRE	AQLIARRVR	0.0713	23121.4	50.00	Sequence
IAs	474	VSSEDAMTADWTRVP	MTADWTRVP	0.0712	23130.4	50.00	Sequence
IAs	52	IRARQPVALVLSGGP	VALVLSGGP	0.0709	23213.1	50.00	Sequence
IAs	493	ERISTRITNEVAEVN	RITNEVAEV	0.0707	23261.9	50.00	Sequence
IAs	85	GVPVLGICYGFQAMA	VPVLGICYG	0.0707	23263.1	50.00	Sequence
IAs	367	KFTLVEPLRLLFKDE	KFTLVEPLR	0.0703	23367.1	50.00	Sequence
IAs	178	HPEVMHTPHGQQVLS	EVMHTPHGQ	0.0698	23504.8	50.00	Sequence
IAs	118	ELKVLGGKLHSDLPE	LKVLGGKLH	0.0696	23548.0	50.00	Sequence
IAs	351	ANIKSHHNVGGLPDD	SHHNVGGLP	0.0690	23696.5	50.00	Sequence
IAs	5	DIDVPETPARPVLVV	ETPARPVLV	0.0690	23706.3	50.00	Sequence
IAs	371	VEPLRLLFKDEVRAV	RLLFKDEVR	0.0686	23801.9	50.00	Sequence
IAs	350	TANIKSHHNVGGLPD	SHHNVGGLP	0.0685	23816.6	50.00	Sequence
IAs	19	VDFGAQYAQLIARRV	QYAQLIARR	0.0685	23822.0	50.00	Sequence
IAs	410	IVGEVTAKRLDTLRH	VTAKRLDTL	0.0684	23860.9	50.00	Sequence
IAs	59	ALVLSGGPASVYADG	ALVLSGGPA	0.0679	23989.8	50.00	Sequence
IAs	270	VQRDFVAATGANLVT	VAATGANLV	0.0678	24005.9	50.00	Sequence
IAs	349	GTANIKSHHNVGGLP	SHHNVGGLP	0.0678	24016.8	50.00	Sequence
IAs	408	IRIVGEVTAKRLDTL	VTAKRLDTL	0.0677	24030.9	50.00	Sequence
IAs	6	IDVPETPARPVLVVD	ETPARPVLV	0.0674	24108.0	50.00	Sequence
IAs	322	DVLDGKTAEFLVQGT	LDGKTAEFL	0.0674	24109.0	50.00	Sequence
IAs	409	RIVGEVTAKRLDTLR	RIVGEVTAK	0.0669	24250.8	50.00	Sequence
IAs	230	GLSGGVDSAVAAALV	DSAVAAALV	0.0665	24338.9	50.00	Sequence
IAs	101	ALGGIVAHTGTREYG	LGGIVAHTG	0.0661	24463.2	50.00	Sequence
IAs	447	VVLLADVRSVGVQGD	ADVRSVGVQ	0.0659	24509.9	50.00	Sequence
IAs	346	GGSGTANIKSHHNVG	SGTANIKSH	0.0655	24627.3	50.00	Sequence
IAs	310	RQFIRAFEGAVRDVL	FEGAVRDVL	0.0654	24637.5	50.00	Sequence
IAs	420	DTLRHADSIVREELT	RHADSIVRE	0.0654	24653.5	50.00	Sequence
IAs	356	HHNVGGLPDDLKFTL	NVGGLPDDL	0.0652	24695.4	50.00	Sequence
IAs	424	HADSIVREELTAAGL	HADSIVREE	0.0652	24699.9	50.00	Sequence
IAs	498	RITNEVAEVNRVVLD	AEVNRVVLD	0.0651	24709.3	50.00	Sequence
IAs	212	NALIEQVRTQIGDGH	ALIEQVRTQ	0.0649	24780.2	50.00	Sequence
IAs	179	PEVMHTPHGQQVLSR	EVMHTPHGQ	0.0647	24825.1	50.00	Sequence
IAs	416	AKRLDTLRHADSIVR	KRLDTLRHA	0.0646	24850.8	50.00	Sequence
IAs	106	VAHTGTREYGRTELK	REYGRTELK	0.0643	24933.5	50.00	Sequence
IAs	406	LGIRIVGEVTAKRLD	GEVTAKRLD	0.0637	25091.0	50.00	Sequence
IAs	419	LDTLRHADSIVREEL	RHADSIVRE	0.0637	25091.3	50.00	Sequence
IAs	61	VLSGGPASVYADGAP	ASVYADGAP	0.0635	25143.0	50.00	Sequence
IAs	415	TAKRLDTLRHADSIV	KRLDTLRHA	0.0635	25149.5	50.00	Sequence
IAs	502	EVAEVNRVVLDITSK	RVVLDITSK	0.0632	25234.8	50.00	Sequence
IAs	492	LERISTRITNEVAEV	RITNEVAEV	0.0628	25336.6	50.00	Sequence
IAs	473	PVSSEDAMTADWTRV	EDAMTADWT	0.0627	25383.2	50.00	Sequence
IAs	40	SEVIPHTASIEEIRA	HTASIEEIR	0.0626	25398.1	50.00	Sequence
IAs	100	QALGGIVAHTGTREY	IVAHTGTRE	0.0622	25511.0	50.00	Sequence
IAs	102	LGGIVAHTGTREYGR	LGGIVAHTG	0.0621	25544.1	50.00	Sequence
IAs	39	FSEVIPHTASIEEIR	HTASIEEIR	0.0620	25569.0	50.00	Sequence
IAs	51	EIRARQPVALVLSGG	IRARQPVAL	0.0616	25667.7	50.00	Sequence
IAs	211	ANALIEQVRTQIGDG	ALIEQVRTQ	0.0609	25864.5	50.00	Sequence
IAs	343	ESGGGSGTANIKSHH	GGGSGTANI	0.0609	25867.9	50.00	Sequence
IAs	309	GRQFIRAFEGAVRDV	RAFEGAVRD	0.0609	25869.0	50.00	Sequence
IAs	348	SGTANIKSHHNVGGL	SGTANIKSH	0.0608	25887.7	50.00	Sequence
IAs	249	GDRLTCVFVDHGLLR	VFVDHGLLR	0.0606	25953.6	50.00	Sequence
IAs	499	ITNEVAEVNRVVLDI	AEVNRVVLD	0.0606	25966.6	50.00	Sequence
IAs	318	GAVRDVLDGKTAEFL	RDVLDGKTA	0.0605	25980.3	50.00	Sequence
IAs	347	GSGTANIKSHHNVGG	SGTANIKSH	0.0603	26042.5	50.00	Sequence
IAs	15	PVLVVDFGAQYAQLI	FGAQYAQLI	0.0598	26188.9	50.00	Sequence
IAs	311	QFIRAFEGAVRDVLD	FEGAVRDVL	0.0596	26227.7	50.00	Sequence
IAs	342	VESGGGSGTANIKSH	SGTANIKSH	0.0595	26267.2	50.00	Sequence
IAs	99	AQALGGIVAHTGTRE	IVAHTGTRE	0.0594	26295.1	50.00	Sequence
IAs	287	AAETFLEALSGVSAP	EALSGVSAP	0.0594	26306.5	50.00	Sequence

IAs	455	SVGVQGDGRTYGHPI	GDGRTYGHP	0.0592	26355.2	50.00	Sequence
IAs	213	ALIEQVRTQIGDGHA	ALIEQVRTQ	0.0591	26377.7	50.00	Sequence
IAs	250	DRLTCVFVDHGLLRA	VFVDHGLLR	0.0589	26432.0	50.00	Sequence
IAs	357	HNVGGLPDDLKFTLV	NVGGLPDDL	0.0588	26461.2	50.00	Sequence
IAs	375	RLLFKDEVRAVGREL	RLLFKDEVR	0.0588	26462.3	50.00	Sequence
IAs	407	GIRIVGEVTAKRLDT	GEVTAKRLD	0.0588	26473.8	50.00	Sequence
IAs	374	LRLLFKDEVRAVGRE	RLLFKDEVR	0.0585	26543.5	50.00	Sequence
IAs	107	AHTGTREYGRTELKV	REYGRTELK	0.0585	26555.8	50.00	Sequence
IAs	340	DVVESGGGSGTANIK	GGSGTANIK	0.0583	26621.7	50.00	Sequence
IAs	23	AQYAQLIARRVREAR	QYAQLIARR	0.0582	26641.6	50.00	Sequence
IAs	497	TRITNEVAEVNRVVL	EVAEVNRVV	0.0582	26651.4	50.00	Sequence
IAs	495	ISTRITNEVAEVNRV	RITNEVAEV	0.0577	26785.3	50.00	Sequence
IAs	307	IIGRQFIRAFEGAVR	QFIRAFEGA	0.0575	26831.7	50.00	Sequence
IAs	229	CGLSGGVDSAVAAAL	SGGVDSAVA	0.0573	26890.1	50.00	Sequence
IAs	22	GAQYAQLIARRVREA	QYAQLIARR	0.0571	26944.0	50.00	Sequence
IAs	373	PLRLLFKDEVRAVGR	RLLFKDEVR	0.0571	26946.9	50.00	Sequence
IAs	226	HAICGLSGGVDSAVA	SGGVDSAVA	0.0571	26961.8	50.00	Sequence
IAs	319	AVRDVLDGKTAEFLV	LDGKTAEFL	0.0569	27012.3	50.00	Sequence
IAs	372	EPLRLLFKDEVRAVG	RLLFKDEVR	0.0568	27030.1	50.00	Sequence
IAs	418	RLDTLRHADSIVREE	RHADSIVRE	0.0565	27126.8	50.00	Sequence
IAs	96	QAMAQALGGIVAHTG	LGGIVAHTG	0.0562	27219.1	50.00	Sequence
IAs	16	VLVVDFGAQYAQLIA	FGAQYAQLI	0.0557	27369.1	50.00	Sequence
IAs	314	RAFEGAVRDVLDGKT	RAFEGAVRD	0.0554	27455.7	50.00	Sequence
IAs	341	VVESGGGSGTANIKS	GGSGTANIK	0.0552	27503.6	50.00	Sequence
IAs	251	RLTCVFVDHGLLRAG	VFVDHGLLR	0.0550	27582.0	50.00	Sequence
IAs	344	SGGGSGTANIKSHHN	SGTANIKSH	0.0547	27666.3	50.00	Sequence
IAs	312	FIRAFEGAVRDVLDG	RAFEGAVRD	0.0547	27666.3	50.00	Sequence
IAs	496	STRITNEVAEVNRVV	EVAEVNRVV	0.0546	27695.9	50.00	Sequence
IAs	227	AICGLSGGVDSAVAA	GGVDSAVAA	0.0544	27765.8	50.00	Sequence
IAs	313	IRAFEGAVRDVLDGK	RAFEGAVRD	0.0540	27860.9	50.00	Sequence
IAs	180	EVMHTPHGQQVLSRF	EVMHTPHGQ	0.0540	27860.9	50.00	Sequence
IAs	113	EYGRTELKVLGGKLH	LKVLGGKLH	0.0539	27920.1	50.00	Sequence
IAs	108	HTGTREYGRTELKVL	REYGRTELK	0.0536	27996.6	50.00	Sequence
IAs	252	LTCVFVDHGLLRAGE	CVFVDHGLL	0.0536	28000.5	50.00	Sequence
IAs	298	VSAPEGKRKIIGRQF	KRKIIGRQF	0.0534	28056.6	50.00	Sequence
IAs	17	LVVDFGAQYAQLIAR	FGAQYAQLI	0.0534	28058.8	50.00	Sequence
IAs	248	IGDRLTCVFVDHGLL	CVFVDHGLL	0.0531	28158.5	50.00	Sequence
IAs	268	AQVQRDFVAATGANL	RDFVAATGA	0.0529	28211.3	50.00	Sequence
IAs	228	ICGLSGGVDSAVAAA	GGVDSAVAA	0.0528	28246.1	50.00	Sequence
IAs	266	ERAQVQRDFVAATGA	RDFVAATGA	0.0520	28489.2	50.00	Sequence
IAs	95	FQAMAQALGGIVAHT	ALGGIVAHT	0.0512	28742.4	50.00	Sequence
IAs	317	EGAVRDVLDGKTAEF	RDVLDGKTA	0.0509	28824.3	50.00	Sequence
IAs	38	VFSEVIPHTASIEEI	VFSEVIPHT	0.0507	28899.3	50.00	Sequence
IAs	97	AMAQALGGIVAHTGT	LGGIVAHTG	0.0504	28967.9	50.00	Sequence
IAs	265	GERAQVQRDFVAATG	ERAQVQRDF	0.0503	29023.7	50.00	Sequence
IAs	114	YGRTELKVLGGKLHS	LKVLGGKLH	0.0500	29113.0	50.00	Sequence
IAs	501	NEVAEVNRVVLDITS	EVAEVNRVV	0.0498	29171.4	50.00	Sequence
IAs	98	MAQALGGIVAHTGTR	LGGIVAHTG	0.0498	29187.1	50.00	Sequence
IAs	368	FTLVEPLRLLFKDEV	FTLVEPLRL	0.0495	29252.9	50.00	Sequence
IAs	264	AGERAQVQRDFVAAT	GERAQVQRD	0.0494	29282.7	50.00	Sequence
IAs	500	TNEVAEVNRVVLDIT	AEVNRVVLD	0.0489	29449.2	50.00	Sequence
IAs	484	WTRVPYEVLERISTR	EVLERISTR	0.0481	29705.2	50.00	Sequence
IAs	115	GRTELKVLGGKLHSD	LKVLGGKLH	0.0479	29770.8	50.00	Sequence
IAs	116	RTELKVLGGKLHSDL	LKVLGGKLH	0.0472	29999.1	50.00	Sequence
IAs	339	PDVVESGGGSGTANI	GGGSGTANI	0.0470	30075.8	50.00	Sequence
IAs	240	AAALVQRAIGDRLTC	AAALVQRAI	0.0463	30306.4	50.00	Sequence
IAs	267	RAQVQRDFVAATGAN	RDFVAATGA	0.0459	30425.0	50.00	Sequence
IAs	486	RVPYEVLERISTRIT	VPYEVLERI	0.0458	30457.6	50.00	Sequence
IAs	117	TELKVLGGKLHSDLP	LKVLGGKLH	0.0457	30498.9	50.00	Sequence
IAs	487	VPYEVLERISTRITN	VPYEVLERI	0.0454	30610.2	50.00	Sequence
IAs	112	REYGRTELKVLGGKL	REYGRTELK	0.0453	30617.2	50.00	Sequence
IAs	491	VLERISTRITNEVAE	RISTRITNE	0.0450	30729.7	50.00	Sequence
IAs	284	TVDAAETFLEALSGV	TFLEALSGV	0.0449	30756.0	50.00	Sequence
IAs	490	EVLERISTRITNEVA	RISTRITNE	0.0449	30767.7	50.00	Sequence
IAs	161	PVAAFEAFDRRLAGV	AAFEAFDRR	0.0445	30881.7	50.00	Sequence
IAs	111	TREYGRTELKVLGGK	REYGRTELK	0.0443	30949.3	50.00	Sequence

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         IAs  485  TRVPYEVLERISTRI  VPYEVLERI        0.0443     30959.0               50.00     Sequence
         IAs  488  PYEVLERISTRITNE  RISTRITNE        0.0443     30965.0               50.00     Sequence
         IAs  483  DWTRVPYEVLERIST  VPYEVLERI        0.0439     31086.9               50.00     Sequence
         IAs  358  NVGGLPDDLKFTLVE  NVGGLPDDL        0.0439     31109.4               50.00     Sequence
         IAs  489  YEVLERISTRITNEV  RISTRITNE        0.0435     31216.3               50.00     Sequence
         IAs  162  VAAFEAFDRRLAGVQ  AAFEAFDRR        0.0432     31337.8               50.00     Sequence
         IAs  192  SRFLHDFAGLGAQWT  FAGLGAQWT        0.0429     31423.7               50.00     Sequence
         IAs  110  GTREYGRTELKVLGG  REYGRTELK        0.0420     31756.9               50.00     Sequence
         IAs  187  GQQVLSRFLHDFAGL  RFLHDFAGL        0.0419     31775.9               50.00     Sequence
         IAs  109  TGTREYGRTELKVLG  REYGRTELK        0.0419     31789.3               50.00     Sequence
         IAs  186  HGQQVLSRFLHDFAG  HGQQVLSRF        0.0411     32038.9               50.00     Sequence
         IAs  215  IEQVRTQIGDGHAIC  TQIGDGHAI        0.0409     32114.6               50.00     Sequence
         IAs  214  LIEQVRTQIGDGHAI  TQIGDGHAI        0.0408     32164.0               50.00     Sequence
         IAs  217  QVRTQIGDGHAICGL  VRTQIGDGH        0.0403     32342.6               50.00     Sequence
         IAs  245  QRAIGDRLTCVFVDH  RLTCVFVDH        0.0402     32352.1               50.00     Sequence
         IAs   60  LVLSGGPASVYADGA  GPASVYADG        0.0402     32358.7               50.00     Sequence
         IAs  185  PHGQQVLSRFLHDFA  QVLSRFLHD        0.0402     32370.6               50.00     Sequence
         IAs  183  HTPHGQQVLSRFLHD  QVLSRFLHD        0.0401     32395.9               50.00     Sequence
         IAs  188  QQVLSRFLHDFAGLG  RFLHDFAGL        0.0400     32417.2               50.00     Sequence
         IAs  184  TPHGQQVLSRFLHDF  QVLSRFLHD        0.0400     32440.4               50.00     Sequence
         IAs  246  RAIGDRLTCVFVDHG  RLTCVFVDH        0.0396     32578.6               50.00     Sequence
         IAs  247  AIGDRLTCVFVDHGL  RLTCVFVDH        0.0389     32826.3               50.00     Sequence
         IAs  297  GVSAPEGKRKIIGRQ  VSAPEGKRK        0.0387     32881.8               50.00     Sequence
         IAs  241  AALVQRAIGDRLTCV  AALVQRAIG        0.0387     32884.3               50.00     Sequence
         IAs  163  AAFEAFDRRLAGVQY  AAFEAFDRR        0.0385     32979.1               50.00     Sequence
         IAs  189  QVLSRFLHDFAGLGA  RFLHDFAGL        0.0378     33219.4               50.00     Sequence
         IAs  377  LFKDEVRAVGRELGL  RAVGRELGL        0.0376     33272.6               50.00     Sequence
         IAs   94  GFQAMAQALGGIVAH  QAMAQALGG        0.0375     33312.2               50.00     Sequence
         IAs  216  EQVRTQIGDGHAICG  VRTQIGDGH        0.0373     33400.6               50.00     Sequence
         IAs  285  VDAAETFLEALSGVS  AAETFLEAL        0.0367     33625.1               50.00     Sequence
         IAs  182  MHTPHGQQVLSRFLH  QQVLSRFLH        0.0362     33779.0               50.00     Sequence
         IAs  218  VRTQIGDGHAICGLS  VRTQIGDGH        0.0353     34141.3               50.00     Sequence
         IAs  103  GGIVAHTGTREYGRT  GIVAHTGTR        0.0351     34193.4               50.00     Sequence
         IAs  104  GIVAHTGTREYGRTE  GIVAHTGTR        0.0351     34208.2               50.00     Sequence
         IAs  244  VQRAIGDRLTCVFVD  IGDRLTCVF        0.0330     34995.9               50.00     Sequence
         IAs  242  ALVQRAIGDRLTCVF  ALVQRAIGD        0.0323     35234.5               50.00     Sequence
         IAs  223  GDGHAICGLSGGVDS  CGLSGGVDS        0.0317     35466.6               50.00     Sequence
         IAs  105  IVAHTGTREYGRTEL  TGTREYGRT        0.0317     35487.0               50.00     Sequence
         IAs  224  DGHAICGLSGGVDSA  HAICGLSGG        0.0307     35885.8               50.00     Sequence
         IAs  243  LVQRAIGDRLTCVFV  IGDRLTCVF        0.0304     35985.8               50.00     Sequence
         IAs  191  LSRFLHDFAGLGAQW  HDFAGLGAQ        0.0300     36122.7               50.00     Sequence
         IAs  337  LYPDVVESGGGSGTA  LYPDVVESG        0.0300     36128.6               50.00     Sequence
         IAs  225  GHAICGLSGGVDSAV  HAICGLSGG        0.0299     36167.3               50.00     Sequence
         IAs  286  DAAETFLEALSGVSA  AAETFLEAL        0.0293     36400.1               50.00     Sequence
         IAs  181  VMHTPHGQQVLSRFL  MHTPHGQQV        0.0288     36601.1               50.00     Sequence
         IAs  376  LLFKDEVRAVGRELG  DEVRAVGRE        0.0283     36806.4               50.00     Sequence
         IAs  336  TLYPDVVESGGGSGT  LYPDVVESG        0.0278     37021.7               50.00     Sequence
         IAs  335  GTLYPDVVESGGGSG  LYPDVVESG        0.0267     37473.9               50.00     Sequence
         IAs  222  IGDGHAICGLSGGVD  ICGLSGGVD        0.0266     37487.6               50.00     Sequence
         IAs  190  VLSRFLHDFAGLGAQ  HDFAGLGAQ        0.0259     37770.6               50.00     Sequence
         IAs  145  TAAPDGFDVVASSAG  FDVVASSAG        0.0251     38124.5               50.00     Sequence
         IAs  144  VTAAPDGFDVVASSA  AAPDGFDVV        0.0245     38376.6               50.00     Sequence
         IAs  359  VGGLPDDLKFTLVEP  VGGLPDDLK        0.0244     38407.7               50.00     Sequence
         IAs  146  AAPDGFDVVASSAGA  AAPDGFDVV        0.0243     38444.7               50.00     Sequence
         IAs  220  TQIGDGHAICGLSGG  HAICGLSGG        0.0238     38649.5               50.00     Sequence
         IAs  338  YPDVVESGGGSGTAN  SGGGSGTAN        0.0226     39146.6               50.00     Sequence
         IAs  221  QIGDGHAICGLSGGV  GDGHAICGL        0.0223     39285.7               50.00     Sequence
         IAs  219  RTQIGDGHAICGLSG  TQIGDGHAI        0.0208     39909.9               50.00     Sequence
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Allele: IAs. Number of high binders 0. Number of weak binders 0. Number of peptides 511

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Explain the output. Go **back**.