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  306  GGLLHHAPSLLAFTN  LHHAPSLLA        0.8742          3.9         SB     0.80     Sequence
   DRB1_0101  305  IGGLLHHAPSLLAFT  LHHAPSLLA        0.8676          4.2         SB     1.00     Sequence
   DRB1_0101  307  GLLHHAPSLLAFTNP  LHHAPSLLA        0.8634          4.4         SB     2.00     Sequence
   DRB1_0101   79  IDPFRAAKTLNINFF  FRAAKTLNI        0.8596          4.6         SB     2.00     Sequence
   DRB1_0101  304  YIGGLLHHAPSLLAF  LHHAPSLLA        0.8525          4.9         SB     2.00     Sequence
   DRB1_0101  308  LLHHAPSLLAFTNPT  LHHAPSLLA        0.8490          5.1         SB     4.00     Sequence
   DRB1_0101  224  QAEINYQFNSLLHAA  INYQFNSLL        0.8465          5.3         SB     4.00     Sequence
   DRB1_0101   78  RIDPFRAAKTLNINF  FRAAKTLNI        0.8431          5.5         SB     4.00     Sequence
   DRB1_0101   80  DPFRAAKTLNINFFV  FRAAKTLNI        0.8364          5.9         SB     4.00     Sequence
   DRB1_0101   77  ARIDPFRAAKTLNIN  FRAAKTLNI        0.8259          6.6         SB     4.00     Sequence
   DRB1_0101  309  LHHAPSLLAFTNPTV  LHHAPSLLA        0.8228          6.8         SB     4.00     Sequence
   DRB1_0101   81  PFRAAKTLNINFFVH  FRAAKTLNI        0.8219          6.9         SB     8.00     Sequence
   DRB1_0101  148  NGSFYEVDAISGWWN  FYEVDAISG        0.8213          6.9         SB     8.00     Sequence
   DRB1_0101   76  TARIDPFRAAKTLNI  FRAAKTLNI        0.8199          7.0         SB     8.00     Sequence
   DRB1_0101  303  HYIGGLLHHAPSLLA  LHHAPSLLA        0.8184          7.1         SB     8.00     Sequence
   DRB1_0101  337  INLVYSQRNRSACVR  VYSQRNRSA        0.8181          7.2         SB     8.00     Sequence
   DRB1_0101  225  AEINYQFNSLLHAAD  INYQFNSLL        0.8176          7.2         SB     8.00     Sequence
   DRB1_0101  223  GQAEINYQFNSLLHA  INYQFNSLL        0.8117          7.7         SB     8.00     Sequence
   DRB1_0101  191  NDQYVDLRDKMLTNL  YVDLRDKML        0.8093          7.9         SB     8.00     Sequence
   DRB1_0101  432  DHEYLTEGGVFTNDL  YLTEGGVFT        0.7992          8.8         SB     8.00     Sequence
   DRB1_0101   82  FRAAKTLNINFFVHD  FRAAKTLNI        0.7956          9.1         SB     8.00     Sequence
   DRB1_0101  147  ANGSFYEVDAISGWW  FYEVDAISG        0.7879          9.9         SB     8.00     Sequence
   DRB1_0101  149  GSFYEVDAISGWWNT  FYEVDAISG        0.7872         10.0         SB     8.00     Sequence
   DRB1_0101  373  GNPYLAFSAMLMAGL  YLAFSAMLM        0.7870         10.0         SB     8.00     Sequence
   DRB1_0101  433  HEYLTEGGVFTNDLI  YLTEGGVFT        0.7816         10.6         SB     8.00     Sequence
   DRB1_0101  376  YLAFSAMLMAGLDGI  FSAMLMAGL        0.7800         10.8         SB     8.00     Sequence
   DRB1_0101  226  EINYQFNSLLHAADD  INYQFNSLL        0.7798         10.8         SB    16.00     Sequence
   DRB1_0101  192  DQYVDLRDKMLTNLI  YVDLRDKML        0.7758         11.3         SB    16.00     Sequence
   DRB1_0101  377  LAFSAMLMAGLDGIK  FSAMLMAGL        0.7737         11.6         SB    16.00     Sequence
   DRB1_0101  338  NLVYSQRNRSACVRI  VYSQRNRSA        0.7736         11.6         SB    16.00     Sequence
   DRB1_0101  336  PINLVYSQRNRSACV  VYSQRNRSA        0.7729         11.7         SB    16.00     Sequence
   DRB1_0101  378  AFSAMLMAGLDGIKN  AMLMAGLDG        0.7711         11.9         SB    16.00     Sequence
   DRB1_0101  374  NPYLAFSAMLMAGLD  FSAMLMAGL        0.7654         12.7         SB    16.00     Sequence
   DRB1_0101  375  PYLAFSAMLMAGLDG  FSAMLMAGL        0.7601         13.4         SB    16.00     Sequence
   DRB1_0101  232  NSLLHAADDMQLYKY  LHAADDMQL        0.7586         13.6         SB    16.00     Sequence
   DRB1_0101  207  NSGFILEKGHHEVGS  FILEKGHHE        0.7569         13.9         SB    16.00     Sequence
   DRB1_0101  401  DKDLYELPPEEAASI  LYELPPEEA        0.7556         14.1         SB    16.00     Sequence
   DRB1_0101  227  INYQFNSLLHAADDM  INYQFNSLL        0.7551         14.1         SB    16.00     Sequence
   DRB1_0101  193  QYVDLRDKMLTNLIN  YVDLRDKML        0.7541         14.3         SB    16.00     Sequence
   DRB1_0101  222  GGQAEINYQFNSLLH  INYQFNSLL        0.7541         14.3         SB    16.00     Sequence
   DRB1_0101  190  PNDQYVDLRDKMLTN  YVDLRDKML        0.7536         14.4         SB    16.00     Sequence
   DRB1_0101    6  DDVFKLAKDEKVEYV  FKLAKDEKV        0.7508         14.8         SB    16.00     Sequence
   DRB1_0101  241  MQLYKYIIKNTAWQN  YKYIIKNTA        0.7507         14.8         SB    16.00     Sequence
   DRB1_0101  150  SFYEVDAISGWWNTG  FYEVDAISG        0.7507         14.8         SB    16.00     Sequence
   DRB1_0101   21  DVRFCDLPGIMQHFT  FCDLPGIMQ        0.7488         15.1         SB    16.00     Sequence
   DRB1_0101  372  SGNPYLAFSAMLMAG  YLAFSAMLM        0.7487         15.2         SB    16.00     Sequence
   DRB1_0101  114  AENYLISTGIADTAY  YLISTGIAD        0.7472         15.4         SB    16.00     Sequence
   DRB1_0101  132  EAEFYIFDSVSFDSR  FYIFDSVSF        0.7454         15.7         SB    16.00     Sequence
   DRB1_0101  379  FSAMLMAGLDGIKNK  AMLMAGLDG        0.7430         16.1         SB    16.00     Sequence
   DRB1_0101  402  KDLYELPPEEAASIP  LYELPPEEA        0.7410         16.5         SB    16.00     Sequence
   DRB1_0101    7  DVFKLAKDEKVEYVD  FKLAKDEKV        0.7395         16.8         SB    16.00     Sequence
   DRB1_0101  339  LVYSQRNRSACVRIP  VYSQRNRSA        0.7393         16.8         SB    16.00     Sequence
   DRB1_0101   22  VRFCDLPGIMQHFTI  FCDLPGIMQ        0.7391         16.8         SB    16.00     Sequence
   DRB1_0101  371  SSGNPYLAFSAMLMA  YLAFSAMLM        0.7353         17.5         SB    16.00     Sequence
   DRB1_0101  430  EADHEYLTEGGVFTN  YLTEGGVFT        0.7351         17.6         SB    16.00     Sequence
   DRB1_0101  431  ADHEYLTEGGVFTND  YLTEGGVFT        0.7330         18.0         SB    16.00     Sequence
   DRB1_0101  434  EYLTEGGVFTNDLIE  YLTEGGVFT        0.7290         18.8         SB    16.00     Sequence
   DRB1_0101  116  NYLISTGIADTAYFG  ISTGIADTA        0.7289         18.8         SB    16.00     Sequence
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DRB1_0101  146  RANGSFYEVDAISGW  FYEVDAISG         0.7280          19.0          SB    16.00      Sequence
DRB1_0101   65  ESDMLLLPDPETARI  MLLLPDPET         0.7275          19.1          SB    16.00      Sequence
DRB1_0101    8  VFKLAKDEKVEYVDV  FKLAKDEKV         0.7260          19.4          SB    16.00      Sequence
DRB1_0101  115  ENYLISTGIADTAYF  YLISTGIAD         0.7210          20.5          SB    16.00      Sequence
DRB1_0101  302  RHYIGGLLHHAPSLL  LLHHAPSLL         0.7199          20.7          SB    16.00      Sequence
DRB1_0101  370  DSSGNPYLAFSAMLM  YLAFSAMLM         0.7187          21.0          SB    16.00      Sequence
DRB1_0101  208  SGFILEKGHHEVGSG  FILEKGHHE         0.7177          21.2          SB    16.00      Sequence
DRB1_0101   75  ETARIDPFRAAKTLN  IDPFRAAKT         0.7174          21.3          SB    16.00      Sequence
DRB1_0101  335  APINLVYSQRNRSAC  VYSQRNRSA         0.7159          21.6          SB    16.00      Sequence
DRB1_0101  113  KAENYLISTGIADTA  YLISTGIAD         0.7150          21.8          SB    16.00      Sequence
DRB1_0101   20  VDVRFCDLPGIMQHF  FCDLPGIMQ         0.7125          22.4          SB    16.00      Sequence
DRB1_0101   89  NINFFVHDPFTLEPY  FFVHDPFTL         0.7113          22.7          SB    16.00      Sequence
DRB1_0101  206  INSGFILEKGHHEVG  FILEKGHHE         0.7104          22.9          SB    16.00      Sequence
DRB1_0101  381  AMLMAGLDGIKNKIE  MAGLDGIKN         0.7100          23.1          SB    32.00      Sequence
DRB1_0101  334  EAPINLVYSQRNRSA  INLVYSQRN         0.7096          23.2          SB    32.00      Sequence
DRB1_0101  233  SLLHAADDMQLYKYI  LHAADDMQL         0.7092          23.2          SB    32.00      Sequence
DRB1_0101  312  APSLLAFTNPTVNSY  LLAFTNPTV         0.7085          23.4          SB    32.00      Sequence
DRB1_0101  240  DMQLYKYIIKNTAWQ  YKYIIKNTA         0.7080          23.5          SB    32.00      Sequence
DRB1_0101  380  SAMLMAGLDGIKNKI  MAGLDGIKN         0.7076          23.7          SB    32.00      Sequence
DRB1_0101  189  APNDQYVDLRDKMLT  YVDLRDKML         0.7053          24.2          SB    32.00      Sequence
DRB1_0101  133  AEFYIFDSVSFDSRA  FYIFDSVSF         0.7034          24.8          SB    32.00      Sequence
DRB1_0101  112  RKAENYLISTGIADT  ENYLISTGI         0.7028          24.9          SB    32.00      Sequence
DRB1_0101  323  VNSYKRLVPGYEAPI  YKRLVPGYE         0.7019          25.2          SB    32.00      Sequence
DRB1_0101   23  RFCDLPGIMQHFTIP  FCDLPGIMQ         0.7015          25.3          SB    32.00      Sequence
DRB1_0101  194  YVDLRDKMLTNLINS  YVDLRDKML         0.6999          25.7          SB    32.00      Sequence
DRB1_0101   57  IRGFQSIHESDMLLL  FQSIHESDM         0.6991          25.9          SB    32.00      Sequence
DRB1_0101   66  SDMLLLPDPETARID  MLLLPDPET         0.6990          26.0          SB    32.00      Sequence
DRB1_0101  242  QLYKYIIKNTAWQNG  YKYIIKNTA         0.6975          26.4          SB    32.00      Sequence
DRB1_0101  151  FYEVDAISGWWNTGA  FYEVDAISG         0.6971          26.5          SB    32.00      Sequence
DRB1_0101  131  AEAEFYIFDSVSFDS  FYIFDSVSF         0.6962          26.8          SB    32.00      Sequence
DRB1_0101  200  KMLTNLINSGFILEK  TNLINSGFI         0.6955          27.0          SB    32.00      Sequence
DRB1_0101  198  RDKMLTNLINSGFIL  MLTNLINSG         0.6942          27.4          SB    32.00      Sequence
DRB1_0101  311  HAPSLLAFTNPTVNS  LLAFTNPTV         0.6901          28.6          SB    32.00      Sequence
DRB1_0101  231  FNSLLHAADDMQLYK  LHAADDMQL         0.6882          29.2          SB    32.00      Sequence
DRB1_0101   74  PETARIDPFRAAKTL  IDPFRAAKT         0.6814          31.4          SB    32.00      Sequence
DRB1_0101  199  DKMLTNLINSGFILE  LTNLINSGF         0.6812          31.5          SB    32.00      Sequence
DRB1_0101  291  ETGYAGLSDTARHYI  YAGLSDTAR         0.6808          31.6          SB    32.00      Sequence
DRB1_0101  324  NSYKRLVPGYEAPIN  KRLVPGYEA         0.6793          32.1          SB    32.00      Sequence
DRB1_0101  429  LEADHEYLTEGGVFT  YLTEGGVFT         0.6790          32.2          SB    32.00      Sequence
DRB1_0101  228  NYQFNSLLHAADDMQ  FNSLLHAAD         0.6768          33.0          SB    32.00      Sequence
DRB1_0101  313  PSLLAFTNPTVNSYK  LLAFTNPTV         0.6751          33.6          SB    32.00      Sequence
DRB1_0101  435  YLTEGGVFTNDLIET  YLTEGGVFT         0.6749          33.7          SB    32.00      Sequence
DRB1_0101  221  SGGQAEINYQFNSLL  INYQFNSLL         0.6745          33.8          SB    32.00      Sequence
DRB1_0101   87  TLNINFFVHDPFTLE  FFVHDPFTL         0.6705          35.3          SB    32.00      Sequence
DRB1_0101   88  LNINFFVHDPFTLEP  FFVHDPFTL         0.6703          35.4          SB    32.00      Sequence
DRB1_0101  117  YLISTGIADTAYFGA  ISTGIADTA         0.6678          36.4          SB    32.00      Sequence
DRB1_0101  205  LINSGFILEKGHHEV  FILEKGHHE         0.6653          37.4          SB    32.00      Sequence
DRB1_0101   90  INFFVHDPFTLEPYS  FFVHDPFTL         0.6649          37.6          SB    32.00      Sequence
DRB1_0101  301  ARHYIGGLLHHAPSL  YIGGLLHHA         0.6641          37.9          SB    32.00      Sequence
DRB1_0101  340  VYSQRNRSACVRIPI  VYSQRNRSA         0.6626          38.5          SB    32.00      Sequence
DRB1_0101  209  GFILEKGHHEVGSGG  FILEKGHHE         0.6607          39.3          SB    32.00      Sequence
DRB1_0101    9  FKLAKDEKVEYVDVR  FKLAKDEKV         0.6595          39.8          SB    32.00      Sequence
DRB1_0101  201  MLTNLINSGFILEKG  NLINSGFIL         0.6586          40.2          SB    32.00      Sequence
DRB1_0101   27  LPGIMQHFTIPASAF  IMQHFTIPA         0.6570          40.9          SB    32.00      Sequence
DRB1_0101  239  DDMQLYKYIIKNTAW  YKYIIKNTA         0.6556          41.5          SB    32.00      Sequence
DRB1_0101   19  YVDVRFCDLPGIMQH  FCDLPGIMQ         0.6540          42.3          SB    32.00      Sequence
DRB1_0101  403  DLYELPPEEAASIPQ  LYELPPEEA         0.6525          43.0          SB    32.00      Sequence
DRB1_0101    5  PDDVFKLAKDEKVEY  FKLAKDEKV         0.6522          43.1          SB    32.00      Sequence
DRB1_0101   86  KTLNINFFVHDPFTL  FFVHDPFTL         0.6512          43.6          SB    32.00      Sequence
DRB1_0101  310  HHAPSLLAFTNPTVN  LLAFTNPTV         0.6492          44.5          SB    32.00      Sequence
DRB1_0101  243  LYKYIIKNTAWQNGK  YKYIIKNTA         0.6481          45.0          SB    32.00      Sequence
DRB1_0101  400  VDKDLYELPPEEAAS  LYELPPEEA         0.6473          45.4          SB    32.00      Sequence
DRB1_0101  230  QFNSLLHAADDMQLY  LHAADDMQL         0.6463          45.9          SB    32.00      Sequence
DRB1_0101  134  EFYIFDSVSFDSRAN  FYIFDSVSF         0.6458          46.2          SB    32.00      Sequence
DRB1_0101  145  SRANGSFYEVDAISG  FYEVDAISG         0.6452          46.5          SB    32.00      Sequence
DRB1_0101   24  FCDLPGIMQHFTIPA  FCDLPGIMQ         0.6440          47.1          SB    32.00      Sequence
DRB1_0101  292  TGYAGLSDTARHYIG  YAGLSDTAR         0.6436          47.3          SB    32.00      Sequence
DRB1_0101   58  RGFQSIHESDMLLLP  FQSIHESDM         0.6428          47.7          SB    32.00      Sequence
DRB1_0101  130  GAEAEFYIFDSVSFD  FYIFDSVSF         0.6399          49.2          SB    32.00      Sequence
DRB1_0101  129  FGAEAEFYIFDSVSF  FYIFDSVSF         0.6398          49.3          SB    32.00      Sequence
DRB1_0101  229  YQFNSLLHAADDMQL  FNSLLHAAD         0.6395          49.4          SB    32.00      Sequence
DRB1_0101  314  SLLAFTNPTVNSYKR  LLAFTNPTV         0.6394          49.5          SB    32.00      Sequence
DRB1_0101  382  MLMAGLDGIKNKIEP  MAGLDGIKN         0.6377          50.4          WB    32.00      Sequence
DRB1_0101  197  LRDKMLTNLINSGFI  DKMLTNLIN         0.6370          50.8          WB    32.00      Sequence
DRB1_0101  326  YKRLVPGYEAPINLV  LVPGYEAPI         0.6369          50.8          WB    32.00      Sequence
DRB1_0101  300  TARHYIGGLLHHAPS  YIGGLLHHA         0.6364          51.1          WB    32.00      Sequence
DRB1_0101  126  TAYFGAEAEFYIFDS  FGAEAEFYI         0.6362          51.3          WB    32.00      Sequence
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DRB1_0101  124  ADTAYFGAEAEFYIF  YFGAEAEFY        0.6337        52.6        WB    32.00      Sequence
DRB1_0101  234  LLHAADDMQLYKYII  LHAADDMQL        0.6324        53.4        WB    32.00      Sequence
DRB1_0101  125  DTAYFGAEAEFYIFD  YFGAEAEFY        0.6321        53.6        WB    32.00      Sequence
DRB1_0101   64  HESDMLLLPDPETAR  MLLLPDPET        0.6282        55.9        WB    32.00      Sequence
DRB1_0101  111  ARKAENYLISTGIAD  ENYLISTGI        0.6268        56.7        WB    32.00      Sequence
DRB1_0101  188  VAPNDQYVDLRDKML  YVDLRDKML        0.6259        57.3        WB    32.00      Sequence
DRB1_0101  196  DLRDKMLTNLINSGF  DKMLTNLIN        0.6250        57.8        WB    32.00      Sequence
DRB1_0101  325  SYKRLVPGYEAPINL  KRLVPGYEA        0.6242        58.3        WB    32.00      Sequence
DRB1_0101  284  GAPLMYDETGYAGLS  MYDETGYAG        0.6238        58.6        WB    32.00      Sequence
DRB1_0101  181  HKGGYFPVAPNDQYV  YFPVAPNDQ        0.6222        59.6        WB    32.00      Sequence
DRB1_0101  244  YKYIIKNTAWQNGKT  IIKNTAWQN        0.6214        60.1        WB    32.00      Sequence
DRB1_0101  404  LYELPPEEAASIPQT  LYELPPEEA        0.6210        60.4        WB    32.00      Sequence
DRB1_0101  285  APLMYDETGYAGLSD  MYDETGYAG        0.6208        60.5        WB    32.00      Sequence
DRB1_0101   73  DPETARIDPFRAAKT  TARIDPFRA        0.6206        60.6        WB    32.00      Sequence
DRB1_0101   67  DMLLLPDPETARIDP  MLLLPDPET        0.6197        61.2        WB    32.00      Sequence
DRB1_0101  254  QNGKTVTFMPKPLFG  TVTFMPKPL        0.6170        63.1        WB    32.00      Sequence
DRB1_0101  182  KGGYFPVAPNDQYVD  YFPVAPNDQ        0.6158        63.9        WB    32.00      Sequence
DRB1_0101  108  RNIARKAENYLISTG  ARKAENYLI        0.6150        64.4        WB    32.00      Sequence
DRB1_0101  255  NGKTVTFMPKPLFGD  TVTFMPKPL        0.6118        66.7        WB    32.00      Sequence
DRB1_0101  298  SDTARHYIGGLLHHA  YIGGLLHHA        0.6083        69.3        WB    32.00      Sequence
DRB1_0101  299  DTARHYIGGLLHHAP  YIGGLLHHA        0.6080        69.5        WB    32.00      Sequence
DRB1_0101  210  FILEKGHHEVGSGGQ  FILEKGHHE        0.6050        71.8        WB    32.00      Sequence
DRB1_0101   91  NFFVHDPFTLEPYSR  FFVHDPFTL        0.6039        72.7        WB    32.00      Sequence
DRB1_0101   29  GIMQHFTIPASAFDK  QHFTIPASA        0.6026        73.6        WB    32.00      Sequence
DRB1_0101  278  QSLWKDGAPLMYDET  WKDGAPLMY        0.6008        75.2        WB    50.00      Sequence
DRB1_0101  202  LTNLINSGFILEKGH  NLINSGFIL        0.6006        75.3        WB    50.00      Sequence
DRB1_0101  158  SGWWNTGAATEADGS  WNTGAATEA        0.5978        77.6        WB    50.00      Sequence
DRB1_0101  135  FYIFDSVSFDSRANG  FYIFDSVSF        0.5965        78.7        WB    50.00      Sequence
DRB1_0101   43  KSVFDDGLAFDGSSI  FDDGLAFDG        0.5942        80.7        WB    50.00      Sequence
DRB1_0101  110  IARKAENYLISTGIA  ENYLISTGI        0.5929        81.8        WB    50.00      Sequence
DRB1_0101  333  YEAPINLVYSQRNRS  INLVYSQRN        0.5917        82.9        WB    50.00      Sequence
DRB1_0101  367  RSPDSSGNPYLAFSA  DSSGNPYLA        0.5917        82.9        WB    50.00      Sequence
DRB1_0101  330  VPGYEAPINLVYSQR  YEAPINLVY        0.5915        83.1        WB    50.00      Sequence
DRB1_0101  315  LLAFTNPTVNSYKRL  LLAFTNPTV        0.5915        83.1        WB    50.00      Sequence
DRB1_0101  290  DETGYAGLSDTARHY  YAGLSDTAR        0.5912        83.4        WB    50.00      Sequence
DRB1_0101  195  VDLRDKMLTNLINSG  RDKMLTNLI        0.5909        83.6        WB    50.00      Sequence
DRB1_0101  322  TVNSYKRLVPGYEAP  YKRLVPGYE        0.5904        84.1        WB    50.00      Sequence
DRB1_0101   68  MLLLPDPETARIDPF  MLLLPDPET        0.5890        85.3        WB    50.00      Sequence
DRB1_0101  204  NLINSGFILEKGHHE  FILEKGHHE        0.5868        87.4        WB    50.00      Sequence
DRB1_0101   18  EYVDVRFCDLPGIMQ  FCDLPGIMQ        0.5867        87.6        WB    50.00      Sequence
DRB1_0101  321  PTVNSYKRLVPGYEA  YKRLVPGYE        0.5864        87.8        WB    50.00      Sequence
DRB1_0101   28  PGIMQHFTIPASAFD  IMQHFTIPA        0.5863        87.9        WB    50.00      Sequence
DRB1_0101  238  ADDMQLYKYIIKNTA  YKYIIKNTA        0.5859        88.3        WB    50.00      Sequence
DRB1_0101   30  IMQHFTIPASAFDKS  HFTIPASAF        0.5847        89.4        WB    50.00      Sequence
DRB1_0101   59  GFQSIHESDMLLLPD  FQSIHESDM        0.5840        90.1        WB    50.00      Sequence
DRB1_0101  253  WQNGKTVTFMPKPLF  TVTFMPKPL        0.5788        95.4        WB    50.00      Sequence
DRB1_0101   31  MQHFTIPASAFDKSV  HFTIPASAF        0.5785        95.6        WB    50.00      Sequence
DRB1_0101  107  PRNIARKAENYLIST  ARKAENYLI        0.5764        97.9        WB    50.00      Sequence
DRB1_0101  256  GKTVTFMPKPLFGDN  TVTFMPKPL        0.5753        99.0        WB    50.00      Sequence
DRB1_0101  329  LVPGYEAPINLVYSQ  GYEAPINLV        0.5738       100.6        WB    50.00      Sequence
DRB1_0101   56  SIRGFQSIHESDMLL  FQSIHESDM        0.5715       103.2        WB    50.00      Sequence
DRB1_0101  127  AYFGAEAEFYIFDSV  YFGAEAEFY        0.5693       105.6        WB    50.00      Sequence
DRB1_0101  327  KRLVPGYEAPINLVY  LVPGYEAPI        0.5680       107.2        WB    50.00      Sequence
DRB1_0101  277  HQSLWKDGAPLMYDE  WKDGAPLMY        0.5669       108.4        WB    50.00      Sequence
DRB1_0101  293  GYAGLSDTARHYIGG  YAGLSDTAR        0.5661       109.4        WB    50.00      Sequence
DRB1_0101  369  PDSSGNPYLAFSAML  PYLAFSAML        0.5659       109.6        WB    50.00      Sequence
DRB1_0101  399  PVDKDLYELPPEEAA  LYELPPEEA        0.5607       116.0        WB    50.00      Sequence
DRB1_0101  328  RLVPGYEAPINLVYS  GYEAPINLV        0.5573       120.3        WB    50.00      Sequence
DRB1_0101   26  DLPGIMQHFTIPASA  IMQHFTIPA        0.5573       120.4        WB    50.00      Sequence
DRB1_0101  109  NIARKAENYLISTGI  ARKAENYLI        0.5525       126.6        WB    50.00      Sequence
DRB1_0101  350  VRIPITGSNPKAKRL  PITGSNPKA        0.5514       128.3        WB    50.00      Sequence
DRB1_0101  123  IADTAYFGAEAEFYI  YFGAEAEFY        0.5508       129.1        WB    50.00      Sequence
DRB1_0101  286  PLMYDETGYAGLSDT  MYDETGYAG        0.5492       131.4        WB    50.00      Sequence
DRB1_0101    4  TPDDVFKLAKDEKVE  FKLAKDEKV        0.5487       132.0        WB    50.00      Sequence
DRB1_0101   92  FFVHDPFTLEPYSRD  FFVHDPFTL        0.5478       133.3        WB    50.00      Sequence
DRB1_0101  283  DGAPLMYDETGYAGL  MYDETGYAG        0.5465       135.1        WB    50.00      Sequence
DRB1_0101  332  GYEAPINLVYSQRNR  INLVYSQRN        0.5461       135.8        WB    50.00      Sequence
DRB1_0101  331  PGYEAPINLVYSQRN  YEAPINLVY        0.5451       137.3        WB    50.00      Sequence
DRB1_0101  257  KTVTFMPKPLFGDNG  TVTFMPKPL        0.5444       138.3        WB    50.00      Sequence
DRB1_0101  276  CHQSLWKDGAPLMYD  WKDGAPLMY        0.5428       140.7        WB    50.00      Sequence
DRB1_0101  275  HCHQSLWKDGAPLMY  WKDGAPLMY        0.5422       141.7        WB    50.00      Sequence
DRB1_0101  463  NIRPHPYEFALYYDV  YEFALYYDV        0.5411       143.3        WB    50.00      Sequence
DRB1_0101  203  TNLINSGFILEKGHH  NLINSGFIL        0.5378       148.5        WB    50.00      Sequence
DRB1_0101   49  GLAFDGSSIRGFQSI  FDGSSIRGF        0.5363       151.0        WB    50.00      Sequence
DRB1_0101  159  GWWNTGAATEADGSP  WNTGAATEA        0.5359       151.7        WB    50.00      Sequence
DRB1_0101  235  LHAADDMQLYKYIIK  LHAADDMQL        0.5357       151.9        WB    50.00      Sequence
DRB1_0101   46  FDDGLAFDGSSIRGF  GLAFDGSSI        0.5354       152.5        WB    50.00      Sequence
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DRB1_0101  118  LISTGIADTAYFGAE  ISTGIADTA         0.5336         155.4          WB    50.00      Sequence
DRB1_0101  383  LMAGLDGIKNKIEPQ  MAGLDGIKN         0.5326         157.1          WB    50.00      Sequence
DRB1_0101  279  SLWKDGAPLMYDETG  WKDGAPLMY         0.5322         157.8          WB    50.00      Sequence
DRB1_0101  183  GGYFPVAPNDQYVDL  YFPVAPNDQ         0.5309         160.1          WB    50.00      Sequence
DRB1_0101   60  FQSIHESDMLLLPDP  SIHESDMLL         0.5307         160.5          WB    50.00      Sequence
DRB1_0101  346  RSACVRIPITGSNPK  CVRIPITGS         0.5286         164.1          WB    50.00      Sequence
DRB1_0101   32  QHFTIPASAFDKSVF  HFTIPASAF         0.5284         164.4          WB    50.00      Sequence
DRB1_0101   63  IHESDMLLLPDPETA  MLLLPDPET         0.5264         168.1          WB    50.00      Sequence
DRB1_0101  157  ISGWWNTGAATEADG  WNTGAATEA         0.5258         169.1          WB    50.00      Sequence
DRB1_0101   25  CDLPGIMQHFTIPAS  PGIMQHFTI         0.5215         177.3          WB    50.00      Sequence
DRB1_0101   44  SVFDDGLAFDGSSIR  FDDGLAFDG         0.5212         177.7          WB    50.00      Sequence
DRB1_0101  180  RHKGGYFPVAPNDQY  YFPVAPNDQ         0.5164         187.3          WB    50.00      Sequence
DRB1_0101  245  KYIIKNTAWQNGKTV  IIKNTAWQN         0.5164         187.3          WB    50.00      Sequence
DRB1_0101    3  KTPDDVFKLAKDEKV  FKLAKDEKV         0.5125         195.4          WB    50.00      Sequence
DRB1_0101  366  FRSPDSSGNPYLAFS  DSSGNPYLA         0.5116         197.3          WB    50.00      Sequence
DRB1_0101   16  KVEYVDVRFCDLPGI  YVDVRFCDL         0.5091         202.7          WB    50.00      Sequence
DRB1_0101   48  DGLAFDGSSIRGFQS  FDGSSIRGF         0.5071         207.0          WB    50.00      Sequence
DRB1_0101  294  YAGLSDTARHYIGGL  YAGLSDTAR         0.5054         211.0          WB    50.00      Sequence
DRB1_0101  368  SPDSSGNPYLAFSAM  DSSGNPYLA         0.5041         213.9          WB    50.00      Sequence
DRB1_0101  106  DPRNIARKAENYLIS  ARKAENYLI         0.5025         217.6          WB    50.00      Sequence
DRB1_0101  287  LMYDETGYAGLSDTA  MYDETGYAG         0.4989         226.4          WB    50.00      Sequence
DRB1_0101  128  YFGAEAEFYIFDSVS  YFGAEAEFY         0.4986         227.1          WB    50.00      Sequence
DRB1_0101   47  DDGLAFDGSSIRGFQ  GLAFDGSSI         0.4967         231.8          WB    50.00      Sequence
DRB1_0101   50  LAFDGSSIRGFQSIH  FDGSSIRGF         0.4951         235.7          WB    50.00      Sequence
DRB1_0101  248  IKNTAWQNGKTVTFM  TAWQNGKTV         0.4923         243.2          WB    50.00      Sequence
DRB1_0101  252  AWQNGKTVTFMPKPL  TVTFMPKPL         0.4920         243.9          WB    50.00      Sequence
DRB1_0101   45  VFDDGLAFDGSSIRG  FDDGLAFDG         0.4906         247.4          WB    50.00      Sequence
DRB1_0101   42  DKSVFDDGLAFDGSS  FDDGLAFDG         0.4901         248.8          WB    50.00      Sequence
DRB1_0101  258  TVTFMPKPLFGDNGS  TVTFMPKPL         0.4900         249.1          WB    50.00      Sequence
DRB1_0101   83  RAAKTLNINFFVHDP  KTLNINFFV         0.4892         251.2          WB    50.00      Sequence
DRB1_0101  155  DAISGWWNTGAATEA  WNTGAATEA         0.4877         255.4          WB    50.00      Sequence
DRB1_0101  289  YDETGYAGLSDTARH  YAGLSDTAR         0.4856         261.4          WB    50.00      Sequence
DRB1_0101  236  HAADDMQLYKYIIKN  DDMQLYKYI         0.4846         264.1          WB    50.00      Sequence
DRB1_0101  156  AISGWWNTGAATEAD  WNTGAATEA         0.4846         264.2          WB    50.00      Sequence
DRB1_0101  160  WWNTGAATEADGSPN  WNTGAATEA         0.4842         265.4          WB    50.00      Sequence
DRB1_0101  344  RNRSACVRIPITGSN  CVRIPITGS         0.4832         268.3          WB    50.00      Sequence
DRB1_0101  237  AADDMQLYKYIIKNT  DMQLYKYII         0.4831         268.6          WB    50.00      Sequence
DRB1_0101   33  HFTIPASAFDKSVFD  HFTIPASAF         0.4803         276.8          WB    50.00      Sequence
DRB1_0101   72  PDPETARIDPFRAAK  TARIDPFRA         0.4772         286.1          WB    50.00      Sequence
DRB1_0101  320  NPTVNSYKRLVPGYE  YKRLVPGYE         0.4737         297.3          WB    50.00      Sequence
DRB1_0101   51  AFDGSSIRGFQSIHE  FDGSSIRGF         0.4728         300.3          WB    50.00      Sequence
DRB1_0101  345  NRSACVRIPITGSNP  CVRIPITGS         0.4708         306.5          WB    50.00      Sequence
DRB1_0101  184  GYFPVAPNDQYVDLR  YFPVAPNDQ         0.4693         311.7          WB    50.00      Sequence
DRB1_0101   55  SSIRGFQSIHESDML  FQSIHESDM         0.4690         312.8          WB    50.00      Sequence
DRB1_0101  351  RIPITGSNPKAKRLE  PITGSNPKA         0.4669         319.8          WB    50.00      Sequence
DRB1_0101  412  AASIPQTPTQLSDVI  SIPQTPTQL         0.4667         320.5          WB    50.00      Sequence
DRB1_0101  411  EAASIPQTPTQLSDV  SIPQTPTQL         0.4645         328.4          WB    50.00      Sequence
DRB1_0101  263  PKPLFGDNGSGMHCH  LFGDNGSGM         0.4622         336.7          WB    50.00      Sequence
DRB1_0101   17  VEYVDVRFCDLPGIM  YVDVRFCDL         0.4583         351.2          WB    50.00      Sequence
DRB1_0101  398  APVDKDLYELPPEEA  LYELPPEEA         0.4571         355.8          WB    50.00      Sequence
DRB1_0101  295  AGLSDTARHYIGGLL  SDTARHYIG         0.4545         366.0          WB    50.00      Sequence
DRB1_0101  343  QRNRSACVRIPITGS  CVRIPITGS         0.4526         373.6          WB    50.00      Sequence
DRB1_0101  363  RLEFRSPDSSGNPYL  FRSPDSSGN         0.4524         374.2          WB    50.00      Sequence
DRB1_0101  119  ISTGIADTAYFGAEA  ISTGIADTA         0.4511         379.5          WB    50.00      Sequence
DRB1_0101  280  LWKDGAPLMYDETGY  WKDGAPLMY         0.4510         380.1          WB    50.00      Sequence
DRB1_0101  297  LSDTARHYIGGLLHH  ARHYIGGLL         0.4496         385.6          WB    50.00      Sequence
DRB1_0101   62  SIHESDMLLLPDPET  MLLLPDPET         0.4484         390.8          WB    50.00      Sequence
DRB1_0101  342  SQRNRSACVRIPITG  NRSACVRIP         0.4437         411.1          WB    50.00      Sequence
DRB1_0101  177  YKVRHKGGYFPVAPN  RHKGGYFPV         0.4435         412.1          WB    50.00      Sequence
DRB1_0101   54  GSSIRGFQSIHESDM  IRGFQSIHE         0.4431         414.0          WB    50.00      Sequence
DRB1_0101   84  AAKTLNINFFVHDPF  KTLNINFFV         0.4410         423.2          WB    50.00      Sequence
DRB1_0101  250  NTAWQNGKTVTFMPK  WQNGKTVTF         0.4407         424.6          WB    50.00      Sequence
DRB1_0101  341  YSQRNRSACVRIPIT  SQRNRSACV         0.4402         427.1          WB    50.00      Sequence
DRB1_0101  296  GLSDTARHYIGGLLH  SDTARHYIG         0.4400         427.8          WB    50.00      Sequence
DRB1_0101   15  EKVEYVDVRFCDLPG  YVDVRFCDL         0.4389         433.0          WB    50.00      Sequence
DRB1_0101  365  EFRSPDSSGNPYLAF  DSSGNPYLA         0.4386         434.3          WB    50.00      Sequence
DRB1_0101  179  VRHKGGYFPVAPNDQ  YFPVAPNDQ         0.4372         440.9          WB    50.00      Sequence
DRB1_0101   52  FDGSSIRGFQSIHES  GSSIRGFQS         0.4366         443.9          WB    50.00      Sequence
DRB1_0101  161  WNTGAATEADGSPNR  WNTGAATEA         0.4340         456.7          WB    50.00      Sequence
DRB1_0101  384  MAGLDGIKNKIEPQA  MAGLDGIKN         0.4338         457.9          WB    50.00      Sequence
DRB1_0101  288  MYDETGYAGLSDTAR  YAGLSDTAR         0.4327         463.1          WB    50.00      Sequence
DRB1_0101  347  SACVRIPITGSNPKA  CVRIPITGS         0.4316         468.6          WB    50.00      Sequence
DRB1_0101  105  RDPRNIARKAENYLI  ARKAENYLI         0.4297         478.6          WB    50.00      Sequence
DRB1_0101  176  GYKVRHKGGYFPVAP  RHKGGYFPV         0.4295         479.7          WB    50.00      Sequence
DRB1_0101  441  VFTNDLIETWISFKR  NDLIETWIS         0.4291         481.7          WB    50.00      Sequence
DRB1_0101  349  CVRIPITGSNPKAKR  PITGSNPKA         0.4288         483.2          WB    50.00      Sequence
DRB1_0101  122  GIADTAYFGAEAEFY  YFGAEAEFY         0.4278         488.6          WB    50.00      Sequence
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DRB1_0101  249  KNTAWQNGKTVTFMP  TAWQNGKTV        0.4273        491.0         WB    50.00      Sequence
DRB1_0101  175  RGYKVRHKGGYFPVA  RHKGGYFPV        0.4269        493.0         WB    50.00      Sequence
DRB1_0101  247  IIKNTAWQNGKTVTF  TAWQNGKTV        0.4259        498.6         WB    50.00      Sequence
DRB1_0101   41  FDKSVFDDGLAFDGS  FDDGLAFDG        0.4193        535.2               50.00      Sequence
DRB1_0101  264  KPLFGDNGSGMHCHQ  LFGDNGSGM        0.4186        539.7               50.00      Sequence
DRB1_0101  246  YIIKNTAWQNGKTVT  IIKNTAWQN        0.4171        548.4               50.00      Sequence
DRB1_0101   61  QSIHESDMLLLPDPE  SIHESDMLL        0.4133        571.2               50.00      Sequence
DRB1_0101  282  KDGAPLMYDETGYAG  MYDETGYAG        0.4089        599.0               50.00      Sequence
DRB1_0101  178  KVRHKGGYFPVAPND  RHKGGYFPV        0.4084        602.4               50.00      Sequence
DRB1_0101   95  HDPFTLEPYSRDPRN  FTLEPYSRD        0.4083        603.2               50.00      Sequence
DRB1_0101  458  EIEPVNIRPHPYEFA  PVNIRPHPY        0.4081        604.1               50.00      Sequence
DRB1_0101   85  AKTLNINFFVHDPFT  KTLNINFFV        0.4063        616.6               50.00      Sequence
DRB1_0101  185  YFPVAPNDQYVDLRD  YFPVAPNDQ        0.4057        620.1               50.00      Sequence
DRB1_0101  259  VTFMPKPLFGDNGSG  TFMPKPLFG        0.4053        622.7               50.00      Sequence
DRB1_0101   14  DEKVEYVDVRFCDLP  YVDVRFCDL        0.4035        634.9               50.00      Sequence
DRB1_0101  461  PVNIRPHPYEFALYY  IRPHPYEFA        0.4032        637.1               50.00      Sequence
DRB1_0101  413  ASIPQTPTQLSDVID  SIPQTPTQL        0.4031        638.1               50.00      Sequence
DRB1_0101  137  IFDSVSFDSRANGSF  SVSFDSRAN        0.4006        655.8               50.00      Sequence
DRB1_0101   13  KDEKVEYVDVRFCDL  YVDVRFCDL        0.3987        668.8               50.00      Sequence
DRB1_0101  364  LEFRSPDSSGNPYLA  FRSPDSSGN        0.3965        685.1               50.00      Sequence
DRB1_0101  348  ACVRIPITGSNPKAK  CVRIPITGS        0.3956        691.8               50.00      Sequence
DRB1_0101   71  LPDPETARIDPFRAA  TARIDPFRA        0.3938        705.7               50.00      Sequence
DRB1_0101  251  TAWQNGKTVTFMPKP  WQNGKTVTF        0.3873        756.7               50.00      Sequence
DRB1_0101  352  IPITGSNPKAKRLEF  PITGSNPKA        0.3868        761.2               50.00      Sequence
DRB1_0101  316  LAFTNPTVNSYKRLV  FTNPTVNSY        0.3864        764.4               50.00      Sequence
DRB1_0101  152  YEVDAISGWWNTGAA  VDAISGWWN        0.3859        768.4               50.00      Sequence
DRB1_0101  442  FTNDLIETWISFKRE  NDLIETWIS        0.3830        792.7               50.00      Sequence
DRB1_0101  440  GVFTNDLIETWISFK  NDLIETWIS        0.3823        799.2               50.00      Sequence
DRB1_0101  439  GGVFTNDLIETWISF  NDLIETWIS        0.3792        826.1               50.00      Sequence
DRB1_0101  459  IEPVNIRPHPYEFAL  PVNIRPHPY        0.3792        826.6               50.00      Sequence
DRB1_0101  168  EADGSPNRGYKVRHK  GSPNRGYKV        0.3790        827.9               50.00      Sequence
DRB1_0101  262  MPKPLFGDNGSGMHC  LFGDNGSGM        0.3764        851.7               50.00      Sequence
DRB1_0101  409  PEEAASIPQTPTQLS  SIPQTPTQL        0.3749        866.1               50.00      Sequence
DRB1_0101  410  EEAASIPQTPTQLSD  SIPQTPTQL        0.3742        872.2               50.00      Sequence
DRB1_0101  281  WKDGAPLMYDETGYA  WKDGAPLMY        0.3734        879.7               50.00      Sequence
DRB1_0101  136  YIFDSVSFDSRANGS  SVSFDSRAN        0.3667        945.6               50.00      Sequence
DRB1_0101  362  KRLEFRSPDSSGNPY  FRSPDSSGN        0.3647        966.7               50.00      Sequence
DRB1_0101   53  DGSSIRGFQSIHESD  IRGFQSIHE        0.3637        977.2               50.00      Sequence
DRB1_0101   94  VHDPFTLEPYSRDPR  FTLEPYSRD        0.3635        978.8               50.00      Sequence
DRB1_0101  436  LTEGGVFTNDLIETW  GGVFTNDLI        0.3623        992.0               50.00      Sequence
DRB1_0101  462  VNIRPHPYEFALYYD  IRPHPYEFA        0.3618        997.9               50.00      Sequence
DRB1_0101  353  PITGSNPKAKRLEFR  GSNPKAKRL        0.3605       1011.9               50.00      Sequence
DRB1_0101   69  LLLPDPETARIDPFR  LLLPDPETA        0.3597       1020.9               50.00      Sequence
DRB1_0101  274  MHCHQSLWKDGAPLM  SLWKDGAPL        0.3558       1064.7               50.00      Sequence
DRB1_0101  460  EPVNIRPHPYEFALY  PVNIRPHPY        0.3553       1070.5               50.00      Sequence
DRB1_0101  174  NRGYKVRHKGGYFPV  RHKGGYFPV        0.3543       1081.8               50.00      Sequence
DRB1_0101  153  EVDAISGWWNTGAAT  ISGWWNTGA        0.3536       1089.6               50.00      Sequence
DRB1_0101   40  AFDKSVFDDGLAFDG  FDDGLAFDG        0.3526       1102.1               50.00      Sequence
DRB1_0101  140  SVSFDSRANGSFYEV  FDSRANGSF        0.3502       1130.8               50.00      Sequence
DRB1_0101  169  ADGSPNRGYKVRHKG  GSPNRGYKV        0.3489       1146.9               50.00      Sequence
DRB1_0101  260  TFMPKPLFGDNGSGM  TFMPKPLFG        0.3457       1187.3               50.00      Sequence
DRB1_0101  154  VDAISGWWNTGAATE  ISGWWNTGA        0.3453       1192.2               50.00      Sequence
DRB1_0101  138  FDSVSFDSRANGSFY  SVSFDSRAN        0.3450       1196.3               50.00      Sequence
DRB1_0101  438  EGGVFTNDLIETWIS  NDLIETWIS        0.3445       1202.8               50.00      Sequence
DRB1_0101  443  TNDLIETWISFKREN  NDLIETWIS        0.3434       1217.5               50.00      Sequence
DRB1_0101   96  DPFTLEPYSRDPRNI  FTLEPYSRD        0.3422       1232.5               50.00      Sequence
DRB1_0101  220  GSGGQAEINYQFNSL  GQAEINYQF        0.3413       1244.6               50.00      Sequence
DRB1_0101  360  KAKRLEFRSPDSSGN  FRSPDSSGN        0.3402       1259.6               50.00      Sequence
DRB1_0101   34  FTIPASAFDKSVFDD  FTIPASAFD        0.3393       1273.0               50.00      Sequence
DRB1_0101  100  LEPYSRDPRNIARKA  YSRDPRNIA        0.3391       1274.7               50.00      Sequence
DRB1_0101  414  SIPQTPTQLSDVIDR  SIPQTPTQL        0.3387       1280.7               50.00      Sequence
DRB1_0101  361  AKRLEFRSPDSSGNP  FRSPDSSGN        0.3380       1290.9               50.00      Sequence
DRB1_0101  261  FMPKPLFGDNGSGMH  LFGDNGSGM        0.3370       1304.4               50.00      Sequence
DRB1_0101  265  PLFGDNGSGMHCHQS  LFGDNGSGM        0.3347       1336.6               50.00      Sequence
DRB1_0101  120  STGIADTAYFGAEAE  GIADTAYFG        0.3336       1353.4               50.00      Sequence
DRB1_0101  317  AFTNPTVNSYKRLVP  FTNPTVNSY        0.3300       1406.5               50.00      Sequence
DRB1_0101   97  PFTLEPYSRDPRNIA  FTLEPYSRD        0.3287       1427.4               50.00      Sequence
DRB1_0101   99  TLEPYSRDPRNIARK  PYSRDPRNI        0.3283       1433.7               50.00      Sequence
DRB1_0101  457  NEIEPVNIRPHPYEF  PVNIRPHPY        0.3266       1459.6               50.00      Sequence
DRB1_0101  444  NDLIETWISFKRENE  IETWISFKR        0.3253       1479.7               50.00      Sequence
DRB1_0101  318  FTNPTVNSYKRLVPG  PTVNSYKRL        0.3245       1492.9               50.00      Sequence
DRB1_0101  167  TEADGSPNRGYKVRH  GSPNRGYKV        0.3225       1526.1               50.00      Sequence
DRB1_0101  143  FDSRANGSFYEVDAI  RANGSFYEV        0.3224       1528.4               50.00      Sequence
DRB1_0101  450  WISFKRENEIEPVNI  FKRENEIEP        0.3207       1555.6               50.00      Sequence
DRB1_0101   70  LLPDPETARIDPFRA  TARIDPFRA        0.3195       1576.0               50.00      Sequence
DRB1_0101  319  TNPTVNSYKRLVPGY  TVNSYKRLV        0.3173       1614.0               50.00      Sequence
DRB1_0101  139  DSVSFDSRANGSFYE  SFDSRANGS        0.3173       1614.1               50.00      Sequence
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DRB1_0101  437  TEGGVFTNDLIETWI  GGVFTNDLI        0.3136       1680.2            50.00     Sequence
DRB1_0101  408  PPEEAASIPQTPTQL  SIPQTPTQL        0.3133       1685.5            50.00     Sequence
DRB1_0101  171  GSPNRGYKVRHKGGY  GSPNRGYKV        0.3122       1706.4            50.00     Sequence
DRB1_0101   98  FTLEPYSRDPRNIAR  FTLEPYSRD        0.3114       1719.9            50.00     Sequence
DRB1_0101  423  SDVIDRLEADHEYLT  IDRLEADHE        0.3092       1761.2            50.00     Sequence
DRB1_0101  268  GDNGSGMHCHQSLWK  GSGMHCHQS        0.3088       1769.0            50.00     Sequence
DRB1_0101  271  GSGMHCHQSLWKDGA  MHCHQSLWK        0.3067       1810.7            50.00     Sequence
DRB1_0101  170  DGSPNRGYKVRHKGG  GSPNRGYKV        0.3061       1821.3            50.00     Sequence
DRB1_0101  266  LFGDNGSGMHCHQSL  LFGDNGSGM        0.3023       1899.6            50.00     Sequence
DRB1_0101  354  ITGSNPKAKRLEFRS  GSNPKAKRL        0.3015       1916.0            50.00     Sequence
DRB1_0101  451  ISFKRENEIEPVNIR  FKRENEIEP        0.2964       2023.6            50.00     Sequence
DRB1_0101  270  NGSGMHCHQSLWKDG  GSGMHCHQS        0.2935       2088.9            50.00     Sequence
DRB1_0101  391  KNKIEPQAPVDKDLY  IEPQAPVDK        0.2930       2099.6            50.00     Sequence
DRB1_0101   93  FVHDPFTLEPYSRDP  FTLEPYSRD        0.2906       2156.0            50.00     Sequence
DRB1_0101  141  VSFDSRANGSFYEVD  FDSRANGSF        0.2903       2161.7            50.00     Sequence
DRB1_0101  173  PNRGYKVRHKGGYFP  GYKVRHKGG        0.2902       2165.4            50.00     Sequence
DRB1_0101  269  DNGSGMHCHQSLWKD  GSGMHCHQS        0.2897       2174.9            50.00     Sequence
DRB1_0101  359  PKAKRLEFRSPDSSG  LEFRSPDSS        0.2897       2175.6            50.00     Sequence
DRB1_0101  172  SPNRGYKVRHKGGYF  GYKVRHKGG        0.2895       2181.6            50.00     Sequence
DRB1_0101  388  DGIKNKIEPQAPVDK  IEPQAPVDK        0.2890       2192.2            50.00     Sequence
DRB1_0101  453  FKRENEIEPVNIRPH  ENEIEPVNI        0.2883       2210.1            50.00     Sequence
DRB1_0101  166  ATEADGSPNRGYKVR  GSPNRGYKV        0.2881       2213.7            50.00     Sequence
DRB1_0101  121  TGIADTAYFGAEAEF  GIADTAYFG        0.2879       2219.4            50.00     Sequence
DRB1_0101  142  SFDSRANGSFYEVDA  RANGSFYEV        0.2835       2327.6            50.00     Sequence
DRB1_0101  389  GIKNKIEPQAPVDKD  IEPQAPVDK        0.2807       2398.8            50.00     Sequence
DRB1_0101  425  VIDRLEADHEYLTEG  IDRLEADHE        0.2800       2417.8            50.00     Sequence
DRB1_0101  103  YSRDPRNIARKAENY  DPRNIARKA        0.2795       2431.0            50.00     Sequence
DRB1_0101  445  DLIETWISFKRENEI  IETWISFKR        0.2781       2465.8            50.00     Sequence
DRB1_0101  424  DVIDRLEADHEYLTE  IDRLEADHE        0.2746       2561.3            50.00     Sequence
DRB1_0101  101  EPYSRDPRNIARKAE  YSRDPRNIA        0.2741       2575.7            50.00     Sequence
DRB1_0101  446  LIETWISFKRENEIE  IETWISFKR        0.2740       2578.5            50.00     Sequence
DRB1_0101  447  IETWISFKRENEIEP  FKRENEIEP        0.2731       2602.9            50.00     Sequence
DRB1_0101  449  TWISFKRENEIEPVN  FKRENEIEP        0.2712       2658.6            50.00     Sequence
DRB1_0101  144  DSRANGSFYEVDAIS  RANGSFYEV        0.2704       2680.9            50.00     Sequence
DRB1_0101  390  IKNKIEPQAPVDKDL  IEPQAPVDK        0.2687       2731.0            50.00     Sequence
DRB1_0101  452  SFKRENEIEPVNIRP  FKRENEIEP        0.2657       2820.0            50.00     Sequence
DRB1_0101  448  ETWISFKRENEIEPV  FKRENEIEP        0.2652       2835.3            50.00     Sequence
DRB1_0101  358  NPKAKRLEFRSPDSS  LEFRSPDSS        0.2646       2854.7            50.00     Sequence
DRB1_0101  422  LSDVIDRLEADHEYL  IDRLEADHE        0.2645       2859.3            50.00     Sequence
DRB1_0101  102  PYSRDPRNIARKAEN  YSRDPRNIA        0.2631       2901.4            50.00     Sequence
DRB1_0101  165  AATEADGSPNRGYKV  GSPNRGYKV        0.2627       2913.2            50.00     Sequence
DRB1_0101  104  SRDPRNIARKAENYL  DPRNIARKA        0.2614       2955.1            50.00     Sequence
DRB1_0101  267  FGDNGSGMHCHQSLW  GSGMHCHQS        0.2611       2965.7            50.00     Sequence
DRB1_0101  385  AGLDGIKNKIEPQAP  LDGIKNKIE        0.2610       2968.2            50.00     Sequence
DRB1_0101  214  KGHHEVGSGGQAEIN  HEVGSGGQA        0.2605       2986.2            50.00     Sequence
DRB1_0101  219  VGSGGQAEINYQFNS  GQAEINYQF        0.2594       3019.8            50.00     Sequence
DRB1_0101  212  LEKGHHEVGSGGQAE  GHHEVGSGG        0.2582       3059.5            50.00     Sequence
DRB1_0101  355  TGSNPKAKRLEFRSP  GSNPKAKRL        0.2563       3124.4            50.00     Sequence
DRB1_0101  273  GMHCHQSLWKDGAPL  SLWKDGAPL        0.2554       3154.6            50.00     Sequence
DRB1_0101  386  GLDGIKNKIEPQAPV  LDGIKNKIE        0.2552       3161.0            50.00     Sequence
DRB1_0101  420  TQLSDVIDRLEADHE  IDRLEADHE        0.2543       3190.9            50.00     Sequence
DRB1_0101  426  IDRLEADHEYLTEGG  LEADHEYLT        0.2539       3204.7            50.00     Sequence
DRB1_0101   11  LAKDEKVEYVDVRFC  DEKVEYVDV        0.2537       3213.1            50.00     Sequence
DRB1_0101  211  ILEKGHHEVGSGGQA  GHHEVGSGG        0.2509       3311.8            50.00     Sequence
DRB1_0101  405  YELPPEEAASIPQTP  YELPPEEAA        0.2507       3319.1            50.00     Sequence
DRB1_0101  456  ENEIEPVNIRPHPYE  PVNIRPHPY        0.2477       3427.8            50.00     Sequence
DRB1_0101  415  IPQTPTQLSDVIDRL  TPTQLSDVI        0.2468       3460.8            50.00     Sequence
DRB1_0101  213  EKGHHEVGSGGQAEI  GHHEVGSGG        0.2456       3507.3            50.00     Sequence
DRB1_0101  421  QLSDVIDRLEADHEY  IDRLEADHE        0.2454       3515.3            50.00     Sequence
DRB1_0101  163  TGAATEADGSPNRGY  ATEADGSPN        0.2454       3515.7            50.00     Sequence
DRB1_0101  272  SGMHCHQSLWKDGAP  MHCHQSLWK        0.2447       3540.9            50.00     Sequence
DRB1_0101   38  ASAFDKSVFDDGLAF  FDKSVFDDG        0.2436       3584.6            50.00     Sequence
DRB1_0101  392  NKIEPQAPVDKDLYE  IEPQAPVDK        0.2431       3601.9            50.00     Sequence
DRB1_0101  164  GAATEADGSPNRGYK  ATEADGSPN        0.2429       3609.3            50.00     Sequence
DRB1_0101  455  RENEIEPVNIRPHPY  PVNIRPHPY        0.2424       3629.8            50.00     Sequence
DRB1_0101  215  GHHEVGSGGQAEINY  EVGSGGQAE        0.2405       3707.2            50.00     Sequence
DRB1_0101  162  NTGAATEADGSPNRG  ATEADGSPN        0.2373       3834.2            50.00     Sequence
DRB1_0101  217  HEVGSGGQAEINYQF  GSGGQAEIN        0.2368       3856.7            50.00     Sequence
DRB1_0101  387  LDGIKNKIEPQAPVD  KNKIEPQAP        0.2368       3857.5            50.00     Sequence
DRB1_0101  417  QTPTQLSDVIDRLEA  TPTQLSDVI        0.2340       3974.6            50.00     Sequence
DRB1_0101  419  PTQLSDVIDRLEADH  LSDVIDRLE        0.2302       4143.0            50.00     Sequence
DRB1_0101  218  EVGSGGQAEINYQFN  GQAEINYQF        0.2294       4178.0            50.00     Sequence
DRB1_0101  454  KRENEIEPVNIRPHP  ENEIEPVNI        0.2276       4261.1            50.00     Sequence
DRB1_0101  418  TPTQLSDVIDRLEAD  QLSDVIDRL        0.2264       4318.6            50.00     Sequence
DRB1_0101   39  SAFDKSVFDDGLAFD  SVFDDGLAF        0.2237       4445.4            50.00     Sequence
DRB1_0101   10  KLAKDEKVEYVDVRF  AKDEKVEYV        0.2235       4454.9            50.00     Sequence
DRB1_0101  356  GSNPKAKRLEFRSPD  GSNPKAKRL        0.2201       4619.3            50.00     Sequence
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   DRB1_0101  416  PQTPTQLSDVIDRLE  TPTQLSDVI        0.2180       4727.4                50.00     Sequence
   DRB1_0101    0  VTEKTPDDVFKLAKD  KTPDDVFKL        0.2155       4854.8                50.00     Sequence
   DRB1_0101  393  KIEPQAPVDKDLYEL  IEPQAPVDK        0.2143       4920.7                50.00     Sequence
   DRB1_0101   12  AKDEKVEYVDVRFCD  DEKVEYVDV        0.2122       5030.5                50.00     Sequence
   DRB1_0101  216  HHEVGSGGQAEINYQ  VGSGGQAEI        0.2101       5148.8                50.00     Sequence
   DRB1_0101   35  TIPASAFDKSVFDDG  TIPASAFDK        0.2080       5264.9                50.00     Sequence
   DRB1_0101   37  PASAFDKSVFDDGLA  FDKSVFDDG        0.2004       5717.6                50.00     Sequence
   DRB1_0101  428  RLEADHEYLTEGGVF  LEADHEYLT        0.1951       6057.0                50.00     Sequence
   DRB1_0101  427  DRLEADHEYLTEGGV  LEADHEYLT        0.1921       6256.0                50.00     Sequence
   DRB1_0101  394  IEPQAPVDKDLYELP  IEPQAPVDK        0.1838       6842.2                50.00     Sequence
   DRB1_0101   36  IPASAFDKSVFDDGL  FDKSVFDDG        0.1837       6850.6                50.00     Sequence
   DRB1_0101  407  LPPEEAASIPQTPTQ  EEAASIPQT        0.1824       6946.5                50.00     Sequence
   DRB1_0101  406  ELPPEEAASIPQTPT  LPPEEAASI        0.1795       7172.2                50.00     Sequence
   DRB1_0101    1  TEKTPDDVFKLAKDE  KTPDDVFKL        0.1722       7758.3                50.00     Sequence
   DRB1_0101    2  EKTPDDVFKLAKDEK  KTPDDVFKL        0.1581       9034.6                50.00     Sequence
   DRB1_0101  186  FPVAPNDQYVDLRDK  FPVAPNDQY        0.1547       9371.8                50.00     Sequence
   DRB1_0101  357  SNPKAKRLEFRSPDS  RLEFRSPDS        0.1536       9484.6                50.00     Sequence
   DRB1_0101  187  PVAPNDQYVDLRDKM  PVAPNDQYV        0.1319      11998.4                50.00     Sequence
   DRB1_0101  397  QAPVDKDLYELPPEE  VDKDLYELP        0.1298      12279.5                50.00     Sequence
   DRB1_0101  396  PQAPVDKDLYELPPE  PVDKDLYEL        0.1257      12827.2                50.00     Sequence
   DRB1_0101  395  EPQAPVDKDLYELPP  PVDKDLYEL        0.1199      13659.4                50.00     Sequence
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Allele: DRB1_0101. Number of high binders 130. Number of weak binders 162. Number of peptides 464

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0301   67  DMLLLPDPETARIDP  DMLLLPDPE        0.7300         18.6         SB     0.40     Sequence
   DRB1_0301   66  SDMLLLPDPETARID  DMLLLPDPE        0.7152         21.8         SB     0.80     Sequence
   DRB1_0301  138  FDSVSFDSRANGSFY  FDSVSFDSR        0.6950         27.1         SB     0.80     Sequence
   DRB1_0301  137  IFDSVSFDSRANGSF  FDSVSFDSR        0.6878         29.3         SB     0.80     Sequence
   DRB1_0301   65  ESDMLLLPDPETARI  DMLLLPDPE        0.6865         29.7         SB     0.80     Sequence
   DRB1_0301  136  YIFDSVSFDSRANGS  FDSVSFDSR        0.6676         36.5         SB     1.00     Sequence
   DRB1_0301  336  PINLVYSQRNRSACV  LVYSQRNRS        0.6475         45.3         SB     2.00     Sequence
   DRB1_0301  135  FYIFDSVSFDSRANG  FDSVSFDSR        0.6379         50.3         WB     2.00     Sequence
   DRB1_0301   64  HESDMLLLPDPETAR  DMLLLPDPE        0.6263         57.0         WB     2.00     Sequence
   DRB1_0301  337  INLVYSQRNRSACVR  INLVYSQRN        0.6245         58.1         WB     2.00     Sequence
   DRB1_0301  335  APINLVYSQRNRSAC  LVYSQRNRS        0.6102         67.8         WB     4.00     Sequence
   DRB1_0301    8  VFKLAKDEKVEYVDV  VFKLAKDEK        0.5905         84.0         WB     4.00     Sequence
   DRB1_0301  134  EFYIFDSVSFDSRAN  FDSVSFDSR        0.5691        105.9         WB     4.00     Sequence
   DRB1_0301    7  DVFKLAKDEKVEYVD  VFKLAKDEK        0.5690        106.0         WB     4.00     Sequence
   DRB1_0301  334  EAPINLVYSQRNRSA  LVYSQRNRS        0.5542        124.4         WB     4.00     Sequence
   DRB1_0301   41  FDKSVFDDGLAFDGS  SVFDDGLAF        0.5517        127.9         WB     4.00     Sequence
   DRB1_0301   47  DDGLAFDGSSIRGFQ  LAFDGSSIR        0.5489        131.7         WB     8.00     Sequence
   DRB1_0301    6  DDVFKLAKDEKVEYV  VFKLAKDEK        0.5445        138.2         WB     8.00     Sequence
   DRB1_0301   40  AFDKSVFDDGLAFDG  SVFDDGLAF        0.5289        163.6         WB     8.00     Sequence
   DRB1_0301   39  SAFDKSVFDDGLAFD  SVFDDGLAF        0.5222        175.8         WB     8.00     Sequence
   DRB1_0301  232  NSLLHAADDMQLYKY  LLHAADDMQ        0.5183        183.4         WB     8.00     Sequence
   DRB1_0301  305  IGGLLHHAPSLLAFT  IGGLLHHAP        0.5101        200.4         WB     8.00     Sequence
   DRB1_0301    5  PDDVFKLAKDEKVEY  VFKLAKDEK        0.5084        204.2         WB     8.00     Sequence
   DRB1_0301  231  FNSLLHAADDMQLYK  LLHAADDMQ        0.5080        205.0         WB     8.00     Sequence
   DRB1_0301   68  MLLLPDPETARIDPF  LLLPDPETA        0.5078        205.6         WB     8.00     Sequence
   DRB1_0301   44  SVFDDGLAFDGSSIR  DDGLAFDGS        0.5029        216.6         WB     8.00     Sequence
   DRB1_0301   46  FDDGLAFDGSSIRGF  LAFDGSSIR        0.5026        217.3         WB     8.00     Sequence
   DRB1_0301  133  AEFYIFDSVSFDSRA  FDSVSFDSR        0.5023        218.2         WB     8.00     Sequence
   DRB1_0301  233  SLLHAADDMQLYKYI  LLHAADDMQ        0.4966        232.0         WB     8.00     Sequence
   DRB1_0301   42  DKSVFDDGLAFDGSS  SVFDDGLAF        0.4940        238.6         WB     8.00     Sequence
   DRB1_0301  304  YIGGLLHHAPSLLAF  IGGLLHHAP        0.4842        265.3         WB     8.00     Sequence
   DRB1_0301  338  NLVYSQRNRSACVRI  LVYSQRNRS        0.4824        270.6         WB     8.00     Sequence
   DRB1_0301   38  ASAFDKSVFDDGLAF  SVFDDGLAF        0.4813        273.9         WB     8.00     Sequence
   DRB1_0301  333  YEAPINLVYSQRNRS  LVYSQRNRS        0.4747        294.1         WB    16.00     Sequence
   DRB1_0301   62  SIHESDMLLLPDPET  DMLLLPDPE        0.4694        311.4         WB    16.00     Sequence
   DRB1_0301   63  IHESDMLLLPDPETA  DMLLLPDPE        0.4686        314.1         WB    16.00     Sequence
   DRB1_0301  352  IPITGSNPKAKRLEF  IPITGSNPK        0.4685        314.5         WB    16.00     Sequence
   DRB1_0301   48  DGLAFDGSSIRGFQS  LAFDGSSIR        0.4610        341.1         WB    16.00     Sequence
   DRB1_0301  230  QFNSLLHAADDMQLY  LLHAADDMQ        0.4595        346.7         WB    16.00     Sequence
   DRB1_0301  198  RDKMLTNLINSGFIL  MLTNLINSG        0.4556        361.7         WB    16.00     Sequence
   DRB1_0301   36  IPASAFDKSVFDDGL  IPASAFDKS        0.4548        364.8         WB    16.00     Sequence
   DRB1_0301   49  GLAFDGSSIRGFQSI  LAFDGSSIR        0.4540        367.8         WB    16.00     Sequence
   DRB1_0301   45  VFDDGLAFDGSSIRG  LAFDGSSIR        0.4538        368.7         WB    16.00     Sequence
   DRB1_0301  351  RIPITGSNPKAKRLE  IPITGSNPK        0.4507        381.0         WB    16.00     Sequence
   DRB1_0301   43  KSVFDDGLAFDGSSI  SVFDDGLAF        0.4507        381.1         WB    16.00     Sequence
   DRB1_0301  420  TQLSDVIDRLEADHE  QLSDVIDRL        0.4484        390.7         WB    16.00     Sequence
   DRB1_0301  382  MLMAGLDGIKNKIEP  MLMAGLDGI        0.4454        403.6         WB    16.00     Sequence
   DRB1_0301  192  DQYVDLRDKMLTNLI  QYVDLRDKM        0.4429        414.6         WB    16.00     Sequence
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DRB1_0301   35  TIPASAFDKSVFDDG  IPASAFDKS         0.4417        420.3          WB    16.00      Sequence
DRB1_0301  292  TGYAGLSDTARHYIG  GYAGLSDTA         0.4385        434.9          WB    16.00      Sequence
DRB1_0301   50  LAFDGSSIRGFQSIH  LAFDGSSIR         0.4366        444.2          WB    16.00      Sequence
DRB1_0301  193  QYVDLRDKMLTNLIN  QYVDLRDKM         0.4346        453.9          WB    16.00      Sequence
DRB1_0301  381  AMLMAGLDGIKNKIE  MLMAGLDGI         0.4338        457.7          WB    16.00      Sequence
DRB1_0301  293  GYAGLSDTARHYIGG  GYAGLSDTA         0.4332        460.5          WB    16.00      Sequence
DRB1_0301  439  GGVFTNDLIETWISF  GGVFTNDLI         0.4331        461.2          WB    16.00      Sequence
DRB1_0301  191  NDQYVDLRDKMLTNL  QYVDLRDKM         0.4286        484.1          WB    16.00      Sequence
DRB1_0301  139  DSVSFDSRANGSFYE  SVSFDSRAN         0.4271        492.0          WB    16.00      Sequence
DRB1_0301  234  LLHAADDMQLYKYII  LLHAADDMQ         0.4261        497.5          WB    16.00      Sequence
DRB1_0301   61  QSIHESDMLLLPDPE  SIHESDMLL         0.4250        503.3                16.00      Sequence
DRB1_0301  350  VRIPITGSNPKAKRL  IPITGSNPK         0.4240        509.0                16.00      Sequence
DRB1_0301   69  LLLPDPETARIDPFR  LLLPDPETA         0.4231        513.8                16.00      Sequence
DRB1_0301  419  PTQLSDVIDRLEADH  QLSDVIDRL         0.4210        525.4                16.00      Sequence
DRB1_0301  339  LVYSQRNRSACVRIP  LVYSQRNRS         0.4208        526.6                16.00      Sequence
DRB1_0301  303  HYIGGLLHHAPSLLA  IGGLLHHAP         0.4172        548.0                16.00      Sequence
DRB1_0301  132  EAEFYIFDSVSFDSR  FDSVSFDSR         0.4151        560.2                16.00      Sequence
DRB1_0301  438  EGGVFTNDLIETWIS  GGVFTNDLI         0.4144        564.8                16.00      Sequence
DRB1_0301   34  FTIPASAFDKSVFDD  IPASAFDKS         0.4139        567.7                16.00      Sequence
DRB1_0301  190  PNDQYVDLRDKMLTN  QYVDLRDKM         0.4127        575.3                16.00      Sequence
DRB1_0301  291  ETGYAGLSDTARHYI  GYAGLSDTA         0.4127        575.3                16.00      Sequence
DRB1_0301  418  TPTQLSDVIDRLEAD  TQLSDVIDR         0.4113        583.7                16.00      Sequence
DRB1_0301  380  SAMLMAGLDGIKNKI  LMAGLDGIK         0.4087        600.3                16.00      Sequence
DRB1_0301  199  DKMLTNLINSGFILE  MLTNLINSG         0.4079        605.8                16.00      Sequence
DRB1_0301  421  QLSDVIDRLEADHEY  QLSDVIDRL         0.4021        645.0                16.00      Sequence
DRB1_0301  200  KMLTNLINSGFILEK  MLTNLINSG         0.3995        663.6                16.00      Sequence
DRB1_0301    4  TPDDVFKLAKDEKVE  VFKLAKDEK         0.3978        675.5                16.00      Sequence
DRB1_0301  306  GGLLHHAPSLLAFTN  GLLHHAPSL         0.3928        713.2                32.00      Sequence
DRB1_0301  197  LRDKMLTNLINSGFI  RDKMLTNLI         0.3925        715.4                32.00      Sequence
DRB1_0301   60  FQSIHESDMLLLPDP  QSIHESDML         0.3881        750.7                32.00      Sequence
DRB1_0301    9  FKLAKDEKVEYVDVR  FKLAKDEKV         0.3879        752.3                32.00      Sequence
DRB1_0301   20  VDVRFCDLPGIMQHF  VDVRFCDLP         0.3851        774.9                32.00      Sequence
DRB1_0301  194  YVDLRDKMLTNLINS  VDLRDKMLT         0.3811        809.6                32.00      Sequence
DRB1_0301  276  CHQSLWKDGAPLMYD  HQSLWKDGA         0.3806        813.9                32.00      Sequence
DRB1_0301  437  TEGGVFTNDLIETWI  GGVFTNDLI         0.3802        817.1                32.00      Sequence
DRB1_0301   59  GFQSIHESDMLLLPD  SIHESDMLL         0.3796        822.7                32.00      Sequence
DRB1_0301   58  RGFQSIHESDMLLLP  SIHESDMLL         0.3777        840.1                32.00      Sequence
DRB1_0301  229  YQFNSLLHAADDMQL  LLHAADDMQ         0.3774        842.6                32.00      Sequence
DRB1_0301  349  CVRIPITGSNPKAKR  IPITGSNPK         0.3753        861.8                32.00      Sequence
DRB1_0301  423  SDVIDRLEADHEYLT  IDRLEADHE         0.3750        865.1                32.00      Sequence
DRB1_0301  417  QTPTQLSDVIDRLEA  TQLSDVIDR         0.3746        868.5                32.00      Sequence
DRB1_0301  284  GAPLMYDETGYAGLS  GAPLMYDET         0.3744        870.4                32.00      Sequence
DRB1_0301  302  RHYIGGLLHHAPSLL  IGGLLHHAP         0.3740        874.4                32.00      Sequence
DRB1_0301  424  DVIDRLEADHEYLTE  IDRLEADHE         0.3739        875.5                32.00      Sequence
DRB1_0301  277  HQSLWKDGAPLMYDE  HQSLWKDGA         0.3729        884.4                32.00      Sequence
DRB1_0301   33  HFTIPASAFDKSVFD  IPASAFDKS         0.3706        907.2                32.00      Sequence
DRB1_0301  195  VDLRDKMLTNLINSG  VDLRDKMLT         0.3691        921.9                32.00      Sequence
DRB1_0301  196  DLRDKMLTNLINSGF  RDKMLTNLI         0.3676        936.8                32.00      Sequence
DRB1_0301  201  MLTNLINSGFILEKG  MLTNLINSG         0.3674        938.5                32.00      Sequence
DRB1_0301  117  YLISTGIADTAYFGA  LISTGIADT         0.3657        956.4                32.00      Sequence
DRB1_0301  425  VIDRLEADHEYLTEG  IDRLEADHE         0.3654        959.1                32.00      Sequence
DRB1_0301   19  YVDVRFCDLPGIMQH  VDVRFCDLP         0.3641        972.8                32.00      Sequence
DRB1_0301   57  IRGFQSIHESDMLLL  IRGFQSIHE         0.3615       1000.6                32.00      Sequence
DRB1_0301  116  NYLISTGIADTAYFG  LISTGIADT         0.3611       1004.7                32.00      Sequence
DRB1_0301  307  GLLHHAPSLLAFTNP  LLHHAPSLL         0.3596       1021.7                32.00      Sequence
DRB1_0301  275  HCHQSLWKDGAPLMY  HQSLWKDGA         0.3564       1057.9                32.00      Sequence
DRB1_0301  320  NPTVNSYKRLVPGYE  NPTVNSYKR         0.3561       1061.1                32.00      Sequence
DRB1_0301  140  SVSFDSRANGSFYEV  VSFDSRANG         0.3541       1083.8                32.00      Sequence
DRB1_0301  379  FSAMLMAGLDGIKNK  MLMAGLDGI         0.3530       1097.2                32.00      Sequence
DRB1_0301  290  DETGYAGLSDTARHY  GYAGLSDTA         0.3509       1122.5                32.00      Sequence
DRB1_0301  189  APNDQYVDLRDKMLT  QYVDLRDKM         0.3506       1126.0                32.00      Sequence
DRB1_0301  294  YAGLSDTARHYIGGL  YAGLSDTAR         0.3450       1196.8                32.00      Sequence
DRB1_0301  283  DGAPLMYDETGYAGL  GAPLMYDET         0.3438       1211.7                32.00      Sequence
DRB1_0301  264  KPLFGDNGSGMHCHQ  LFGDNGSGM         0.3428       1225.3                32.00      Sequence
DRB1_0301   18  EYVDVRFCDLPGIMQ  VDVRFCDLP         0.3426       1227.2                32.00      Sequence
DRB1_0301  115  ENYLISTGIADTAYF  YLISTGIAD         0.3421       1234.2                32.00      Sequence
DRB1_0301  319  TNPTVNSYKRLVPGY  NPTVNSYKR         0.3404       1257.7                32.00      Sequence
DRB1_0301   88  LNINFFVHDPFTLEP  INFFVHDPF         0.3400       1262.9                32.00      Sequence
DRB1_0301  422  LSDVIDRLEADHEYL  SDVIDRLEA         0.3380       1289.8                32.00      Sequence
DRB1_0301  426  IDRLEADHEYLTEGG  IDRLEADHE         0.3377       1294.0                32.00      Sequence
DRB1_0301  118  LISTGIADTAYFGAE  LISTGIADT         0.3377       1294.9                32.00      Sequence
DRB1_0301   89  NINFFVHDPFTLEPY  INFFVHDPF         0.3371       1302.6                32.00      Sequence
DRB1_0301  263  PKPLFGDNGSGMHCH  LFGDNGSGM         0.3329       1363.7                32.00      Sequence
DRB1_0301   17  VEYVDVRFCDLPGIM  VDVRFCDLP         0.3298       1409.9                32.00      Sequence
DRB1_0301    3  KTPDDVFKLAKDEKV  VFKLAKDEK         0.3297       1412.3                32.00      Sequence
DRB1_0301   90  INFFVHDPFTLEPYS  INFFVHDPF         0.3292       1418.6                32.00      Sequence
DRB1_0301  440  GVFTNDLIETWISFK  VFTNDLIET         0.3274       1447.1                32.00      Sequence
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DRB1_0301  383  LMAGLDGIKNKIEPQ  LMAGLDGIK        0.3267       1457.6              32.00     Sequence
DRB1_0301  278  QSLWKDGAPLMYDET  SLWKDGAPL        0.3255       1476.6              32.00     Sequence
DRB1_0301  279  SLWKDGAPLMYDETG  SLWKDGAPL        0.3244       1495.2              32.00     Sequence
DRB1_0301  241  MQLYKYIIKNTAWQN  MQLYKYIIK        0.3232       1514.3              32.00     Sequence
DRB1_0301  318  FTNPTVNSYKRLVPG  NPTVNSYKR        0.3228       1521.3              32.00     Sequence
DRB1_0301  436  LTEGGVFTNDLIETW  GGVFTNDLI        0.3208       1554.8              32.00     Sequence
DRB1_0301   87  TLNINFFVHDPFTLE  INFFVHDPF        0.3207       1556.2              32.00     Sequence
DRB1_0301  228  NYQFNSLLHAADDMQ  LLHAADDMQ        0.3193       1580.3              32.00     Sequence
DRB1_0301  235  LHAADDMQLYKYIIK  LHAADDMQL        0.3185       1593.6              32.00     Sequence
DRB1_0301  203  TNLINSGFILEKGHH  TNLINSGFI        0.3180       1601.4              32.00     Sequence
DRB1_0301   37  PASAFDKSVFDDGLA  PASAFDKSV        0.3177       1607.3              32.00     Sequence
DRB1_0301  416  PQTPTQLSDVIDRLE  TQLSDVIDR        0.3149       1656.6              32.00     Sequence
DRB1_0301   32  QHFTIPASAFDKSVF  IPASAFDKS        0.3144       1666.0              32.00     Sequence
DRB1_0301  274  MHCHQSLWKDGAPLM  HQSLWKDGA        0.3141       1670.6              32.00     Sequence
DRB1_0301  374  NPYLAFSAMLMAGLD  NPYLAFSAM        0.3134       1683.4              32.00     Sequence
DRB1_0301  262  MPKPLFGDNGSGMHC  LFGDNGSGM        0.3133       1685.2              32.00     Sequence
DRB1_0301  202  LTNLINSGFILEKGH  TNLINSGFI        0.3110       1728.3              32.00     Sequence
DRB1_0301  205  LINSGFILEKGHHEV  LINSGFILE        0.3091       1765.0              32.00     Sequence
DRB1_0301  240  DMQLYKYIIKNTAWQ  MQLYKYIIK        0.3047       1850.9              32.00     Sequence
DRB1_0301  243  LYKYIIKNTAWQNGK  YKYIIKNTA        0.3037       1870.4              32.00     Sequence
DRB1_0301  415  IPQTPTQLSDVIDRL  TQLSDVIDR        0.3031       1882.0              32.00     Sequence
DRB1_0301   70  LLPDPETARIDPFRA  LLPDPETAR        0.3026       1891.8              32.00     Sequence
DRB1_0301  317  AFTNPTVNSYKRLVP  NPTVNSYKR        0.3003       1940.4              32.00     Sequence
DRB1_0301  114  AENYLISTGIADTAY  NYLISTGIA        0.2990       1968.5              50.00     Sequence
DRB1_0301  204  NLINSGFILEKGHHE  LINSGFILE        0.2974       2001.1              50.00     Sequence
DRB1_0301  373  GNPYLAFSAMLMAGL  NPYLAFSAM        0.2962       2028.1              50.00     Sequence
DRB1_0301  119  ISTGIADTAYFGAEA  ISTGIADTA        0.2956       2042.0              50.00     Sequence
DRB1_0301   56  SIRGFQSIHESDMLL  SIHESDMLL        0.2955       2043.4              50.00     Sequence
DRB1_0301  282  KDGAPLMYDETGYAG  GAPLMYDET        0.2950       2054.0              50.00     Sequence
DRB1_0301  224  QAEINYQFNSLLHAA  QAEINYQFN        0.2949       2058.0              50.00     Sequence
DRB1_0301  332  GYEAPINLVYSQRNR  INLVYSQRN        0.2947       2061.9              50.00     Sequence
DRB1_0301   79  IDPFRAAKTLNINFF  IDPFRAAKT        0.2928       2104.1              50.00     Sequence
DRB1_0301   22  VRFCDLPGIMQHFTI  RFCDLPGIM        0.2893       2185.0              50.00     Sequence
DRB1_0301  242  QLYKYIIKNTAWQNG  YKYIIKNTA        0.2879       2219.1              50.00     Sequence
DRB1_0301  314  SLLAFTNPTVNSYKR  SLLAFTNPT        0.2878       2222.4              50.00     Sequence
DRB1_0301  227  INYQFNSLLHAADDM  NYQFNSLLH        0.2865       2252.7              50.00     Sequence
DRB1_0301  207  NSGFILEKGHHEVGS  FILEKGHHE        0.2839       2316.8              50.00     Sequence
DRB1_0301  208  SGFILEKGHHEVGSG  FILEKGHHE        0.2836       2323.9              50.00     Sequence
DRB1_0301  301  ARHYIGGLLHHAPSL  IGGLLHHAP        0.2830       2339.4              50.00     Sequence
DRB1_0301  206  INSGFILEKGHHEVG  FILEKGHHE        0.2811       2388.2              50.00     Sequence
DRB1_0301   15  EKVEYVDVRFCDLPG  KVEYVDVRF        0.2805       2404.0              50.00     Sequence
DRB1_0301  226  EINYQFNSLLHAADD  NYQFNSLLH        0.2801       2413.1              50.00     Sequence
DRB1_0301  261  FMPKPLFGDNGSGMH  KPLFGDNGS        0.2801       2415.2              50.00     Sequence
DRB1_0301  446  LIETWISFKRENEIE  LIETWISFK        0.2798       2422.0              50.00     Sequence
DRB1_0301  188  VAPNDQYVDLRDKML  QYVDLRDKM        0.2789       2445.5              50.00     Sequence
DRB1_0301   78  RIDPFRAAKTLNINF  IDPFRAAKT        0.2786       2452.8              50.00     Sequence
DRB1_0301  441  VFTNDLIETWISFKR  VFTNDLIET        0.2775       2481.9              50.00     Sequence
DRB1_0301   23  RFCDLPGIMQHFTIP  RFCDLPGIM        0.2771       2494.7              50.00     Sequence
DRB1_0301   10  KLAKDEKVEYVDVRF  LAKDEKVEY        0.2761       2520.8              50.00     Sequence
DRB1_0301  313  PSLLAFTNPTVNSYK  SLLAFTNPT        0.2760       2523.7              50.00     Sequence
DRB1_0301  316  LAFTNPTVNSYKRLV  LAFTNPTVN        0.2753       2542.1              50.00     Sequence
DRB1_0301  225  AEINYQFNSLLHAAD  NYQFNSLLH        0.2749       2554.7              50.00     Sequence
DRB1_0301  244  YKYIIKNTAWQNGKT  YKYIIKNTA        0.2748       2556.1              50.00     Sequence
DRB1_0301  372  SGNPYLAFSAMLMAG  NPYLAFSAM        0.2745       2564.7              50.00     Sequence
DRB1_0301   11  LAKDEKVEYVDVRFC  LAKDEKVEY        0.2744       2568.8              50.00     Sequence
DRB1_0301   31  MQHFTIPASAFDKSV  MQHFTIPAS        0.2739       2581.3              50.00     Sequence
DRB1_0301  308  LLHHAPSLLAFTNPT  LLHHAPSLL        0.2736       2591.0              50.00     Sequence
DRB1_0301   14  DEKVEYVDVRFCDLP  EKVEYVDVR        0.2728       2612.5              50.00     Sequence
DRB1_0301   76  TARIDPFRAAKTLNI  TARIDPFRA        0.2714       2653.4              50.00     Sequence
DRB1_0301  285  APLMYDETGYAGLSD  LMYDETGYA        0.2710       2665.4              50.00     Sequence
DRB1_0301  238  ADDMQLYKYIIKNTA  MQLYKYIIK        0.2705       2679.1              50.00     Sequence
DRB1_0301  239  DDMQLYKYIIKNTAW  MQLYKYIIK        0.2703       2684.0              50.00     Sequence
DRB1_0301   16  KVEYVDVRFCDLPGI  KVEYVDVRF        0.2701       2688.9              50.00     Sequence
DRB1_0301   86  KTLNINFFVHDPFTL  LNINFFVHD        0.2698       2698.3              50.00     Sequence
DRB1_0301   27  LPGIMQHFTIPASAF  LPGIMQHFT        0.2691       2719.5              50.00     Sequence
DRB1_0301  100  LEPYSRDPRNIARKA  LEPYSRDPR        0.2659       2816.6              50.00     Sequence
DRB1_0301  348  ACVRIPITGSNPKAK  IPITGSNPK        0.2658       2818.3              50.00     Sequence
DRB1_0301  281  WKDGAPLMYDETGYA  GAPLMYDET        0.2644       2860.8              50.00     Sequence
DRB1_0301  289  YDETGYAGLSDTARH  YAGLSDTAR        0.2641       2869.9              50.00     Sequence
DRB1_0301  378  AFSAMLMAGLDGIKN  LMAGLDGIK        0.2637       2882.4              50.00     Sequence
DRB1_0301  315  LLAFTNPTVNSYKRL  LAFTNPTVN        0.2619       2939.7              50.00     Sequence
DRB1_0301   21  DVRFCDLPGIMQHFT  RFCDLPGIM        0.2611       2964.1              50.00     Sequence
DRB1_0301  141  VSFDSRANGSFYEVD  VSFDSRANG        0.2608       2975.4              50.00     Sequence
DRB1_0301  223  GQAEINYQFNSLLHA  QAEINYQFN        0.2595       3018.1              50.00     Sequence
DRB1_0301  399  PVDKDLYELPPEEAA  VDKDLYELP        0.2571       3097.6              50.00     Sequence
DRB1_0301  113  KAENYLISTGIADTA  NYLISTGIA        0.2569       3103.8              50.00     Sequence
DRB1_0301  326  YKRLVPGYEAPINLV  LVPGYEAPI        0.2550       3166.9              50.00     Sequence
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DRB1_0301    0  VTEKTPDDVFKLAKD  VTEKTPDDV         0.2544       3189.8             50.00     Sequence
DRB1_0301  371  SSGNPYLAFSAMLMA  NPYLAFSAM         0.2541       3197.4             50.00     Sequence
DRB1_0301  280  LWKDGAPLMYDETGY  LWKDGAPLM         0.2527       3247.1             50.00     Sequence
DRB1_0301  445  DLIETWISFKRENEI  LIETWISFK         0.2509       3310.8             50.00     Sequence
DRB1_0301   77  ARIDPFRAAKTLNIN  IDPFRAAKT         0.2505       3326.5             50.00     Sequence
DRB1_0301  400  VDKDLYELPPEEAAS  VDKDLYELP         0.2504       3330.5             50.00     Sequence
DRB1_0301  435  YLTEGGVFTNDLIET  GGVFTNDLI         0.2496       3359.5             50.00     Sequence
DRB1_0301  327  KRLVPGYEAPINLVY  RLVPGYEAP         0.2494       3365.7             50.00     Sequence
DRB1_0301   13  KDEKVEYVDVRFCDL  EKVEYVDVR         0.2491       3377.6             50.00     Sequence
DRB1_0301  286  PLMYDETGYAGLSDT  LMYDETGYA         0.2489       3384.9             50.00     Sequence
DRB1_0301  342  SQRNRSACVRIPITG  RNRSACVRI         0.2484       3400.9             50.00     Sequence
DRB1_0301   99  TLEPYSRDPRNIARK  LEPYSRDPR         0.2473       3441.2             50.00     Sequence
DRB1_0301   30  IMQHFTIPASAFDKS  MQHFTIPAS         0.2467       3466.1             50.00     Sequence
DRB1_0301  312  APSLLAFTNPTVNSY  SLLAFTNPT         0.2418       3653.1             50.00     Sequence
DRB1_0301  265  PLFGDNGSGMHCHQS  LFGDNGSGM         0.2408       3692.3             50.00     Sequence
DRB1_0301  398  APVDKDLYELPPEEA  VDKDLYELP         0.2408       3694.4             50.00     Sequence
DRB1_0301  328  RLVPGYEAPINLVYS  RLVPGYEAP         0.2406       3700.3             50.00     Sequence
DRB1_0301  448  ETWISFKRENEIEPV  WISFKRENE         0.2390       3766.6             50.00     Sequence
DRB1_0301  340  VYSQRNRSACVRIPI  VYSQRNRSA         0.2371       3844.5             50.00     Sequence
DRB1_0301  447  IETWISFKRENEIEP  ISFKRENEI         0.2361       3886.3             50.00     Sequence
DRB1_0301  341  YSQRNRSACVRIPIT  RNRSACVRI         0.2353       3919.3             50.00     Sequence
DRB1_0301  321  PTVNSYKRLVPGYEA  PTVNSYKRL         0.2350       3931.6             50.00     Sequence
DRB1_0301  171  GSPNRGYKVRHKGGY  SPNRGYKVR         0.2345       3954.0             50.00     Sequence
DRB1_0301  287  LMYDETGYAGLSDTA  LMYDETGYA         0.2343       3962.2             50.00     Sequence
DRB1_0301  450  WISFKRENEIEPVNI  ISFKRENEI         0.2311       4104.4             50.00     Sequence
DRB1_0301  172  SPNRGYKVRHKGGYF  SPNRGYKVR         0.2308       4116.8             50.00     Sequence
DRB1_0301   26  DLPGIMQHFTIPASA  LPGIMQHFT         0.2290       4194.9             50.00     Sequence
DRB1_0301  397  QAPVDKDLYELPPEE  VDKDLYELP         0.2278       4249.5             50.00     Sequence
DRB1_0301  131  AEAEFYIFDSVSFDS  EFYIFDSVS         0.2267       4303.9             50.00     Sequence
DRB1_0301  449  TWISFKRENEIEPVN  ISFKRENEI         0.2251       4377.1             50.00     Sequence
DRB1_0301  343  QRNRSACVRIPITGS  RNRSACVRI         0.2248       4390.2             50.00     Sequence
DRB1_0301   98  FTLEPYSRDPRNIAR  LEPYSRDPR         0.2247       4398.1             50.00     Sequence
DRB1_0301  112  RKAENYLISTGIADT  YLISTGIAD         0.2243       4415.6             50.00     Sequence
DRB1_0301  353  PITGSNPKAKRLEFR  ITGSNPKAK         0.2234       4457.3             50.00     Sequence
DRB1_0301  236  HAADDMQLYKYIIKN  HAADDMQLY         0.2234       4457.4             50.00     Sequence
DRB1_0301  222  GGQAEINYQFNSLLH  QAEINYQFN         0.2232       4466.4             50.00     Sequence
DRB1_0301   24  FCDLPGIMQHFTIPA  LPGIMQHFT         0.2211       4573.1             50.00     Sequence
DRB1_0301  377  LAFSAMLMAGLDGIK  LMAGLDGIK         0.2203       4611.5             50.00     Sequence
DRB1_0301  260  TFMPKPLFGDNGSGM  KPLFGDNGS         0.2201       4621.0             50.00     Sequence
DRB1_0301   96  DPFTLEPYSRDPRNI  LEPYSRDPR         0.2195       4653.4             50.00     Sequence
DRB1_0301  325  SYKRLVPGYEAPINL  YKRLVPGYE         0.2189       4683.1             50.00     Sequence
DRB1_0301   28  PGIMQHFTIPASAFD  MQHFTIPAS         0.2179       4731.3             50.00     Sequence
DRB1_0301  344  RNRSACVRIPITGSN  RNRSACVRI         0.2175       4753.4             50.00     Sequence
DRB1_0301   97  PFTLEPYSRDPRNIA  LEPYSRDPR         0.2173       4760.8             50.00     Sequence
DRB1_0301  375  PYLAFSAMLMAGLDG  PYLAFSAML         0.2169       4785.0             50.00     Sequence
DRB1_0301  266  LFGDNGSGMHCHQSL  LFGDNGSGM         0.2164       4809.0             50.00     Sequence
DRB1_0301  170  DGSPNRGYKVRHKGG  SPNRGYKVR         0.2150       4883.0             50.00     Sequence
DRB1_0301   91  NFFVHDPFTLEPYSR  NFFVHDPFT         0.2131       4985.4             50.00     Sequence
DRB1_0301   85  AKTLNINFFVHDPFT  LNINFFVHD         0.2121       5040.5             50.00     Sequence
DRB1_0301  295  AGLSDTARHYIGGLL  AGLSDTARH         0.2118       5054.6             50.00     Sequence
DRB1_0301  363  RLEFRSPDSSGNPYL  LEFRSPDSS         0.2115       5071.9             50.00     Sequence
DRB1_0301   12  AKDEKVEYVDVRFCD  EKVEYVDVR         0.2113       5083.8             50.00     Sequence
DRB1_0301  149  GSFYEVDAISGWWNT  SFYEVDAIS         0.2108       5111.5             50.00     Sequence
DRB1_0301  237  AADDMQLYKYIIKNT  MQLYKYIIK         0.2106       5120.1             50.00     Sequence
DRB1_0301    2  EKTPDDVFKLAKDEK  VFKLAKDEK         0.2092       5200.5             50.00     Sequence
DRB1_0301  271  GSGMHCHQSLWKDGA  GSGMHCHQS         0.2079       5275.2             50.00     Sequence
DRB1_0301  311  HAPSLLAFTNPTVNS  SLLAFTNPT         0.2078       5281.2             50.00     Sequence
DRB1_0301  403  DLYELPPEEAASIPQ  LYELPPEEA         0.2077       5285.6             50.00     Sequence
DRB1_0301  187  PVAPNDQYVDLRDKM  QYVDLRDKM         0.2069       5331.5             50.00     Sequence
DRB1_0301  362  KRLEFRSPDSSGNPY  LEFRSPDSS         0.2057       5400.3             50.00     Sequence
DRB1_0301  209  GFILEKGHHEVGSGG  FILEKGHHE         0.2049       5446.9             50.00     Sequence
DRB1_0301   25  CDLPGIMQHFTIPAS  LPGIMQHFT         0.2040       5499.3             50.00     Sequence
DRB1_0301  150  SFYEVDAISGWWNTG  SFYEVDAIS         0.2028       5574.3             50.00     Sequence
DRB1_0301  404  LYELPPEEAASIPQT  LYELPPEEA         0.2027       5579.2             50.00     Sequence
DRB1_0301  444  NDLIETWISFKRENE  LIETWISFK         0.2019       5623.7             50.00     Sequence
DRB1_0301  331  PGYEAPINLVYSQRN  PINLVYSQR         0.2019       5629.2             50.00     Sequence
DRB1_0301  370  DSSGNPYLAFSAMLM  NPYLAFSAM         0.2014       5658.6             50.00     Sequence
DRB1_0301   55  SSIRGFQSIHESDML  IRGFQSIHE         0.2012       5669.8             50.00     Sequence
DRB1_0301   92  FFVHDPFTLEPYSRD  DPFTLEPYS         0.2007       5698.7             50.00     Sequence
DRB1_0301   75  ETARIDPFRAAKTLN  TARIDPFRA         0.2004       5718.2             50.00     Sequence
DRB1_0301   29  GIMQHFTIPASAFDK  MQHFTIPAS         0.2004       5720.7             50.00     Sequence
DRB1_0301  148  NGSFYEVDAISGWWN  SFYEVDAIS         0.1995       5773.3             50.00     Sequence
DRB1_0301  396  PQAPVDKDLYELPPE  VDKDLYELP         0.1968       5947.4             50.00     Sequence
DRB1_0301  329  LVPGYEAPINLVYSQ  LVPGYEAPI         0.1962       5984.5             50.00     Sequence
DRB1_0301  402  KDLYELPPEEAASIP  LYELPPEEA         0.1960       5996.4             50.00     Sequence
DRB1_0301   93  FVHDPFTLEPYSRDP  FVHDPFTLE         0.1935       6162.3             50.00     Sequence
DRB1_0301  414  SIPQTPTQLSDVIDR  TQLSDVIDR         0.1930       6197.0             50.00     Sequence
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DRB1_0301  347  SACVRIPITGSNPKA  IPITGSNPK         0.1916      6287.6              50.00     Sequence
DRB1_0301  221  SGGQAEINYQFNSLL  QAEINYQFN         0.1916      6291.7              50.00     Sequence
DRB1_0301  169  ADGSPNRGYKVRHKG  SPNRGYKVR         0.1909      6341.1              50.00     Sequence
DRB1_0301  270  NGSGMHCHQSLWKDG  GSGMHCHQS         0.1901      6396.3              50.00     Sequence
DRB1_0301  273  GMHCHQSLWKDGAPL  HQSLWKDGA         0.1881      6536.0              50.00     Sequence
DRB1_0301   95  HDPFTLEPYSRDPRN  PFTLEPYSR         0.1866      6641.0              50.00     Sequence
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DRB1_0301  361  AKRLEFRSPDSSGNP  LEFRSPDSS         0.1851      6747.9              50.00     Sequence
DRB1_0301  401  DKDLYELPPEEAASI  LYELPPEEA         0.1846      6787.3              50.00     Sequence
DRB1_0301  210  FILEKGHHEVGSGGQ  FILEKGHHE         0.1827      6923.2              50.00     Sequence
DRB1_0301  364  LEFRSPDSSGNPYLA  LEFRSPDSS         0.1825      6938.1              50.00     Sequence
DRB1_0301   82  FRAAKTLNINFFVHD  FRAAKTLNI         0.1823      6958.0              50.00     Sequence
DRB1_0301  288  MYDETGYAGLSDTAR  YAGLSDTAR         0.1813      7029.5              50.00     Sequence
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DRB1_0301  395  EPQAPVDKDLYELPP  VDKDLYELP         0.1797      7157.8              50.00     Sequence
DRB1_0301   74  PETARIDPFRAAKTL  TARIDPFRA         0.1792      7191.3              50.00     Sequence
DRB1_0301   54  GSSIRGFQSIHESDM  IRGFQSIHE         0.1790      7211.9              50.00     Sequence
DRB1_0301  434  EYLTEGGVFTNDLIE  GGVFTNDLI         0.1788      7223.2              50.00     Sequence
DRB1_0301   94  VHDPFTLEPYSRDPR  PFTLEPYSR         0.1770      7363.1              50.00     Sequence
DRB1_0301   80  DPFRAAKTLNINFFV  FRAAKTLNI         0.1770      7363.2              50.00     Sequence
DRB1_0301  111  ARKAENYLISTGIAD  YLISTGIAD         0.1770      7365.3              50.00     Sequence
DRB1_0301  376  YLAFSAMLMAGLDGI  LAFSAMLMA         0.1768      7378.4              50.00     Sequence
DRB1_0301  130  GAEAEFYIFDSVSFD  EFYIFDSVS         0.1758      7464.7              50.00     Sequence
DRB1_0301  322  TVNSYKRLVPGYEAP  TVNSYKRLV         0.1757      7472.2              50.00     Sequence
DRB1_0301  164  GAATEADGSPNRGYK  GAATEADGS         0.1745      7566.4              50.00     Sequence
DRB1_0301   84  AAKTLNINFFVHDPF  LNINFFVHD         0.1741      7604.2              50.00     Sequence
DRB1_0301  269  DNGSGMHCHQSLWKD  GSGMHCHQS         0.1740      7608.4              50.00     Sequence
DRB1_0301  427  DRLEADHEYLTEGGV  LEADHEYLT         0.1735      7649.3              50.00     Sequence
DRB1_0301  184  GYFPVAPNDQYVDLR  FPVAPNDQY         0.1731      7683.1              50.00     Sequence
DRB1_0301  324  NSYKRLVPGYEAPIN  LVPGYEAPI         0.1727      7713.7              50.00     Sequence
DRB1_0301  323  VNSYKRLVPGYEAPI  LVPGYEAPI         0.1723      7748.0              50.00     Sequence
DRB1_0301  147  ANGSFYEVDAISGWW  SFYEVDAIS         0.1722      7758.4              50.00     Sequence
DRB1_0301  309  LHHAPSLLAFTNPTV  LHHAPSLLA         0.1722      7761.3              50.00     Sequence
DRB1_0301  173  PNRGYKVRHKGGYFP  NRGYKVRHK         0.1702      7925.6              50.00     Sequence
DRB1_0301  330  VPGYEAPINLVYSQR  PGYEAPINL         0.1696      7977.2              50.00     Sequence
DRB1_0301   81  PFRAAKTLNINFFVH  FRAAKTLNI         0.1696      7977.7              50.00     Sequence
DRB1_0301  360  KAKRLEFRSPDSSGN  LEFRSPDSS         0.1690      8030.9              50.00     Sequence
DRB1_0301  310  HHAPSLLAFTNPTVN  SLLAFTNPT         0.1685      8074.8              50.00     Sequence
DRB1_0301  185  YFPVAPNDQYVDLRD  FPVAPNDQY         0.1681      8111.4              50.00     Sequence
DRB1_0301  394  IEPQAPVDKDLYELP  QAPVDKDLY         0.1655      8343.4              50.00     Sequence
DRB1_0301  168  EADGSPNRGYKVRHK  SPNRGYKVR         0.1631      8559.7              50.00     Sequence
DRB1_0301  443  TNDLIETWISFKREN  LIETWISFK         0.1622      8643.3              50.00     Sequence
DRB1_0301  101  EPYSRDPRNIARKAE  YSRDPRNIA         0.1613      8731.9              50.00     Sequence
DRB1_0301  186  FPVAPNDQYVDLRDK  FPVAPNDQY         0.1612      8740.0              50.00     Sequence
DRB1_0301  354  ITGSNPKAKRLEFRS  ITGSNPKAK         0.1612      8744.0              50.00     Sequence
DRB1_0301  183  GGYFPVAPNDQYVDL  FPVAPNDQY         0.1596      8894.1              50.00     Sequence
DRB1_0301  126  TAYFGAEAEFYIFDS  TAYFGAEAE         0.1573      9119.6              50.00     Sequence
DRB1_0301  167  TEADGSPNRGYKVRH  TEADGSPNR         0.1552      9328.7              50.00     Sequence
DRB1_0301  163  TGAATEADGSPNRGY  GAATEADGS         0.1544      9401.9              50.00     Sequence
DRB1_0301  268  GDNGSGMHCHQSLWK  GSGMHCHQS         0.1537      9473.4              50.00     Sequence
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DRB1_0301  125  DTAYFGAEAEFYIFD  TAYFGAEAE         0.1525      9603.8              50.00     Sequence
DRB1_0301   73  DPETARIDPFRAAKT  TARIDPFRA         0.1522      9634.0              50.00     Sequence
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DRB1_0301  124  ADTAYFGAEAEFYIF  TAYFGAEAE         0.1458     10319.6              50.00     Sequence
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DRB1_0301  460  EPVNIRPHPYEFALY  PVNIRPHPY         0.1450     10415.3              50.00     Sequence
DRB1_0301  428  RLEADHEYLTEGGVF  LEADHEYLT         0.1448     10439.9              50.00     Sequence
DRB1_0301  151  FYEVDAISGWWNTGA  FYEVDAISG         0.1439     10538.3              50.00     Sequence
DRB1_0301  104  SRDPRNIARKAENYL  SRDPRNIAR         0.1429     10652.5              50.00     Sequence
DRB1_0301   53  DGSSIRGFQSIHESD  GSSIRGFQS         0.1419     10764.8              50.00     Sequence
DRB1_0301  442  FTNDLIETWISFKRE  FTNDLIETW         0.1410     10872.4              50.00     Sequence
DRB1_0301  272  SGMHCHQSLWKDGAP  HQSLWKDGA         0.1407     10905.5              50.00     Sequence
DRB1_0301  103  YSRDPRNIARKAENY  SRDPRNIAR         0.1393     11077.0              50.00     Sequence
DRB1_0301  296  GLSDTARHYIGGLLH  GLSDTARHY         0.1376     11284.1              50.00     Sequence
DRB1_0301  162  NTGAATEADGSPNRG  GAATEADGS         0.1362     11454.6              50.00     Sequence
DRB1_0301  120  STGIADTAYFGAEAE  TGIADTAYF         0.1350     11608.4              50.00     Sequence
DRB1_0301  174  NRGYKVRHKGGYFPV  NRGYKVRHK         0.1345     11668.5              50.00     Sequence
DRB1_0301  458  EIEPVNIRPHPYEFA  PVNIRPHPY         0.1343     11689.3              50.00     Sequence
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DRB1_0301  432  DHEYLTEGGVFTNDL  HEYLTEGGV         0.1334       11806.9                50.00      Sequence
DRB1_0301  461  PVNIRPHPYEFALYY  PVNIRPHPY         0.1327       11893.2                50.00      Sequence
DRB1_0301  105  RDPRNIARKAENYLI  RDPRNIARK         0.1318       12008.9                50.00      Sequence
DRB1_0301   71  LPDPETARIDPFRAA  LPDPETARI         0.1310       12118.2                50.00      Sequence
DRB1_0301  142  SFDSRANGSFYEVDA  SFDSRANGS         0.1307       12151.0                50.00      Sequence
DRB1_0301  393  KIEPQAPVDKDLYEL  QAPVDKDLY         0.1305       12180.0                50.00      Sequence
DRB1_0301  346  RSACVRIPITGSNPK  IPITGSNPK         0.1299       12267.1                50.00      Sequence
DRB1_0301  429  LEADHEYLTEGGVFT  LEADHEYLT         0.1296       12303.5                50.00      Sequence
DRB1_0301  106  DPRNIARKAENYLIS  DPRNIARKA         0.1287       12416.7                50.00      Sequence
DRB1_0301  359  PKAKRLEFRSPDSSG  RLEFRSPDS         0.1287       12419.4                50.00      Sequence
DRB1_0301  123  IADTAYFGAEAEFYI  IADTAYFGA         0.1263       12743.9                50.00      Sequence
DRB1_0301  259  VTFMPKPLFGDNGSG  KPLFGDNGS         0.1261       12781.2                50.00      Sequence
DRB1_0301  129  FGAEAEFYIFDSVSF  EFYIFDSVS         0.1259       12804.0                50.00      Sequence
DRB1_0301  166  ATEADGSPNRGYKVR  TEADGSPNR         0.1251       12919.1                50.00      Sequence
DRB1_0301  182  KGGYFPVAPNDQYVD  FPVAPNDQY         0.1247       12969.2                50.00      Sequence
DRB1_0301  175  RGYKVRHKGGYFPVA  YKVRHKGGY         0.1237       13111.9                50.00      Sequence
DRB1_0301  457  NEIEPVNIRPHPYEF  PVNIRPHPY         0.1234       13160.5                50.00      Sequence
DRB1_0301  161  WNTGAATEADGSPNR  GAATEADGS         0.1233       13167.2                50.00      Sequence
DRB1_0301  108  RNIARKAENYLISTG  NIARKAENY         0.1224       13305.0                50.00      Sequence
DRB1_0301  109  NIARKAENYLISTGI  NIARKAENY         0.1213       13453.0                50.00      Sequence
DRB1_0301  107  PRNIARKAENYLIST  NIARKAENY         0.1208       13527.6                50.00      Sequence
DRB1_0301  220  GSGGQAEINYQFNSL  QAEINYQFN         0.1206       13564.1                50.00      Sequence
DRB1_0301  267  FGDNGSGMHCHQSLW  GSGMHCHQS         0.1199       13657.5                50.00      Sequence
DRB1_0301  110  IARKAENYLISTGIA  RKAENYLIS         0.1175       14023.6                50.00      Sequence
DRB1_0301  145  SRANGSFYEVDAISG  SFYEVDAIS         0.1168       14131.8                50.00      Sequence
DRB1_0301   72  PDPETARIDPFRAAK  TARIDPFRA         0.1165       14177.5                50.00      Sequence
DRB1_0301  211  ILEKGHHEVGSGGQA  ILEKGHHEV         0.1152       14379.5                50.00      Sequence
DRB1_0301  181  HKGGYFPVAPNDQYV  FPVAPNDQY         0.1141       14542.2                50.00      Sequence
DRB1_0301  413  ASIPQTPTQLSDVID  IPQTPTQLS         0.1141       14553.2                50.00      Sequence
DRB1_0301  127  AYFGAEAEFYIFDSV  AYFGAEAEF         0.1137       14607.9                50.00      Sequence
DRB1_0301  358  NPKAKRLEFRSPDSS  KRLEFRSPD         0.1134       14660.7                50.00      Sequence
DRB1_0301  298  SDTARHYIGGLLHHA  RHYIGGLLH         0.1120       14882.7                50.00      Sequence
DRB1_0301  431  ADHEYLTEGGVFTND  HEYLTEGGV         0.1107       15089.7                50.00      Sequence
DRB1_0301  256  GKTVTFMPKPLFGDN  GKTVTFMPK         0.1101       15194.1                50.00      Sequence
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DRB1_0301  121  TGIADTAYFGAEAEF  TGIADTAYF         0.1087       15418.3                50.00      Sequence
DRB1_0301  386  GLDGIKNKIEPQAPV  GLDGIKNKI         0.1080       15538.1                50.00      Sequence
DRB1_0301  385  AGLDGIKNKIEPQAP  AGLDGIKNK         0.1078       15572.4                50.00      Sequence
DRB1_0301  128  YFGAEAEFYIFDSVS  FGAEAEFYI         0.1065       15790.1                50.00      Sequence
DRB1_0301  355  TGSNPKAKRLEFRSP  TGSNPKAKR         0.1049       16066.5                50.00      Sequence
DRB1_0301  176  GYKVRHKGGYFPVAP  GYKVRHKGG         0.1039       16237.4                50.00      Sequence
DRB1_0301  456  ENEIEPVNIRPHPYE  NEIEPVNIR         0.1033       16358.6                50.00      Sequence
DRB1_0301  366  FRSPDSSGNPYLAFS  FRSPDSSGN         0.1031       16382.5                50.00      Sequence
DRB1_0301  122  GIADTAYFGAEAEFY  IADTAYFGA         0.1025       16501.5                50.00      Sequence
DRB1_0301  258  TVTFMPKPLFGDNGS  VTFMPKPLF         0.1009       16785.5                50.00      Sequence
DRB1_0301  368  SPDSSGNPYLAFSAM  SPDSSGNPY         0.1008       16796.2                50.00      Sequence
DRB1_0301  245  KYIIKNTAWQNGKTV  KYIIKNTAW         0.1004       16880.9                50.00      Sequence
DRB1_0301  412  AASIPQTPTQLSDVI  IPQTPTQLS         0.1002       16902.3                50.00      Sequence
DRB1_0301  257  KTVTFMPKPLFGDNG  VTFMPKPLF         0.0992       17097.8                50.00      Sequence
DRB1_0301  165  AATEADGSPNRGYKV  TEADGSPNR         0.0990       17121.7                50.00      Sequence
DRB1_0301  365  EFRSPDSSGNPYLAF  FRSPDSSGN         0.0989       17144.9                50.00      Sequence
DRB1_0301  430  EADHEYLTEGGVFTN  HEYLTEGGV         0.0970       17510.6                50.00      Sequence
DRB1_0301  254  QNGKTVTFMPKPLFG  GKTVTFMPK         0.0967       17571.2                50.00      Sequence
DRB1_0301  392  NKIEPQAPVDKDLYE  QAPVDKDLY         0.0960       17699.4                50.00      Sequence
DRB1_0301  144  DSRANGSFYEVDAIS  SFYEVDAIS         0.0954       17807.5                50.00      Sequence
DRB1_0301  455  RENEIEPVNIRPHPY  NEIEPVNIR         0.0944       18008.5                50.00      Sequence
DRB1_0301  453  FKRENEIEPVNIRPH  FKRENEIEP         0.0933       18212.6                50.00      Sequence
DRB1_0301  297  LSDTARHYIGGLLHH  LSDTARHYI         0.0933       18212.6                50.00      Sequence
DRB1_0301  253  WQNGKTVTFMPKPLF  GKTVTFMPK         0.0930       18271.3                50.00      Sequence
DRB1_0301  357  SNPKAKRLEFRSPDS  NPKAKRLEF         0.0910       18673.4                50.00      Sequence
DRB1_0301  367  RSPDSSGNPYLAFSA  SPDSSGNPY         0.0899       18901.7                50.00      Sequence
DRB1_0301  180  RHKGGYFPVAPNDQY  FPVAPNDQY         0.0898       18918.6                50.00      Sequence
DRB1_0301  391  KNKIEPQAPVDKDLY  KNKIEPQAP         0.0883       19241.7                50.00      Sequence
DRB1_0301  216  HHEVGSGGQAEINYQ  HHEVGSGGQ         0.0876       19378.8                50.00      Sequence
DRB1_0301  411  EAASIPQTPTQLSDV  EAASIPQTP         0.0871       19478.8                50.00      Sequence
DRB1_0301  219  VGSGGQAEINYQFNS  VGSGGQAEI         0.0861       19701.0                50.00      Sequence
DRB1_0301  160  WWNTGAATEADGSPN  WWNTGAATE         0.0858       19764.8                50.00      Sequence
DRB1_0301  345  NRSACVRIPITGSNP  RSACVRIPI         0.0857       19772.5                50.00      Sequence
DRB1_0301  390  IKNKIEPQAPVDKDL  KNKIEPQAP         0.0850       19939.2                50.00      Sequence
DRB1_0301  452  SFKRENEIEPVNIRP  FKRENEIEP         0.0845       20032.2                50.00      Sequence
DRB1_0301  387  LDGIKNKIEPQAPVD  LDGIKNKIE         0.0840       20152.4                50.00      Sequence
DRB1_0301  356  GSNPKAKRLEFRSPD  GSNPKAKRL         0.0833       20296.4                50.00      Sequence
DRB1_0301  250  NTAWQNGKTVTFMPK  TAWQNGKTV         0.0831       20353.8                50.00      Sequence
DRB1_0301  158  SGWWNTGAATEADGS  WWNTGAATE         0.0827       20442.3                50.00      Sequence
DRB1_0301  389  GIKNKIEPQAPVDKD  KNKIEPQAP         0.0826       20448.1                50.00      Sequence
DRB1_0301  454  KRENEIEPVNIRPHP  KRENEIEPV         0.0822       20551.8                50.00      Sequence
DRB1_0301  157  ISGWWNTGAATEADG  SGWWNTGAA         0.0821       20557.4                50.00      Sequence
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   DRB1_0301  217  HEVGSGGQAEINYQF  VGSGGQAEI        0.0813      20752.5               50.00     Sequence
   DRB1_0301  218  EVGSGGQAEINYQFN  VGSGGQAEI        0.0801      21016.7               50.00     Sequence
   DRB1_0301  388  DGIKNKIEPQAPVDK  GIKNKIEPQ        0.0796      21140.7               50.00     Sequence
   DRB1_0301  249  KNTAWQNGKTVTFMP  TAWQNGKTV        0.0792      21224.6               50.00     Sequence
   DRB1_0301  463  NIRPHPYEFALYYDV  NIRPHPYEF        0.0787      21331.4               50.00     Sequence
   DRB1_0301  215  GHHEVGSGGQAEINY  HHEVGSGGQ        0.0780      21502.4               50.00     Sequence
   DRB1_0301  177  YKVRHKGGYFPVAPN  VRHKGGYFP        0.0779      21514.3               50.00     Sequence
   DRB1_0301  251  TAWQNGKTVTFMPKP  TAWQNGKTV        0.0766      21836.5               50.00     Sequence
   DRB1_0301  246  YIIKNTAWQNGKTVT  YIIKNTAWQ        0.0763      21897.8               50.00     Sequence
   DRB1_0301  156  AISGWWNTGAATEAD  SGWWNTGAA        0.0752      22169.8               50.00     Sequence
   DRB1_0301  143  FDSRANGSFYEVDAI  FDSRANGSF        0.0746      22297.8               50.00     Sequence
   DRB1_0301  248  IKNTAWQNGKTVTFM  TAWQNGKTV        0.0746      22314.5               50.00     Sequence
   DRB1_0301  247  IIKNTAWQNGKTVTF  IIKNTAWQN        0.0743      22381.9               50.00     Sequence
   DRB1_0301  159  GWWNTGAATEADGSP  GWWNTGAAT        0.0729      22708.1               50.00     Sequence
   DRB1_0301  462  VNIRPHPYEFALYYD  NIRPHPYEF        0.0681      23935.7               50.00     Sequence
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   DRB1_0301  179  VRHKGGYFPVAPNDQ  VRHKGGYFP        0.0591      26378.9               50.00     Sequence
   DRB1_0301  409  PEEAASIPQTPTQLS  PEEAASIPQ        0.0587      26495.0               50.00     Sequence
   DRB1_0301  214  KGHHEVGSGGQAEIN  HHEVGSGGQ        0.0582      26632.1               50.00     Sequence
   DRB1_0301  406  ELPPEEAASIPQTPT  LPPEEAASI        0.0523      28388.6               50.00     Sequence
   DRB1_0301  405  YELPPEEAASIPQTP  LPPEEAASI        0.0523      28390.1               50.00     Sequence
   DRB1_0301  213  EKGHHEVGSGGQAEI  HHEVGSGGQ        0.0517      28580.3               50.00     Sequence
   DRB1_0301  408  PPEEAASIPQTPTQL  EAASIPQTP        0.0511      28754.3               50.00     Sequence
   DRB1_0301  407  LPPEEAASIPQTPTQ  LPPEEAASI        0.0493      29342.0               50.00     Sequence
   DRB1_0301  154  VDAISGWWNTGAATE  GWWNTGAAT        0.0492      29346.7               50.00     Sequence
   DRB1_0301  212  LEKGHHEVGSGGQAE  LEKGHHEVG        0.0429      31435.3               50.00     Sequence
   DRB1_0301  153  EVDAISGWWNTGAAT  GWWNTGAAT        0.0349      34262.3               50.00     Sequence
   DRB1_0301  152  YEVDAISGWWNTGAA  YEVDAISGW        0.0279      36966.5               50.00     Sequence
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Allele: DRB1_0301. Number of high binders 7. Number of weak binders 51. Number of peptides 464

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0401  198  RDKMLTNLINSGFIL  KMLTNLINS        0.7685         12.2         SB     0.40     Sequence
   DRB1_0401  197  LRDKMLTNLINSGFI  KMLTNLINS        0.7570         13.9         SB     0.80     Sequence
   DRB1_0401  309  LHHAPSLLAFTNPTV  LHHAPSLLA        0.7531         14.5         SB     0.80     Sequence
   DRB1_0401  199  DKMLTNLINSGFILE  KMLTNLINS        0.7411         16.5         SB     0.80     Sequence
   DRB1_0401  196  DLRDKMLTNLINSGF  KMLTNLINS        0.7342         17.7         SB     1.00     Sequence
   DRB1_0401  308  LLHHAPSLLAFTNPT  LHHAPSLLA        0.7117         22.6         SB     2.00     Sequence
   DRB1_0401  313  PSLLAFTNPTVNSYK  LLAFTNPTV        0.7036         24.7         SB     2.00     Sequence
   DRB1_0401  195  VDLRDKMLTNLINSG  KMLTNLINS        0.6822         31.1         SB     4.00     Sequence
   DRB1_0401  307  GLLHHAPSLLAFTNP  LHHAPSLLA        0.6754         33.5         SB     4.00     Sequence
   DRB1_0401  312  APSLLAFTNPTVNSY  LLAFTNPTV        0.6742         34.0         SB     4.00     Sequence
   DRB1_0401  336  PINLVYSQRNRSACV  INLVYSQRN        0.6668         36.8         SB     4.00     Sequence
   DRB1_0401  314  SLLAFTNPTVNSYKR  LLAFTNPTV        0.6666         36.9         SB     4.00     Sequence
   DRB1_0401  337  INLVYSQRNRSACVR  LVYSQRNRS        0.6632         38.2         SB     4.00     Sequence
   DRB1_0401  242  QLYKYIIKNTAWQNG  YKYIIKNTA        0.6595         39.8         SB     4.00     Sequence
   DRB1_0401  241  MQLYKYIIKNTAWQN  QLYKYIIKN        0.6565         41.1         SB     4.00     Sequence
   DRB1_0401  200  KMLTNLINSGFILEK  KMLTNLINS        0.6485         44.8         SB     4.00     Sequence
   DRB1_0401  335  APINLVYSQRNRSAC  INLVYSQRN        0.6404         49.0         SB     4.00     Sequence
   DRB1_0401  306  GGLLHHAPSLLAFTN  LHHAPSLLA        0.6359         51.4         WB     4.00     Sequence
   DRB1_0401  311  HAPSLLAFTNPTVNS  LLAFTNPTV        0.6345         52.2         WB     4.00     Sequence
   DRB1_0401   80  DPFRAAKTLNINFFV  FRAAKTLNI        0.6274         56.3         WB     8.00     Sequence
   DRB1_0401  240  DMQLYKYIIKNTAWQ  QLYKYIIKN        0.6266         56.8         WB     8.00     Sequence
   DRB1_0401  194  YVDLRDKMLTNLINS  KMLTNLINS        0.6246         58.1         WB     8.00     Sequence
   DRB1_0401  226  EINYQFNSLLHAADD  YQFNSLLHA        0.6229         59.2         WB     8.00     Sequence
   DRB1_0401  225  AEINYQFNSLLHAAD  NYQFNSLLH        0.6170         63.0         WB     8.00     Sequence
   DRB1_0401   79  IDPFRAAKTLNINFF  FRAAKTLNI        0.6157         64.0         WB     8.00     Sequence
   DRB1_0401   81  PFRAAKTLNINFFVH  FRAAKTLNI        0.6140         65.2         WB     8.00     Sequence
   DRB1_0401  334  EAPINLVYSQRNRSA  INLVYSQRN        0.6126         66.1         WB     8.00     Sequence
   DRB1_0401  363  RLEFRSPDSSGNPYL  LEFRSPDSS        0.6085         69.1         WB     8.00     Sequence
   DRB1_0401  243  LYKYIIKNTAWQNGK  YKYIIKNTA        0.6048         71.9         WB     8.00     Sequence
   DRB1_0401  362  KRLEFRSPDSSGNPY  LEFRSPDSS        0.5995         76.2         WB     8.00     Sequence
   DRB1_0401  338  NLVYSQRNRSACVRI  LVYSQRNRS        0.5898         84.6         WB     8.00     Sequence
   DRB1_0401  315  LLAFTNPTVNSYKRL  LAFTNPTVN        0.5893         85.1         WB     8.00     Sequence
   DRB1_0401  244  YKYIIKNTAWQNGKT  YKYIIKNTA        0.5889         85.5         WB     8.00     Sequence
   DRB1_0401  224  QAEINYQFNSLLHAA  YQFNSLLHA        0.5872         87.1         WB     8.00     Sequence
   DRB1_0401  133  AEFYIFDSVSFDSRA  FYIFDSVSF        0.5848         89.3         WB     8.00     Sequence
   DRB1_0401  310  HHAPSLLAFTNPTVN  LLAFTNPTV        0.5831         91.0         WB     8.00     Sequence
   DRB1_0401  361  AKRLEFRSPDSSGNP  LEFRSPDSS        0.5812         92.8         WB     8.00     Sequence
   DRB1_0401  305  IGGLLHHAPSLLAFT  LHHAPSLLA        0.5812         92.8         WB     8.00     Sequence
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DRB1_0401  374  NPYLAFSAMLMAGLD  YLAFSAMLM         0.5797          94.4           WB     8.00      Sequence
DRB1_0401  375  PYLAFSAMLMAGLDG  YLAFSAMLM         0.5766          97.6           WB     8.00      Sequence
DRB1_0401   78  RIDPFRAAKTLNINF  FRAAKTLNI         0.5763          97.9           WB     8.00      Sequence
DRB1_0401  134  EFYIFDSVSFDSRAN  FYIFDSVSF         0.5748          99.5           WB     8.00      Sequence
DRB1_0401  227  INYQFNSLLHAADDM  YQFNSLLHA         0.5696         105.3           WB     8.00      Sequence
DRB1_0401  135  FYIFDSVSFDSRANG  FYIFDSVSF         0.5683         106.8           WB    16.00      Sequence
DRB1_0401  376  YLAFSAMLMAGLDGI  YLAFSAMLM         0.5676         107.6           WB    16.00      Sequence
DRB1_0401  333  YEAPINLVYSQRNRS  INLVYSQRN         0.5653         110.3           WB    16.00      Sequence
DRB1_0401  132  EAEFYIFDSVSFDSR  FYIFDSVSF         0.5647         111.1           WB    16.00      Sequence
DRB1_0401  239  DDMQLYKYIIKNTAW  QLYKYIIKN         0.5633         112.8           WB    16.00      Sequence
DRB1_0401  149  GSFYEVDAISGWWNT  SFYEVDAIS         0.5555         122.7           WB    16.00      Sequence
DRB1_0401  304  YIGGLLHHAPSLLAF  LHHAPSLLA         0.5536         125.3           WB    16.00      Sequence
DRB1_0401  373  GNPYLAFSAMLMAGL  YLAFSAMLM         0.5528         126.2           WB    16.00      Sequence
DRB1_0401   55  SSIRGFQSIHESDML  IRGFQSIHE         0.5524         126.9           WB    16.00      Sequence
DRB1_0401  148  NGSFYEVDAISGWWN  SFYEVDAIS         0.5516         127.9           WB    16.00      Sequence
DRB1_0401  115  ENYLISTGIADTAYF  YLISTGIAD         0.5493         131.2           WB    16.00      Sequence
DRB1_0401  228  NYQFNSLLHAADDMQ  NYQFNSLLH         0.5471         134.3           WB    16.00      Sequence
DRB1_0401  360  KAKRLEFRSPDSSGN  LEFRSPDSS         0.5467         135.0           WB    16.00      Sequence
DRB1_0401   28  PGIMQHFTIPASAFD  MQHFTIPAS         0.5463         135.5           WB    16.00      Sequence
DRB1_0401   66  SDMLLLPDPETARID  MLLLPDPET         0.5460         135.9           WB    16.00      Sequence
DRB1_0401   30  IMQHFTIPASAFDKS  MQHFTIPAS         0.5444         138.2           WB    16.00      Sequence
DRB1_0401   29  GIMQHFTIPASAFDK  MQHFTIPAS         0.5443         138.5           WB    16.00      Sequence
DRB1_0401  303  HYIGGLLHHAPSLLA  LHHAPSLLA         0.5408         143.7           WB    16.00      Sequence
DRB1_0401  114  AENYLISTGIADTAY  YLISTGIAD         0.5360         151.4           WB    16.00      Sequence
DRB1_0401   67  DMLLLPDPETARIDP  MLLLPDPET         0.5336         155.5           WB    16.00      Sequence
DRB1_0401  116  NYLISTGIADTAYFG  YLISTGIAD         0.5306         160.6           WB    16.00      Sequence
DRB1_0401   82  FRAAKTLNINFFVHD  FRAAKTLNI         0.5301         161.4           WB    16.00      Sequence
DRB1_0401   65  ESDMLLLPDPETARI  MLLLPDPET         0.5293         162.8           WB    16.00      Sequence
DRB1_0401   54  GSSIRGFQSIHESDM  IRGFQSIHE         0.5272         166.5           WB    16.00      Sequence
DRB1_0401  223  GQAEINYQFNSLLHA  EINYQFNSL         0.5264         168.0           WB    16.00      Sequence
DRB1_0401   56  SIRGFQSIHESDMLL  IRGFQSIHE         0.5248         170.9           WB    16.00      Sequence
DRB1_0401   57  IRGFQSIHESDMLLL  IRGFQSIHE         0.5206         178.9           WB    16.00      Sequence
DRB1_0401   77  ARIDPFRAAKTLNIN  FRAAKTLNI         0.5186         182.9           WB    16.00      Sequence
DRB1_0401  364  LEFRSPDSSGNPYLA  LEFRSPDSS         0.5171         185.8           WB    16.00      Sequence
DRB1_0401  147  ANGSFYEVDAISGWW  SFYEVDAIS         0.5151         189.8           WB    16.00      Sequence
DRB1_0401   31  MQHFTIPASAFDKSV  MQHFTIPAS         0.5134         193.3           WB    16.00      Sequence
DRB1_0401  253  WQNGKTVTFMPKPLF  WQNGKTVTF         0.5078         205.4           WB    16.00      Sequence
DRB1_0401  332  GYEAPINLVYSQRNR  INLVYSQRN         0.5075         206.2           WB    16.00      Sequence
DRB1_0401   64  HESDMLLLPDPETAR  MLLLPDPET         0.5059         209.9           WB    16.00      Sequence
DRB1_0401   27  LPGIMQHFTIPASAF  MQHFTIPAS         0.5036         215.2           WB    16.00      Sequence
DRB1_0401  359  PKAKRLEFRSPDSSG  LEFRSPDSS         0.4950         236.1           WB    16.00      Sequence
DRB1_0401  372  SGNPYLAFSAMLMAG  YLAFSAMLM         0.4938         239.0           WB    16.00      Sequence
DRB1_0401   68  MLLLPDPETARIDPF  MLLLPDPET         0.4930         241.2           WB    16.00      Sequence
DRB1_0401  131  AEAEFYIFDSVSFDS  FYIFDSVSF         0.4903         248.3           WB    16.00      Sequence
DRB1_0401  150  SFYEVDAISGWWNTG  SFYEVDAIS         0.4883         253.8           WB    32.00      Sequence
DRB1_0401  113  KAENYLISTGIADTA  YLISTGIAD         0.4879         254.8           WB    32.00      Sequence
DRB1_0401  339  LVYSQRNRSACVRIP  LVYSQRNRS         0.4870         257.4           WB    32.00      Sequence
DRB1_0401  302  RHYIGGLLHHAPSLL  RHYIGGLLH         0.4846         264.2           WB    32.00      Sequence
DRB1_0401   21  DVRFCDLPGIMQHFT  RFCDLPGIM         0.4823         270.7           WB    32.00      Sequence
DRB1_0401   63  IHESDMLLLPDPETA  MLLLPDPET         0.4801         277.4           WB    32.00      Sequence
DRB1_0401  316  LAFTNPTVNSYKRLV  LAFTNPTVN         0.4768         287.4           WB    32.00      Sequence
DRB1_0401   20  VDVRFCDLPGIMQHF  VRFCDLPGI         0.4737         297.1           WB    32.00      Sequence
DRB1_0401  193  QYVDLRDKMLTNLIN  DLRDKMLTN         0.4717         303.8           WB    32.00      Sequence
DRB1_0401   76  TARIDPFRAAKTLNI  FRAAKTLNI         0.4707         307.1           WB    32.00      Sequence
DRB1_0401  301  ARHYIGGLLHHAPSL  RHYIGGLLH         0.4698         310.0           WB    32.00      Sequence
DRB1_0401  381  AMLMAGLDGIKNKIE  MAGLDGIKN         0.4684         314.9           WB    32.00      Sequence
DRB1_0401  238  ADDMQLYKYIIKNTA  QLYKYIIKN         0.4682         315.4           WB    32.00      Sequence
DRB1_0401   90  INFFVHDPFTLEPYS  FFVHDPFTL         0.4678         316.6           WB    32.00      Sequence
DRB1_0401   53  DGSSIRGFQSIHESD  IRGFQSIHE         0.4657         324.1           WB    32.00      Sequence
DRB1_0401   91  NFFVHDPFTLEPYSR  FFVHDPFTL         0.4624         335.9           WB    32.00      Sequence
DRB1_0401  331  PGYEAPINLVYSQRN  YEAPINLVY         0.4606         342.3           WB    32.00      Sequence
DRB1_0401   89  NINFFVHDPFTLEPY  FFVHDPFTL         0.4571         355.7           WB    32.00      Sequence
DRB1_0401  112  RKAENYLISTGIADT  RKAENYLIS         0.4542         366.9           WB    32.00      Sequence
DRB1_0401  146  RANGSFYEVDAISGW  SFYEVDAIS         0.4526         373.3           WB    32.00      Sequence
DRB1_0401  252  AWQNGKTVTFMPKPL  WQNGKTVTF         0.4521         375.5           WB    32.00      Sequence
DRB1_0401  229  YQFNSLLHAADDMQL  YQFNSLLHA         0.4499         384.5           WB    32.00      Sequence
DRB1_0401   62  SIHESDMLLLPDPET  MLLLPDPET         0.4476         394.1           WB    32.00      Sequence
DRB1_0401   19  YVDVRFCDLPGIMQH  VRFCDLPGI         0.4433         412.9           WB    32.00      Sequence
DRB1_0401   92  FFVHDPFTLEPYSRD  FFVHDPFTL         0.4395         430.4           WB    32.00      Sequence
DRB1_0401  251  TAWQNGKTVTFMPKP  WQNGKTVTF         0.4392         431.5           WB    32.00      Sequence
DRB1_0401  291  ETGYAGLSDTARHYI  YAGLSDTAR         0.4387         434.0           WB    32.00      Sequence
DRB1_0401   22  VRFCDLPGIMQHFTI  RFCDLPGIM         0.4383         436.2           WB    32.00      Sequence
DRB1_0401  300  TARHYIGGLLHHAPS  RHYIGGLLH         0.4371         441.8           WB    32.00      Sequence
DRB1_0401   26  DLPGIMQHFTIPASA  MQHFTIPAS         0.4355         449.5           WB    32.00      Sequence
DRB1_0401  274  MHCHQSLWKDGAPLM  MHCHQSLWK         0.4345         454.4           WB    32.00      Sequence
DRB1_0401  377  LAFSAMLMAGLDGIK  LAFSAMLMA         0.4340         456.5           WB    32.00      Sequence
DRB1_0401   49  GLAFDGSSIRGFQSI  LAFDGSSIR         0.4336         458.8           WB    32.00      Sequence
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DRB1_0401  256  GKTVTFMPKPLFGDN  VTFMPKPLF        0.4333        460.3          WB    32.00      Sequence
DRB1_0401   88  LNINFFVHDPFTLEP  FFVHDPFTL        0.4319        467.2          WB    32.00      Sequence
DRB1_0401  136  YIFDSVSFDSRANGS  YIFDSVSFD        0.4299        477.3          WB    32.00      Sequence
DRB1_0401  358  NPKAKRLEFRSPDSS  LEFRSPDSS        0.4299        477.4          WB    32.00      Sequence
DRB1_0401  380  SAMLMAGLDGIKNKI  MAGLDGIKN        0.4296        479.2          WB    32.00      Sequence
DRB1_0401  292  TGYAGLSDTARHYIG  YAGLSDTAR        0.4293        480.5          WB    32.00      Sequence
DRB1_0401  445  DLIETWISFKRENEI  IETWISFKR        0.4279        487.6          WB    32.00      Sequence
DRB1_0401  156  AISGWWNTGAATEAD  ISGWWNTGA        0.4270        492.5          WB    32.00      Sequence
DRB1_0401   32  QHFTIPASAFDKSVF  QHFTIPASA        0.4260        498.0          WB    32.00      Sequence
DRB1_0401  255  NGKTVTFMPKPLFGD  VTFMPKPLF        0.4254        501.0                32.00      Sequence
DRB1_0401  117  YLISTGIADTAYFGA  YLISTGIAD        0.4247        505.3                32.00      Sequence
DRB1_0401  155  DAISGWWNTGAATEA  ISGWWNTGA        0.4240        508.9                32.00      Sequence
DRB1_0401  273  GMHCHQSLWKDGAPL  MHCHQSLWK        0.4238        510.1                32.00      Sequence
DRB1_0401  444  NDLIETWISFKRENE  IETWISFKR        0.4234        512.0                32.00      Sequence
DRB1_0401  130  GAEAEFYIFDSVSFD  FYIFDSVSF        0.4226        516.4                32.00      Sequence
DRB1_0401  382  MLMAGLDGIKNKIEP  MAGLDGIKN        0.4220        520.1                32.00      Sequence
DRB1_0401  272  SGMHCHQSLWKDGAP  MHCHQSLWK        0.4204        529.3                32.00      Sequence
DRB1_0401   48  DGLAFDGSSIRGFQS  LAFDGSSIR        0.4174        546.3                32.00      Sequence
DRB1_0401   87  TLNINFFVHDPFTLE  FFVHDPFTL        0.4157        556.9                32.00      Sequence
DRB1_0401  250  NTAWQNGKTVTFMPK  WQNGKTVTF        0.4154        558.2                32.00      Sequence
DRB1_0401   18  EYVDVRFCDLPGIMQ  VRFCDLPGI        0.4150        560.7                32.00      Sequence
DRB1_0401  245  KYIIKNTAWQNGKTV  KYIIKNTAW        0.4137        568.8                32.00      Sequence
DRB1_0401  290  DETGYAGLSDTARHY  GYAGLSDTA        0.4123        577.4                32.00      Sequence
DRB1_0401  286  PLMYDETGYAGLSDT  LMYDETGYA        0.4097        594.2                32.00      Sequence
DRB1_0401  371  SSGNPYLAFSAMLMA  YLAFSAMLM        0.4073        609.8                32.00      Sequence
DRB1_0401   86  KTLNINFFVHDPFTL  FFVHDPFTL        0.4068        613.1                32.00      Sequence
DRB1_0401  327  KRLVPGYEAPINLVY  KRLVPGYEA        0.4066        614.1                32.00      Sequence
DRB1_0401   47  DDGLAFDGSSIRGFQ  LAFDGSSIR        0.4061        617.8                32.00      Sequence
DRB1_0401   52  FDGSSIRGFQSIHES  IRGFQSIHE        0.4052        623.9                32.00      Sequence
DRB1_0401  151  FYEVDAISGWWNTGA  FYEVDAISG        0.4050        625.1                32.00      Sequence
DRB1_0401  330  VPGYEAPINLVYSQR  YEAPINLVY        0.4024        643.0                32.00      Sequence
DRB1_0401  254  QNGKTVTFMPKPLFG  KTVTFMPKP        0.4006        655.7                32.00      Sequence
DRB1_0401   50  LAFDGSSIRGFQSIH  LAFDGSSIR        0.3991        666.2                32.00      Sequence
DRB1_0401  154  VDAISGWWNTGAATE  ISGWWNTGA        0.3977        676.7                32.00      Sequence
DRB1_0401  157  ISGWWNTGAATEADG  ISGWWNTGA        0.3963        686.4                32.00      Sequence
DRB1_0401  378  AFSAMLMAGLDGIKN  MAGLDGIKN        0.3954        693.4                32.00      Sequence
DRB1_0401  379  FSAMLMAGLDGIKNK  MAGLDGIKN        0.3945        700.1                32.00      Sequence
DRB1_0401  299  DTARHYIGGLLHHAP  RHYIGGLLH        0.3942        702.5                32.00      Sequence
DRB1_0401  285  APLMYDETGYAGLSD  LMYDETGYA        0.3925        715.8                32.00      Sequence
DRB1_0401  111  ARKAENYLISTGIAD  RKAENYLIS        0.3880        750.8                32.00      Sequence
DRB1_0401  192  DQYVDLRDKMLTNLI  DLRDKMLTN        0.3874        756.1                32.00      Sequence
DRB1_0401    6  DDVFKLAKDEKVEYV  FKLAKDEKV        0.3852        774.5                50.00      Sequence
DRB1_0401  329  LVPGYEAPINLVYSQ  PGYEAPINL        0.3810        810.3                50.00      Sequence
DRB1_0401  447  IETWISFKRENEIEP  IETWISFKR        0.3805        814.5                50.00      Sequence
DRB1_0401  271  GSGMHCHQSLWKDGA  MHCHQSLWK        0.3801        818.6                50.00      Sequence
DRB1_0401  328  RLVPGYEAPINLVYS  PGYEAPINL        0.3785        832.4                50.00      Sequence
DRB1_0401    7  DVFKLAKDEKVEYVD  FKLAKDEKV        0.3779        837.7                50.00      Sequence
DRB1_0401  284  GAPLMYDETGYAGLS  LMYDETGYA        0.3778        839.3                50.00      Sequence
DRB1_0401  443  TNDLIETWISFKREN  IETWISFKR        0.3775        841.9                50.00      Sequence
DRB1_0401  326  YKRLVPGYEAPINLV  KRLVPGYEA        0.3768        847.9                50.00      Sequence
DRB1_0401  287  LMYDETGYAGLSDTA  LMYDETGYA        0.3768        848.2                50.00      Sequence
DRB1_0401  249  KNTAWQNGKTVTFMP  WQNGKTVTF        0.3734        879.3                50.00      Sequence
DRB1_0401  137  IFDSVSFDSRANGSF  IFDSVSFDS        0.3731        882.5                50.00      Sequence
DRB1_0401  145  SRANGSFYEVDAISG  SFYEVDAIS        0.3717        896.2                50.00      Sequence
DRB1_0401  340  VYSQRNRSACVRIPI  VYSQRNRSA        0.3714        898.9                50.00      Sequence
DRB1_0401  293  GYAGLSDTARHYIGG  YAGLSDTAR        0.3694        919.0                50.00      Sequence
DRB1_0401    8  VFKLAKDEKVEYVDV  FKLAKDEKV        0.3684        928.6                50.00      Sequence
DRB1_0401   23  RFCDLPGIMQHFTIP  RFCDLPGIM        0.3683        929.5                50.00      Sequence
DRB1_0401  257  KTVTFMPKPLFGDNG  VTFMPKPLF        0.3671        941.4                50.00      Sequence
DRB1_0401   51  AFDGSSIRGFQSIHE  IRGFQSIHE        0.3666        946.7                50.00      Sequence
DRB1_0401  288  MYDETGYAGLSDTAR  YAGLSDTAR        0.3648        965.9                50.00      Sequence
DRB1_0401  383  LMAGLDGIKNKIEPQ  MAGLDGIKN        0.3639        975.2                50.00      Sequence
DRB1_0401  289  YDETGYAGLSDTARH  GYAGLSDTA        0.3638        975.8                50.00      Sequence
DRB1_0401   61  QSIHESDMLLLPDPE  IHESDMLLL        0.3632        982.3                50.00      Sequence
DRB1_0401  222  GGQAEINYQFNSLLH  EINYQFNSL        0.3632        982.5                50.00      Sequence
DRB1_0401  343  QRNRSACVRIPITGS  SACVRIPIT        0.3617        998.8                50.00      Sequence
DRB1_0401  441  VFTNDLIETWISFKR  VFTNDLIET        0.3599       1018.5                50.00      Sequence
DRB1_0401  344  RNRSACVRIPITGSN  SACVRIPIT        0.3599       1018.5                50.00      Sequence
DRB1_0401   44  SVFDDGLAFDGSSIR  SVFDDGLAF        0.3598       1019.6                50.00      Sequence
DRB1_0401    5  PDDVFKLAKDEKVEY  FKLAKDEKV        0.3590       1027.7                50.00      Sequence
DRB1_0401  153  EVDAISGWWNTGAAT  ISGWWNTGA        0.3583       1035.6                50.00      Sequence
DRB1_0401   46  FDDGLAFDGSSIRGF  LAFDGSSIR        0.3579       1040.2                50.00      Sequence
DRB1_0401  450  WISFKRENEIEPVNI  FKRENEIEP        0.3549       1074.9                50.00      Sequence
DRB1_0401  191  NDQYVDLRDKMLTNL  QYVDLRDKM        0.3547       1076.7                50.00      Sequence
DRB1_0401  442  FTNDLIETWISFKRE  DLIETWISF        0.3542       1083.3                50.00      Sequence
DRB1_0401  345  NRSACVRIPITGSNP  SACVRIPIT        0.3537       1088.3                50.00      Sequence
DRB1_0401  446  LIETWISFKRENEIE  IETWISFKR        0.3535       1090.8                50.00      Sequence
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DRB1_0401  237  AADDMQLYKYIIKNT  MQLYKYIIK        0.3517       1113.0                50.00      Sequence
DRB1_0401  180  RHKGGYFPVAPNDQY  KGGYFPVAP        0.3486       1151.0                50.00      Sequence
DRB1_0401  346  RSACVRIPITGSNPK  SACVRIPIT        0.3483       1154.3                50.00      Sequence
DRB1_0401  451  ISFKRENEIEPVNIR  FKRENEIEP        0.3461       1182.1                50.00      Sequence
DRB1_0401  325  SYKRLVPGYEAPINL  KRLVPGYEA        0.3450       1196.5                50.00      Sequence
DRB1_0401  190  PNDQYVDLRDKMLTN  QYVDLRDKM        0.3444       1203.7                50.00      Sequence
DRB1_0401  248  IKNTAWQNGKTVTFM  WQNGKTVTF        0.3406       1254.5                50.00      Sequence
DRB1_0401  129  FGAEAEFYIFDSVSF  FYIFDSVSF        0.3381       1288.6                50.00      Sequence
DRB1_0401  283  DGAPLMYDETGYAGL  LMYDETGYA        0.3379       1292.0                50.00      Sequence
DRB1_0401  278  QSLWKDGAPLMYDET  WKDGAPLMY        0.3374       1299.1                50.00      Sequence
DRB1_0401  452  SFKRENEIEPVNIRP  FKRENEIEP        0.3372       1301.0                50.00      Sequence
DRB1_0401  298  SDTARHYIGGLLHHA  RHYIGGLLH        0.3335       1354.9                50.00      Sequence
DRB1_0401   25  CDLPGIMQHFTIPAS  IMQHFTIPA        0.3321       1376.1                50.00      Sequence
DRB1_0401  270  NGSGMHCHQSLWKDG  MHCHQSLWK        0.3307       1397.1                50.00      Sequence
DRB1_0401   43  KSVFDDGLAFDGSSI  SVFDDGLAF        0.3297       1412.2                50.00      Sequence
DRB1_0401  179  VRHKGGYFPVAPNDQ  RHKGGYFPV        0.3292       1419.2                50.00      Sequence
DRB1_0401  342  SQRNRSACVRIPITG  SACVRIPIT        0.3283       1433.1                50.00      Sequence
DRB1_0401  277  HQSLWKDGAPLMYDE  QSLWKDGAP        0.3278       1441.0                50.00      Sequence
DRB1_0401   24  FCDLPGIMQHFTIPA  FCDLPGIMQ        0.3278       1441.2                50.00      Sequence
DRB1_0401  152  YEVDAISGWWNTGAA  ISGWWNTGA        0.3273       1448.9                50.00      Sequence
DRB1_0401   17  VEYVDVRFCDLPGIM  VRFCDLPGI        0.3255       1477.4                50.00      Sequence
DRB1_0401  324  NSYKRLVPGYEAPIN  KRLVPGYEA        0.3243       1495.8                50.00      Sequence
DRB1_0401  110  IARKAENYLISTGIA  RKAENYLIS        0.3230       1518.3                50.00      Sequence
DRB1_0401   58  RGFQSIHESDMLLLP  RGFQSIHES        0.3224       1528.1                50.00      Sequence
DRB1_0401   83  RAAKTLNINFFVHDP  KTLNINFFV        0.3219       1535.2                50.00      Sequence
DRB1_0401  317  AFTNPTVNSYKRLVP  AFTNPTVNS        0.3210       1550.3                50.00      Sequence
DRB1_0401  453  FKRENEIEPVNIRPH  FKRENEIEP        0.3204       1561.8                50.00      Sequence
DRB1_0401  449  TWISFKRENEIEPVN  FKRENEIEP        0.3196       1574.2                50.00      Sequence
DRB1_0401  178  KVRHKGGYFPVAPND  RHKGGYFPV        0.3193       1579.6                50.00      Sequence
DRB1_0401  247  IIKNTAWQNGKTVTF  IIKNTAWQN        0.3191       1583.6                50.00      Sequence
DRB1_0401   69  LLLPDPETARIDPFR  LLLPDPETA        0.3176       1608.4                50.00      Sequence
DRB1_0401  433  HEYLTEGGVFTNDLI  YLTEGGVFT        0.3148       1658.6                50.00      Sequence
DRB1_0401  435  YLTEGGVFTNDLIET  YLTEGGVFT        0.3139       1674.0                50.00      Sequence
DRB1_0401  370  DSSGNPYLAFSAMLM  YLAFSAMLM        0.3139       1674.9                50.00      Sequence
DRB1_0401   33  HFTIPASAFDKSVFD  HFTIPASAF        0.3124       1702.9                50.00      Sequence
DRB1_0401  347  SACVRIPITGSNPKA  SACVRIPIT        0.3122       1705.4                50.00      Sequence
DRB1_0401  182  KGGYFPVAPNDQYVD  KGGYFPVAP        0.3119       1710.9                50.00      Sequence
DRB1_0401   60  FQSIHESDMLLLPDP  IHESDMLLL        0.3117       1715.8                50.00      Sequence
DRB1_0401  384  MAGLDGIKNKIEPQA  MAGLDGIKN        0.3091       1763.6                50.00      Sequence
DRB1_0401    4  TPDDVFKLAKDEKVE  FKLAKDEKV        0.3088       1770.5                50.00      Sequence
DRB1_0401  233  SLLHAADDMQLYKYI  LHAADDMQL        0.3083       1779.1                50.00      Sequence
DRB1_0401  177  YKVRHKGGYFPVAPN  RHKGGYFPV        0.3065       1814.8                50.00      Sequence
DRB1_0401  246  YIIKNTAWQNGKTVT  YIIKNTAWQ        0.3058       1827.6                50.00      Sequence
DRB1_0401  181  HKGGYFPVAPNDQYV  GGYFPVAPN        0.3055       1833.6                50.00      Sequence
DRB1_0401   45  VFDDGLAFDGSSIRG  LAFDGSSIR        0.3053       1838.9                50.00      Sequence
DRB1_0401   16  KVEYVDVRFCDLPGI  KVEYVDVRF        0.3030       1883.7                50.00      Sequence
DRB1_0401  201  MLTNLINSGFILEKG  MLTNLINSG        0.3025       1895.5                50.00      Sequence
DRB1_0401  281  WKDGAPLMYDETGYA  WKDGAPLMY        0.3020       1904.5                50.00      Sequence
DRB1_0401  232  NSLLHAADDMQLYKY  LHAADDMQL        0.3007       1931.3                50.00      Sequence
DRB1_0401   85  AKTLNINFFVHDPFT  KTLNINFFV        0.3007       1932.3                50.00      Sequence
DRB1_0401  439  GGVFTNDLIETWISF  VFTNDLIET        0.3006       1934.5                50.00      Sequence
DRB1_0401  401  DKDLYELPPEEAASI  LYELPPEEA        0.3005       1936.0                50.00      Sequence
DRB1_0401  432  DHEYLTEGGVFTNDL  YLTEGGVFT        0.2999       1948.1                50.00      Sequence
DRB1_0401  231  FNSLLHAADDMQLYK  LLHAADDMQ        0.2983       1983.2                50.00      Sequence
DRB1_0401  402  KDLYELPPEEAASIP  LYELPPEEA        0.2983       1983.6                50.00      Sequence
DRB1_0401  341  YSQRNRSACVRIPIT  SACVRIPIT        0.2964       2023.3                50.00      Sequence
DRB1_0401   42  DKSVFDDGLAFDGSS  SVFDDGLAF        0.2947       2062.4                50.00      Sequence
DRB1_0401  264  KPLFGDNGSGMHCHQ  LFGDNGSGM        0.2941       2073.9                50.00      Sequence
DRB1_0401  434  EYLTEGGVFTNDLIE  YLTEGGVFT        0.2933       2092.8                50.00      Sequence
DRB1_0401  282  KDGAPLMYDETGYAG  LMYDETGYA        0.2925       2110.3                50.00      Sequence
DRB1_0401  276  CHQSLWKDGAPLMYD  QSLWKDGAP        0.2925       2111.8                50.00      Sequence
DRB1_0401  174  NRGYKVRHKGGYFPV  NRGYKVRHK        0.2924       2114.2                50.00      Sequence
DRB1_0401  230  QFNSLLHAADDMQLY  QFNSLLHAA        0.2908       2151.3                50.00      Sequence
DRB1_0401   84  AAKTLNINFFVHDPF  KTLNINFFV        0.2903       2162.0                50.00      Sequence
DRB1_0401  448  ETWISFKRENEIEPV  FKRENEIEP        0.2896       2179.3                50.00      Sequence
DRB1_0401  323  VNSYKRLVPGYEAPI  KRLVPGYEA        0.2886       2201.6                50.00      Sequence
DRB1_0401   97  PFTLEPYSRDPRNIA  PFTLEPYSR        0.2876       2225.7                50.00      Sequence
DRB1_0401  263  PKPLFGDNGSGMHCH  LFGDNGSGM        0.2875       2228.0                50.00      Sequence
DRB1_0401  275  HCHQSLWKDGAPLMY  QSLWKDGAP        0.2875       2228.4                50.00      Sequence
DRB1_0401  269  DNGSGMHCHQSLWKD  MHCHQSLWK        0.2854       2278.5                50.00      Sequence
DRB1_0401  258  TVTFMPKPLFGDNGS  VTFMPKPLF        0.2851       2288.3                50.00      Sequence
DRB1_0401  440  GVFTNDLIETWISFK  VFTNDLIET        0.2847       2295.9                50.00      Sequence
DRB1_0401  109  NIARKAENYLISTGI  RKAENYLIS        0.2836       2324.5                50.00      Sequence
DRB1_0401  265  PLFGDNGSGMHCHQS  LFGDNGSGM        0.2831       2337.6                50.00      Sequence
DRB1_0401  438  EGGVFTNDLIETWIS  VFTNDLIET        0.2818       2370.4                50.00      Sequence
DRB1_0401  294  YAGLSDTARHYIGGL  YAGLSDTAR        0.2809       2393.0                50.00      Sequence
DRB1_0401  189  APNDQYVDLRDKMLT  QYVDLRDKM        0.2784       2460.3                50.00      Sequence
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DRB1_0401  297  LSDTARHYIGGLLHH  RHYIGGLLH         0.2779       2472.9                50.00      Sequence
DRB1_0401  221  SGGQAEINYQFNSLL  EINYQFNSL         0.2777       2477.0                50.00      Sequence
DRB1_0401  138  FDSVSFDSRANGSFY  SVSFDSRAN         0.2773       2487.6                50.00      Sequence
DRB1_0401  234  LLHAADDMQLYKYII  LHAADDMQL         0.2760       2523.0                50.00      Sequence
DRB1_0401   75  ETARIDPFRAAKTLN  TARIDPFRA         0.2759       2526.9                50.00      Sequence
DRB1_0401  357  SNPKAKRLEFRSPDS  RLEFRSPDS         0.2754       2541.3                50.00      Sequence
DRB1_0401   96  DPFTLEPYSRDPRNI  PFTLEPYSR         0.2743       2571.5                50.00      Sequence
DRB1_0401  280  LWKDGAPLMYDETGY  WKDGAPLMY         0.2742       2573.7                50.00      Sequence
DRB1_0401    3  KTPDDVFKLAKDEKV  FKLAKDEKV         0.2730       2608.4                50.00      Sequence
DRB1_0401   41  FDKSVFDDGLAFDGS  SVFDDGLAF         0.2718       2639.8                50.00      Sequence
DRB1_0401  140  SVSFDSRANGSFYEV  SVSFDSRAN         0.2717       2644.3                50.00      Sequence
DRB1_0401  102  PYSRDPRNIARKAEN  YSRDPRNIA         0.2716       2646.1                50.00      Sequence
DRB1_0401  173  PNRGYKVRHKGGYFP  NRGYKVRHK         0.2713       2656.3                50.00      Sequence
DRB1_0401  236  HAADDMQLYKYIIKN  MQLYKYIIK         0.2691       2719.5                50.00      Sequence
DRB1_0401  139  DSVSFDSRANGSFYE  SVSFDSRAN         0.2678       2757.9                50.00      Sequence
DRB1_0401    9  FKLAKDEKVEYVDVR  FKLAKDEKV         0.2670       2781.3                50.00      Sequence
DRB1_0401  158  SGWWNTGAATEADGS  SGWWNTGAA         0.2668       2788.3                50.00      Sequence
DRB1_0401  235  LHAADDMQLYKYIIK  LHAADDMQL         0.2645       2857.0                50.00      Sequence
DRB1_0401  128  YFGAEAEFYIFDSVS  YFGAEAEFY         0.2641       2869.2                50.00      Sequence
DRB1_0401  101  EPYSRDPRNIARKAE  PYSRDPRNI         0.2632       2899.9                50.00      Sequence
DRB1_0401   93  FVHDPFTLEPYSRDP  PFTLEPYSR         0.2609       2970.7                50.00      Sequence
DRB1_0401  176  GYKVRHKGGYFPVAP  RHKGGYFPV         0.2602       2995.0                50.00      Sequence
DRB1_0401  100  LEPYSRDPRNIARKA  YSRDPRNIA         0.2589       3036.6                50.00      Sequence
DRB1_0401   59  GFQSIHESDMLLLPD  SIHESDMLL         0.2586       3047.5                50.00      Sequence
DRB1_0401  172  SPNRGYKVRHKGGYF  NRGYKVRHK         0.2585       3050.0                50.00      Sequence
DRB1_0401  400  VDKDLYELPPEEAAS  LYELPPEEA         0.2580       3066.9                50.00      Sequence
DRB1_0401  365  EFRSPDSSGNPYLAF  EFRSPDSSG         0.2575       3082.9                50.00      Sequence
DRB1_0401  126  TAYFGAEAEFYIFDS  YFGAEAEFY         0.2573       3091.1                50.00      Sequence
DRB1_0401  125  DTAYFGAEAEFYIFD  YFGAEAEFY         0.2565       3118.2                50.00      Sequence
DRB1_0401  431  ADHEYLTEGGVFTND  YLTEGGVFT         0.2555       3149.5                50.00      Sequence
DRB1_0401   95  HDPFTLEPYSRDPRN  PFTLEPYSR         0.2554       3154.4                50.00      Sequence
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DRB1_0401   94  VHDPFTLEPYSRDPR  PFTLEPYSR         0.2519       3275.5                50.00      Sequence
DRB1_0401  144  DSRANGSFYEVDAIS  SFYEVDAIS         0.2514       3294.1                50.00      Sequence
DRB1_0401  171  GSPNRGYKVRHKGGY  NRGYKVRHK         0.2506       3322.4                50.00      Sequence
DRB1_0401  437  TEGGVFTNDLIETWI  VFTNDLIET         0.2504       3328.3                50.00      Sequence
DRB1_0401  127  AYFGAEAEFYIFDSV  YFGAEAEFY         0.2480       3416.8                50.00      Sequence
DRB1_0401  208  SGFILEKGHHEVGSG  FILEKGHHE         0.2470       3452.6                50.00      Sequence
DRB1_0401  262  MPKPLFGDNGSGMHC  LFGDNGSGM         0.2450       3528.4                50.00      Sequence
DRB1_0401  322  TVNSYKRLVPGYEAP  KRLVPGYEA         0.2410       3684.3                50.00      Sequence
DRB1_0401  207  NSGFILEKGHHEVGS  FILEKGHHE         0.2405       3706.2                50.00      Sequence
DRB1_0401  436  LTEGGVFTNDLIETW  VFTNDLIET         0.2343       3960.7                50.00      Sequence
DRB1_0401  183  GGYFPVAPNDQYVDL  GGYFPVAPN         0.2339       3978.8                50.00      Sequence
DRB1_0401  188  VAPNDQYVDLRDKML  QYVDLRDKM         0.2331       4016.4                50.00      Sequence
DRB1_0401  220  GSGGQAEINYQFNSL  EINYQFNSL         0.2327       4031.9                50.00      Sequence
DRB1_0401  403  DLYELPPEEAASIPQ  LYELPPEEA         0.2324       4044.7                50.00      Sequence
DRB1_0401  266  LFGDNGSGMHCHQSL  LFGDNGSGM         0.2318       4071.0                50.00      Sequence
DRB1_0401  268  GDNGSGMHCHQSLWK  MHCHQSLWK         0.2312       4096.6                50.00      Sequence
DRB1_0401  124  ADTAYFGAEAEFYIF  YFGAEAEFY         0.2288       4207.8                50.00      Sequence
DRB1_0401  108  RNIARKAENYLISTG  RKAENYLIS         0.2275       4263.4                50.00      Sequence
DRB1_0401  209  GFILEKGHHEVGSGG  FILEKGHHE         0.2268       4299.1                50.00      Sequence
DRB1_0401  204  NLINSGFILEKGHHE  NLINSGFIL         0.2267       4301.9                50.00      Sequence
DRB1_0401  350  VRIPITGSNPKAKRL  VRIPITGSN         0.2258       4344.6                50.00      Sequence
DRB1_0401   99  TLEPYSRDPRNIARK  YSRDPRNIA         0.2254       4364.2                50.00      Sequence
DRB1_0401  119  ISTGIADTAYFGAEA  ISTGIADTA         0.2230       4476.8                50.00      Sequence
DRB1_0401  296  GLSDTARHYIGGLLH  RHYIGGLLH         0.2228       4489.0                50.00      Sequence
DRB1_0401  206  INSGFILEKGHHEVG  GFILEKGHH         0.2211       4571.8                50.00      Sequence
DRB1_0401  399  PVDKDLYELPPEEAA  LYELPPEEA         0.2208       4588.2                50.00      Sequence
DRB1_0401   39  SAFDKSVFDDGLAFD  SVFDDGLAF         0.2207       4592.6                50.00      Sequence
DRB1_0401  348  ACVRIPITGSNPKAK  VRIPITGSN         0.2200       4623.7                50.00      Sequence
DRB1_0401  118  LISTGIADTAYFGAE  ISTGIADTA         0.2199       4628.7                50.00      Sequence
DRB1_0401   40  AFDKSVFDDGLAFDG  SVFDDGLAF         0.2195       4653.2                50.00      Sequence
DRB1_0401   74  PETARIDPFRAAKTL  TARIDPFRA         0.2192       4668.5                50.00      Sequence
DRB1_0401  103  YSRDPRNIARKAENY  YSRDPRNIA         0.2186       4696.6                50.00      Sequence
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DRB1_0401  430  EADHEYLTEGGVFTN  YLTEGGVFT         0.2154       4860.2                50.00      Sequence
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DRB1_0401   70  LLPDPETARIDPFRA  LLPDPETAR         0.2139       4940.2                50.00      Sequence
DRB1_0401  175  RGYKVRHKGGYFPVA  VRHKGGYFP         0.2133       4975.6                50.00      Sequence
DRB1_0401  455  RENEIEPVNIRPHPY  NEIEPVNIR         0.2129       4997.5                50.00      Sequence
DRB1_0401  349  CVRIPITGSNPKAKR  VRIPITGSN         0.2127       5006.6                50.00      Sequence
DRB1_0401   38  ASAFDKSVFDDGLAF  SAFDKSVFD         0.2104       5129.6                50.00      Sequence
DRB1_0401  120  STGIADTAYFGAEAE  TGIADTAYF         0.2103       5140.4                50.00      Sequence
DRB1_0401  123  IADTAYFGAEAEFYI  TAYFGAEAE         0.2098       5167.1                50.00      Sequence
DRB1_0401   98  FTLEPYSRDPRNIAR  YSRDPRNIA         0.2096       5177.9                50.00      Sequence
DRB1_0401  261  FMPKPLFGDNGSGMH  LFGDNGSGM         0.2089       5217.4                50.00      Sequence
DRB1_0401  420  TQLSDVIDRLEADHE  TQLSDVIDR         0.2077       5284.0                50.00      Sequence
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    DRB1_0401  170  DGSPNRGYKVRHKGG  NRGYKVRHK        0.2071      5321.1            50.00     Sequence
    DRB1_0401  454  KRENEIEPVNIRPHP  NEIEPVNIR        0.2060      5384.9            50.00     Sequence
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    DRB1_0401  457  NEIEPVNIRPHPYEF  NEIEPVNIR        0.2034      5537.4            50.00     Sequence
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    DRB1_0401  122  GIADTAYFGAEAEFY  TAYFGAEAE        0.1845      6793.3            50.00     Sequence
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    DRB1_0401  106  DPRNIARKAENYLIS  RKAENYLIS        0.1809      7059.6            50.00     Sequence
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    DRB1_0401  351  RIPITGSNPKAKRLE  PITGSNPKA        0.1802      7115.1            50.00     Sequence
    DRB1_0401  159  GWWNTGAATEADGSP  WNTGAATEA        0.1774      7332.2            50.00     Sequence
    DRB1_0401  415  IPQTPTQLSDVIDRL  IPQTPTQLS        0.1769      7373.1            50.00     Sequence
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    DRB1_0401  219  VGSGGQAEINYQFNS  SGGQAEINY        0.1757      7468.4            50.00     Sequence
    DRB1_0401  417  QTPTQLSDVIDRLEA  TQLSDVIDR        0.1753      7501.0            50.00     Sequence
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    DRB1_0401  366  FRSPDSSGNPYLAFS  FRSPDSSGN        0.1728      7706.6            50.00     Sequence
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    DRB1_0401  214  KGHHEVGSGGQAEIN  KGHHEVGSG        0.1649      8397.6            50.00     Sequence
    DRB1_0401  398  APVDKDLYELPPEEA  LYELPPEEA        0.1636      8516.0            50.00     Sequence
    DRB1_0401  218  EVGSGGQAEINYQFN  SGGQAEINY        0.1632      8553.1            50.00     Sequence
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    DRB1_0401  421  QLSDVIDRLEADHEY  QLSDVIDRL        0.1507      9791.7            50.00     Sequence
    DRB1_0401  212  LEKGHHEVGSGGQAE  KGHHEVGSG        0.1504      9827.0            50.00     Sequence
    DRB1_0401  105  RDPRNIARKAENYLI  RNIARKAEN        0.1493      9942.9            50.00     Sequence
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    DRB1_0401  161  WNTGAATEADGSPNR  WNTGAATEA        0.1478     10103.7            50.00     Sequence
    DRB1_0401  217  HEVGSGGQAEINYQF  GSGGQAEIN        0.1476     10121.2            50.00     Sequence
    DRB1_0401  424  DVIDRLEADHEYLTE  DVIDRLEAD        0.1470     10188.4            50.00     Sequence
    DRB1_0401  416  PQTPTQLSDVIDRLE  TQLSDVIDR        0.1467     10220.2            50.00     Sequence
    DRB1_0401  185  YFPVAPNDQYVDLRD  YFPVAPNDQ        0.1465     10246.7            50.00     Sequence
    DRB1_0401   12  AKDEKVEYVDVRFCD  KVEYVDVRF        0.1463     10267.6            50.00     Sequence
    DRB1_0401  458  EIEPVNIRPHPYEFA  EIEPVNIRP        0.1460     10298.7            50.00     Sequence
    DRB1_0401  413  ASIPQTPTQLSDVID  IPQTPTQLS        0.1440     10528.5            50.00     Sequence
    DRB1_0401  104  SRDPRNIARKAENYL  RNIARKAEN        0.1431     10627.1            50.00     Sequence
    DRB1_0401  422  LSDVIDRLEADHEYL  DVIDRLEAD        0.1418     10782.6            50.00     Sequence
    DRB1_0401   10  KLAKDEKVEYVDVRF  LAKDEKVEY        0.1406     10918.6            50.00     Sequence
    DRB1_0401  160  WWNTGAATEADGSPN  WNTGAATEA        0.1402     10964.3            50.00     Sequence
    DRB1_0401  405  YELPPEEAASIPQTP  YELPPEEAA        0.1352     11577.3            50.00     Sequence
    DRB1_0401  411  EAASIPQTPTQLSDV  EAASIPQTP        0.1348     11634.0            50.00     Sequence
    DRB1_0401  211  ILEKGHHEVGSGGQA  KGHHEVGSG        0.1347     11644.2            50.00     Sequence
    DRB1_0401  143  FDSRANGSFYEVDAI  GSFYEVDAI        0.1339     11737.4            50.00     Sequence
    DRB1_0401  409  PEEAASIPQTPTQLS  EEAASIPQT        0.1336     11777.5            50.00     Sequence
    DRB1_0401  369  PDSSGNPYLAFSAML  PYLAFSAML        0.1323     11943.0            50.00     Sequence
    DRB1_0401  410  EEAASIPQTPTQLSD  EEAASIPQT        0.1312     12093.6            50.00     Sequence
    DRB1_0401  216  HHEVGSGGQAEINYQ  GSGGQAEIN        0.1311     12108.6            50.00     Sequence
    DRB1_0401  267  FGDNGSGMHCHQSLW  FGDNGSGMH        0.1300     12255.5            50.00     Sequence
    DRB1_0401  428  RLEADHEYLTEGGVF  HEYLTEGGV        0.1288     12409.8            50.00     Sequence
    DRB1_0401  353  PITGSNPKAKRLEFR  PITGSNPKA        0.1269     12669.4            50.00     Sequence
    DRB1_0401  427  DRLEADHEYLTEGGV  LEADHEYLT        0.1260     12787.3            50.00     Sequence
    DRB1_0401    2  EKTPDDVFKLAKDEK  VFKLAKDEK        0.1259     12810.1            50.00     Sequence
    DRB1_0401   71  LPDPETARIDPFRAA  TARIDPFRA        0.1255     12853.8            50.00     Sequence
    DRB1_0401  168  EADGSPNRGYKVRHK  NRGYKVRHK        0.1248     12952.1            50.00     Sequence
    DRB1_0401  215  GHHEVGSGGQAEINY  GHHEVGSGG        0.1248     12964.5            50.00     Sequence
    DRB1_0401  187  PVAPNDQYVDLRDKM  QYVDLRDKM        0.1239     13084.4            50.00     Sequence
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   DRB1_0401  142  SFDSRANGSFYEVDA  SFDSRANGS        0.1196      13703.8                50.00     Sequence
   DRB1_0401  386  GLDGIKNKIEPQAPV  LDGIKNKIE        0.1196      13707.1                50.00     Sequence
   DRB1_0401  164  GAATEADGSPNRGYK  TEADGSPNR        0.1159      14266.8                50.00     Sequence
   DRB1_0401  387  LDGIKNKIEPQAPVD  LDGIKNKIE        0.1140      14565.6                50.00     Sequence
   DRB1_0401  462  VNIRPHPYEFALYYD  PHPYEFALY        0.1136      14629.0                50.00     Sequence
   DRB1_0401  318  FTNPTVNSYKRLVPG  FTNPTVNSY        0.1127      14768.3                50.00     Sequence
   DRB1_0401  165  AATEADGSPNRGYKV  TEADGSPNR        0.1122      14854.5                50.00     Sequence
   DRB1_0401  408  PPEEAASIPQTPTQL  EAASIPQTP        0.1109      15066.7                50.00     Sequence
   DRB1_0401  385  AGLDGIKNKIEPQAP  LDGIKNKIE        0.1104      15149.3                50.00     Sequence
   DRB1_0401  407  LPPEEAASIPQTPTQ  EEAASIPQT        0.1101      15200.2                50.00     Sequence
   DRB1_0401  320  NPTVNSYKRLVPGYE  VNSYKRLVP        0.1098      15240.3                50.00     Sequence
   DRB1_0401  186  FPVAPNDQYVDLRDK  FPVAPNDQY        0.1094      15313.4                50.00     Sequence
   DRB1_0401  356  GSNPKAKRLEFRSPD  KAKRLEFRS        0.1078      15572.9                50.00     Sequence
   DRB1_0401  368  SPDSSGNPYLAFSAM  SSGNPYLAF        0.1042      16187.1                50.00     Sequence
   DRB1_0401  163  TGAATEADGSPNRGY  GAATEADGS        0.1041      16202.3                50.00     Sequence
   DRB1_0401  319  TNPTVNSYKRLVPGY  NSYKRLVPG        0.1041      16202.5                50.00     Sequence
   DRB1_0401  388  DGIKNKIEPQAPVDK  IKNKIEPQA        0.1031      16392.0                50.00     Sequence
   DRB1_0401  406  ELPPEEAASIPQTPT  PEEAASIPQ        0.1016      16655.6                50.00     Sequence
   DRB1_0401  397  QAPVDKDLYELPPEE  DKDLYELPP        0.1001      16929.2                50.00     Sequence
   DRB1_0401  426  IDRLEADHEYLTEGG  LEADHEYLT        0.1000      16940.9                50.00     Sequence
   DRB1_0401  425  VIDRLEADHEYLTEG  LEADHEYLT        0.0996      17026.5                50.00     Sequence
   DRB1_0401  166  ATEADGSPNRGYKVR  TEADGSPNR        0.0972      17467.9                50.00     Sequence
   DRB1_0401  162  NTGAATEADGSPNRG  GAATEADGS        0.0967      17556.5                50.00     Sequence
   DRB1_0401  295  AGLSDTARHYIGGLL  AGLSDTARH        0.0963      17638.6                50.00     Sequence
   DRB1_0401  367  RSPDSSGNPYLAFSA  RSPDSSGNP        0.0933      18214.8                50.00     Sequence
   DRB1_0401  167  TEADGSPNRGYKVRH  TEADGSPNR        0.0929      18292.6                50.00     Sequence
   DRB1_0401  461  PVNIRPHPYEFALYY  PVNIRPHPY        0.0928      18324.9                50.00     Sequence
   DRB1_0401    1  TEKTPDDVFKLAKDE  TEKTPDDVF        0.0911      18652.4                50.00     Sequence
   DRB1_0401  355  TGSNPKAKRLEFRSP  KAKRLEFRS        0.0893      19018.8                50.00     Sequence
   DRB1_0401  354  ITGSNPKAKRLEFRS  ITGSNPKAK        0.0883      19225.3                50.00     Sequence
   DRB1_0401  391  KNKIEPQAPVDKDLY  NKIEPQAPV        0.0868      19557.2                50.00     Sequence
   DRB1_0401  460  EPVNIRPHPYEFALY  PVNIRPHPY        0.0866      19588.7                50.00     Sequence
   DRB1_0401  459  IEPVNIRPHPYEFAL  IEPVNIRPH        0.0858      19765.7                50.00     Sequence
   DRB1_0401  389  GIKNKIEPQAPVDKD  NKIEPQAPV        0.0853      19874.6                50.00     Sequence
   DRB1_0401    0  VTEKTPDDVFKLAKD  TEKTPDDVF        0.0839      20162.9                50.00     Sequence
   DRB1_0401  390  IKNKIEPQAPVDKDL  NKIEPQAPV        0.0836      20240.7                50.00     Sequence
   DRB1_0401  396  PQAPVDKDLYELPPE  DKDLYELPP        0.0796      21122.0                50.00     Sequence
   DRB1_0401  392  NKIEPQAPVDKDLYE  NKIEPQAPV        0.0743      22383.6                50.00     Sequence
   DRB1_0401  393  KIEPQAPVDKDLYEL  IEPQAPVDK        0.0631      25267.3                50.00     Sequence
   DRB1_0401  394  IEPQAPVDKDLYELP  IEPQAPVDK        0.0624      25446.7                50.00     Sequence
   DRB1_0401  395  EPQAPVDKDLYELPP  QAPVDKDLY        0.0423      31642.4                50.00     Sequence
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Allele: DRB1_0401. Number of high binders 17. Number of weak binders 107. Number of peptides 464

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0404  312  APSLLAFTNPTVNSY  SLLAFTNPT        0.8493          5.1         SB     0.05     Sequence
   DRB1_0404  313  PSLLAFTNPTVNSYK  SLLAFTNPT        0.8488          5.1         SB     0.05     Sequence
   DRB1_0404  311  HAPSLLAFTNPTVNS  SLLAFTNPT        0.8409          5.6         SB     0.10     Sequence
   DRB1_0404  314  SLLAFTNPTVNSYKR  SLLAFTNPT        0.8059          8.2         SB     0.30     Sequence
   DRB1_0404  310  HHAPSLLAFTNPTVN  SLLAFTNPT        0.8050          8.2         SB     0.30     Sequence
   DRB1_0404  309  LHHAPSLLAFTNPTV  SLLAFTNPT        0.7525         14.6         SB     1.00     Sequence
   DRB1_0404  197  LRDKMLTNLINSGFI  MLTNLINSG        0.7448         15.8         SB     2.00     Sequence
   DRB1_0404  198  RDKMLTNLINSGFIL  MLTNLINSG        0.7446         15.9         SB     2.00     Sequence
   DRB1_0404  196  DLRDKMLTNLINSGF  DKMLTNLIN        0.7193         20.8         SB     2.00     Sequence
   DRB1_0404  199  DKMLTNLINSGFILE  MLTNLINSG        0.7168         21.4         SB     2.00     Sequence
   DRB1_0404  226  EINYQFNSLLHAADD  EINYQFNSL        0.7160         21.6         SB     2.00     Sequence
   DRB1_0404  225  AEINYQFNSLLHAAD  EINYQFNSL        0.7050         24.3         SB     4.00     Sequence
   DRB1_0404  195  VDLRDKMLTNLINSG  DKMLTNLIN        0.6834         30.7         SB     4.00     Sequence
   DRB1_0404  224  QAEINYQFNSLLHAA  EINYQFNSL        0.6804         31.8         SB     4.00     Sequence
   DRB1_0404  308  LLHHAPSLLAFTNPT  SLLAFTNPT        0.6734         34.2         SB     4.00     Sequence
   DRB1_0404  200  KMLTNLINSGFILEK  MLTNLINSG        0.6709         35.2         SB     4.00     Sequence
   DRB1_0404  223  GQAEINYQFNSLLHA  EINYQFNSL        0.6441         47.0         SB     8.00     Sequence
   DRB1_0404   54  GSSIRGFQSIHESDM  SIRGFQSIH        0.6423         48.0         SB     8.00     Sequence
   DRB1_0404   53  DGSSIRGFQSIHESD  SIRGFQSIH        0.6318         53.7         WB     8.00     Sequence
   DRB1_0404   55  SSIRGFQSIHESDML  SIRGFQSIH        0.6315         53.9         WB     8.00     Sequence
   DRB1_0404  154  VDAISGWWNTGAATE  AISGWWNTG        0.6052         71.6         WB    16.00     Sequence
   DRB1_0404  194  YVDLRDKMLTNLINS  LRDKMLTNL        0.6051         71.7         WB    16.00     Sequence
   DRB1_0404  155  DAISGWWNTGAATEA  AISGWWNTG        0.5995         76.2         WB    16.00     Sequence
   DRB1_0404  153  EVDAISGWWNTGAAT  AISGWWNTG        0.5972         78.1         WB    16.00     Sequence
   DRB1_0404   66  SDMLLLPDPETARID  DMLLLPDPE        0.5941         80.8         WB    16.00     Sequence
   DRB1_0404   28  PGIMQHFTIPASAFD  IMQHFTIPA        0.5877         86.6         WB    16.00     Sequence
   DRB1_0404  380  SAMLMAGLDGIKNKI  MLMAGLDGI        0.5837         90.4         WB    16.00     Sequence
   DRB1_0404   67  DMLLLPDPETARIDP  MLLLPDPET        0.5832         90.9         WB    16.00     Sequence
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DRB1_0404   65  ESDMLLLPDPETARI  DMLLLPDPE        0.5826        91.5        WB    16.00      Sequence
DRB1_0404  227  INYQFNSLLHAADDM  QFNSLLHAA        0.5812        92.9        WB    16.00      Sequence
DRB1_0404   27  LPGIMQHFTIPASAF  IMQHFTIPA        0.5798        94.3        WB    16.00      Sequence
DRB1_0404   52  FDGSSIRGFQSIHES  SIRGFQSIH        0.5796        94.5        WB    16.00      Sequence
DRB1_0404  443  TNDLIETWISFKREN  DLIETWISF        0.5780        96.1        WB    16.00      Sequence
DRB1_0404  378  AFSAMLMAGLDGIKN  MLMAGLDGI        0.5780        96.2        WB    16.00      Sequence
DRB1_0404  444  NDLIETWISFKRENE  DLIETWISF        0.5768        97.4        WB    16.00      Sequence
DRB1_0404  379  FSAMLMAGLDGIKNK  MLMAGLDGI        0.5749        99.4        WB    16.00      Sequence
DRB1_0404  375  PYLAFSAMLMAGLDG  PYLAFSAML        0.5688       106.2        WB    16.00      Sequence
DRB1_0404  381  AMLMAGLDGIKNKIE  MLMAGLDGI        0.5665       108.8        WB    16.00      Sequence
DRB1_0404   29  GIMQHFTIPASAFDK  GIMQHFTIP        0.5649       110.8        WB    16.00      Sequence
DRB1_0404  374  NPYLAFSAMLMAGLD  PYLAFSAML        0.5620       114.3        WB    16.00      Sequence
DRB1_0404  241  MQLYKYIIKNTAWQN  YKYIIKNTA        0.5587       118.4        WB    16.00      Sequence
DRB1_0404  442  FTNDLIETWISFKRE  DLIETWISF        0.5539       124.8        WB    16.00      Sequence
DRB1_0404   26  DLPGIMQHFTIPASA  GIMQHFTIP        0.5512       128.5        WB    16.00      Sequence
DRB1_0404  152  YEVDAISGWWNTGAA  AISGWWNTG        0.5502       129.9        WB    16.00      Sequence
DRB1_0404   64  HESDMLLLPDPETAR  DMLLLPDPE        0.5482       132.7        WB    16.00      Sequence
DRB1_0404  240  DMQLYKYIIKNTAWQ  QLYKYIIKN        0.5460       135.9        WB    16.00      Sequence
DRB1_0404  228  NYQFNSLLHAADDMQ  QFNSLLHAA        0.5441       138.8        WB    16.00      Sequence
DRB1_0404  201  MLTNLINSGFILEKG  MLTNLINSG        0.5422       141.6        WB    16.00      Sequence
DRB1_0404  377  LAFSAMLMAGLDGIK  MLMAGLDGI        0.5397       145.5        WB    16.00      Sequence
DRB1_0404  445  DLIETWISFKRENEI  DLIETWISF        0.5367       150.3        WB    16.00      Sequence
DRB1_0404  133  AEFYIFDSVSFDSRA  FYIFDSVSF        0.5358       151.7        WB    16.00      Sequence
DRB1_0404  222  GGQAEINYQFNSLLH  EINYQFNSL        0.5355       152.3        WB    16.00      Sequence
DRB1_0404  373  GNPYLAFSAMLMAGL  PYLAFSAML        0.5331       156.3        WB    16.00      Sequence
DRB1_0404  132  EAEFYIFDSVSFDSR  FYIFDSVSF        0.5328       156.8        WB    16.00      Sequence
DRB1_0404  307  GLLHHAPSLLAFTNP  GLLHHAPSL        0.5300       161.6        WB    16.00      Sequence
DRB1_0404  382  MLMAGLDGIKNKIEP  MLMAGLDGI        0.5260       168.7        WB    16.00      Sequence
DRB1_0404  242  QLYKYIIKNTAWQNG  YKYIIKNTA        0.5226       175.1        WB    32.00      Sequence
DRB1_0404   51  AFDGSSIRGFQSIHE  SIRGFQSIH        0.5210       178.2        WB    32.00      Sequence
DRB1_0404  239  DDMQLYKYIIKNTAW  QLYKYIIKN        0.5198       180.5        WB    32.00      Sequence
DRB1_0404  441  VFTNDLIETWISFKR  DLIETWISF        0.5177       184.7        WB    32.00      Sequence
DRB1_0404  306  GGLLHHAPSLLAFTN  GLLHHAPSL        0.5174       185.2        WB    32.00      Sequence
DRB1_0404  376  YLAFSAMLMAGLDGI  FSAMLMAGL        0.5152       189.7        WB    32.00      Sequence
DRB1_0404  131  AEAEFYIFDSVSFDS  FYIFDSVSF        0.5100       200.6        WB    32.00      Sequence
DRB1_0404  305  IGGLLHHAPSLLAFT  GLLHHAPSL        0.5094       202.0        WB    32.00      Sequence
DRB1_0404  113  KAENYLISTGIADTA  YLISTGIAD        0.5081       204.9        WB    32.00      Sequence
DRB1_0404  114  AENYLISTGIADTAY  YLISTGIAD        0.5076       206.1        WB    32.00      Sequence
DRB1_0404  115  ENYLISTGIADTAYF  YLISTGIAD        0.5068       207.8        WB    32.00      Sequence
DRB1_0404   56  SIRGFQSIHESDMLL  SIRGFQSIH        0.5067       207.9        WB    32.00      Sequence
DRB1_0404  372  SGNPYLAFSAMLMAG  PYLAFSAML        0.5003       223.0        WB    32.00      Sequence
DRB1_0404  193  QYVDLRDKMLTNLIN  LRDKMLTNL        0.4996       224.7        WB    32.00      Sequence
DRB1_0404   25  CDLPGIMQHFTIPAS  IMQHFTIPA        0.4971       230.8        WB    32.00      Sequence
DRB1_0404  229  YQFNSLLHAADDMQL  QFNSLLHAA        0.4960       233.6        WB    32.00      Sequence
DRB1_0404  134  EFYIFDSVSFDSRAN  FYIFDSVSF        0.4934       240.0        WB    32.00      Sequence
DRB1_0404  151  FYEVDAISGWWNTGA  AISGWWNTG        0.4916       244.9        WB    32.00      Sequence
DRB1_0404  112  RKAENYLISTGIADT  YLISTGIAD        0.4909       246.7        WB    32.00      Sequence
DRB1_0404  304  YIGGLLHHAPSLLAF  GLLHHAPSL        0.4880       254.5        WB    32.00      Sequence
DRB1_0404  238  ADDMQLYKYIIKNTA  MQLYKYIIK        0.4840       265.7        WB    32.00      Sequence
DRB1_0404   30  IMQHFTIPASAFDKS  IMQHFTIPA        0.4825       270.2        WB    32.00      Sequence
DRB1_0404   63  IHESDMLLLPDPETA  DMLLLPDPE        0.4806       275.8        WB    32.00      Sequence
DRB1_0404  116  NYLISTGIADTAYFG  YLISTGIAD        0.4793       279.8        WB    32.00      Sequence
DRB1_0404  156  AISGWWNTGAATEAD  AISGWWNTG        0.4770       286.8        WB    32.00      Sequence
DRB1_0404  315  LLAFTNPTVNSYKRL  LLAFTNPTV        0.4744       294.9        WB    32.00      Sequence
DRB1_0404  303  HYIGGLLHHAPSLLA  LLHHAPSLL        0.4736       297.5        WB    32.00      Sequence
DRB1_0404   80  DPFRAAKTLNINFFV  FRAAKTLNI        0.4734       298.0        WB    32.00      Sequence
DRB1_0404   81  PFRAAKTLNINFFVH  FRAAKTLNI        0.4728       300.2        WB    32.00      Sequence
DRB1_0404   68  MLLLPDPETARIDPF  MLLLPDPET        0.4718       303.3        WB    32.00      Sequence
DRB1_0404   19  YVDVRFCDLPGIMQH  RFCDLPGIM        0.4699       309.8        WB    32.00      Sequence
DRB1_0404  130  GAEAEFYIFDSVSFD  FYIFDSVSF        0.4670       319.6        WB    32.00      Sequence
DRB1_0404   50  LAFDGSSIRGFQSIH  SIRGFQSIH        0.4645       328.1        WB    32.00      Sequence
DRB1_0404   79  IDPFRAAKTLNINFF  FRAAKTLNI        0.4639       330.6        WB    32.00      Sequence
DRB1_0404  347  SACVRIPITGSNPKA  RIPITGSNP        0.4625       335.7        WB    32.00      Sequence
DRB1_0404   78  RIDPFRAAKTLNINF  FRAAKTLNI        0.4597       345.8        WB    32.00      Sequence
DRB1_0404   77  ARIDPFRAAKTLNIN  DPFRAAKTL        0.4595       346.4        WB    32.00      Sequence
DRB1_0404  440  GVFTNDLIETWISFK  DLIETWISF        0.4587       349.4        WB    32.00      Sequence
DRB1_0404  243  LYKYIIKNTAWQNGK  YKYIIKNTA        0.4583       350.9        WB    32.00      Sequence
DRB1_0404  371  SSGNPYLAFSAMLMA  PYLAFSAML        0.4536       369.5        WB    32.00      Sequence
DRB1_0404   21  DVRFCDLPGIMQHFT  RFCDLPGIM        0.4524       374.1        WB    32.00      Sequence
DRB1_0404   20  VDVRFCDLPGIMQHF  RFCDLPGIM        0.4523       374.7        WB    32.00      Sequence
DRB1_0404   24  FCDLPGIMQHFTIPA  GIMQHFTIP        0.4517       376.9        WB    32.00      Sequence
DRB1_0404  346  RSACVRIPITGSNPK  ACVRIPITG        0.4511       379.5        WB    32.00      Sequence
DRB1_0404   82  FRAAKTLNINFFVHD  FRAAKTLNI        0.4509       380.5        WB    32.00      Sequence
DRB1_0404  348  ACVRIPITGSNPKAK  RIPITGSNP        0.4483       391.4        WB    32.00      Sequence
DRB1_0404  111  ARKAENYLISTGIAD  YLISTGIAD        0.4464       399.3        WB    32.00      Sequence
DRB1_0404  257  KTVTFMPKPLFGDNG  TVTFMPKPL        0.4453       404.3        WB    32.00      Sequence
DRB1_0404  135  FYIFDSVSFDSRANG  FYIFDSVSF        0.4432       413.5        WB    32.00      Sequence
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DRB1_0404  256  GKTVTFMPKPLFGDN  TVTFMPKPL        0.4418        419.9          WB    32.00      Sequence
DRB1_0404  221  SGGQAEINYQFNSLL  EINYQFNSL        0.4415        421.1          WB    32.00      Sequence
DRB1_0404  345  NRSACVRIPITGSNP  ACVRIPITG        0.4357        448.1          WB    32.00      Sequence
DRB1_0404  258  TVTFMPKPLFGDNGS  TVTFMPKPL        0.4350        451.6          WB    32.00      Sequence
DRB1_0404   18  EYVDVRFCDLPGIMQ  RFCDLPGIM        0.4331        461.0          WB    32.00      Sequence
DRB1_0404   22  VRFCDLPGIMQHFTI  RFCDLPGIM        0.4330        461.7          WB    32.00      Sequence
DRB1_0404  117  YLISTGIADTAYFGA  YLISTGIAD        0.4326        463.7          WB    32.00      Sequence
DRB1_0404  302  RHYIGGLLHHAPSLL  HYIGGLLHH        0.4325        464.4          WB    32.00      Sequence
DRB1_0404  349  CVRIPITGSNPKAKR  RIPITGSNP        0.4313        470.2          WB    32.00      Sequence
DRB1_0404   23  RFCDLPGIMQHFTIP  RFCDLPGIM        0.4287        483.9          WB    32.00      Sequence
DRB1_0404   76  TARIDPFRAAKTLNI  DPFRAAKTL        0.4272        491.4          WB    32.00      Sequence
DRB1_0404  150  SFYEVDAISGWWNTG  AISGWWNTG        0.4240        509.1                32.00      Sequence
DRB1_0404  255  NGKTVTFMPKPLFGD  TVTFMPKPL        0.4232        513.4                32.00      Sequence
DRB1_0404  230  QFNSLLHAADDMQLY  QFNSLLHAA        0.4168        549.9                32.00      Sequence
DRB1_0404  244  YKYIIKNTAWQNGKT  YKYIIKNTA        0.4147        562.7                32.00      Sequence
DRB1_0404   87  TLNINFFVHDPFTLE  LNINFFVHD        0.4137        569.1                32.00      Sequence
DRB1_0404   62  SIHESDMLLLPDPET  DMLLLPDPE        0.4134        570.4                32.00      Sequence
DRB1_0404  334  EAPINLVYSQRNRSA  PINLVYSQR        0.4130        573.0                32.00      Sequence
DRB1_0404  328  RLVPGYEAPINLVYS  LVPGYEAPI        0.4130        573.2                32.00      Sequence
DRB1_0404  300  TARHYIGGLLHHAPS  TARHYIGGL        0.4097        594.1                32.00      Sequence
DRB1_0404  129  FGAEAEFYIFDSVSF  FYIFDSVSF        0.4056        621.2                50.00      Sequence
DRB1_0404   88  LNINFFVHDPFTLEP  LNINFFVHD        0.3997        662.0                50.00      Sequence
DRB1_0404  333  YEAPINLVYSQRNRS  PINLVYSQR        0.3985        670.7                50.00      Sequence
DRB1_0404  350  VRIPITGSNPKAKRL  RIPITGSNP        0.3981        673.6                50.00      Sequence
DRB1_0404   31  MQHFTIPASAFDKSV  HFTIPASAF        0.3954        693.7                50.00      Sequence
DRB1_0404  299  DTARHYIGGLLHHAP  TARHYIGGL        0.3953        694.5                50.00      Sequence
DRB1_0404  327  KRLVPGYEAPINLVY  LVPGYEAPI        0.3944        700.9                50.00      Sequence
DRB1_0404  237  AADDMQLYKYIIKNT  MQLYKYIIK        0.3943        701.4                50.00      Sequence
DRB1_0404  411  EAASIPQTPTQLSDV  SIPQTPTQL        0.3939        704.8                50.00      Sequence
DRB1_0404  326  YKRLVPGYEAPINLV  LVPGYEAPI        0.3934        708.9                50.00      Sequence
DRB1_0404   86  KTLNINFFVHDPFTL  LNINFFVHD        0.3908        728.5                50.00      Sequence
DRB1_0404  344  RNRSACVRIPITGSN  ACVRIPITG        0.3900        735.3                50.00      Sequence
DRB1_0404  412  AASIPQTPTQLSDVI  SIPQTPTQL        0.3886        746.6                50.00      Sequence
DRB1_0404  301  ARHYIGGLLHHAPSL  HYIGGLLHH        0.3875        755.6                50.00      Sequence
DRB1_0404  335  APINLVYSQRNRSAC  PINLVYSQR        0.3874        756.3                50.00      Sequence
DRB1_0404  414  SIPQTPTQLSDVIDR  SIPQTPTQL        0.3855        772.0                50.00      Sequence
DRB1_0404   17  VEYVDVRFCDLPGIM  RFCDLPGIM        0.3808        811.9                50.00      Sequence
DRB1_0404  370  DSSGNPYLAFSAMLM  PYLAFSAML        0.3773        843.4                50.00      Sequence
DRB1_0404  110  IARKAENYLISTGIA  KAENYLIST        0.3730        884.0                50.00      Sequence
DRB1_0404  413  ASIPQTPTQLSDVID  SIPQTPTQL        0.3713        899.5                50.00      Sequence
DRB1_0404   32  QHFTIPASAFDKSVF  HFTIPASAF        0.3694        918.8                50.00      Sequence
DRB1_0404  351  RIPITGSNPKAKRLE  RIPITGSNP        0.3690        922.5                50.00      Sequence
DRB1_0404  298  SDTARHYIGGLLHHA  TARHYIGGL        0.3679        933.7                50.00      Sequence
DRB1_0404   89  NINFFVHDPFTLEPY  NFFVHDPFT        0.3678        934.6                50.00      Sequence
DRB1_0404   16  KVEYVDVRFCDLPGI  YVDVRFCDL        0.3669        943.6                50.00      Sequence
DRB1_0404  325  SYKRLVPGYEAPINL  LVPGYEAPI        0.3659        954.3                50.00      Sequence
DRB1_0404  336  PINLVYSQRNRSACV  PINLVYSQR        0.3626        988.7                50.00      Sequence
DRB1_0404   49  GLAFDGSSIRGFQSI  SSIRGFQSI        0.3611       1005.5                50.00      Sequence
DRB1_0404   85  AKTLNINFFVHDPFT  LNINFFVHD        0.3604       1012.3                50.00      Sequence
DRB1_0404  332  GYEAPINLVYSQRNR  PINLVYSQR        0.3596       1021.7                50.00      Sequence
DRB1_0404  192  DQYVDLRDKMLTNLI  RDKMLTNLI        0.3588       1029.8                50.00      Sequence
DRB1_0404  291  ETGYAGLSDTARHYI  TGYAGLSDT        0.3587       1031.2                50.00      Sequence
DRB1_0404  362  KRLEFRSPDSSGNPY  EFRSPDSSG        0.3581       1037.6                50.00      Sequence
DRB1_0404  254  QNGKTVTFMPKPLFG  TVTFMPKPL        0.3568       1052.8                50.00      Sequence
DRB1_0404  292  TGYAGLSDTARHYIG  TGYAGLSDT        0.3548       1075.6                50.00      Sequence
DRB1_0404   84  AAKTLNINFFVHDPF  TLNINFFVH        0.3538       1087.5                50.00      Sequence
DRB1_0404   90  INFFVHDPFTLEPYS  NFFVHDPFT        0.3531       1095.5                50.00      Sequence
DRB1_0404  361  AKRLEFRSPDSSGNP  EFRSPDSSG        0.3526       1101.5                50.00      Sequence
DRB1_0404  410  EEAASIPQTPTQLSD  SIPQTPTQL        0.3506       1125.6                50.00      Sequence
DRB1_0404  231  FNSLLHAADDMQLYK  LLHAADDMQ        0.3498       1135.6                50.00      Sequence
DRB1_0404  232  NSLLHAADDMQLYKY  LLHAADDMQ        0.3482       1155.9                50.00      Sequence
DRB1_0404  329  LVPGYEAPINLVYSQ  LVPGYEAPI        0.3473       1166.7                50.00      Sequence
DRB1_0404  290  DETGYAGLSDTARHY  TGYAGLSDT        0.3471       1169.4                50.00      Sequence
DRB1_0404  149  GSFYEVDAISGWWNT  FYEVDAISG        0.3469       1171.3                50.00      Sequence
DRB1_0404  439  GGVFTNDLIETWISF  DLIETWISF        0.3442       1206.4                50.00      Sequence
DRB1_0404   83  RAAKTLNINFFVHDP  AAKTLNINF        0.3437       1212.9                50.00      Sequence
DRB1_0404  343  QRNRSACVRIPITGS  ACVRIPITG        0.3392       1273.4                50.00      Sequence
DRB1_0404  324  NSYKRLVPGYEAPIN  LVPGYEAPI        0.3386       1281.6                50.00      Sequence
DRB1_0404  316  LAFTNPTVNSYKRLV  LAFTNPTVN        0.3374       1298.4                50.00      Sequence
DRB1_0404   33  HFTIPASAFDKSVFD  HFTIPASAF        0.3349       1334.4                50.00      Sequence
DRB1_0404  360  KAKRLEFRSPDSSGN  KRLEFRSPD        0.3346       1339.2                50.00      Sequence
DRB1_0404  233  SLLHAADDMQLYKYI  LHAADDMQL        0.3318       1380.1                50.00      Sequence
DRB1_0404  363  RLEFRSPDSSGNPYL  EFRSPDSSG        0.3314       1385.7                50.00      Sequence
DRB1_0404  297  LSDTARHYIGGLLHH  TARHYIGGL        0.3279       1439.0                50.00      Sequence
DRB1_0404   48  DGLAFDGSSIRGFQS  GLAFDGSSI        0.3267       1457.9                50.00      Sequence
DRB1_0404  236  HAADDMQLYKYIIKN  MQLYKYIIK        0.3239       1502.6                50.00      Sequence
DRB1_0404  183  GGYFPVAPNDQYVDL  FPVAPNDQY        0.3230       1517.2                50.00      Sequence
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DRB1_0404  109  NIARKAENYLISTGI  KAENYLIST         0.3226        1524.4              50.00     Sequence
DRB1_0404   75  ETARIDPFRAAKTLN  DPFRAAKTL         0.3213        1545.8              50.00     Sequence
DRB1_0404  202  LTNLINSGFILEKGH  LINSGFILE         0.3170        1619.4              50.00     Sequence
DRB1_0404   57  IRGFQSIHESDMLLL  GFQSIHESD         0.3156        1644.0              50.00     Sequence
DRB1_0404   15  EKVEYVDVRFCDLPG  YVDVRFCDL         0.3152        1651.0              50.00     Sequence
DRB1_0404  337  INLVYSQRNRSACVR  NLVYSQRNR         0.3132        1687.5              50.00     Sequence
DRB1_0404   47  DDGLAFDGSSIRGFQ  GLAFDGSSI         0.3130        1691.1              50.00     Sequence
DRB1_0404  289  YDETGYAGLSDTARH  TGYAGLSDT         0.3116        1717.6              50.00     Sequence
DRB1_0404  272  SGMHCHQSLWKDGAP  SGMHCHQSL         0.3108        1732.0              50.00     Sequence
DRB1_0404  182  KGGYFPVAPNDQYVD  FPVAPNDQY         0.3104        1739.9              50.00     Sequence
DRB1_0404  271  GSGMHCHQSLWKDGA  SGMHCHQSL         0.3096        1755.1              50.00     Sequence
DRB1_0404  409  PEEAASIPQTPTQLS  SIPQTPTQL         0.3069        1805.9              50.00     Sequence
DRB1_0404  220  GSGGQAEINYQFNSL  EINYQFNSL         0.3061        1822.5              50.00     Sequence
DRB1_0404  446  LIETWISFKRENEIE  TWISFKREN         0.3059        1826.3              50.00     Sequence
DRB1_0404  369  PDSSGNPYLAFSAML  PYLAFSAML         0.3052        1840.0              50.00     Sequence
DRB1_0404  184  GYFPVAPNDQYVDLR  FPVAPNDQY         0.3050        1844.7              50.00     Sequence
DRB1_0404   61  QSIHESDMLLLPDPE  SIHESDMLL         0.3049        1845.2              50.00     Sequence
DRB1_0404  359  PKAKRLEFRSPDSSG  KRLEFRSPD         0.3038        1867.7              50.00     Sequence
DRB1_0404  323  VNSYKRLVPGYEAPI  SYKRLVPGY         0.3030        1885.1              50.00     Sequence
DRB1_0404  148  NGSFYEVDAISGWWN  FYEVDAISG         0.3021        1903.4              50.00     Sequence
DRB1_0404   91  NFFVHDPFTLEPYSR  FFVHDPFTL         0.3020        1904.1              50.00     Sequence
DRB1_0404  331  PGYEAPINLVYSQRN  PINLVYSQR         0.3018        1909.1              50.00     Sequence
DRB1_0404  245  KYIIKNTAWQNGKTV  KYIIKNTAW         0.2976        1998.0              50.00     Sequence
DRB1_0404   14  DEKVEYVDVRFCDLP  YVDVRFCDL         0.2965        2021.0              50.00     Sequence
DRB1_0404  203  TNLINSGFILEKGHH  LINSGFILE         0.2947        2061.2              50.00     Sequence
DRB1_0404   58  RGFQSIHESDMLLLP  SIHESDMLL         0.2937        2084.8              50.00     Sequence
DRB1_0404  383  LMAGLDGIKNKIEPQ  LMAGLDGIK         0.2926        2108.4              50.00     Sequence
DRB1_0404   59  GFQSIHESDMLLLPD  SIHESDMLL         0.2925        2110.8              50.00     Sequence
DRB1_0404    6  DDVFKLAKDEKVEYV  FKLAKDEKV         0.2925        2111.5              50.00     Sequence
DRB1_0404  234  LLHAADDMQLYKYII  LLHAADDMQ         0.2914        2137.5              50.00     Sequence
DRB1_0404  147  ANGSFYEVDAISGWW  FYEVDAISG         0.2908        2151.0              50.00     Sequence
DRB1_0404   46  FDDGLAFDGSSIRGF  GLAFDGSSI         0.2864        2254.4              50.00     Sequence
DRB1_0404    7  DVFKLAKDEKVEYVD  FKLAKDEKV         0.2860        2265.6              50.00     Sequence
DRB1_0404  253  WQNGKTVTFMPKPLF  TVTFMPKPL         0.2855        2278.1              50.00     Sequence
DRB1_0404  338  NLVYSQRNRSACVRI  NLVYSQRNR         0.2848        2294.8              50.00     Sequence
DRB1_0404  108  RNIARKAENYLISTG  KAENYLIST         0.2839        2316.3              50.00     Sequence
DRB1_0404    5  PDDVFKLAKDEKVEY  FKLAKDEKV         0.2806        2402.5              50.00     Sequence
DRB1_0404  270  NGSGMHCHQSLWKDG  SGMHCHQSL         0.2790        2443.1              50.00     Sequence
DRB1_0404   13  KDEKVEYVDVRFCDL  KVEYVDVRF         0.2789        2444.9              50.00     Sequence
DRB1_0404  322  TVNSYKRLVPGYEAP  SYKRLVPGY         0.2787        2451.1              50.00     Sequence
DRB1_0404   60  FQSIHESDMLLLPDP  SIHESDMLL         0.2774        2485.8              50.00     Sequence
DRB1_0404   92  FFVHDPFTLEPYSRD  FFVHDPFTL         0.2768        2501.0              50.00     Sequence
DRB1_0404  146  RANGSFYEVDAISGW  FYEVDAISG         0.2759        2526.2              50.00     Sequence
DRB1_0404  364  LEFRSPDSSGNPYLA  EFRSPDSSG         0.2740        2578.6              50.00     Sequence
DRB1_0404  284  GAPLMYDETGYAGLS  APLMYDETG         0.2738        2585.2              50.00     Sequence
DRB1_0404  191  NDQYVDLRDKMLTNL  QYVDLRDKM         0.2727        2614.3              50.00     Sequence
DRB1_0404  181  HKGGYFPVAPNDQYV  YFPVAPNDQ         0.2716        2646.9              50.00     Sequence
DRB1_0404  128  YFGAEAEFYIFDSVS  EFYIFDSVS         0.2713        2655.8              50.00     Sequence
DRB1_0404  185  YFPVAPNDQYVDLRD  FPVAPNDQY         0.2673        2772.5              50.00     Sequence
DRB1_0404  342  SQRNRSACVRIPITG  SACVRIPIT         0.2668        2787.2              50.00     Sequence
DRB1_0404  283  DGAPLMYDETGYAGL  APLMYDETG         0.2660        2811.1              50.00     Sequence
DRB1_0404  259  VTFMPKPLFGDNGSG  VTFMPKPLF         0.2655        2827.6              50.00     Sequence
DRB1_0404  118  LISTGIADTAYFGAE  LISTGIADT         0.2626        2918.4              50.00     Sequence
DRB1_0404  246  YIIKNTAWQNGKTVT  IIKNTAWQN         0.2622        2928.7              50.00     Sequence
DRB1_0404  285  APLMYDETGYAGLSD  APLMYDETG         0.2602        2995.0              50.00     Sequence
DRB1_0404  204  NLINSGFILEKGHHE  LINSGFILE         0.2598        3008.7              50.00     Sequence
DRB1_0404   74  PETARIDPFRAAKTL  RIDPFRAAK         0.2584        3051.7              50.00     Sequence
DRB1_0404  235  LHAADDMQLYKYIIK  LHAADDMQL         0.2575        3082.4              50.00     Sequence
DRB1_0404  288  MYDETGYAGLSDTAR  TGYAGLSDT         0.2568        3106.4              50.00     Sequence
DRB1_0404  282  KDGAPLMYDETGYAG  APLMYDETG         0.2557        3145.0              50.00     Sequence
DRB1_0404    4  TPDDVFKLAKDEKVE  FKLAKDEKV         0.2556        3146.1              50.00     Sequence
DRB1_0404    8  VFKLAKDEKVEYVDV  FKLAKDEKV         0.2555        3149.1              50.00     Sequence
DRB1_0404  408  PPEEAASIPQTPTQL  SIPQTPTQL         0.2547        3178.0              50.00     Sequence
DRB1_0404  296  GLSDTARHYIGGLLH  TARHYIGGL         0.2541        3197.5              50.00     Sequence
DRB1_0404   69  LLLPDPETARIDPFR  LLLPDPETA         0.2529        3239.4              50.00     Sequence
DRB1_0404  330  VPGYEAPINLVYSQR  PINLVYSQR         0.2507        3317.5              50.00     Sequence
DRB1_0404  273  GMHCHQSLWKDGAPL  HCHQSLWKD         0.2503        3331.5              50.00     Sequence
DRB1_0404  293  GYAGLSDTARHYIGG  YAGLSDTAR         0.2497        3356.2              50.00     Sequence
DRB1_0404  321  PTVNSYKRLVPGYEA  TVNSYKRLV         0.2490        3378.9              50.00     Sequence
DRB1_0404   45  VFDDGLAFDGSSIRG  DGLAFDGSS         0.2483        3407.3              50.00     Sequence
DRB1_0404  180  RHKGGYFPVAPNDQY  FPVAPNDQY         0.2451        3523.9              50.00     Sequence
DRB1_0404  145  SRANGSFYEVDAISG  FYEVDAISG         0.2446        3545.8              50.00     Sequence
DRB1_0404  418  TPTQLSDVIDRLEAD  TQLSDVIDR         0.2434        3590.4              50.00     Sequence
DRB1_0404  274  MHCHQSLWKDGAPLM  SLWKDGAPL         0.2432        3597.0              50.00     Sequence
DRB1_0404  269  DNGSGMHCHQSLWKD  SGMHCHQSL         0.2420        3644.3              50.00     Sequence
DRB1_0404  417  QTPTQLSDVIDRLEA  TPTQLSDVI         0.2390        3767.5              50.00     Sequence
DRB1_0404  107  PRNIARKAENYLIST  IARKAENYL         0.2375        3827.4              50.00     Sequence
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DRB1_0404   44  SVFDDGLAFDGSSIR  GLAFDGSSI         0.2319        4065.5             50.00     Sequence
DRB1_0404  420  TQLSDVIDRLEADHE  TQLSDVIDR         0.2310        4105.4             50.00     Sequence
DRB1_0404  365  EFRSPDSSGNPYLAF  EFRSPDSSG         0.2309        4110.6             50.00     Sequence
DRB1_0404  320  NPTVNSYKRLVPGYE  TVNSYKRLV         0.2296        4171.3             50.00     Sequence
DRB1_0404    3  KTPDDVFKLAKDEKV  FKLAKDEKV         0.2250        4380.2             50.00     Sequence
DRB1_0404  352  IPITGSNPKAKRLEF  IPITGSNPK         0.2224        4505.1             50.00     Sequence
DRB1_0404  449  TWISFKRENEIEPVN  TWISFKREN         0.2214        4554.3             50.00     Sequence
DRB1_0404  275  HCHQSLWKDGAPLMY  SLWKDGAPL         0.2202        4613.5             50.00     Sequence
DRB1_0404  416  PQTPTQLSDVIDRLE  TPTQLSDVI         0.2183        4711.1             50.00     Sequence
DRB1_0404  261  FMPKPLFGDNGSGMH  PKPLFGDNG         0.2182        4718.7             50.00     Sequence
DRB1_0404  205  LINSGFILEKGHHEV  LINSGFILE         0.2179        4733.7             50.00     Sequence
DRB1_0404  419  PTQLSDVIDRLEADH  TQLSDVIDR         0.2171        4775.1             50.00     Sequence
DRB1_0404  423  SDVIDRLEADHEYLT  DVIDRLEAD         0.2169        4784.5             50.00     Sequence
DRB1_0404  317  AFTNPTVNSYKRLVP  FTNPTVNSY         0.2166        4797.4             50.00     Sequence
DRB1_0404  415  IPQTPTQLSDVIDRL  TPTQLSDVI         0.2165        4804.8             50.00     Sequence
DRB1_0404  260  TFMPKPLFGDNGSGM  FMPKPLFGD         0.2164        4810.5             50.00     Sequence
DRB1_0404  358  NPKAKRLEFRSPDSS  KRLEFRSPD         0.2163        4812.6             50.00     Sequence
DRB1_0404  252  AWQNGKTVTFMPKPL  TVTFMPKPL         0.2163        4812.6             50.00     Sequence
DRB1_0404  186  FPVAPNDQYVDLRDK  FPVAPNDQY         0.2160        4833.0             50.00     Sequence
DRB1_0404  319  TNPTVNSYKRLVPGY  TVNSYKRLV         0.2157        4844.2             50.00     Sequence
DRB1_0404   12  AKDEKVEYVDVRFCD  EKVEYVDVR         0.2154        4863.3             50.00     Sequence
DRB1_0404  190  PNDQYVDLRDKMLTN  YVDLRDKML         0.2148        4891.7             50.00     Sequence
DRB1_0404  247  IIKNTAWQNGKTVTF  IIKNTAWQN         0.2125        5014.9             50.00     Sequence
DRB1_0404  448  ETWISFKRENEIEPV  TWISFKREN         0.2118        5053.3             50.00     Sequence
DRB1_0404  339  LVYSQRNRSACVRIP  LVYSQRNRS         0.2116        5064.2             50.00     Sequence
DRB1_0404   73  DPETARIDPFRAAKT  RIDPFRAAK         0.2113        5084.6             50.00     Sequence
DRB1_0404  294  YAGLSDTARHYIGGL  YAGLSDTAR         0.2102        5141.7             50.00     Sequence
DRB1_0404  281  WKDGAPLMYDETGYA  APLMYDETG         0.2102        5145.9             50.00     Sequence
DRB1_0404  384  MAGLDGIKNKIEPQA  GLDGIKNKI         0.2077        5282.7             50.00     Sequence
DRB1_0404   34  FTIPASAFDKSVFDD  FTIPASAFD         0.2076        5292.0             50.00     Sequence
DRB1_0404  447  IETWISFKRENEIEP  TWISFKREN         0.2074        5299.5             50.00     Sequence
DRB1_0404  422  LSDVIDRLEADHEYL  DVIDRLEAD         0.2073        5307.5             50.00     Sequence
DRB1_0404  136  YIFDSVSFDSRANGS  YIFDSVSFD         0.2068        5337.4             50.00     Sequence
DRB1_0404    9  FKLAKDEKVEYVDVR  FKLAKDEKV         0.2049        5446.2             50.00     Sequence
DRB1_0404  318  FTNPTVNSYKRLVPG  FTNPTVNSY         0.2042        5486.8             50.00     Sequence
DRB1_0404  463  NIRPHPYEFALYYDV  YEFALYYDV         0.2041        5491.4             50.00     Sequence
DRB1_0404  286  PLMYDETGYAGLSDT  PLMYDETGY         0.2035        5527.5             50.00     Sequence
DRB1_0404   35  TIPASAFDKSVFDDG  PASAFDKSV         0.2035        5530.7             50.00     Sequence
DRB1_0404  424  DVIDRLEADHEYLTE  DVIDRLEAD         0.2026        5587.0             50.00     Sequence
DRB1_0404  438  EGGVFTNDLIETWIS  VFTNDLIET         0.1975        5900.2             50.00     Sequence
DRB1_0404   36  IPASAFDKSVFDDGL  PASAFDKSV         0.1971        5928.3             50.00     Sequence
DRB1_0404  268  GDNGSGMHCHQSLWK  SGMHCHQSL         0.1969        5942.5             50.00     Sequence
DRB1_0404  179  VRHKGGYFPVAPNDQ  HKGGYFPVA         0.1968        5945.8             50.00     Sequence
DRB1_0404   41  FDKSVFDDGLAFDGS  SVFDDGLAF         0.1967        5952.4             50.00     Sequence
DRB1_0404  276  CHQSLWKDGAPLMYD  SLWKDGAPL         0.1956        6022.8             50.00     Sequence
DRB1_0404  341  YSQRNRSACVRIPIT  SACVRIPIT         0.1956        6023.7             50.00     Sequence
DRB1_0404  421  QLSDVIDRLEADHEY  DVIDRLEAD         0.1936        6152.2             50.00     Sequence
DRB1_0404  457  NEIEPVNIRPHPYEF  IEPVNIRPH         0.1925        6230.1             50.00     Sequence
DRB1_0404   42  DKSVFDDGLAFDGSS  SVFDDGLAF         0.1923        6242.5             50.00     Sequence
DRB1_0404  262  MPKPLFGDNGSGMHC  PLFGDNGSG         0.1918        6278.0             50.00     Sequence
DRB1_0404  263  PKPLFGDNGSGMHCH  PLFGDNGSG         0.1915        6296.8             50.00     Sequence
DRB1_0404   43  KSVFDDGLAFDGSSI  SVFDDGLAF         0.1915        6297.4             50.00     Sequence
DRB1_0404   40  AFDKSVFDDGLAFDG  SVFDDGLAF         0.1908        6343.5             50.00     Sequence
DRB1_0404  287  LMYDETGYAGLSDTA  TGYAGLSDT         0.1905        6366.8             50.00     Sequence
DRB1_0404   37  PASAFDKSVFDDGLA  PASAFDKSV         0.1903        6378.4             50.00     Sequence
DRB1_0404  456  ENEIEPVNIRPHPYE  IEPVNIRPH         0.1850        6753.2             50.00     Sequence
DRB1_0404  106  DPRNIARKAENYLIS  IARKAENYL         0.1833        6883.9             50.00     Sequence
DRB1_0404  459  IEPVNIRPHPYEFAL  IEPVNIRPH         0.1831        6892.9             50.00     Sequence
DRB1_0404  189  APNDQYVDLRDKMLT  YVDLRDKML         0.1821        6974.6             50.00     Sequence
DRB1_0404   97  PFTLEPYSRDPRNIA  FTLEPYSRD         0.1818        6993.4             50.00     Sequence
DRB1_0404  458  EIEPVNIRPHPYEFA  IEPVNIRPH         0.1815        7014.0             50.00     Sequence
DRB1_0404   38  ASAFDKSVFDDGLAF  FDKSVFDDG         0.1811        7048.0             50.00     Sequence
DRB1_0404  279  SLWKDGAPLMYDETG  SLWKDGAPL         0.1810        7053.3             50.00     Sequence
DRB1_0404   39  SAFDKSVFDDGLAFD  FDKSVFDDG         0.1806        7088.4             50.00     Sequence
DRB1_0404   11  LAKDEKVEYVDVRFC  EKVEYVDVR         0.1775        7326.6             50.00     Sequence
DRB1_0404  277  HQSLWKDGAPLMYDE  SLWKDGAPL         0.1760        7448.8             50.00     Sequence
DRB1_0404   96  DPFTLEPYSRDPRNI  LEPYSRDPR         0.1749        7534.8             50.00     Sequence
DRB1_0404  248  IKNTAWQNGKTVTFM  IKNTAWQNG         0.1749        7538.0             50.00     Sequence
DRB1_0404  433  HEYLTEGGVFTNDLI  EYLTEGGVF         0.1745        7569.4             50.00     Sequence
DRB1_0404  437  TEGGVFTNDLIETWI  VFTNDLIET         0.1744        7578.2             50.00     Sequence
DRB1_0404  434  EYLTEGGVFTNDLIE  EYLTEGGVF         0.1726        7722.0             50.00     Sequence
DRB1_0404   98  FTLEPYSRDPRNIAR  FTLEPYSRD         0.1721        7769.8             50.00     Sequence
DRB1_0404  432  DHEYLTEGGVFTNDL  YLTEGGVFT         0.1718        7791.5             50.00     Sequence
DRB1_0404  178  KVRHKGGYFPVAPND  HKGGYFPVA         0.1716        7808.0             50.00     Sequence
DRB1_0404  295  AGLSDTARHYIGGLL  TARHYIGGL         0.1690        8030.0             50.00     Sequence
DRB1_0404  340  VYSQRNRSACVRIPI  VYSQRNRSA         0.1689        8042.2             50.00     Sequence
DRB1_0404  357  SNPKAKRLEFRSPDS  KRLEFRSPD         0.1686        8063.1             50.00     Sequence
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DRB1_0404  157  ISGWWNTGAATEADG  ISGWWNTGA         0.1680       8124.0                50.00     Sequence
DRB1_0404  264  KPLFGDNGSGMHCHQ  PLFGDNGSG         0.1675       8159.6                50.00     Sequence
DRB1_0404  455  RENEIEPVNIRPHPY  EIEPVNIRP         0.1663       8269.9                50.00     Sequence
DRB1_0404   93  FVHDPFTLEPYSRDP  FVHDPFTLE         0.1645       8429.4                50.00     Sequence
DRB1_0404  460  EPVNIRPHPYEFALY  EPVNIRPHP         0.1639       8491.5                50.00     Sequence
DRB1_0404   95  HDPFTLEPYSRDPRN  PFTLEPYSR         0.1635       8525.5                50.00     Sequence
DRB1_0404  278  QSLWKDGAPLMYDET  SLWKDGAPL         0.1633       8538.8                50.00     Sequence
DRB1_0404  280  LWKDGAPLMYDETGY  APLMYDETG         0.1612       8741.2                50.00     Sequence
DRB1_0404  392  NKIEPQAPVDKDLYE  NKIEPQAPV         0.1612       8743.3                50.00     Sequence
DRB1_0404  144  DSRANGSFYEVDAIS  SFYEVDAIS         0.1604       8814.1                50.00     Sequence
DRB1_0404  207  NSGFILEKGHHEVGS  FILEKGHHE         0.1596       8891.9                50.00     Sequence
DRB1_0404   94  VHDPFTLEPYSRDPR  PFTLEPYSR         0.1592       8935.7                50.00     Sequence
DRB1_0404  188  VAPNDQYVDLRDKML  YVDLRDKML         0.1581       9040.8                50.00     Sequence
DRB1_0404  431  ADHEYLTEGGVFTND  EYLTEGGVF         0.1579       9061.7                50.00     Sequence
DRB1_0404  462  VNIRPHPYEFALYYD  RPHPYEFAL         0.1575       9093.1                50.00     Sequence
DRB1_0404  127  AYFGAEAEFYIFDSV  AEFYIFDSV         0.1570       9146.5                50.00     Sequence
DRB1_0404  436  LTEGGVFTNDLIETW  GGVFTNDLI         0.1569       9154.5                50.00     Sequence
DRB1_0404  425  VIDRLEADHEYLTEG  VIDRLEADH         0.1569       9159.0                50.00     Sequence
DRB1_0404  450  WISFKRENEIEPVNI  ISFKRENEI         0.1567       9180.2                50.00     Sequence
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DRB1_0404  435  YLTEGGVFTNDLIET  YLTEGGVFT         0.1542       9427.2                50.00     Sequence
DRB1_0404  177  YKVRHKGGYFPVAPN  HKGGYFPVA         0.1532       9526.2                50.00     Sequence
DRB1_0404  206  INSGFILEKGHHEVG  GFILEKGHH         0.1532       9532.6                50.00     Sequence
DRB1_0404  401  DKDLYELPPEEAASI  DLYELPPEE         0.1524       9613.5                50.00     Sequence
DRB1_0404   72  PDPETARIDPFRAAK  RIDPFRAAK         0.1516       9699.0                50.00     Sequence
DRB1_0404  137  IFDSVSFDSRANGSF  SVSFDSRAN         0.1513       9725.6                50.00     Sequence
DRB1_0404  249  KNTAWQNGKTVTFMP  WQNGKTVTF         0.1510       9763.0                50.00     Sequence
DRB1_0404  461  PVNIRPHPYEFALYY  IRPHPYEFA         0.1506       9806.1                50.00     Sequence
DRB1_0404  407  LPPEEAASIPQTPTQ  EAASIPQTP         0.1498       9891.4                50.00     Sequence
DRB1_0404  402  KDLYELPPEEAASIP  DLYELPPEE         0.1498       9892.1                50.00     Sequence
DRB1_0404  267  FGDNGSGMHCHQSLW  SGMHCHQSL         0.1492       9951.8                50.00     Sequence
DRB1_0404  454  KRENEIEPVNIRPHP  NEIEPVNIR         0.1480      10080.7                50.00     Sequence
DRB1_0404  120  STGIADTAYFGAEAE  TGIADTAYF         0.1475      10139.1                50.00     Sequence
DRB1_0404  138  FDSVSFDSRANGSFY  SVSFDSRAN         0.1458      10327.2                50.00     Sequence
DRB1_0404  251  TAWQNGKTVTFMPKP  WQNGKTVTF         0.1455      10354.0                50.00     Sequence
DRB1_0404  393  KIEPQAPVDKDLYEL  KIEPQAPVD         0.1454      10371.5                50.00     Sequence
DRB1_0404  451  ISFKRENEIEPVNIR  ISFKRENEI         0.1452      10386.9                50.00     Sequence
DRB1_0404    2  EKTPDDVFKLAKDEK  DVFKLAKDE         0.1434      10601.1                50.00     Sequence
DRB1_0404  265  PLFGDNGSGMHCHQS  PLFGDNGSG         0.1433      10603.0                50.00     Sequence
DRB1_0404   99  TLEPYSRDPRNIARK  LEPYSRDPR         0.1428      10667.6                50.00     Sequence
DRB1_0404  105  RDPRNIARKAENYLI  IARKAENYL         0.1424      10710.9                50.00     Sequence
DRB1_0404  250  NTAWQNGKTVTFMPK  WQNGKTVTF         0.1407      10904.8                50.00     Sequence
DRB1_0404  400  VDKDLYELPPEEAAS  DLYELPPEE         0.1406      10919.8                50.00     Sequence
DRB1_0404  266  LFGDNGSGMHCHQSL  LFGDNGSGM         0.1399      11003.5                50.00     Sequence
DRB1_0404  368  SPDSSGNPYLAFSAM  NPYLAFSAM         0.1397      11031.3                50.00     Sequence
DRB1_0404   10  KLAKDEKVEYVDVRF  EKVEYVDVR         0.1387      11144.8                50.00     Sequence
DRB1_0404  390  IKNKIEPQAPVDKDL  NKIEPQAPV         0.1381      11215.6                50.00     Sequence
DRB1_0404  121  TGIADTAYFGAEAEF  TGIADTAYF         0.1373      11323.4                50.00     Sequence
DRB1_0404  399  PVDKDLYELPPEEAA  DLYELPPEE         0.1357      11511.9                50.00     Sequence
DRB1_0404  403  DLYELPPEEAASIPQ  DLYELPPEE         0.1349      11622.6                50.00     Sequence
DRB1_0404  430  EADHEYLTEGGVFTN  EYLTEGGVF         0.1320      11990.2                50.00     Sequence
DRB1_0404  453  FKRENEIEPVNIRPH  FKRENEIEP         0.1313      12071.9                50.00     Sequence
DRB1_0404  139  DSVSFDSRANGSFYE  SVSFDSRAN         0.1312      12095.0                50.00     Sequence
DRB1_0404  140  SVSFDSRANGSFYEV  SVSFDSRAN         0.1304      12198.2                50.00     Sequence
DRB1_0404  389  GIKNKIEPQAPVDKD  NKIEPQAPV         0.1294      12323.1                50.00     Sequence
DRB1_0404  385  AGLDGIKNKIEPQAP  GLDGIKNKI         0.1291      12363.2                50.00     Sequence
DRB1_0404  209  GFILEKGHHEVGSGG  FILEKGHHE         0.1291      12365.3                50.00     Sequence
DRB1_0404  406  ELPPEEAASIPQTPT  EAASIPQTP         0.1276      12571.6                50.00     Sequence
DRB1_0404  176  GYKVRHKGGYFPVAP  RHKGGYFPV         0.1253      12886.3                50.00     Sequence
DRB1_0404  397  QAPVDKDLYELPPEE  QAPVDKDLY         0.1248      12954.4                50.00     Sequence
DRB1_0404  104  SRDPRNIARKAENYL  IARKAENYL         0.1242      13048.1                50.00     Sequence
DRB1_0404  398  APVDKDLYELPPEEA  DLYELPPEE         0.1208      13523.8                50.00     Sequence
DRB1_0404  366  FRSPDSSGNPYLAFS  FRSPDSSGN         0.1208      13526.5                50.00     Sequence
DRB1_0404  405  YELPPEEAASIPQTP  EAASIPQTP         0.1204      13590.3                50.00     Sequence
DRB1_0404  386  GLDGIKNKIEPQAPV  GLDGIKNKI         0.1202      13615.9                50.00     Sequence
DRB1_0404  394  IEPQAPVDKDLYELP  IEPQAPVDK         0.1198      13673.0                50.00     Sequence
DRB1_0404  388  DGIKNKIEPQAPVDK  IKNKIEPQA         0.1194      13743.8                50.00     Sequence
DRB1_0404  395  EPQAPVDKDLYELPP  QAPVDKDLY         0.1184      13888.8                50.00     Sequence
DRB1_0404  426  IDRLEADHEYLTEGG  RLEADHEYL         0.1181      13934.2                50.00     Sequence
DRB1_0404  100  LEPYSRDPRNIARKA  LEPYSRDPR         0.1179      13966.7                50.00     Sequence
DRB1_0404  396  PQAPVDKDLYELPPE  PVDKDLYEL         0.1165      14172.8                50.00     Sequence
DRB1_0404  452  SFKRENEIEPVNIRP  SFKRENEIE         0.1164      14191.1                50.00     Sequence
DRB1_0404  428  RLEADHEYLTEGGVF  RLEADHEYL         0.1158      14285.2                50.00     Sequence
DRB1_0404  175  RGYKVRHKGGYFPVA  HKGGYFPVA         0.1152      14378.4                50.00     Sequence
DRB1_0404  427  DRLEADHEYLTEGGV  RLEADHEYL         0.1124      14813.1                50.00     Sequence
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   DRB1_0404   71  LPDPETARIDPFRAA  PETARIDPF        0.1103      15154.3               50.00     Sequence
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   DRB1_0404  429  LEADHEYLTEGGVFT  EYLTEGGVF        0.1088      15404.0               50.00     Sequence
   DRB1_0404  356  GSNPKAKRLEFRSPD  AKRLEFRSP        0.1083      15486.4               50.00     Sequence
   DRB1_0404  126  TAYFGAEAEFYIFDS  AYFGAEAEF        0.1076      15616.9               50.00     Sequence
   DRB1_0404  404  LYELPPEEAASIPQT  YELPPEEAA        0.1062      15847.9               50.00     Sequence
   DRB1_0404  143  FDSRANGSFYEVDAI  RANGSFYEV        0.1058      15912.0               50.00     Sequence
   DRB1_0404   70  LLPDPETARIDPFRA  LLPDPETAR        0.1056      15951.0               50.00     Sequence
   DRB1_0404  187  PVAPNDQYVDLRDKM  QYVDLRDKM        0.1041      16206.9               50.00     Sequence
   DRB1_0404  141  VSFDSRANGSFYEVD  SFDSRANGS        0.1021      16572.5               50.00     Sequence
   DRB1_0404  158  SGWWNTGAATEADGS  WWNTGAATE        0.1004      16871.8               50.00     Sequence
   DRB1_0404  125  DTAYFGAEAEFYIFD  AYFGAEAEF        0.0998      16978.2               50.00     Sequence
   DRB1_0404  210  FILEKGHHEVGSGGQ  FILEKGHHE        0.0989      17149.5               50.00     Sequence
   DRB1_0404  103  YSRDPRNIARKAENY  RNIARKAEN        0.0984      17243.1               50.00     Sequence
   DRB1_0404  159  GWWNTGAATEADGSP  WWNTGAATE        0.0975      17418.4               50.00     Sequence
   DRB1_0404  102  PYSRDPRNIARKAEN  PYSRDPRNI        0.0945      17985.3               50.00     Sequence
   DRB1_0404  173  PNRGYKVRHKGGYFP  PNRGYKVRH        0.0935      18174.6               50.00     Sequence
   DRB1_0404  160  WWNTGAATEADGSPN  WWNTGAATE        0.0908      18721.7               50.00     Sequence
   DRB1_0404  172  SPNRGYKVRHKGGYF  PNRGYKVRH        0.0906      18754.2               50.00     Sequence
   DRB1_0404  124  ADTAYFGAEAEFYIF  AYFGAEAEF        0.0903      18829.6               50.00     Sequence
   DRB1_0404  142  SFDSRANGSFYEVDA  SFDSRANGS        0.0895      18989.4               50.00     Sequence
   DRB1_0404  174  NRGYKVRHKGGYFPV  KVRHKGGYF        0.0882      19252.5               50.00     Sequence
   DRB1_0404    1  TEKTPDDVFKLAKDE  DVFKLAKDE        0.0873      19440.7               50.00     Sequence
   DRB1_0404  355  TGSNPKAKRLEFRSP  AKRLEFRSP        0.0803      20963.5               50.00     Sequence
   DRB1_0404  101  EPYSRDPRNIARKAE  PYSRDPRNI        0.0798      21092.3               50.00     Sequence
   DRB1_0404  353  PITGSNPKAKRLEFR  PITGSNPKA        0.0796      21142.3               50.00     Sequence
   DRB1_0404  219  VGSGGQAEINYQFNS  QAEINYQFN        0.0792      21214.0               50.00     Sequence
   DRB1_0404  217  HEVGSGGQAEINYQF  HEVGSGGQA        0.0790      21275.9               50.00     Sequence
   DRB1_0404  123  IADTAYFGAEAEFYI  AYFGAEAEF        0.0787      21334.2               50.00     Sequence
   DRB1_0404  367  RSPDSSGNPYLAFSA  SPDSSGNPY        0.0784      21408.0               50.00     Sequence
   DRB1_0404  171  GSPNRGYKVRHKGGY  PNRGYKVRH        0.0783      21426.5               50.00     Sequence
   DRB1_0404  218  EVGSGGQAEINYQFN  EVGSGGQAE        0.0773      21657.3               50.00     Sequence
   DRB1_0404  214  KGHHEVGSGGQAEIN  HEVGSGGQA        0.0756      22072.2               50.00     Sequence
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   DRB1_0404  161  WNTGAATEADGSPNR  WNTGAATEA        0.0730      22707.8               50.00     Sequence
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   DRB1_0404  213  EKGHHEVGSGGQAEI  KGHHEVGSG        0.0714      23097.4               50.00     Sequence
   DRB1_0404  168  EADGSPNRGYKVRHK  PNRGYKVRH        0.0706      23288.3               50.00     Sequence
   DRB1_0404  164  GAATEADGSPNRGYK  TEADGSPNR        0.0706      23297.9               50.00     Sequence
   DRB1_0404  163  TGAATEADGSPNRGY  TEADGSPNR        0.0701      23413.1               50.00     Sequence
   DRB1_0404  122  GIADTAYFGAEAEFY  YFGAEAEFY        0.0691      23684.7               50.00     Sequence
   DRB1_0404  162  NTGAATEADGSPNRG  AATEADGSP        0.0686      23800.8               50.00     Sequence
   DRB1_0404  215  GHHEVGSGGQAEINY  HEVGSGGQA        0.0680      23957.4               50.00     Sequence
   DRB1_0404  354  ITGSNPKAKRLEFRS  ITGSNPKAK        0.0671      24186.1               50.00     Sequence
   DRB1_0404  169  ADGSPNRGYKVRHKG  PNRGYKVRH        0.0662      24427.0               50.00     Sequence
   DRB1_0404  211  ILEKGHHEVGSGGQA  KGHHEVGSG        0.0660      24482.0               50.00     Sequence
   DRB1_0404  167  TEADGSPNRGYKVRH  TEADGSPNR        0.0652      24683.1               50.00     Sequence
   DRB1_0404  212  LEKGHHEVGSGGQAE  KGHHEVGSG        0.0651      24709.6               50.00     Sequence
   DRB1_0404  166  ATEADGSPNRGYKVR  TEADGSPNR        0.0641      25001.3               50.00     Sequence
   DRB1_0404    0  VTEKTPDDVFKLAKD  TEKTPDDVF        0.0621      25525.6               50.00     Sequence
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Allele: DRB1_0404. Number of high binders 18. Number of weak binders 98. Number of peptides 464

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0405  133  AEFYIFDSVSFDSRA  YIFDSVSFD        0.7278         19.0         SB     2.00     Sequence
   DRB1_0405  226  EINYQFNSLLHAADD  YQFNSLLHA        0.7247         19.7         SB     2.00     Sequence
   DRB1_0405  132  EAEFYIFDSVSFDSR  YIFDSVSFD        0.7220         20.3         SB     2.00     Sequence
   DRB1_0405   28  PGIMQHFTIPASAFD  MQHFTIPAS        0.7191         20.9         SB     2.00     Sequence
   DRB1_0405  225  AEINYQFNSLLHAAD  YQFNSLLHA        0.7160         21.6         SB     2.00     Sequence
   DRB1_0405   54  GSSIRGFQSIHESDM  SSIRGFQSI        0.7120         22.5         SB     2.00     Sequence
   DRB1_0405  197  LRDKMLTNLINSGFI  DKMLTNLIN        0.7108         22.8         SB     4.00     Sequence
   DRB1_0405  131  AEAEFYIFDSVSFDS  YIFDSVSFD        0.7099         23.1         SB     4.00     Sequence
   DRB1_0405   53  DGSSIRGFQSIHESD  SSIRGFQSI        0.7077         23.6         SB     4.00     Sequence
   DRB1_0405   29  GIMQHFTIPASAFDK  MQHFTIPAS        0.7055         24.2         SB     4.00     Sequence
   DRB1_0405  198  RDKMLTNLINSGFIL  KMLTNLINS        0.7032         24.8         SB     4.00     Sequence
   DRB1_0405  196  DLRDKMLTNLINSGF  DKMLTNLIN        0.7030         24.9         SB     4.00     Sequence
   DRB1_0405   27  LPGIMQHFTIPASAF  MQHFTIPAS        0.6977         26.3         SB     4.00     Sequence
   DRB1_0405   52  FDGSSIRGFQSIHES  SIRGFQSIH        0.6968         26.6         SB     4.00     Sequence
   DRB1_0405  306  GGLLHHAPSLLAFTN  LHHAPSLLA        0.6959         26.8         SB     4.00     Sequence
   DRB1_0405   55  SSIRGFQSIHESDML  SSIRGFQSI        0.6951         27.1         SB     4.00     Sequence
   DRB1_0405  334  EAPINLVYSQRNRSA  INLVYSQRN        0.6938         27.5         SB     4.00     Sequence
   DRB1_0405  305  IGGLLHHAPSLLAFT  LHHAPSLLA        0.6907         28.4         SB     4.00     Sequence
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DRB1_0405  130  GAEAEFYIFDSVSFD  AEFYIFDSV          0.6873          29.5           SB     4.00      Sequence
DRB1_0405  335  APINLVYSQRNRSAC  INLVYSQRN          0.6849          30.2           SB     4.00      Sequence
DRB1_0405  307  GLLHHAPSLLAFTNP  LHHAPSLLA          0.6797          32.0           SB     4.00      Sequence
DRB1_0405  224  QAEINYQFNSLLHAA  YQFNSLLHA          0.6796          32.0           SB     4.00      Sequence
DRB1_0405  195  VDLRDKMLTNLINSG  DKMLTNLIN          0.6789          32.3           SB     4.00      Sequence
DRB1_0405  304  YIGGLLHHAPSLLAF  GLLHHAPSL          0.6761          33.3           SB     4.00      Sequence
DRB1_0405  333  YEAPINLVYSQRNRS  INLVYSQRN          0.6758          33.4           SB     4.00      Sequence
DRB1_0405  134  EFYIFDSVSFDSRAN  YIFDSVSFD          0.6707          35.3           SB     8.00      Sequence
DRB1_0405   26  DLPGIMQHFTIPASA  IMQHFTIPA          0.6699          35.6           SB     8.00      Sequence
DRB1_0405  240  DMQLYKYIIKNTAWQ  QLYKYIIKN          0.6688          36.0           SB     8.00      Sequence
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DRB1_0405  332  GYEAPINLVYSQRNR  INLVYSQRN          0.6659          37.1           SB     8.00      Sequence
DRB1_0405   51  AFDGSSIRGFQSIHE  SSIRGFQSI          0.6655          37.3           SB     8.00      Sequence
DRB1_0405  199  DKMLTNLINSGFILE  MLTNLINSG          0.6639          38.0           SB     8.00      Sequence
DRB1_0405   78  RIDPFRAAKTLNINF  FRAAKTLNI          0.6634          38.1           SB     8.00      Sequence
DRB1_0405  223  GQAEINYQFNSLLHA  EINYQFNSL          0.6633          38.2           SB     8.00      Sequence
DRB1_0405   79  IDPFRAAKTLNINFF  FRAAKTLNI          0.6582          40.4           SB     8.00      Sequence
DRB1_0405  228  NYQFNSLLHAADDMQ  YQFNSLLHA          0.6577          40.6           SB     8.00      Sequence
DRB1_0405   62  SIHESDMLLLPDPET  SIHESDMLL          0.6575          40.7           SB     8.00      Sequence
DRB1_0405  194  YVDLRDKMLTNLINS  DKMLTNLIN          0.6569          41.0           SB     8.00      Sequence
DRB1_0405  227  INYQFNSLLHAADDM  YQFNSLLHA          0.6562          41.2           SB     8.00      Sequence
DRB1_0405  238  ADDMQLYKYIIKNTA  DMQLYKYII          0.6538          42.3           SB     8.00      Sequence
DRB1_0405  303  HYIGGLLHHAPSLLA  LLHHAPSLL          0.6502          44.0           SB     8.00      Sequence
DRB1_0405  241  MQLYKYIIKNTAWQN  QLYKYIIKN          0.6448          46.7           SB     8.00      Sequence
DRB1_0405   77  ARIDPFRAAKTLNIN  FRAAKTLNI          0.6434          47.4           SB     8.00      Sequence
DRB1_0405  373  GNPYLAFSAMLMAGL  YLAFSAMLM          0.6406          48.8           SB     8.00      Sequence
DRB1_0405  336  PINLVYSQRNRSACV  INLVYSQRN          0.6405          48.9           SB     8.00      Sequence
DRB1_0405  237  AADDMQLYKYIIKNT  DMQLYKYII          0.6404          49.0           SB     8.00      Sequence
DRB1_0405  374  NPYLAFSAMLMAGLD  YLAFSAMLM          0.6404          49.0           SB     8.00      Sequence
DRB1_0405   30  IMQHFTIPASAFDKS  MQHFTIPAS          0.6401          49.1           SB     8.00      Sequence
DRB1_0405   80  DPFRAAKTLNINFFV  FRAAKTLNI          0.6343          52.3           WB     8.00      Sequence
DRB1_0405  376  YLAFSAMLMAGLDGI  YLAFSAMLM          0.6337          52.6           WB     8.00      Sequence
DRB1_0405   25  CDLPGIMQHFTIPAS  IMQHFTIPA          0.6280          56.0           WB     8.00      Sequence
DRB1_0405  242  QLYKYIIKNTAWQNG  QLYKYIIKN          0.6195          61.3           WB    16.00      Sequence
DRB1_0405  331  PGYEAPINLVYSQRN  INLVYSQRN          0.6168          63.2           WB    16.00      Sequence
DRB1_0405  193  QYVDLRDKMLTNLIN  DKMLTNLIN          0.6139          65.2           WB    16.00      Sequence
DRB1_0405  135  FYIFDSVSFDSRANG  YIFDSVSFD          0.6099          68.1           WB    16.00      Sequence
DRB1_0405  236  HAADDMQLYKYIIKN  DMQLYKYII          0.6094          68.5           WB    16.00      Sequence
DRB1_0405  375  PYLAFSAMLMAGLDG  LAFSAMLMA          0.6090          68.8           WB    16.00      Sequence
DRB1_0405   76  TARIDPFRAAKTLNI  FRAAKTLNI          0.6072          70.1           WB    16.00      Sequence
DRB1_0405  372  SGNPYLAFSAMLMAG  YLAFSAMLM          0.6070          70.3           WB    16.00      Sequence
DRB1_0405  382  MLMAGLDGIKNKIEP  MLMAGLDGI          0.6037          72.8           WB    16.00      Sequence
DRB1_0405  371  SSGNPYLAFSAMLMA  YLAFSAMLM          0.6028          73.5           WB    16.00      Sequence
DRB1_0405  200  KMLTNLINSGFILEK  KMLTNLINS          0.6011          74.9           WB    16.00      Sequence
DRB1_0405  381  AMLMAGLDGIKNKIE  MLMAGLDGI          0.5963          78.9           WB    16.00      Sequence
DRB1_0405  113  KAENYLISTGIADTA  YLISTGIAD          0.5954          79.6           WB    16.00      Sequence
DRB1_0405  114  AENYLISTGIADTAY  YLISTGIAD          0.5942          80.7           WB    16.00      Sequence
DRB1_0405   56  SIRGFQSIHESDMLL  IRGFQSIHE          0.5898          84.6           WB    16.00      Sequence
DRB1_0405  377  LAFSAMLMAGLDGIK  LAFSAMLMA          0.5892          85.2           WB    16.00      Sequence
DRB1_0405  337  INLVYSQRNRSACVR  LVYSQRNRS          0.5856          88.5           WB    16.00      Sequence
DRB1_0405   63  IHESDMLLLPDPETA  SDMLLLPDP          0.5849          89.3           WB    16.00      Sequence
DRB1_0405   49  GLAFDGSSIRGFQSI  GLAFDGSSI          0.5837          90.4           WB    16.00      Sequence
DRB1_0405  380  SAMLMAGLDGIKNKI  MLMAGLDGI          0.5826          91.4           WB    16.00      Sequence
DRB1_0405   50  LAFDGSSIRGFQSIH  SSIRGFQSI          0.5819          92.2           WB    16.00      Sequence
DRB1_0405  229  YQFNSLLHAADDMQL  YQFNSLLHA          0.5818          92.3           WB    16.00      Sequence
DRB1_0405  115  ENYLISTGIADTAYF  YLISTGIAD          0.5804          93.7           WB    16.00      Sequence
DRB1_0405  378  AFSAMLMAGLDGIKN  MLMAGLDGI          0.5799          94.2           WB    16.00      Sequence
DRB1_0405  148  NGSFYEVDAISGWWN  GSFYEVDAI          0.5792          94.9           WB    16.00      Sequence
DRB1_0405  129  FGAEAEFYIFDSVSF  AEFYIFDSV          0.5786          95.5           WB    16.00      Sequence
DRB1_0405  112  RKAENYLISTGIADT  YLISTGIAD          0.5748          99.5           WB    16.00      Sequence
DRB1_0405   90  INFFVHDPFTLEPYS  FVHDPFTLE          0.5724         102.2           WB    16.00      Sequence
DRB1_0405  379  FSAMLMAGLDGIKNK  MLMAGLDGI          0.5702         104.6           WB    16.00      Sequence
DRB1_0405   21  DVRFCDLPGIMQHFT  VRFCDLPGI          0.5664         109.0           WB    16.00      Sequence
DRB1_0405   65  ESDMLLLPDPETARI  MLLLPDPET          0.5663         109.1           WB    16.00      Sequence
DRB1_0405   64  HESDMLLLPDPETAR  SDMLLLPDP          0.5657         109.9           WB    16.00      Sequence
DRB1_0405   92  FFVHDPFTLEPYSRD  FVHDPFTLE          0.5656         110.0           WB    16.00      Sequence
DRB1_0405  147  ANGSFYEVDAISGWW  SFYEVDAIS          0.5641         111.8           WB    16.00      Sequence
DRB1_0405  370  DSSGNPYLAFSAMLM  YLAFSAMLM          0.5640         111.8           WB    16.00      Sequence
DRB1_0405   61  QSIHESDMLLLPDPE  SIHESDMLL          0.5637         112.2           WB    32.00      Sequence
DRB1_0405  222  GGQAEINYQFNSLLH  EINYQFNSL          0.5632         112.8           WB    32.00      Sequence
DRB1_0405  149  GSFYEVDAISGWWNT  GSFYEVDAI          0.5618         114.6           WB    32.00      Sequence
DRB1_0405  243  LYKYIIKNTAWQNGK  YKYIIKNTA          0.5609         115.7           WB    32.00      Sequence
DRB1_0405  308  LLHHAPSLLAFTNPT  LLHHAPSLL          0.5592         117.9           WB    32.00      Sequence
DRB1_0405   91  NFFVHDPFTLEPYSR  FVHDPFTLE          0.5586         118.7           WB    32.00      Sequence
DRB1_0405  362  KRLEFRSPDSSGNPY  LEFRSPDSS          0.5575         120.1           WB    32.00      Sequence
DRB1_0405   57  IRGFQSIHESDMLLL  IRGFQSIHE          0.5573         120.3           WB    32.00      Sequence
DRB1_0405  438  EGGVFTNDLIETWIS  GVFTNDLIE          0.5561         121.9           WB    32.00      Sequence
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DRB1_0405  439  GGVFTNDLIETWISF  GVFTNDLIE         0.5550         123.4          WB    32.00      Sequence
DRB1_0405   20  VDVRFCDLPGIMQHF  VRFCDLPGI         0.5542         124.4          WB    32.00      Sequence
DRB1_0405  116  NYLISTGIADTAYFG  YLISTGIAD         0.5531         125.9          WB    32.00      Sequence
DRB1_0405   66  SDMLLLPDPETARID  MLLLPDPET         0.5527         126.4          WB    32.00      Sequence
DRB1_0405  146  RANGSFYEVDAISGW  GSFYEVDAI         0.5499         130.3          WB    32.00      Sequence
DRB1_0405   93  FVHDPFTLEPYSRDP  FVHDPFTLE         0.5484         132.4          WB    32.00      Sequence
DRB1_0405  437  TEGGVFTNDLIETWI  GVFTNDLIE         0.5477         133.5          WB    32.00      Sequence
DRB1_0405  361  AKRLEFRSPDSSGNP  RLEFRSPDS         0.5473         134.1          WB    32.00      Sequence
DRB1_0405   19  YVDVRFCDLPGIMQH  VRFCDLPGI         0.5470         134.5          WB    32.00      Sequence
DRB1_0405  313  PSLLAFTNPTVNSYK  LLAFTNPTV         0.5468         134.8          WB    32.00      Sequence
DRB1_0405  312  APSLLAFTNPTVNSY  LLAFTNPTV         0.5457         136.4          WB    32.00      Sequence
DRB1_0405  111  ARKAENYLISTGIAD  YLISTGIAD         0.5448         137.7          WB    32.00      Sequence
DRB1_0405  136  YIFDSVSFDSRANGS  YIFDSVSFD         0.5437         139.4          WB    32.00      Sequence
DRB1_0405  363  RLEFRSPDSSGNPYL  LEFRSPDSS         0.5406         144.0          WB    32.00      Sequence
DRB1_0405   60  FQSIHESDMLLLPDP  SIHESDMLL         0.5389         146.8          WB    32.00      Sequence
DRB1_0405   81  PFRAAKTLNINFFVH  FRAAKTLNI         0.5383         147.8          WB    32.00      Sequence
DRB1_0405   24  FCDLPGIMQHFTIPA  IMQHFTIPA         0.5376         148.8          WB    32.00      Sequence
DRB1_0405  302  RHYIGGLLHHAPSLL  LLHHAPSLL         0.5375         149.0          WB    32.00      Sequence
DRB1_0405  360  KAKRLEFRSPDSSGN  RLEFRSPDS         0.5371         149.6          WB    32.00      Sequence
DRB1_0405   89  NINFFVHDPFTLEPY  FVHDPFTLE         0.5367         150.3          WB    32.00      Sequence
DRB1_0405  383  LMAGLDGIKNKIEPQ  AGLDGIKNK         0.5354         152.4          WB    32.00      Sequence
DRB1_0405  311  HAPSLLAFTNPTVNS  LLAFTNPTV         0.5346         153.8          WB    32.00      Sequence
DRB1_0405  384  MAGLDGIKNKIEPQA  AGLDGIKNK         0.5343         154.2          WB    32.00      Sequence
DRB1_0405  235  LHAADDMQLYKYIIK  DMQLYKYII         0.5328         156.8          WB    32.00      Sequence
DRB1_0405   22  VRFCDLPGIMQHFTI  FCDLPGIMQ         0.5283         164.7          WB    32.00      Sequence
DRB1_0405  436  LTEGGVFTNDLIETW  GVFTNDLIE         0.5282         164.8          WB    32.00      Sequence
DRB1_0405  314  SLLAFTNPTVNSYKR  LAFTNPTVN         0.5263         168.2          WB    32.00      Sequence
DRB1_0405   31  MQHFTIPASAFDKSV  MQHFTIPAS         0.5207         178.8          WB    32.00      Sequence
DRB1_0405  310  HHAPSLLAFTNPTVN  LLAFTNPTV         0.5195         181.0          WB    32.00      Sequence
DRB1_0405   18  EYVDVRFCDLPGIMQ  VRFCDLPGI         0.5179         184.1          WB    32.00      Sequence
DRB1_0405  330  VPGYEAPINLVYSQR  PINLVYSQR         0.5167         186.6          WB    32.00      Sequence
DRB1_0405  271  GSGMHCHQSLWKDGA  GMHCHQSLW         0.5166         186.9          WB    32.00      Sequence
DRB1_0405  128  YFGAEAEFYIFDSVS  EFYIFDSVS         0.5162         187.6          WB    32.00      Sequence
DRB1_0405  410  EEAASIPQTPTQLSD  IPQTPTQLS         0.5160         188.0          WB    32.00      Sequence
DRB1_0405  244  YKYIIKNTAWQNGKT  YKYIIKNTA         0.5160         188.1          WB    32.00      Sequence
DRB1_0405  413  ASIPQTPTQLSDVID  SIPQTPTQL         0.5154         189.4          WB    32.00      Sequence
DRB1_0405  272  SGMHCHQSLWKDGAP  GMHCHQSLW         0.5142         191.7          WB    32.00      Sequence
DRB1_0405  145  SRANGSFYEVDAISG  SFYEVDAIS         0.5141         191.9          WB    32.00      Sequence
DRB1_0405  309  LHHAPSLLAFTNPTV  LLAFTNPTV         0.5136         193.0          WB    32.00      Sequence
DRB1_0405  117  YLISTGIADTAYFGA  YLISTGIAD         0.5135         193.2          WB    32.00      Sequence
DRB1_0405  192  DQYVDLRDKMLTNLI  YVDLRDKML         0.5128         194.7          WB    32.00      Sequence
DRB1_0405  411  EAASIPQTPTQLSDV  IPQTPTQLS         0.5073         206.6          WB    32.00      Sequence
DRB1_0405   59  GFQSIHESDMLLLPD  SIHESDMLL         0.5067         207.9          WB    32.00      Sequence
DRB1_0405   88  LNINFFVHDPFTLEP  FVHDPFTLE         0.5058         210.0          WB    32.00      Sequence
DRB1_0405   48  DGLAFDGSSIRGFQS  GLAFDGSSI         0.5057         210.1          WB    32.00      Sequence
DRB1_0405  270  NGSGMHCHQSLWKDG  GMHCHQSLW         0.5029         216.8          WB    32.00      Sequence
DRB1_0405   23  RFCDLPGIMQHFTIP  FCDLPGIMQ         0.5028         216.9          WB    32.00      Sequence
DRB1_0405  385  AGLDGIKNKIEPQAP  GLDGIKNKI         0.5017         219.6          WB    32.00      Sequence
DRB1_0405  359  PKAKRLEFRSPDSSG  RLEFRSPDS         0.4998         224.2          WB    32.00      Sequence
DRB1_0405  412  AASIPQTPTQLSDVI  IPQTPTQLS         0.4988         226.5          WB    32.00      Sequence
DRB1_0405  290  DETGYAGLSDTARHY  TGYAGLSDT         0.4986         227.0          WB    32.00      Sequence
DRB1_0405  287  LMYDETGYAGLSDTA  LMYDETGYA         0.4960         233.5          WB    32.00      Sequence
DRB1_0405   47  DDGLAFDGSSIRGFQ  GLAFDGSSI         0.4913         245.6          WB    32.00      Sequence
DRB1_0405  289  YDETGYAGLSDTARH  TGYAGLSDT         0.4910         246.6          WB    32.00      Sequence
DRB1_0405  181  HKGGYFPVAPNDQYV  GGYFPVAPN         0.4893         250.9          WB    32.00      Sequence
DRB1_0405  440  GVFTNDLIETWISFK  GVFTNDLIE         0.4883         253.7          WB    32.00      Sequence
DRB1_0405  182  KGGYFPVAPNDQYVD  GGYFPVAPN         0.4882         254.0          WB    32.00      Sequence
DRB1_0405  435  YLTEGGVFTNDLIET  GVFTNDLIE         0.4874         256.1          WB    32.00      Sequence
DRB1_0405  409  PEEAASIPQTPTQLS  IPQTPTQLS         0.4857         261.0          WB    32.00      Sequence
DRB1_0405  269  DNGSGMHCHQSLWKD  GMHCHQSLW         0.4854         261.8          WB    32.00      Sequence
DRB1_0405  414  SIPQTPTQLSDVIDR  SIPQTPTQL         0.4850         263.0          WB    32.00      Sequence
DRB1_0405  201  MLTNLINSGFILEKG  MLTNLINSG         0.4850         263.1          WB    32.00      Sequence
DRB1_0405  191  NDQYVDLRDKMLTNL  YVDLRDKML         0.4848         263.7          WB    32.00      Sequence
DRB1_0405   67  DMLLLPDPETARIDP  MLLLPDPET         0.4845         264.3          WB    32.00      Sequence
DRB1_0405   58  RGFQSIHESDMLLLP  SIHESDMLL         0.4843         265.0          WB    32.00      Sequence
DRB1_0405  291  ETGYAGLSDTARHYI  TGYAGLSDT         0.4840         265.9          WB    32.00      Sequence
DRB1_0405  190  PNDQYVDLRDKMLTN  DQYVDLRDK         0.4830         268.9          WB    32.00      Sequence
DRB1_0405  183  GGYFPVAPNDQYVDL  GGYFPVAPN         0.4810         274.5          WB    32.00      Sequence
DRB1_0405  257  KTVTFMPKPLFGDNG  FMPKPLFGD         0.4802         277.1          WB    32.00      Sequence
DRB1_0405  284  GAPLMYDETGYAGLS  LMYDETGYA         0.4790         280.8          WB    32.00      Sequence
DRB1_0405  286  PLMYDETGYAGLSDT  LMYDETGYA         0.4768         287.5          WB    32.00      Sequence
DRB1_0405  180  RHKGGYFPVAPNDQY  GGYFPVAPN         0.4738         296.9          WB    50.00      Sequence
DRB1_0405  329  LVPGYEAPINLVYSQ  GYEAPINLV         0.4729         299.9          WB    50.00      Sequence
DRB1_0405  256  GKTVTFMPKPLFGDN  TVTFMPKPL         0.4710         306.0          WB    50.00      Sequence
DRB1_0405  221  SGGQAEINYQFNSLL  EINYQFNSL         0.4703         308.3          WB    50.00      Sequence
DRB1_0405   46  FDDGLAFDGSSIRGF  GLAFDGSSI         0.4698         310.0          WB    50.00      Sequence
DRB1_0405  315  LLAFTNPTVNSYKRL  LAFTNPTVN         0.4690         312.6          WB    50.00      Sequence
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DRB1_0405  338  NLVYSQRNRSACVRI  LVYSQRNRS         0.4686         314.2          WB    50.00      Sequence
DRB1_0405  285  APLMYDETGYAGLSD  LMYDETGYA         0.4684         314.6          WB    50.00      Sequence
DRB1_0405  110  IARKAENYLISTGIA  NYLISTGIA         0.4683         315.1          WB    50.00      Sequence
DRB1_0405  144  DSRANGSFYEVDAIS  SFYEVDAIS         0.4676         317.7          WB    50.00      Sequence
DRB1_0405  189  APNDQYVDLRDKMLT  YVDLRDKML         0.4671         319.4          WB    50.00      Sequence
DRB1_0405  255  NGKTVTFMPKPLFGD  KTVTFMPKP         0.4643         329.1          WB    50.00      Sequence
DRB1_0405  358  NPKAKRLEFRSPDSS  RLEFRSPDS         0.4630         333.6          WB    50.00      Sequence
DRB1_0405   87  TLNINFFVHDPFTLE  FVHDPFTLE         0.4622         336.6          WB    50.00      Sequence
DRB1_0405  258  TVTFMPKPLFGDNGS  FMPKPLFGD         0.4620         337.4          WB    50.00      Sequence
DRB1_0405  288  MYDETGYAGLSDTAR  TGYAGLSDT         0.4619         337.6          WB    50.00      Sequence
DRB1_0405  234  LLHAADDMQLYKYII  DDMQLYKYI         0.4617         338.5          WB    50.00      Sequence
DRB1_0405   16  KVEYVDVRFCDLPGI  VRFCDLPGI         0.4611         340.7          WB    50.00      Sequence
DRB1_0405    6  DDVFKLAKDEKVEYV  FKLAKDEKV         0.4600         344.6          WB    50.00      Sequence
DRB1_0405  434  EYLTEGGVFTNDLIE  GVFTNDLIE         0.4600         344.7          WB    50.00      Sequence
DRB1_0405  273  GMHCHQSLWKDGAPL  GMHCHQSLW         0.4583         351.2          WB    50.00      Sequence
DRB1_0405    5  PDDVFKLAKDEKVEY  FKLAKDEKV         0.4580         352.3          WB    50.00      Sequence
DRB1_0405  415  IPQTPTQLSDVIDRL  PTQLSDVID         0.4578         353.1          WB    50.00      Sequence
DRB1_0405  328  RLVPGYEAPINLVYS  VPGYEAPIN         0.4506         381.7          WB    50.00      Sequence
DRB1_0405  188  VAPNDQYVDLRDKML  DQYVDLRDK         0.4502         383.1          WB    50.00      Sequence
DRB1_0405  245  KYIIKNTAWQNGKTV  YIIKNTAWQ         0.4502         383.2          WB    50.00      Sequence
DRB1_0405  150  SFYEVDAISGWWNTG  SFYEVDAIS         0.4483         391.1          WB    50.00      Sequence
DRB1_0405   17  VEYVDVRFCDLPGIM  VRFCDLPGI         0.4483         391.3          WB    50.00      Sequence
DRB1_0405   95  HDPFTLEPYSRDPRN  FTLEPYSRD         0.4476         394.2          WB    50.00      Sequence
DRB1_0405   96  DPFTLEPYSRDPRNI  FTLEPYSRD         0.4468         397.5          WB    50.00      Sequence
DRB1_0405  283  DGAPLMYDETGYAGL  LMYDETGYA         0.4449         406.0          WB    50.00      Sequence
DRB1_0405  417  QTPTQLSDVIDRLEA  PTQLSDVID         0.4444         408.3          WB    50.00      Sequence
DRB1_0405  444  NDLIETWISFKRENE  LIETWISFK         0.4437         411.0          WB    50.00      Sequence
DRB1_0405  386  GLDGIKNKIEPQAPV  GLDGIKNKI         0.4430         414.1          WB    50.00      Sequence
DRB1_0405  433  HEYLTEGGVFTNDLI  HEYLTEGGV         0.4422         417.9          WB    50.00      Sequence
DRB1_0405  327  KRLVPGYEAPINLVY  VPGYEAPIN         0.4403         426.7          WB    50.00      Sequence
DRB1_0405  416  PQTPTQLSDVIDRLE  PTQLSDVID         0.4391         432.1          WB    50.00      Sequence
DRB1_0405  418  TPTQLSDVIDRLEAD  PTQLSDVID         0.4382         436.2          WB    50.00      Sequence
DRB1_0405  204  NLINSGFILEKGHHE  NLINSGFIL         0.4372         441.3          WB    50.00      Sequence
DRB1_0405    4  TPDDVFKLAKDEKVE  FKLAKDEKV         0.4370         442.1          WB    50.00      Sequence
DRB1_0405  292  TGYAGLSDTARHYIG  TGYAGLSDT         0.4356         448.6          WB    50.00      Sequence
DRB1_0405   82  FRAAKTLNINFFVHD  FRAAKTLNI         0.4352         450.6          WB    50.00      Sequence
DRB1_0405    7  DVFKLAKDEKVEYVD  FKLAKDEKV         0.4349         452.1          WB    50.00      Sequence
DRB1_0405  443  TNDLIETWISFKREN  LIETWISFK         0.4334         459.6          WB    50.00      Sequence
DRB1_0405   75  ETARIDPFRAAKTLN  DPFRAAKTL         0.4315         469.4          WB    50.00      Sequence
DRB1_0405  246  YIIKNTAWQNGKTVT  YIIKNTAWQ         0.4293         480.3          WB    50.00      Sequence
DRB1_0405  364  LEFRSPDSSGNPYLA  EFRSPDSSG         0.4282         486.1          WB    50.00      Sequence
DRB1_0405   94  VHDPFTLEPYSRDPR  FTLEPYSRD         0.4265         495.3          WB    50.00      Sequence
DRB1_0405   15  EKVEYVDVRFCDLPG  KVEYVDVRF         0.4255         500.9                50.00      Sequence
DRB1_0405  316  LAFTNPTVNSYKRLV  LAFTNPTVN         0.4234         512.3                50.00      Sequence
DRB1_0405  346  RSACVRIPITGSNPK  CVRIPITGS         0.4231         513.7                50.00      Sequence
DRB1_0405  419  PTQLSDVIDRLEADH  TQLSDVIDR         0.4229         515.2                50.00      Sequence
DRB1_0405  445  DLIETWISFKRENEI  LIETWISFK         0.4225         517.3                50.00      Sequence
DRB1_0405  442  FTNDLIETWISFKRE  LIETWISFK         0.4219         520.5                50.00      Sequence
DRB1_0405  205  LINSGFILEKGHHEV  LINSGFILE         0.4211         524.9                50.00      Sequence
DRB1_0405  326  YKRLVPGYEAPINLV  YKRLVPGYE         0.4183         541.0                50.00      Sequence
DRB1_0405   14  DEKVEYVDVRFCDLP  KVEYVDVRF         0.4139         567.7                50.00      Sequence
DRB1_0405   13  KDEKVEYVDVRFCDL  KVEYVDVRF         0.4135         570.2                50.00      Sequence
DRB1_0405  109  NIARKAENYLISTGI  IARKAENYL         0.4132         572.1                50.00      Sequence
DRB1_0405  282  KDGAPLMYDETGYAG  LMYDETGYA         0.4126         575.5                50.00      Sequence
DRB1_0405  220  GSGGQAEINYQFNSL  EINYQFNSL         0.4110         585.8                50.00      Sequence
DRB1_0405  441  VFTNDLIETWISFKR  LIETWISFK         0.4108         586.9                50.00      Sequence
DRB1_0405   68  MLLLPDPETARIDPF  MLLLPDPET         0.4091         598.0                50.00      Sequence
DRB1_0405  325  SYKRLVPGYEAPINL  YKRLVPGYE         0.4084         602.6                50.00      Sequence
DRB1_0405    3  KTPDDVFKLAKDEKV  FKLAKDEKV         0.4069         612.1                50.00      Sequence
DRB1_0405  347  SACVRIPITGSNPKA  CVRIPITGS         0.4058         619.5                50.00      Sequence
DRB1_0405  345  NRSACVRIPITGSNP  CVRIPITGS         0.4017         647.7                50.00      Sequence
DRB1_0405  127  AYFGAEAEFYIFDSV  FGAEAEFYI         0.3996         663.0                50.00      Sequence
DRB1_0405  324  NSYKRLVPGYEAPIN  YKRLVPGYE         0.3993         664.5                50.00      Sequence
DRB1_0405  268  GDNGSGMHCHQSLWK  SGMHCHQSL         0.3987         669.1                50.00      Sequence
DRB1_0405  446  LIETWISFKRENEIE  LIETWISFK         0.3985         670.5                50.00      Sequence
DRB1_0405  233  SLLHAADDMQLYKYI  LLHAADDMQ         0.3980         674.3                50.00      Sequence
DRB1_0405  186  FPVAPNDQYVDLRDK  FPVAPNDQY         0.3980         674.5                50.00      Sequence
DRB1_0405  344  RNRSACVRIPITGSN  CVRIPITGS         0.3975         678.1                50.00      Sequence
DRB1_0405  179  VRHKGGYFPVAPNDQ  GGYFPVAPN         0.3966         684.8                50.00      Sequence
DRB1_0405  339  LVYSQRNRSACVRIP  LVYSQRNRS         0.3954         693.4                50.00      Sequence
DRB1_0405  321  PTVNSYKRLVPGYEA  TVNSYKRLV         0.3948         698.2                50.00      Sequence
DRB1_0405  281  WKDGAPLMYDETGYA  LMYDETGYA         0.3944         701.1                50.00      Sequence
DRB1_0405  184  GYFPVAPNDQYVDLR  FPVAPNDQY         0.3938         705.4                50.00      Sequence
DRB1_0405  207  NSGFILEKGHHEVGS  FILEKGHHE         0.3932         710.0                50.00      Sequence
DRB1_0405  301  ARHYIGGLLHHAPSL  GLLHHAPSL         0.3930         711.9                50.00      Sequence
DRB1_0405  202  LTNLINSGFILEKGH  LINSGFILE         0.3921         718.3                50.00      Sequence
DRB1_0405  348  ACVRIPITGSNPKAK  CVRIPITGS         0.3921         718.9                50.00      Sequence
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DRB1_0405   12  AKDEKVEYVDVRFCD  KVEYVDVRF         0.3913         725.0               50.00     Sequence
DRB1_0405  231  FNSLLHAADDMQLYK  LLHAADDMQ         0.3907         729.3               50.00     Sequence
DRB1_0405   98  FTLEPYSRDPRNIAR  FTLEPYSRD         0.3895         739.0               50.00     Sequence
DRB1_0405  156  AISGWWNTGAATEAD  SGWWNTGAA         0.3890         743.1               50.00     Sequence
DRB1_0405  208  SGFILEKGHHEVGSG  FILEKGHHE         0.3889         744.2               50.00     Sequence
DRB1_0405   37  PASAFDKSVFDDGLA  SAFDKSVFD         0.3866         762.4               50.00     Sequence
DRB1_0405  432  DHEYLTEGGVFTNDL  YLTEGGVFT         0.3865         763.3               50.00     Sequence
DRB1_0405  322  TVNSYKRLVPGYEAP  YKRLVPGYE         0.3853         773.8               50.00     Sequence
DRB1_0405  247  IIKNTAWQNGKTVTF  IIKNTAWQN         0.3852         774.4               50.00     Sequence
DRB1_0405  230  QFNSLLHAADDMQLY  FNSLLHAAD         0.3843         781.9               50.00     Sequence
DRB1_0405  323  VNSYKRLVPGYEAPI  YKRLVPGYE         0.3841         783.5               50.00     Sequence
DRB1_0405  157  ISGWWNTGAATEADG  SGWWNTGAA         0.3839         785.5               50.00     Sequence
DRB1_0405    8  VFKLAKDEKVEYVDV  FKLAKDEKV         0.3832         791.4               50.00     Sequence
DRB1_0405   45  VFDDGLAFDGSSIRG  GLAFDGSSI         0.3831         792.3               50.00     Sequence
DRB1_0405  250  NTAWQNGKTVTFMPK  TAWQNGKTV         0.3814         806.8               50.00     Sequence
DRB1_0405  254  QNGKTVTFMPKPLFG  KTVTFMPKP         0.3813         807.5               50.00     Sequence
DRB1_0405  178  KVRHKGGYFPVAPND  GGYFPVAPN         0.3808         811.8               50.00     Sequence
DRB1_0405  259  VTFMPKPLFGDNGSG  FMPKPLFGD         0.3802         817.3               50.00     Sequence
DRB1_0405  343  QRNRSACVRIPITGS  CVRIPITGS         0.3796         822.7               50.00     Sequence
DRB1_0405  155  DAISGWWNTGAATEA  SGWWNTGAA         0.3796         823.0               50.00     Sequence
DRB1_0405  249  KNTAWQNGKTVTFMP  TAWQNGKTV         0.3782         835.6               50.00     Sequence
DRB1_0405  206  INSGFILEKGHHEVG  FILEKGHHE         0.3779         838.3               50.00     Sequence
DRB1_0405   97  PFTLEPYSRDPRNIA  FTLEPYSRD         0.3776         840.3               50.00     Sequence
DRB1_0405  408  PPEEAASIPQTPTQL  EEAASIPQT         0.3750         864.5               50.00     Sequence
DRB1_0405  431  ADHEYLTEGGVFTND  HEYLTEGGV         0.3750         864.6               50.00     Sequence
DRB1_0405  154  VDAISGWWNTGAATE  SGWWNTGAA         0.3748         867.0               50.00     Sequence
DRB1_0405   38  ASAFDKSVFDDGLAF  SAFDKSVFD         0.3733         881.0               50.00     Sequence
DRB1_0405  251  TAWQNGKTVTFMPKP  TAWQNGKTV         0.3723         890.0               50.00     Sequence
DRB1_0405  448  ETWISFKRENEIEPV  WISFKRENE         0.3722         891.1               50.00     Sequence
DRB1_0405  449  TWISFKRENEIEPVN  WISFKRENE         0.3713         899.8               50.00     Sequence
DRB1_0405  369  PDSSGNPYLAFSAML  NPYLAFSAM         0.3704         909.1               50.00     Sequence
DRB1_0405  357  SNPKAKRLEFRSPDS  AKRLEFRSP         0.3681         931.8               50.00     Sequence
DRB1_0405   86  KTLNINFFVHDPFTL  LNINFFVHD         0.3664         949.2               50.00     Sequence
DRB1_0405  450  WISFKRENEIEPVNI  FKRENEIEP         0.3658         955.3               50.00     Sequence
DRB1_0405  253  WQNGKTVTFMPKPLF  VTFMPKPLF         0.3646         967.7               50.00     Sequence
DRB1_0405  158  SGWWNTGAATEADGS  SGWWNTGAA         0.3644         969.8               50.00     Sequence
DRB1_0405   36  IPASAFDKSVFDDGL  SAFDKSVFD         0.3644         970.1               50.00     Sequence
DRB1_0405  349  CVRIPITGSNPKAKR  CVRIPITGS         0.3641         972.9               50.00     Sequence
DRB1_0405  187  PVAPNDQYVDLRDKM  DQYVDLRDK         0.3631         983.3               50.00     Sequence
DRB1_0405   39  SAFDKSVFDDGLAFD  SAFDKSVFD         0.3616         999.3               50.00     Sequence
DRB1_0405  203  TNLINSGFILEKGHH  NLINSGFIL         0.3603        1014.1               50.00     Sequence
DRB1_0405  430  EADHEYLTEGGVFTN  HEYLTEGGV         0.3595        1022.2               50.00     Sequence
DRB1_0405   11  LAKDEKVEYVDVRFC  KVEYVDVRF         0.3578        1041.8               50.00     Sequence
DRB1_0405  143  FDSRANGSFYEVDAI  GSFYEVDAI         0.3575        1044.4               50.00     Sequence
DRB1_0405  185  YFPVAPNDQYVDLRD  FPVAPNDQY         0.3555        1068.2               50.00     Sequence
DRB1_0405  451  ISFKRENEIEPVNIR  FKRENEIEP         0.3552        1071.7               50.00     Sequence
DRB1_0405  248  IKNTAWQNGKTVTFM  TAWQNGKTV         0.3549        1074.4               50.00     Sequence
DRB1_0405   44  SVFDDGLAFDGSSIR  GLAFDGSSI         0.3549        1074.5               50.00     Sequence
DRB1_0405  320  NPTVNSYKRLVPGYE  TVNSYKRLV         0.3543        1081.6               50.00     Sequence
DRB1_0405  387  LDGIKNKIEPQAPVD  GIKNKIEPQ         0.3521        1107.9               50.00     Sequence
DRB1_0405  232  NSLLHAADDMQLYKY  LLHAADDMQ         0.3519        1110.5               50.00     Sequence
DRB1_0405  177  YKVRHKGGYFPVAPN  GGYFPVAPN         0.3513        1116.9               50.00     Sequence
DRB1_0405  400  VDKDLYELPPEEAAS  KDLYELPPE         0.3504        1128.1               50.00     Sequence
DRB1_0405  108  RNIARKAENYLISTG  IARKAENYL         0.3499        1134.5               50.00     Sequence
DRB1_0405  401  DKDLYELPPEEAASI  DLYELPPEE         0.3489        1147.4               50.00     Sequence
DRB1_0405  447  IETWISFKRENEIEP  WISFKRENE         0.3469        1171.4               50.00     Sequence
DRB1_0405   74  PETARIDPFRAAKTL  DPFRAAKTL         0.3469        1172.2               50.00     Sequence
DRB1_0405  300  TARHYIGGLLHHAPS  RHYIGGLLH         0.3469        1172.2               50.00     Sequence
DRB1_0405  267  FGDNGSGMHCHQSLW  SGMHCHQSL         0.3454        1190.5               50.00     Sequence
DRB1_0405  299  DTARHYIGGLLHHAP  RHYIGGLLH         0.3453        1192.7               50.00     Sequence
DRB1_0405   34  FTIPASAFDKSVFDD  FTIPASAFD         0.3440        1209.6               50.00     Sequence
DRB1_0405  317  AFTNPTVNSYKRLVP  FTNPTVNSY         0.3425        1228.6               50.00     Sequence
DRB1_0405  399  PVDKDLYELPPEEAA  KDLYELPPE         0.3396        1268.5               50.00     Sequence
DRB1_0405  151  FYEVDAISGWWNTGA  FYEVDAISG         0.3385        1283.0               50.00     Sequence
DRB1_0405  153  EVDAISGWWNTGAAT  SGWWNTGAA         0.3374        1298.8               50.00     Sequence
DRB1_0405   85  AKTLNINFFVHDPFT  LNINFFVHD         0.3361        1317.9               50.00     Sequence
DRB1_0405  402  KDLYELPPEEAASIP  LYELPPEEA         0.3357        1323.5               50.00     Sequence
DRB1_0405   32  QHFTIPASAFDKSVF  FTIPASAFD         0.3356        1324.1               50.00     Sequence
DRB1_0405    9  FKLAKDEKVEYVDVR  FKLAKDEKV         0.3346        1338.3               50.00     Sequence
DRB1_0405  260  TFMPKPLFGDNGSGM  FMPKPLFGD         0.3317        1381.9               50.00     Sequence
DRB1_0405   35  TIPASAFDKSVFDDG  SAFDKSVFD         0.3316        1382.4               50.00     Sequence
DRB1_0405  429  LEADHEYLTEGGVFT  HEYLTEGGV         0.3313        1387.7               50.00     Sequence
DRB1_0405  298  SDTARHYIGGLLHHA  RHYIGGLLH         0.3312        1389.1               50.00     Sequence
DRB1_0405  452  SFKRENEIEPVNIRP  FKRENEIEP         0.3292        1418.6               50.00     Sequence
DRB1_0405  107  PRNIARKAENYLIST  IARKAENYL         0.3288        1425.6               50.00     Sequence
DRB1_0405  407  LPPEEAASIPQTPTQ  EEAASIPQT         0.3288        1425.7               50.00     Sequence
DRB1_0405  100  LEPYSRDPRNIARKA  YSRDPRNIA         0.3273        1448.6               50.00     Sequence
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DRB1_0405   43  KSVFDDGLAFDGSSI  GLAFDGSSI         0.3270        1452.8               50.00      Sequence
DRB1_0405   33  HFTIPASAFDKSVFD  FTIPASAFD         0.3267        1458.2               50.00      Sequence
DRB1_0405  275  HCHQSLWKDGAPLMY  HCHQSLWKD         0.3241        1499.8               50.00      Sequence
DRB1_0405  456  ENEIEPVNIRPHPYE  EIEPVNIRP         0.3234        1511.4               50.00      Sequence
DRB1_0405  137  IFDSVSFDSRANGSF  SVSFDSRAN         0.3225        1525.6               50.00      Sequence
DRB1_0405  453  FKRENEIEPVNIRPH  FKRENEIEP         0.3222        1530.8               50.00      Sequence
DRB1_0405  101  EPYSRDPRNIARKAE  YSRDPRNIA         0.3222        1531.3               50.00      Sequence
DRB1_0405   99  TLEPYSRDPRNIARK  EPYSRDPRN         0.3220        1534.2               50.00      Sequence
DRB1_0405  252  AWQNGKTVTFMPKPL  KTVTFMPKP         0.3213        1545.8               50.00      Sequence
DRB1_0405  318  FTNPTVNSYKRLVPG  FTNPTVNSY         0.3204        1560.2               50.00      Sequence
DRB1_0405  274  MHCHQSLWKDGAPLM  LWKDGAPLM         0.3202        1564.6               50.00      Sequence
DRB1_0405  319  TNPTVNSYKRLVPGY  TVNSYKRLV         0.3192        1581.8               50.00      Sequence
DRB1_0405  209  GFILEKGHHEVGSGG  FILEKGHHE         0.3191        1582.9               50.00      Sequence
DRB1_0405  420  TQLSDVIDRLEADHE  TQLSDVIDR         0.3181        1599.9               50.00      Sequence
DRB1_0405  342  SQRNRSACVRIPITG  SACVRIPIT         0.3167        1625.6               50.00      Sequence
DRB1_0405  125  DTAYFGAEAEFYIFD  TAYFGAEAE         0.3163        1632.5               50.00      Sequence
DRB1_0405  454  KRENEIEPVNIRPHP  EIEPVNIRP         0.3150        1655.0               50.00      Sequence
DRB1_0405  124  ADTAYFGAEAEFYIF  TAYFGAEAE         0.3146        1662.2               50.00      Sequence
DRB1_0405  457  NEIEPVNIRPHPYEF  EIEPVNIRP         0.3139        1674.9               50.00      Sequence
DRB1_0405  126  TAYFGAEAEFYIFDS  TAYFGAEAE         0.3136        1679.7               50.00      Sequence
DRB1_0405  398  APVDKDLYELPPEEA  KDLYELPPE         0.3129        1693.2               50.00      Sequence
DRB1_0405  123  IADTAYFGAEAEFYI  TAYFGAEAE         0.3128        1694.2               50.00      Sequence
DRB1_0405  463  NIRPHPYEFALYYDV  YEFALYYDV         0.3124        1702.8               50.00      Sequence
DRB1_0405  455  RENEIEPVNIRPHPY  EIEPVNIRP         0.3113        1723.0               50.00      Sequence
DRB1_0405  152  YEVDAISGWWNTGAA  SGWWNTGAA         0.3109        1731.0               50.00      Sequence
DRB1_0405  341  YSQRNRSACVRIPIT  RNRSACVRI         0.3106        1734.9               50.00      Sequence
DRB1_0405   10  KLAKDEKVEYVDVRF  KVEYVDVRF         0.3095        1756.1               50.00      Sequence
DRB1_0405  138  FDSVSFDSRANGSFY  SVSFDSRAN         0.3077        1791.5               50.00      Sequence
DRB1_0405  389  GIKNKIEPQAPVDKD  IKNKIEPQA         0.3073        1797.9               50.00      Sequence
DRB1_0405  428  RLEADHEYLTEGGVF  HEYLTEGGV         0.3055        1834.2               50.00      Sequence
DRB1_0405  458  EIEPVNIRPHPYEFA  EIEPVNIRP         0.3048        1848.2               50.00      Sequence
DRB1_0405  293  GYAGLSDTARHYIGG  YAGLSDTAR         0.3045        1853.4               50.00      Sequence
DRB1_0405  122  GIADTAYFGAEAEFY  TAYFGAEAE         0.3006        1934.0               50.00      Sequence
DRB1_0405   40  AFDKSVFDDGLAFDG  KSVFDDGLA         0.3002        1943.2               50.00      Sequence
DRB1_0405  278  QSLWKDGAPLMYDET  SLWKDGAPL         0.2992        1963.7               50.00      Sequence
DRB1_0405  427  DRLEADHEYLTEGGV  HEYLTEGGV         0.2988        1971.7               50.00      Sequence
DRB1_0405  365  EFRSPDSSGNPYLAF  EFRSPDSSG         0.2967        2017.3               50.00      Sequence
DRB1_0405  406  ELPPEEAASIPQTPT  EEAASIPQT         0.2965        2022.1               50.00      Sequence
DRB1_0405  219  VGSGGQAEINYQFNS  GGQAEINYQ         0.2962        2028.2               50.00      Sequence
DRB1_0405  280  LWKDGAPLMYDETGY  WKDGAPLMY         0.2962        2028.7               50.00      Sequence
DRB1_0405  404  LYELPPEEAASIPQT  LYELPPEEA         0.2958        2036.6               50.00      Sequence
DRB1_0405  462  VNIRPHPYEFALYYD  VNIRPHPYE         0.2954        2045.5               50.00      Sequence
DRB1_0405   41  FDKSVFDDGLAFDGS  SVFDDGLAF         0.2951        2052.2               50.00      Sequence
DRB1_0405  118  LISTGIADTAYFGAE  LISTGIADT         0.2941        2074.6               50.00      Sequence
DRB1_0405  403  DLYELPPEEAASIPQ  LYELPPEEA         0.2920        2121.7               50.00      Sequence
DRB1_0405  279  SLWKDGAPLMYDETG  SLWKDGAPL         0.2909        2147.5               50.00      Sequence
DRB1_0405  106  DPRNIARKAENYLIS  IARKAENYL         0.2889        2196.2               50.00      Sequence
DRB1_0405  121  TGIADTAYFGAEAEF  GIADTAYFG         0.2874        2230.0               50.00      Sequence
DRB1_0405  210  FILEKGHHEVGSGGQ  FILEKGHHE         0.2866        2250.5               50.00      Sequence
DRB1_0405   84  AAKTLNINFFVHDPF  LNINFFVHD         0.2838        2320.6               50.00      Sequence
DRB1_0405  277  HQSLWKDGAPLMYDE  SLWKDGAPL         0.2830        2339.2               50.00      Sequence
DRB1_0405  388  DGIKNKIEPQAPVDK  GIKNKIEPQ         0.2829        2342.2               50.00      Sequence
DRB1_0405  297  LSDTARHYIGGLLHH  RHYIGGLLH         0.2829        2343.0               50.00      Sequence
DRB1_0405   83  RAAKTLNINFFVHDP  KTLNINFFV         0.2829        2343.2               50.00      Sequence
DRB1_0405  461  PVNIRPHPYEFALYY  VNIRPHPYE         0.2807        2397.8               50.00      Sequence
DRB1_0405  350  VRIPITGSNPKAKRL  VRIPITGSN         0.2793        2434.2               50.00      Sequence
DRB1_0405  368  SPDSSGNPYLAFSAM  NPYLAFSAM         0.2793        2435.1               50.00      Sequence
DRB1_0405  120  STGIADTAYFGAEAE  TGIADTAYF         0.2789        2445.0               50.00      Sequence
DRB1_0405    2  EKTPDDVFKLAKDEK  DVFKLAKDE         0.2786        2454.0               50.00      Sequence
DRB1_0405  390  IKNKIEPQAPVDKDL  NKIEPQAPV         0.2759        2525.9               50.00      Sequence
DRB1_0405  159  GWWNTGAATEADGSP  GWWNTGAAT         0.2697        2701.6               50.00      Sequence
DRB1_0405  139  DSVSFDSRANGSFYE  SVSFDSRAN         0.2691        2718.2               50.00      Sequence
DRB1_0405  276  CHQSLWKDGAPLMYD  SLWKDGAPL         0.2690        2722.8               50.00      Sequence
DRB1_0405  405  YELPPEEAASIPQTP  EEAASIPQT         0.2661        2809.2               50.00      Sequence
DRB1_0405  261  FMPKPLFGDNGSGMH  FMPKPLFGD         0.2654        2831.1               50.00      Sequence
DRB1_0405  397  QAPVDKDLYELPPEE  KDLYELPPE         0.2640        2873.6               50.00      Sequence
DRB1_0405   42  DKSVFDDGLAFDGSS  KSVFDDGLA         0.2637        2881.7               50.00      Sequence
DRB1_0405  460  EPVNIRPHPYEFALY  VNIRPHPYE         0.2624        2924.4               50.00      Sequence
DRB1_0405  459  IEPVNIRPHPYEFAL  VNIRPHPYE         0.2615        2953.1               50.00      Sequence
DRB1_0405  218  EVGSGGQAEINYQFN  SGGQAEINY         0.2610        2967.8               50.00      Sequence
DRB1_0405  168  EADGSPNRGYKVRHK  NRGYKVRHK         0.2561        3131.1               50.00      Sequence
DRB1_0405  140  SVSFDSRANGSFYEV  SVSFDSRAN         0.2546        3180.2               50.00      Sequence
DRB1_0405    1  TEKTPDDVFKLAKDE  DVFKLAKDE         0.2531        3232.0               50.00      Sequence
DRB1_0405  105  RDPRNIARKAENYLI  IARKAENYL         0.2489        3383.8               50.00      Sequence
DRB1_0405  340  VYSQRNRSACVRIPI  RNRSACVRI         0.2478        3424.0               50.00      Sequence
DRB1_0405  102  PYSRDPRNIARKAEN  YSRDPRNIA         0.2467        3466.1               50.00      Sequence
DRB1_0405  119  ISTGIADTAYFGAEA  TGIADTAYF         0.2423        3634.5               50.00      Sequence
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   DRB1_0405  421  QLSDVIDRLEADHEY  DVIDRLEAD        0.2400       3725.9                 50.00     Sequence
   DRB1_0405  217  HEVGSGGQAEINYQF  GGQAEINYQ        0.2381       3805.2                 50.00     Sequence
   DRB1_0405  173  PNRGYKVRHKGGYFP  YKVRHKGGY        0.2365       3871.7                 50.00     Sequence
   DRB1_0405  296  GLSDTARHYIGGLLH  ARHYIGGLL        0.2364       3873.4                 50.00     Sequence
   DRB1_0405  167  TEADGSPNRGYKVRH  TEADGSPNR        0.2362       3880.4                 50.00     Sequence
   DRB1_0405  174  NRGYKVRHKGGYFPV  YKVRHKGGY        0.2360       3890.0                 50.00     Sequence
   DRB1_0405   73  DPETARIDPFRAAKT  TARIDPFRA        0.2358       3897.1                 50.00     Sequence
   DRB1_0405  166  ATEADGSPNRGYKVR  TEADGSPNR        0.2346       3948.5                 50.00     Sequence
   DRB1_0405  165  AATEADGSPNRGYKV  TEADGSPNR        0.2309       4113.0                 50.00     Sequence
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   DRB1_0405  172  SPNRGYKVRHKGGYF  NRGYKVRHK        0.2268       4296.5                 50.00     Sequence
   DRB1_0405  103  YSRDPRNIARKAENY  YSRDPRNIA        0.2215       4551.8                 50.00     Sequence
   DRB1_0405  424  DVIDRLEADHEYLTE  DVIDRLEAD        0.2203       4612.1                 50.00     Sequence
   DRB1_0405  422  LSDVIDRLEADHEYL  DVIDRLEAD        0.2198       4636.8                 50.00     Sequence
   DRB1_0405  176  GYKVRHKGGYFPVAP  KVRHKGGYF        0.2184       4704.2                 50.00     Sequence
   DRB1_0405  351  RIPITGSNPKAKRLE  IPITGSNPK        0.2182       4717.6                 50.00     Sequence
   DRB1_0405  171  GSPNRGYKVRHKGGY  NRGYKVRHK        0.2182       4718.8                 50.00     Sequence
   DRB1_0405  392  NKIEPQAPVDKDLYE  NKIEPQAPV        0.2166       4800.0                 50.00     Sequence
   DRB1_0405  164  GAATEADGSPNRGYK  EADGSPNRG        0.2164       4807.8                 50.00     Sequence
   DRB1_0405  141  VSFDSRANGSFYEVD  VSFDSRANG        0.2156       4850.8                 50.00     Sequence
   DRB1_0405  266  LFGDNGSGMHCHQSL  SGMHCHQSL        0.2115       5068.9                 50.00     Sequence
   DRB1_0405  423  SDVIDRLEADHEYLT  DVIDRLEAD        0.2100       5155.7                 50.00     Sequence
   DRB1_0405  175  RGYKVRHKGGYFPVA  KVRHKGGYF        0.2097       5168.7                 50.00     Sequence
   DRB1_0405  142  SFDSRANGSFYEVDA  FDSRANGSF        0.2086       5234.5                 50.00     Sequence
   DRB1_0405  396  PQAPVDKDLYELPPE  KDLYELPPE        0.2063       5364.3                 50.00     Sequence
   DRB1_0405  169  ADGSPNRGYKVRHKG  NRGYKVRHK        0.2041       5493.3                 50.00     Sequence
   DRB1_0405  170  DGSPNRGYKVRHKGG  NRGYKVRHK        0.2009       5688.8                 50.00     Sequence
   DRB1_0405  264  KPLFGDNGSGMHCHQ  PLFGDNGSG        0.1955       6032.7                 50.00     Sequence
   DRB1_0405    0  VTEKTPDDVFKLAKD  DDVFKLAKD        0.1953       6045.9                 50.00     Sequence
   DRB1_0405  356  GSNPKAKRLEFRSPD  AKRLEFRSP        0.1952       6049.1                 50.00     Sequence
   DRB1_0405  425  VIDRLEADHEYLTEG  RLEADHEYL        0.1943       6109.7                 50.00     Sequence
   DRB1_0405  263  PKPLFGDNGSGMHCH  PLFGDNGSG        0.1940       6126.6                 50.00     Sequence
   DRB1_0405  265  PLFGDNGSGMHCHQS  PLFGDNGSG        0.1929       6199.6                 50.00     Sequence
   DRB1_0405  426  IDRLEADHEYLTEGG  RLEADHEYL        0.1920       6263.1                 50.00     Sequence
   DRB1_0405  366  FRSPDSSGNPYLAFS  FRSPDSSGN        0.1902       6386.9                 50.00     Sequence
   DRB1_0405  163  TGAATEADGSPNRGY  TEADGSPNR        0.1896       6429.2                 50.00     Sequence
   DRB1_0405   72  PDPETARIDPFRAAK  TARIDPFRA        0.1881       6536.0                 50.00     Sequence
   DRB1_0405  104  SRDPRNIARKAENYL  IARKAENYL        0.1868       6621.8                 50.00     Sequence
   DRB1_0405  262  MPKPLFGDNGSGMHC  PLFGDNGSG        0.1845       6792.5                 50.00     Sequence
   DRB1_0405  216  HHEVGSGGQAEINYQ  GGQAEINYQ        0.1767       7388.3                 50.00     Sequence
   DRB1_0405  393  KIEPQAPVDKDLYEL  KIEPQAPVD        0.1759       7454.4                 50.00     Sequence
   DRB1_0405   69  LLLPDPETARIDPFR  LLLPDPETA        0.1733       7664.7                 50.00     Sequence
   DRB1_0405  160  WWNTGAATEADGSPN  WWNTGAATE        0.1728       7709.2                 50.00     Sequence
   DRB1_0405  212  LEKGHHEVGSGGQAE  KGHHEVGSG        0.1723       7748.7                 50.00     Sequence
   DRB1_0405  294  YAGLSDTARHYIGGL  YAGLSDTAR        0.1720       7777.4                 50.00     Sequence
   DRB1_0405  213  EKGHHEVGSGGQAEI  KGHHEVGSG        0.1719       7781.7                 50.00     Sequence
   DRB1_0405  162  NTGAATEADGSPNRG  TEADGSPNR        0.1695       7988.4                 50.00     Sequence
   DRB1_0405  352  IPITGSNPKAKRLEF  IPITGSNPK        0.1659       8305.6                 50.00     Sequence
   DRB1_0405  295  AGLSDTARHYIGGLL  ARHYIGGLL        0.1635       8523.4                 50.00     Sequence
   DRB1_0405  214  KGHHEVGSGGQAEIN  HEVGSGGQA        0.1634       8532.3                 50.00     Sequence
   DRB1_0405  367  RSPDSSGNPYLAFSA  PDSSGNPYL        0.1624       8629.0                 50.00     Sequence
   DRB1_0405  211  ILEKGHHEVGSGGQA  KGHHEVGSG        0.1619       8674.2                 50.00     Sequence
   DRB1_0405   71  LPDPETARIDPFRAA  TARIDPFRA        0.1584       9012.9                 50.00     Sequence
   DRB1_0405  161  WNTGAATEADGSPNR  WNTGAATEA        0.1530       9554.0                 50.00     Sequence
   DRB1_0405  395  EPQAPVDKDLYELPP  APVDKDLYE        0.1365      11419.1                 50.00     Sequence
   DRB1_0405  215  GHHEVGSGGQAEINY  HEVGSGGQA        0.1328      11881.0                 50.00     Sequence
   DRB1_0405   70  LLPDPETARIDPFRA  LLPDPETAR        0.1306      12165.4                 50.00     Sequence
   DRB1_0405  394  IEPQAPVDKDLYELP  EPQAPVDKD        0.1229      13225.2                 50.00     Sequence
   DRB1_0405  353  PITGSNPKAKRLEFR  PITGSNPKA        0.1171      14088.1                 50.00     Sequence
   DRB1_0405  355  TGSNPKAKRLEFRSP  AKRLEFRSP        0.1127      14772.1                 50.00     Sequence
   DRB1_0405  354  ITGSNPKAKRLEFRS  ITGSNPKAK        0.0872      19466.2                 50.00     Sequence
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Allele: DRB1_0405. Number of high binders 48. Number of weak binders 166. Number of peptides 464

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0701   76  TARIDPFRAAKTLNI  FRAAKTLNI        0.9516          1.7          SB     0.05     Sequence
   DRB1_0701   77  ARIDPFRAAKTLNIN  FRAAKTLNI        0.9485          1.7          SB     0.05     Sequence
   DRB1_0701   78  RIDPFRAAKTLNINF  FRAAKTLNI        0.9442          1.8          SB     0.05     Sequence
   DRB1_0701   79  IDPFRAAKTLNINFF  FRAAKTLNI        0.9364          2.0          SB     0.10     Sequence
   DRB1_0701   80  DPFRAAKTLNINFFV  FRAAKTLNI        0.9297          2.1          SB     0.15     Sequence
   DRB1_0701   81  PFRAAKTLNINFFVH  FRAAKTLNI        0.9201          2.4          SB     0.20     Sequence
   DRB1_0701   82  FRAAKTLNINFFVHD  FRAAKTLNI        0.9085          2.7          SB     0.40     Sequence
   DRB1_0701  303  HYIGGLLHHAPSLLA  LHHAPSLLA        0.8676          4.2          SB     1.00     Sequence
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DRB1_0701    3  KTPDDVFKLAKDEKV  FKLAKDEKV         0.8607         4.5         SB     2.00       Sequence
DRB1_0701  304  YIGGLLHHAPSLLAF  LHHAPSLLA         0.8556         4.8         SB     2.00       Sequence
DRB1_0701  305  IGGLLHHAPSLLAFT  LHHAPSLLA         0.8396         5.7         SB     2.00       Sequence
DRB1_0701    4  TPDDVFKLAKDEKVE  FKLAKDEKV         0.8362         5.9         SB     2.00       Sequence
DRB1_0701  306  GGLLHHAPSLLAFTN  LHHAPSLLA         0.8174         7.2         SB     4.00       Sequence
DRB1_0701   56  SIRGFQSIHESDMLL  FQSIHESDM         0.8064         8.1         SB     4.00       Sequence
DRB1_0701    5  PDDVFKLAKDEKVEY  FKLAKDEKV         0.8047         8.3         SB     4.00       Sequence
DRB1_0701  307  GLLHHAPSLLAFTNP  LHHAPSLLA         0.8030         8.4         SB     4.00       Sequence
DRB1_0701  338  NLVYSQRNRSACVRI  RNRSACVRI         0.8017         8.6         SB     4.00       Sequence
DRB1_0701   57  IRGFQSIHESDMLLL  FQSIHESDM         0.7940         9.3         SB     4.00       Sequence
DRB1_0701  229  YQFNSLLHAADDMQL  LHAADDMQL         0.7909         9.6         SB     4.00       Sequence
DRB1_0701  308  LLHHAPSLLAFTNPT  LHHAPSLLA         0.7890         9.8         SB     4.00       Sequence
DRB1_0701  302  RHYIGGLLHHAPSLL  LLHHAPSLL         0.7749        11.4         SB     8.00       Sequence
DRB1_0701  221  SGGQAEINYQFNSLL  INYQFNSLL         0.7712        11.9         SB     8.00       Sequence
DRB1_0701  230  QFNSLLHAADDMQLY  LHAADDMQL         0.7708        11.9         SB     8.00       Sequence
DRB1_0701    6  DDVFKLAKDEKVEYV  FKLAKDEKV         0.7681        12.3         SB     8.00       Sequence
DRB1_0701  339  LVYSQRNRSACVRIP  RNRSACVRI         0.7617        13.2         SB     8.00       Sequence
DRB1_0701   58  RGFQSIHESDMLLLP  FQSIHESDM         0.7595        13.5         SB     8.00       Sequence
DRB1_0701  105  RDPRNIARKAENYLI  ARKAENYLI         0.7554        14.1         SB     8.00       Sequence
DRB1_0701    7  DVFKLAKDEKVEYVD  FKLAKDEKV         0.7442        15.9         SB     8.00       Sequence
DRB1_0701  309  LHHAPSLLAFTNPTV  LHHAPSLLA         0.7386        16.9         SB     8.00       Sequence
DRB1_0701  222  GGQAEINYQFNSLLH  INYQFNSLL         0.7383        17.0         SB     8.00       Sequence
DRB1_0701  231  FNSLLHAADDMQLYK  LHAADDMQL         0.7364        17.3         SB     8.00       Sequence
DRB1_0701  340  VYSQRNRSACVRIPI  RNRSACVRI         0.7324        18.1         SB     8.00       Sequence
DRB1_0701  106  DPRNIARKAENYLIS  ARKAENYLI         0.7229        20.0         SB     8.00       Sequence
DRB1_0701   59  GFQSIHESDMLLLPD  FQSIHESDM         0.7190        20.9         SB     8.00       Sequence
DRB1_0701  223  GQAEINYQFNSLLHA  INYQFNSLL         0.7162        21.6         SB     8.00       Sequence
DRB1_0701    8  VFKLAKDEKVEYVDV  FKLAKDEKV         0.7151        21.8         SB     8.00       Sequence
DRB1_0701   54  GSSIRGFQSIHESDM  FQSIHESDM         0.7029        24.9         SB    16.00       Sequence
DRB1_0701   55  SSIRGFQSIHESDML  FQSIHESDM         0.7002        25.6         SB    16.00       Sequence
DRB1_0701  232  NSLLHAADDMQLYKY  LHAADDMQL         0.6946        27.2         SB    16.00       Sequence
DRB1_0701   60  FQSIHESDMLLLPDP  FQSIHESDM         0.6901        28.6         SB    16.00       Sequence
DRB1_0701  205  LINSGFILEKGHHEV  ILEKGHHEV         0.6870        29.6         SB    16.00       Sequence
DRB1_0701  341  YSQRNRSACVRIPIT  RNRSACVRI         0.6864        29.7         SB    16.00       Sequence
DRB1_0701    9  FKLAKDEKVEYVDVR  FKLAKDEKV         0.6805        31.7         SB    16.00       Sequence
DRB1_0701  107  PRNIARKAENYLIST  ARKAENYLI         0.6796        32.0         SB    16.00       Sequence
DRB1_0701  197  LRDKMLTNLINSGFI  TNLINSGFI         0.6767        33.1         SB    16.00       Sequence
DRB1_0701  233  SLLHAADDMQLYKYI  LHAADDMQL         0.6654        37.3         SB    16.00       Sequence
DRB1_0701  188  VAPNDQYVDLRDKML  YVDLRDKML         0.6604        39.4         SB    16.00       Sequence
DRB1_0701  224  QAEINYQFNSLLHAA  INYQFNSLL         0.6588        40.1         SB    16.00       Sequence
DRB1_0701  198  RDKMLTNLINSGFIL  TNLINSGFI         0.6571        40.9         SB    16.00       Sequence
DRB1_0701  189  APNDQYVDLRDKMLT  YVDLRDKML         0.6518        43.3         SB    16.00       Sequence
DRB1_0701  342  SQRNRSACVRIPITG  RNRSACVRI         0.6441        47.0         SB    16.00       Sequence
DRB1_0701  234  LLHAADDMQLYKYII  LHAADDMQL         0.6400        49.2         SB    16.00       Sequence
DRB1_0701  445  DLIETWISFKRENEI  ISFKRENEI         0.6317        53.8         WB    16.00       Sequence
DRB1_0701  331  PGYEAPINLVYSQRN  INLVYSQRN         0.6312        54.0         WB    16.00       Sequence
DRB1_0701  206  INSGFILEKGHHEVG  ILEKGHHEV         0.6291        55.3         WB    16.00       Sequence
DRB1_0701  108  RNIARKAENYLISTG  ARKAENYLI         0.6279        56.1         WB    16.00       Sequence
DRB1_0701  225  AEINYQFNSLLHAAD  INYQFNSLL         0.6235        58.8         WB    16.00       Sequence
DRB1_0701  109  NIARKAENYLISTGI  ARKAENYLI         0.6213        60.2         WB    16.00       Sequence
DRB1_0701  291  ETGYAGLSDTARHYI  LSDTARHYI         0.6120        66.5         WB    16.00       Sequence
DRB1_0701  343  QRNRSACVRIPITGS  RNRSACVRI         0.6061        70.9         WB    16.00       Sequence
DRB1_0701  190  PNDQYVDLRDKMLTN  YVDLRDKML         0.6045        72.2         WB    16.00       Sequence
DRB1_0701  199  DKMLTNLINSGFILE  TNLINSGFI         0.6042        72.4         WB    16.00       Sequence
DRB1_0701  123  IADTAYFGAEAEFYI  FGAEAEFYI         0.6041        72.5         WB    16.00       Sequence
DRB1_0701  370  DSSGNPYLAFSAMLM  YLAFSAMLM         0.5977        77.7         WB    32.00       Sequence
DRB1_0701  235  LHAADDMQLYKYIIK  LHAADDMQL         0.5901        84.4         WB    32.00       Sequence
DRB1_0701  110  IARKAENYLISTGIA  ARKAENYLI         0.5879        86.4         WB    32.00       Sequence
DRB1_0701  332  GYEAPINLVYSQRNR  INLVYSQRN         0.5857        88.5         WB    32.00       Sequence
DRB1_0701  124  ADTAYFGAEAEFYIF  FGAEAEFYI         0.5830        91.1         WB    32.00       Sequence
DRB1_0701  316  LAFTNPTVNSYKRLV  TVNSYKRLV         0.5792        94.9         WB    32.00       Sequence
DRB1_0701  226  EINYQFNSLLHAADD  INYQFNSLL         0.5767        97.5         WB    32.00       Sequence
DRB1_0701  446  LIETWISFKRENEIE  ISFKRENEI         0.5737       100.7         WB    32.00       Sequence
DRB1_0701  207  NSGFILEKGHHEVGS  ILEKGHHEV         0.5723       102.3         WB    32.00       Sequence
DRB1_0701  191  NDQYVDLRDKMLTNL  YVDLRDKML         0.5693       105.6         WB    32.00       Sequence
DRB1_0701  292  TGYAGLSDTARHYIG  LSDTARHYI         0.5688       106.2         WB    32.00       Sequence
DRB1_0701  327  KRLVPGYEAPINLVY  GYEAPINLV         0.5662       109.3         WB    32.00       Sequence
DRB1_0701  371  SSGNPYLAFSAMLMA  YLAFSAMLM         0.5642       111.6         WB    32.00       Sequence
DRB1_0701  344  RNRSACVRIPITGSN  RNRSACVRI         0.5602       116.5         WB    32.00       Sequence
DRB1_0701  104  SRDPRNIARKAENYL  IARKAENYL         0.5571       120.6         WB    32.00       Sequence
DRB1_0701  326  YKRLVPGYEAPINLV  GYEAPINLV         0.5523       126.9         WB    32.00       Sequence
DRB1_0701  192  DQYVDLRDKMLTNLI  YVDLRDKML         0.5479       133.1         WB    32.00       Sequence
DRB1_0701  241  MQLYKYIIKNTAWQN  IIKNTAWQN         0.5443       138.5         WB    32.00       Sequence
DRB1_0701  200  KMLTNLINSGFILEK  TNLINSGFI         0.5421       141.8         WB    32.00       Sequence
DRB1_0701  310  HHAPSLLAFTNPTVN  LLAFTNPTV         0.5415       142.7         WB    32.00       Sequence
DRB1_0701  125  DTAYFGAEAEFYIFD  FGAEAEFYI         0.5410       143.4         WB    32.00       Sequence
DRB1_0701  227  INYQFNSLLHAADDM  INYQFNSLL         0.5348       153.5         WB    32.00       Sequence
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DRB1_0701  317  AFTNPTVNSYKRLVP  TVNSYKRLV        0.5344        154.1          WB    32.00      Sequence
DRB1_0701  295  AGLSDTARHYIGGLL  LSDTARHYI        0.5337        155.3          WB    32.00      Sequence
DRB1_0701  376  YLAFSAMLMAGLDGI  MLMAGLDGI        0.5315        159.1          WB    32.00      Sequence
DRB1_0701   13  KDEKVEYVDVRFCDL  YVDVRFCDL        0.5287        163.8          WB    32.00      Sequence
DRB1_0701  373  GNPYLAFSAMLMAGL  YLAFSAMLM        0.5197        180.8          WB    32.00      Sequence
DRB1_0701  328  RLVPGYEAPINLVYS  GYEAPINLV        0.5168        186.4          WB    32.00      Sequence
DRB1_0701   61  QSIHESDMLLLPDPE  SIHESDMLL        0.5152        189.7          WB    32.00      Sequence
DRB1_0701  293  GYAGLSDTARHYIGG  LSDTARHYI        0.5147        190.8          WB    32.00      Sequence
DRB1_0701  193  QYVDLRDKMLTNLIN  YVDLRDKML        0.5144        191.4          WB    32.00      Sequence
DRB1_0701  208  SGFILEKGHHEVGSG  ILEKGHHEV        0.5075        206.3          WB    32.00      Sequence
DRB1_0701  333  YEAPINLVYSQRNRS  INLVYSQRN        0.5051        211.6          WB    32.00      Sequence
DRB1_0701  372  SGNPYLAFSAMLMAG  YLAFSAMLM        0.5047        212.5          WB    32.00      Sequence
DRB1_0701  201  MLTNLINSGFILEKG  TNLINSGFI        0.5038        214.5          WB    32.00      Sequence
DRB1_0701  126  TAYFGAEAEFYIFDS  FGAEAEFYI        0.5033        215.8          WB    32.00      Sequence
DRB1_0701  447  IETWISFKRENEIEP  ISFKRENEI        0.5014        220.1          WB    32.00      Sequence
DRB1_0701   62  SIHESDMLLLPDPET  SIHESDMLL        0.5005        222.3          WB    32.00      Sequence
DRB1_0701  111  ARKAENYLISTGIAD  ARKAENYLI        0.4967        231.6          WB    32.00      Sequence
DRB1_0701  296  GLSDTARHYIGGLLH  LSDTARHYI        0.4954        235.1          WB    32.00      Sequence
DRB1_0701  311  HAPSLLAFTNPTVNS  LLAFTNPTV        0.4917        244.6          WB    32.00      Sequence
DRB1_0701  242  QLYKYIIKNTAWQNG  IIKNTAWQN        0.4897        250.1          WB    32.00      Sequence
DRB1_0701  321  PTVNSYKRLVPGYEA  TVNSYKRLV        0.4895        250.5          WB    32.00      Sequence
DRB1_0701  294  YAGLSDTARHYIGGL  LSDTARHYI        0.4892        251.3          WB    32.00      Sequence
DRB1_0701  112  RKAENYLISTGIADT  LISTGIADT        0.4885        253.3          WB    32.00      Sequence
DRB1_0701   14  DEKVEYVDVRFCDLP  YVDVRFCDL        0.4857        261.1          WB    32.00      Sequence
DRB1_0701   28  PGIMQHFTIPASAFD  FTIPASAFD        0.4856        261.4          WB    32.00      Sequence
DRB1_0701  127  AYFGAEAEFYIFDSV  FGAEAEFYI        0.4829        269.0          WB    32.00      Sequence
DRB1_0701  247  IIKNTAWQNGKTVTF  WQNGKTVTF        0.4822        271.1          WB    32.00      Sequence
DRB1_0701  318  FTNPTVNSYKRLVPG  TVNSYKRLV        0.4792        279.9          WB    32.00      Sequence
DRB1_0701  204  NLINSGFILEKGHHE  FILEKGHHE        0.4750        293.0          WB    32.00      Sequence
DRB1_0701  374  NPYLAFSAMLMAGLD  YLAFSAMLM        0.4721        302.4          WB    32.00      Sequence
DRB1_0701  202  LTNLINSGFILEKGH  TNLINSGFI        0.4703        308.2          WB    32.00      Sequence
DRB1_0701  275  HCHQSLWKDGAPLMY  LWKDGAPLM        0.4699        309.7          WB    32.00      Sequence
DRB1_0701  312  APSLLAFTNPTVNSY  LLAFTNPTV        0.4689        313.2          WB    32.00      Sequence
DRB1_0701   86  KTLNINFFVHDPFTL  FFVHDPFTL        0.4686        314.1          WB    32.00      Sequence
DRB1_0701  209  GFILEKGHHEVGSGG  ILEKGHHEV        0.4676        317.5          WB    32.00      Sequence
DRB1_0701  329  LVPGYEAPINLVYSQ  GYEAPINLV        0.4667        320.5          WB    32.00      Sequence
DRB1_0701   87  TLNINFFVHDPFTLE  FFVHDPFTL        0.4652        325.8          WB    32.00      Sequence
DRB1_0701  253  WQNGKTVTFMPKPLF  VTFMPKPLF        0.4625        335.3          WB    32.00      Sequence
DRB1_0701  194  YVDLRDKMLTNLINS  YVDLRDKML        0.4620        337.2          WB    32.00      Sequence
DRB1_0701  301  ARHYIGGLLHHAPSL  GLLHHAPSL        0.4619        337.8          WB    32.00      Sequence
DRB1_0701  128  YFGAEAEFYIFDSVS  FGAEAEFYI        0.4595        346.5          WB    32.00      Sequence
DRB1_0701  322  TVNSYKRLVPGYEAP  TVNSYKRLV        0.4553        362.8          WB    32.00      Sequence
DRB1_0701  320  NPTVNSYKRLVPGYE  TVNSYKRLV        0.4527        372.9          WB    50.00      Sequence
DRB1_0701  334  EAPINLVYSQRNRSA  INLVYSQRN        0.4501        383.7          WB    50.00      Sequence
DRB1_0701  248  IKNTAWQNGKTVTFM  WQNGKTVTF        0.4497        385.4          WB    50.00      Sequence
DRB1_0701   46  FDDGLAFDGSSIRGF  FDGSSIRGF        0.4495        386.3          WB    50.00      Sequence
DRB1_0701  448  ETWISFKRENEIEPV  ISFKRENEI        0.4486        389.9          WB    50.00      Sequence
DRB1_0701  336  PINLVYSQRNRSACV  INLVYSQRN        0.4455        403.3          WB    50.00      Sequence
DRB1_0701  113  KAENYLISTGIADTA  LISTGIADT        0.4449        405.8          WB    50.00      Sequence
DRB1_0701   29  GIMQHFTIPASAFDK  FTIPASAFD        0.4446        407.0          WB    50.00      Sequence
DRB1_0701  274  MHCHQSLWKDGAPLM  LWKDGAPLM        0.4416        420.7          WB    50.00      Sequence
DRB1_0701  319  TNPTVNSYKRLVPGY  TVNSYKRLV        0.4363        445.3          WB    50.00      Sequence
DRB1_0701  243  LYKYIIKNTAWQNGK  IIKNTAWQN        0.4354        449.9          WB    50.00      Sequence
DRB1_0701  122  GIADTAYFGAEAEFY  YFGAEAEFY        0.4335        459.0          WB    50.00      Sequence
DRB1_0701  276  CHQSLWKDGAPLMYD  LWKDGAPLM        0.4331        460.9          WB    50.00      Sequence
DRB1_0701   15  EKVEYVDVRFCDLPG  YVDVRFCDL        0.4327        463.2          WB    50.00      Sequence
DRB1_0701  210  FILEKGHHEVGSGGQ  ILEKGHHEV        0.4319        467.4          WB    50.00      Sequence
DRB1_0701  375  PYLAFSAMLMAGLDG  YLAFSAMLM        0.4276        489.4          WB    50.00      Sequence
DRB1_0701  297  LSDTARHYIGGLLHH  ARHYIGGLL        0.4273        491.1          WB    50.00      Sequence
DRB1_0701  203  TNLINSGFILEKGHH  TNLINSGFI        0.4264        495.7          WB    50.00      Sequence
DRB1_0701  173  PNRGYKVRHKGGYFP  KVRHKGGYF        0.4241        508.4                50.00      Sequence
DRB1_0701  337  INLVYSQRNRSACVR  INLVYSQRN        0.4235        511.5                50.00      Sequence
DRB1_0701  330  VPGYEAPINLVYSQR  GYEAPINLV        0.4231        514.1                50.00      Sequence
DRB1_0701  423  SDVIDRLEADHEYLT  RLEADHEYL        0.4215        522.6                50.00      Sequence
DRB1_0701  313  PSLLAFTNPTVNSYK  LLAFTNPTV        0.4206        528.1                50.00      Sequence
DRB1_0701   16  KVEYVDVRFCDLPGI  YVDVRFCDL        0.4165        551.8                50.00      Sequence
DRB1_0701  463  NIRPHPYEFALYYDV  YEFALYYDV        0.4161        554.3                50.00      Sequence
DRB1_0701  174  NRGYKVRHKGGYFPV  KVRHKGGYF        0.4146        563.5                50.00      Sequence
DRB1_0701  449  TWISFKRENEIEPVN  ISFKRENEI        0.4123        577.4                50.00      Sequence
DRB1_0701   88  LNINFFVHDPFTLEP  FFVHDPFTL        0.4112        584.5                50.00      Sequence
DRB1_0701  335  APINLVYSQRNRSAC  INLVYSQRN        0.4110        585.5                50.00      Sequence
DRB1_0701  457  NEIEPVNIRPHPYEF  NIRPHPYEF        0.4100        592.2                50.00      Sequence
DRB1_0701  172  SPNRGYKVRHKGGYF  KVRHKGGYF        0.4075        608.1                50.00      Sequence
DRB1_0701   31  MQHFTIPASAFDKSV  FTIPASAFD        0.4053        623.1                50.00      Sequence
DRB1_0701  422  LSDVIDRLEADHEYL  RLEADHEYL        0.4033        636.6                50.00      Sequence
DRB1_0701   47  DDGLAFDGSSIRGFQ  FDGSSIRGF        0.4012        651.2                50.00      Sequence
DRB1_0701  450  WISFKRENEIEPVNI  ISFKRENEI        0.4003        657.5                50.00      Sequence
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DRB1_0701  114  AENYLISTGIADTAY  LISTGIADT         0.3987         668.8                50.00     Sequence
DRB1_0701   30  IMQHFTIPASAFDKS  FTIPASAFD         0.3972         680.0                50.00     Sequence
DRB1_0701  129  FGAEAEFYIFDSVSF  FGAEAEFYI         0.3956         691.7                50.00     Sequence
DRB1_0701  277  HQSLWKDGAPLMYDE  LWKDGAPLM         0.3939         704.4                50.00     Sequence
DRB1_0701  254  QNGKTVTFMPKPLFG  VTFMPKPLF         0.3932         710.0                50.00     Sequence
DRB1_0701  458  EIEPVNIRPHPYEFA  NIRPHPYEF         0.3929         712.6                50.00     Sequence
DRB1_0701  323  VNSYKRLVPGYEAPI  LVPGYEAPI         0.3911         726.5                50.00     Sequence
DRB1_0701   32  QHFTIPASAFDKSVF  FTIPASAFD         0.3890         742.9                50.00     Sequence
DRB1_0701  249  KNTAWQNGKTVTFMP  WQNGKTVTF         0.3886         746.4                50.00     Sequence
DRB1_0701  137  IFDSVSFDSRANGSF  FDSRANGSF         0.3882         749.9                50.00     Sequence
DRB1_0701  377  LAFSAMLMAGLDGIK  MLMAGLDGI         0.3873         757.1                50.00     Sequence
DRB1_0701  314  SLLAFTNPTVNSYKR  LLAFTNPTV         0.3840         784.7                50.00     Sequence
DRB1_0701  424  DVIDRLEADHEYLTE  RLEADHEYL         0.3806         814.1                50.00     Sequence
DRB1_0701   17  VEYVDVRFCDLPGIM  YVDVRFCDL         0.3780         836.7                50.00     Sequence
DRB1_0701  244  YKYIIKNTAWQNGKT  IIKNTAWQN         0.3774         842.7                50.00     Sequence
DRB1_0701  175  RGYKVRHKGGYFPVA  KVRHKGGYF         0.3764         851.7                50.00     Sequence
DRB1_0701   48  DGLAFDGSSIRGFQS  FDGSSIRGF         0.3741         873.2                50.00     Sequence
DRB1_0701  267  FGDNGSGMHCHQSLW  GMHCHQSLW         0.3699         914.2                50.00     Sequence
DRB1_0701  115  ENYLISTGIADTAYF  LISTGIADT         0.3681         931.4                50.00     Sequence
DRB1_0701   33  HFTIPASAFDKSVFD  FTIPASAFD         0.3677         935.8                50.00     Sequence
DRB1_0701  268  GDNGSGMHCHQSLWK  GMHCHQSLW         0.3661         951.7                50.00     Sequence
DRB1_0701  459  IEPVNIRPHPYEFAL  NIRPHPYEF         0.3658         955.2                50.00     Sequence
DRB1_0701  138  FDSVSFDSRANGSFY  FDSRANGSF         0.3656         957.6                50.00     Sequence
DRB1_0701  363  RLEFRSPDSSGNPYL  FRSPDSSGN         0.3632         982.3                50.00     Sequence
DRB1_0701   89  NINFFVHDPFTLEPY  FFVHDPFTL         0.3625         989.4                50.00     Sequence
DRB1_0701  278  QSLWKDGAPLMYDET  LWKDGAPLM         0.3620         994.8                50.00     Sequence
DRB1_0701   63  IHESDMLLLPDPETA  IHESDMLLL         0.3620         995.0                50.00     Sequence
DRB1_0701  181  HKGGYFPVAPNDQYV  FPVAPNDQY         0.3564        1057.5                50.00     Sequence
DRB1_0701  116  NYLISTGIADTAYFG  LISTGIADT         0.3531        1095.6                50.00     Sequence
DRB1_0701  451  ISFKRENEIEPVNIR  ISFKRENEI         0.3528        1099.6                50.00     Sequence
DRB1_0701  429  LEADHEYLTEGGVFT  YLTEGGVFT         0.3487        1149.0                50.00     Sequence
DRB1_0701  324  NSYKRLVPGYEAPIN  LVPGYEAPI         0.3481        1156.8                50.00     Sequence
DRB1_0701  255  NGKTVTFMPKPLFGD  VTFMPKPLF         0.3474        1165.1                50.00     Sequence
DRB1_0701   49  GLAFDGSSIRGFQSI  FDGSSIRGF         0.3463        1180.0                50.00     Sequence
DRB1_0701  252  AWQNGKTVTFMPKPL  WQNGKTVTF         0.3444        1203.6                50.00     Sequence
DRB1_0701  238  ADDMQLYKYIIKNTA  YKYIIKNTA         0.3397        1266.9                50.00     Sequence
DRB1_0701  315  LLAFTNPTVNSYKRL  LLAFTNPTV         0.3382        1288.0                50.00     Sequence
DRB1_0701  279  SLWKDGAPLMYDETG  LWKDGAPLM         0.3365        1311.5                50.00     Sequence
DRB1_0701  325  SYKRLVPGYEAPINL  LVPGYEAPI         0.3361        1317.2                50.00     Sequence
DRB1_0701  176  GYKVRHKGGYFPVAP  KVRHKGGYF         0.3360        1318.5                50.00     Sequence
DRB1_0701  139  DSVSFDSRANGSFYE  FDSRANGSF         0.3360        1319.3                50.00     Sequence
DRB1_0701  250  NTAWQNGKTVTFMPK  WQNGKTVTF         0.3333        1357.9                50.00     Sequence
DRB1_0701   18  EYVDVRFCDLPGIMQ  YVDVRFCDL         0.3330        1361.9                50.00     Sequence
DRB1_0701  364  LEFRSPDSSGNPYLA  FRSPDSSGN         0.3327        1366.3                50.00     Sequence
DRB1_0701   27  LPGIMQHFTIPASAF  HFTIPASAF         0.3291        1420.2                50.00     Sequence
DRB1_0701  425  VIDRLEADHEYLTEG  RLEADHEYL         0.3273        1448.9                50.00     Sequence
DRB1_0701  460  EPVNIRPHPYEFALY  NIRPHPYEF         0.3268        1456.3                50.00     Sequence
DRB1_0701  148  NGSFYEVDAISGWWN  FYEVDAISG         0.3267        1457.8                50.00     Sequence
DRB1_0701  378  AFSAMLMAGLDGIKN  MLMAGLDGI         0.3266        1460.4                50.00     Sequence
DRB1_0701   90  INFFVHDPFTLEPYS  FFVHDPFTL         0.3256        1474.9                50.00     Sequence
DRB1_0701  269  DNGSGMHCHQSLWKD  GMHCHQSLW         0.3255        1476.7                50.00     Sequence
DRB1_0701   50  LAFDGSSIRGFQSIH  FDGSSIRGF         0.3221        1532.0                50.00     Sequence
DRB1_0701  245  KYIIKNTAWQNGKTV  IIKNTAWQN         0.3214        1543.8                50.00     Sequence
DRB1_0701  360  KAKRLEFRSPDSSGN  FRSPDSSGN         0.3197        1572.1                50.00     Sequence
DRB1_0701   51  AFDGSSIRGFQSIHE  FDGSSIRGF         0.3169        1621.7                50.00     Sequence
DRB1_0701  117  YLISTGIADTAYFGA  LISTGIADT         0.3155        1645.3                50.00     Sequence
DRB1_0701  369  PDSSGNPYLAFSAML  PYLAFSAML         0.3142        1669.8                50.00     Sequence
DRB1_0701  180  RHKGGYFPVAPNDQY  FPVAPNDQY         0.3107        1733.2                50.00     Sequence
DRB1_0701  182  KGGYFPVAPNDQYVD  FPVAPNDQY         0.3099        1749.8                50.00     Sequence
DRB1_0701  430  EADHEYLTEGGVFTN  YLTEGGVFT         0.3098        1750.9                50.00     Sequence
DRB1_0701  239  DDMQLYKYIIKNTAW  YKYIIKNTA         0.3096        1754.8                50.00     Sequence
DRB1_0701  434  EYLTEGGVFTNDLIE  GVFTNDLIE         0.3091        1763.5                50.00     Sequence
DRB1_0701   97  PFTLEPYSRDPRNIA  YSRDPRNIA         0.3091        1763.9                50.00     Sequence
DRB1_0701  290  DETGYAGLSDTARHY  GLSDTARHY         0.3073        1799.2                50.00     Sequence
DRB1_0701  155  DAISGWWNTGAATEA  WNTGAATEA         0.3071        1803.5                50.00     Sequence
DRB1_0701   44  SVFDDGLAFDGSSIR  LAFDGSSIR         0.3060        1825.2                50.00     Sequence
DRB1_0701  461  PVNIRPHPYEFALYY  NIRPHPYEF         0.3053        1837.3                50.00     Sequence
DRB1_0701  365  EFRSPDSSGNPYLAF  FRSPDSSGN         0.3035        1873.3                50.00     Sequence
DRB1_0701  251  TAWQNGKTVTFMPKP  WQNGKTVTF         0.3032        1879.7                50.00     Sequence
DRB1_0701  428  RLEADHEYLTEGGVF  RLEADHEYL         0.3026        1892.5                50.00     Sequence
DRB1_0701  140  SVSFDSRANGSFYEV  FDSRANGSF         0.3024        1896.7                50.00     Sequence
DRB1_0701  228  NYQFNSLLHAADDMQ  LLHAADDMQ         0.3024        1897.1                50.00     Sequence
DRB1_0701   19  YVDVRFCDLPGIMQH  YVDVRFCDL         0.3022        1900.0                50.00     Sequence
DRB1_0701   34  FTIPASAFDKSVFDD  FTIPASAFD         0.3021        1902.4                50.00     Sequence
DRB1_0701  149  GSFYEVDAISGWWNT  FYEVDAISG         0.3000        1945.6                50.00     Sequence
DRB1_0701  177  YKVRHKGGYFPVAPN  KVRHKGGYF         0.2986        1975.3                50.00     Sequence
DRB1_0701  426  IDRLEADHEYLTEGG  RLEADHEYL         0.2986        1975.9                50.00     Sequence
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DRB1_0701  256  GKTVTFMPKPLFGDN  VTFMPKPLF        0.2978       1992.8            50.00     Sequence
DRB1_0701  280  LWKDGAPLMYDETGY  LWKDGAPLM        0.2964       2023.5            50.00     Sequence
DRB1_0701  350  VRIPITGSNPKAKRL  GSNPKAKRL        0.2964       2023.5            50.00     Sequence
DRB1_0701   11  LAKDEKVEYVDVRFC  VEYVDVRFC        0.2956       2041.4            50.00     Sequence
DRB1_0701   84  AAKTLNINFFVHDPF  INFFVHDPF        0.2948       2058.5            50.00     Sequence
DRB1_0701  427  DRLEADHEYLTEGGV  RLEADHEYL        0.2938       2081.6            50.00     Sequence
DRB1_0701  361  AKRLEFRSPDSSGNP  FRSPDSSGN        0.2936       2086.5            50.00     Sequence
DRB1_0701  240  DMQLYKYIIKNTAWQ  YKYIIKNTA        0.2919       2125.0            50.00     Sequence
DRB1_0701  211  ILEKGHHEVGSGGQA  ILEKGHHEV        0.2912       2141.4            50.00     Sequence
DRB1_0701  147  ANGSFYEVDAISGWW  FYEVDAISG        0.2898       2173.3            50.00     Sequence
DRB1_0701  456  ENEIEPVNIRPHPYE  PVNIRPHPY        0.2894       2184.1            50.00     Sequence
DRB1_0701   92  FFVHDPFTLEPYSRD  FFVHDPFTL        0.2873       2232.7            50.00     Sequence
DRB1_0701  246  YIIKNTAWQNGKTVT  IIKNTAWQN        0.2854       2278.5            50.00     Sequence
DRB1_0701  270  NGSGMHCHQSLWKDG  GMHCHQSLW        0.2808       2395.5            50.00     Sequence
DRB1_0701  298  SDTARHYIGGLLHHA  ARHYIGGLL        0.2802       2410.8            50.00     Sequence
DRB1_0701   91  NFFVHDPFTLEPYSR  FFVHDPFTL        0.2797       2424.8            50.00     Sequence
DRB1_0701   52  FDGSSIRGFQSIHES  FDGSSIRGF        0.2795       2429.9            50.00     Sequence
DRB1_0701  362  KRLEFRSPDSSGNPY  FRSPDSSGN        0.2791       2439.7            50.00     Sequence
DRB1_0701  141  VSFDSRANGSFYEVD  FDSRANGSF        0.2774       2486.8            50.00     Sequence
DRB1_0701  379  FSAMLMAGLDGIKNK  MLMAGLDGI        0.2772       2491.5            50.00     Sequence
DRB1_0701  183  GGYFPVAPNDQYVDL  FPVAPNDQY        0.2769       2499.8            50.00     Sequence
DRB1_0701  462  VNIRPHPYEFALYYD  NIRPHPYEF        0.2765       2509.4            50.00     Sequence
DRB1_0701  366  FRSPDSSGNPYLAFS  FRSPDSSGN        0.2747       2559.6            50.00     Sequence
DRB1_0701  435  YLTEGGVFTNDLIET  YLTEGGVFT        0.2742       2573.1            50.00     Sequence
DRB1_0701  432  DHEYLTEGGVFTNDL  YLTEGGVFT        0.2725       2620.0            50.00     Sequence
DRB1_0701  130  GAEAEFYIFDSVSFD  FYIFDSVSF        0.2691       2720.4            50.00     Sequence
DRB1_0701   98  FTLEPYSRDPRNIAR  YSRDPRNIA        0.2690       2721.8            50.00     Sequence
DRB1_0701  145  SRANGSFYEVDAISG  FYEVDAISG        0.2680       2753.3            50.00     Sequence
DRB1_0701  150  SFYEVDAISGWWNTG  FYEVDAISG        0.2656       2824.8            50.00     Sequence
DRB1_0701  431  ADHEYLTEGGVFTND  YLTEGGVFT        0.2651       2839.4            50.00     Sequence
DRB1_0701  433  HEYLTEGGVFTNDLI  YLTEGGVFT        0.2646       2854.8            50.00     Sequence
DRB1_0701   12  AKDEKVEYVDVRFCD  VEYVDVRFC        0.2638       2880.8            50.00     Sequence
DRB1_0701  351  RIPITGSNPKAKRLE  GSNPKAKRL        0.2624       2923.9            50.00     Sequence
DRB1_0701  131  AEAEFYIFDSVSFDS  FYIFDSVSF        0.2624       2924.2            50.00     Sequence
DRB1_0701  156  AISGWWNTGAATEAD  WNTGAATEA        0.2617       2946.3            50.00     Sequence
DRB1_0701   85  AKTLNINFFVHDPFT  INFFVHDPF        0.2617       2946.7            50.00     Sequence
DRB1_0701  257  KTVTFMPKPLFGDNG  VTFMPKPLF        0.2603       2992.6            50.00     Sequence
DRB1_0701  142  SFDSRANGSFYEVDA  FDSRANGSF        0.2597       3009.7            50.00     Sequence
DRB1_0701  271  GSGMHCHQSLWKDGA  GMHCHQSLW        0.2589       3038.2            50.00     Sequence
DRB1_0701  283  DGAPLMYDETGYAGL  YDETGYAGL        0.2573       3089.1            50.00     Sequence
DRB1_0701  440  GVFTNDLIETWISFK  LIETWISFK        0.2554       3153.3            50.00     Sequence
DRB1_0701  178  KVRHKGGYFPVAPND  KVRHKGGYF        0.2552       3159.4            50.00     Sequence
DRB1_0701  273  GMHCHQSLWKDGAPL  GMHCHQSLW        0.2542       3193.9            50.00     Sequence
DRB1_0701   45  VFDDGLAFDGSSIRG  LAFDGSSIR        0.2524       3256.7            50.00     Sequence
DRB1_0701   75  ETARIDPFRAAKTLN  PFRAAKTLN        0.2519       3276.6            50.00     Sequence
DRB1_0701  441  VFTNDLIETWISFKR  LIETWISFK        0.2503       3333.7            50.00     Sequence
DRB1_0701  381  AMLMAGLDGIKNKIE  MLMAGLDGI        0.2501       3339.8            50.00     Sequence
DRB1_0701  184  GYFPVAPNDQYVDLR  FPVAPNDQY        0.2488       3385.8            50.00     Sequence
DRB1_0701  299  DTARHYIGGLLHHAP  ARHYIGGLL        0.2483       3404.4            50.00     Sequence
DRB1_0701   24  FCDLPGIMQHFTIPA  IMQHFTIPA        0.2482       3408.6            50.00     Sequence
DRB1_0701  146  RANGSFYEVDAISGW  FYEVDAISG        0.2465       3473.8            50.00     Sequence
DRB1_0701  171  GSPNRGYKVRHKGGY  YKVRHKGGY        0.2465       3474.4            50.00     Sequence
DRB1_0701  143  FDSRANGSFYEVDAI  FDSRANGSF        0.2421       3640.9            50.00     Sequence
DRB1_0701  118  LISTGIADTAYFGAE  LISTGIADT        0.2409       3688.5            50.00     Sequence
DRB1_0701  151  FYEVDAISGWWNTGA  FYEVDAISG        0.2395       3744.6            50.00     Sequence
DRB1_0701  132  EAEFYIFDSVSFDSR  YIFDSVSFD        0.2385       3787.0            50.00     Sequence
DRB1_0701  352  IPITGSNPKAKRLEF  GSNPKAKRL        0.2364       3873.9            50.00     Sequence
DRB1_0701  380  SAMLMAGLDGIKNKI  MLMAGLDGI        0.2361       3887.9            50.00     Sequence
DRB1_0701  272  SGMHCHQSLWKDGAP  GMHCHQSLW        0.2333       4006.7            50.00     Sequence
DRB1_0701  185  YFPVAPNDQYVDLRD  FPVAPNDQY        0.2324       4044.2            50.00     Sequence
DRB1_0701  196  DLRDKMLTNLINSGF  LTNLINSGF        0.2308       4116.8            50.00     Sequence
DRB1_0701  165  AATEADGSPNRGYKV  GSPNRGYKV        0.2286       4215.2            50.00     Sequence
DRB1_0701  442  FTNDLIETWISFKRE  LIETWISFK        0.2278       4249.5            50.00     Sequence
DRB1_0701  154  VDAISGWWNTGAATE  WWNTGAATE        0.2278       4252.1            50.00     Sequence
DRB1_0701  300  TARHYIGGLLHHAPS  ARHYIGGLL        0.2251       4378.2            50.00     Sequence
DRB1_0701   99  TLEPYSRDPRNIARK  YSRDPRNIA        0.2246       4400.5            50.00     Sequence
DRB1_0701  258  TVTFMPKPLFGDNGS  VTFMPKPLF        0.2244       4410.9            50.00     Sequence
DRB1_0701   96  DPFTLEPYSRDPRNI  PYSRDPRNI        0.2225       4502.6            50.00     Sequence
DRB1_0701   64  HESDMLLLPDPETAR  MLLLPDPET        0.2196       4644.8            50.00     Sequence
DRB1_0701  284  GAPLMYDETGYAGLS  YDETGYAGL        0.2166       4797.8            50.00     Sequence
DRB1_0701  382  MLMAGLDGIKNKIEP  MLMAGLDGI        0.2138       4949.2            50.00     Sequence
DRB1_0701  157  ISGWWNTGAATEADG  WNTGAATEA        0.2126       5010.5            50.00     Sequence
DRB1_0701  133  AEFYIFDSVSFDSRA  FYIFDSVSF        0.2122       5035.2            50.00     Sequence
DRB1_0701  444  NDLIETWISFKRENE  LIETWISFK        0.2121       5039.3            50.00     Sequence
DRB1_0701   25  CDLPGIMQHFTIPAS  IMQHFTIPA        0.2094       5190.7            50.00     Sequence
DRB1_0701  179  VRHKGGYFPVAPNDQ  YFPVAPNDQ        0.2090       5209.6            50.00     Sequence
DRB1_0701  436  LTEGGVFTNDLIETW  GVFTNDLIE        0.2074       5303.0            50.00     Sequence
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DRB1_0701   65  ESDMLLLPDPETARI  MLLLPDPET         0.2065       5352.3                 50.00     Sequence
DRB1_0701  443  TNDLIETWISFKREN  LIETWISFK         0.2061       5374.7                 50.00     Sequence
DRB1_0701  186  FPVAPNDQYVDLRDK  FPVAPNDQY         0.2029       5568.3                 50.00     Sequence
DRB1_0701  353  PITGSNPKAKRLEFR  GSNPKAKRL         0.1989       5811.9                 50.00     Sequence
DRB1_0701  281  WKDGAPLMYDETGYA  LMYDETGYA         0.1981       5863.2                 50.00     Sequence
DRB1_0701  100  LEPYSRDPRNIARKA  YSRDPRNIA         0.1970       5936.1                 50.00     Sequence
DRB1_0701  455  RENEIEPVNIRPHPY  PVNIRPHPY         0.1946       6088.2                 50.00     Sequence
DRB1_0701  166  ATEADGSPNRGYKVR  GSPNRGYKV         0.1930       6196.1                 50.00     Sequence
DRB1_0701  134  EFYIFDSVSFDSRAN  FYIFDSVSF         0.1906       6361.6                 50.00     Sequence
DRB1_0701  213  EKGHHEVGSGGQAEI  VGSGGQAEI         0.1890       6470.5                 50.00     Sequence
DRB1_0701  354  ITGSNPKAKRLEFRS  GSNPKAKRL         0.1889       6479.2                 50.00     Sequence
DRB1_0701  437  TEGGVFTNDLIETWI  GVFTNDLIE         0.1850       6753.0                 50.00     Sequence
DRB1_0701  158  SGWWNTGAATEADGS  WNTGAATEA         0.1834       6870.2                 50.00     Sequence
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DRB1_0701   43  KSVFDDGLAFDGSSI  GLAFDGSSI         0.1784       7256.9                 50.00     Sequence
DRB1_0701  285  APLMYDETGYAGLSD  YDETGYAGL         0.1767       7387.9                 50.00     Sequence
DRB1_0701  259  VTFMPKPLFGDNGSG  VTFMPKPLF         0.1756       7482.1                 50.00     Sequence
DRB1_0701   26  DLPGIMQHFTIPASA  IMQHFTIPA         0.1743       7585.5                 50.00     Sequence
DRB1_0701  102  PYSRDPRNIARKAEN  YSRDPRNIA         0.1740       7608.9                 50.00     Sequence
DRB1_0701  355  TGSNPKAKRLEFRSP  GSNPKAKRL         0.1734       7660.3                 50.00     Sequence
DRB1_0701  195  VDLRDKMLTNLINSG  RDKMLTNLI         0.1725       7731.5                 50.00     Sequence
DRB1_0701   93  FVHDPFTLEPYSRDP  FTLEPYSRD         0.1715       7817.5                 50.00     Sequence
DRB1_0701  135  FYIFDSVSFDSRANG  FYIFDSVSF         0.1714       7825.2                 50.00     Sequence
DRB1_0701  159  GWWNTGAATEADGSP  WNTGAATEA         0.1661       8292.2                 50.00     Sequence
DRB1_0701  438  EGGVFTNDLIETWIS  GVFTNDLIE         0.1650       8389.6                 50.00     Sequence
DRB1_0701   35  TIPASAFDKSVFDDG  PASAFDKSV         0.1644       8445.1                 50.00     Sequence
DRB1_0701  214  KGHHEVGSGGQAEIN  VGSGGQAEI         0.1634       8537.4                 50.00     Sequence
DRB1_0701  167  TEADGSPNRGYKVRH  GSPNRGYKV         0.1631       8563.4                 50.00     Sequence
DRB1_0701   36  IPASAFDKSVFDDGL  DKSVFDDGL         0.1621       8654.2                 50.00     Sequence
DRB1_0701  346  RSACVRIPITGSNPK  IPITGSNPK         0.1620       8663.9                 50.00     Sequence
DRB1_0701  367  RSPDSSGNPYLAFSA  PDSSGNPYL         0.1614       8716.4                 50.00     Sequence
DRB1_0701  356  GSNPKAKRLEFRSPD  GSNPKAKRL         0.1614       8722.8                 50.00     Sequence
DRB1_0701  152  YEVDAISGWWNTGAA  VDAISGWWN         0.1604       8811.9                 50.00     Sequence
DRB1_0701  160  WWNTGAATEADGSPN  WNTGAATEA         0.1603       8824.4                 50.00     Sequence
DRB1_0701   74  PETARIDPFRAAKTL  IDPFRAAKT         0.1588       8972.3                 50.00     Sequence
DRB1_0701   67  DMLLLPDPETARIDP  MLLLPDPET         0.1576       9088.7                 50.00     Sequence
DRB1_0701   68  MLLLPDPETARIDPF  MLLLPDPET         0.1563       9211.8                 50.00     Sequence
DRB1_0701  416  PQTPTQLSDVIDRLE  LSDVIDRLE         0.1559       9252.5                 50.00     Sequence
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DRB1_0701   53  DGSSIRGFQSIHESD  IRGFQSIHE         0.1534       9509.7                 50.00     Sequence
DRB1_0701  170  DGSPNRGYKVRHKGG  GSPNRGYKV         0.1507       9792.3                 50.00     Sequence
DRB1_0701  153  EVDAISGWWNTGAAT  VDAISGWWN         0.1500       9869.5                 50.00     Sequence
DRB1_0701  452  SFKRENEIEPVNIRP  FKRENEIEP         0.1490       9969.4                 50.00     Sequence
DRB1_0701  286  PLMYDETGYAGLSDT  YDETGYAGL         0.1473      10160.8                 50.00     Sequence
DRB1_0701  368  SPDSSGNPYLAFSAM  PDSSGNPYL         0.1460      10302.6                 50.00     Sequence
DRB1_0701  345  NRSACVRIPITGSNP  RSACVRIPI         0.1447      10443.3                 50.00     Sequence
DRB1_0701  410  EEAASIPQTPTQLSD  IPQTPTQLS         0.1444      10484.4                 50.00     Sequence
DRB1_0701   37  PASAFDKSVFDDGLA  DKSVFDDGL         0.1439      10542.9                 50.00     Sequence
DRB1_0701  262  MPKPLFGDNGSGMHC  LFGDNGSGM         0.1414      10827.7                 50.00     Sequence
DRB1_0701  217  HEVGSGGQAEINYQF  GQAEINYQF         0.1402      10969.2                 50.00     Sequence
DRB1_0701  411  EAASIPQTPTQLSDV  IPQTPTQLS         0.1402      10974.3                 50.00     Sequence
DRB1_0701  408  PPEEAASIPQTPTQL  SIPQTPTQL         0.1393      11071.9                 50.00     Sequence
DRB1_0701  288  MYDETGYAGLSDTAR  YDETGYAGL         0.1393      11071.9                 50.00     Sequence
DRB1_0701  136  YIFDSVSFDSRANGS  IFDSVSFDS         0.1391      11097.6                 50.00     Sequence
DRB1_0701  215  GHHEVGSGGQAEINY  VGSGGQAEI         0.1390      11115.2                 50.00     Sequence
DRB1_0701  348  ACVRIPITGSNPKAK  ITGSNPKAK         0.1389      11119.6                 50.00     Sequence
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DRB1_0701  261  FMPKPLFGDNGSGMH  LFGDNGSGM         0.1348      11630.6                 50.00     Sequence
DRB1_0701  168  EADGSPNRGYKVRHK  GSPNRGYKV         0.1347      11641.3                 50.00     Sequence
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DRB1_0701  103  YSRDPRNIARKAENY  YSRDPRNIA         0.1316      12032.6                 50.00     Sequence
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DRB1_0701    0  VTEKTPDDVFKLAKD  TEKTPDDVF         0.1280      12512.3                 50.00     Sequence
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DRB1_0701   83  RAAKTLNINFFVHDP  AAKTLNINF         0.1266      12702.3                 50.00     Sequence
DRB1_0701  412  AASIPQTPTQLSDVI  IPQTPTQLS         0.1256      12841.2                 50.00     Sequence
DRB1_0701  263  PKPLFGDNGSGMHCH  LFGDNGSGM         0.1249      12946.1                 50.00     Sequence
DRB1_0701  386  GLDGIKNKIEPQAPV  NKIEPQAPV         0.1242      13042.0                 50.00     Sequence
DRB1_0701  413  ASIPQTPTQLSDVID  IPQTPTQLS         0.1238      13101.4                 50.00     Sequence
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   DRB1_0701  349  CVRIPITGSNPKAKR  ITGSNPKAK        0.1209      13513.3               50.00     Sequence
   DRB1_0701  421  QLSDVIDRLEADHEY  IDRLEADHE        0.1202      13612.9               50.00     Sequence
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   DRB1_0701  414  SIPQTPTQLSDVIDR  SIPQTPTQL        0.1154      14341.2               50.00     Sequence
   DRB1_0701  289  YDETGYAGLSDTARH  YDETGYAGL        0.1147      14459.8               50.00     Sequence
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   DRB1_0701  454  KRENEIEPVNIRPHP  IEPVNIRPH        0.1110      15042.0               50.00     Sequence
   DRB1_0701  403  DLYELPPEEAASIPQ  PEEAASIPQ        0.1101      15191.5               50.00     Sequence
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   DRB1_0701   21  DVRFCDLPGIMQHFT  FCDLPGIMQ        0.1090      15369.0               50.00     Sequence
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   DRB1_0701  384  MAGLDGIKNKIEPQA  LDGIKNKIE        0.1050      16059.7               50.00     Sequence
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   DRB1_0701   70  LLPDPETARIDPFRA  PETARIDPF        0.1036      16301.5               50.00     Sequence
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   DRB1_0701  393  KIEPQAPVDKDLYEL  PQAPVDKDL        0.0925      18370.6               50.00     Sequence
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   DRB1_0701  402  KDLYELPPEEAASIP  LPPEEAASI        0.0833      20296.0               50.00     Sequence
   DRB1_0701  407  LPPEEAASIPQTPTQ  AASIPQTPT        0.0805      20916.8               50.00     Sequence
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   DRB1_0701  359  PKAKRLEFRSPDSSG  EFRSPDSSG        0.0617      25656.0               50.00     Sequence
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   DRB1_0701  396  PQAPVDKDLYELPPE  PQAPVDKDL        0.0564      27146.5               50.00     Sequence
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Allele: DRB1_0701. Number of high binders 52. Number of weak binders 93. Number of peptides 464

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0802  321  PTVNSYKRLVPGYEA  TVNSYKRLV         0.6919         28.0         SB     0.80     Sequence
   DRB1_0802  173  PNRGYKVRHKGGYFP  RGYKVRHKG         0.6915         28.2         SB     0.80     Sequence
   DRB1_0802  322  TVNSYKRLVPGYEAP  TVNSYKRLV         0.6901         28.6         SB     0.80     Sequence
   DRB1_0802  175  RGYKVRHKGGYFPVA  RGYKVRHKG         0.6873         29.5         SB     0.80     Sequence
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   DRB1_0802  242  QLYKYIIKNTAWQNG  YKYIIKNTA         0.6804         31.7         SB     0.80     Sequence
   DRB1_0802  241  MQLYKYIIKNTAWQN  YKYIIKNTA         0.6644         37.8         SB     0.80     Sequence
   DRB1_0802  172  SPNRGYKVRHKGGYF  RGYKVRHKG         0.6550         41.8         SB     1.00     Sequence
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   DRB1_0802  227  INYQFNSLLHAADDM  QFNSLLHAA         0.6113         67.1         WB     2.00     Sequence
   DRB1_0802  318  FTNPTVNSYKRLVPG  TVNSYKRLV         0.6110         67.3         WB     2.00     Sequence
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   DRB1_0802  226  EINYQFNSLLHAADD  QFNSLLHAA         0.5907         83.8         WB     4.00     Sequence
   DRB1_0802  225  AEINYQFNSLLHAAD  QFNSLLHAA         0.5725        102.0         WB     4.00     Sequence
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   DRB1_0802  304  YIGGLLHHAPSLLAF  YIGGLLHHA         0.5025        217.6         WB     8.00     Sequence
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   DRB1_0802   53  DGSSIRGFQSIHESD  GSSIRGFQS         0.3893        740.5               32.00     Sequence
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   DRB1_0802  389  GIKNKIEPQAPVDKD  IKNKIEPQA         0.3711        901.8               32.00     Sequence
   DRB1_0802  388  DGIKNKIEPQAPVDK  IKNKIEPQA         0.3710        903.0               32.00     Sequence
   DRB1_0802  153  EVDAISGWWNTGAAT  VDAISGWWN         0.3694        918.6               32.00     Sequence
   DRB1_0802   52  FDGSSIRGFQSIHES  GSSIRGFQS         0.3681        931.6               32.00     Sequence
   DRB1_0802   80  DPFRAAKTLNINFFV  PFRAAKTLN         0.3664        949.0               32.00     Sequence
   DRB1_0802   51  AFDGSSIRGFQSIHE  GSSIRGFQS         0.3624        990.6               32.00     Sequence
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DRB1_0802  274  MHCHQSLWKDGAPLM  LWKDGAPLM         0.3604        1012.8              32.00     Sequence
DRB1_0802  275  HCHQSLWKDGAPLMY  CHQSLWKDG         0.3601        1016.4              32.00     Sequence
DRB1_0802  386  GLDGIKNKIEPQAPV  IKNKIEPQA         0.3550        1073.1              32.00     Sequence
DRB1_0802  387  LDGIKNKIEPQAPVD  IKNKIEPQA         0.3547        1076.8              32.00     Sequence
DRB1_0802  385  AGLDGIKNKIEPQAP  IKNKIEPQA         0.3539        1086.4              32.00     Sequence
DRB1_0802  193  QYVDLRDKMLTNLIN  YVDLRDKML         0.3539        1086.7              32.00     Sequence
DRB1_0802  305  IGGLLHHAPSLLAFT  IGGLLHHAP         0.3486        1150.3              32.00     Sequence
DRB1_0802  276  CHQSLWKDGAPLMYD  CHQSLWKDG         0.3471        1169.1              32.00     Sequence
DRB1_0802  194  YVDLRDKMLTNLINS  YVDLRDKML         0.3465        1176.6              32.00     Sequence
DRB1_0802  178  KVRHKGGYFPVAPND  VRHKGGYFP         0.3446        1201.0              32.00     Sequence
DRB1_0802   50  LAFDGSSIRGFQSIH  GSSIRGFQS         0.3425        1229.4              32.00     Sequence
DRB1_0802   81  PFRAAKTLNINFFVH  PFRAAKTLN         0.3386        1282.1              32.00     Sequence
DRB1_0802  384  MAGLDGIKNKIEPQA  IKNKIEPQA         0.3380        1290.2              32.00     Sequence
DRB1_0802  443  TNDLIETWISFKREN  IETWISFKR         0.3335        1354.4              32.00     Sequence
DRB1_0802  154  VDAISGWWNTGAATE  VDAISGWWN         0.3316        1382.5              32.00     Sequence
DRB1_0802  442  FTNDLIETWISFKRE  IETWISFKR         0.3314        1386.2              32.00     Sequence
DRB1_0802  273  GMHCHQSLWKDGAPL  MHCHQSLWK         0.3285        1429.5              32.00     Sequence
DRB1_0802  344  RNRSACVRIPITGSN  RNRSACVRI         0.3263        1463.8              32.00     Sequence
DRB1_0802  152  YEVDAISGWWNTGAA  VDAISGWWN         0.3260        1468.9              32.00     Sequence
DRB1_0802  151  FYEVDAISGWWNTGA  VDAISGWWN         0.3256        1475.5              32.00     Sequence
DRB1_0802  192  DQYVDLRDKMLTNLI  YVDLRDKML         0.3254        1479.5              32.00     Sequence
DRB1_0802  332  GYEAPINLVYSQRNR  YEAPINLVY         0.3253        1480.4              32.00     Sequence
DRB1_0802  209  GFILEKGHHEVGSGG  GFILEKGHH         0.3247        1490.8              32.00     Sequence
DRB1_0802  223  GQAEINYQFNSLLHA  INYQFNSLL         0.3155        1646.0              50.00     Sequence
DRB1_0802  390  IKNKIEPQAPVDKDL  IKNKIEPQA         0.3128        1695.6              50.00     Sequence
DRB1_0802  150  SFYEVDAISGWWNTG  VDAISGWWN         0.3119        1711.2              50.00     Sequence
DRB1_0802  195  VDLRDKMLTNLINSG  VDLRDKMLT         0.3113        1722.8              50.00     Sequence
DRB1_0802  450  WISFKRENEIEPVNI  WISFKRENE         0.3096        1754.2              50.00     Sequence
DRB1_0802  296  GLSDTARHYIGGLLH  GLSDTARHY         0.3095        1757.1              50.00     Sequence
DRB1_0802   27  LPGIMQHFTIPASAF  GIMQHFTIP         0.3069        1806.0              50.00     Sequence
DRB1_0802  250  NTAWQNGKTVTFMPK  GKTVTFMPK         0.3061        1822.0              50.00     Sequence
DRB1_0802  373  GNPYLAFSAMLMAGL  YLAFSAMLM         0.3048        1848.8              50.00     Sequence
DRB1_0802  237  AADDMQLYKYIIKNT  QLYKYIIKN         0.3043        1857.5              50.00     Sequence
DRB1_0802  375  PYLAFSAMLMAGLDG  YLAFSAMLM         0.3029        1887.5              50.00     Sequence
DRB1_0802  208  SGFILEKGHHEVGSG  ILEKGHHEV         0.3018        1908.8              50.00     Sequence
DRB1_0802  325  SYKRLVPGYEAPINL  YKRLVPGYE         0.3014        1916.8              50.00     Sequence
DRB1_0802  441  VFTNDLIETWISFKR  IETWISFKR         0.3007        1931.1              50.00     Sequence
DRB1_0802   74  PETARIDPFRAAKTL  RIDPFRAAK         0.2998        1950.0              50.00     Sequence
DRB1_0802  272  SGMHCHQSLWKDGAP  MHCHQSLWK         0.2996        1954.9              50.00     Sequence
DRB1_0802   29  GIMQHFTIPASAFDK  GIMQHFTIP         0.2989        1970.1              50.00     Sequence
DRB1_0802  102  PYSRDPRNIARKAEN  YSRDPRNIA         0.2979        1991.1              50.00     Sequence
DRB1_0802  374  NPYLAFSAMLMAGLD  YLAFSAMLM         0.2978        1994.3              50.00     Sequence
DRB1_0802   28  PGIMQHFTIPASAFD  IMQHFTIPA         0.2962        2029.0              50.00     Sequence
DRB1_0802  191  NDQYVDLRDKMLTNL  YVDLRDKML         0.2960        2032.7              50.00     Sequence
DRB1_0802  345  NRSACVRIPITGSNP  RSACVRIPI         0.2951        2053.1              50.00     Sequence
DRB1_0802  351  RIPITGSNPKAKRLE  PITGSNPKA         0.2950        2055.8              50.00     Sequence
DRB1_0802  350  VRIPITGSNPKAKRL  RIPITGSNP         0.2943        2071.5              50.00     Sequence
DRB1_0802  271  GSGMHCHQSLWKDGA  HQSLWKDGA         0.2939        2079.8              50.00     Sequence
DRB1_0802  360  KAKRLEFRSPDSSGN  KAKRLEFRS         0.2924        2112.4              50.00     Sequence
DRB1_0802  343  QRNRSACVRIPITGS  RNRSACVRI         0.2917        2129.4              50.00     Sequence
DRB1_0802  277  HQSLWKDGAPLMYDE  SLWKDGAPL         0.2912        2140.3              50.00     Sequence
DRB1_0802  155  DAISGWWNTGAATEA  AISGWWNTG         0.2895        2181.7              50.00     Sequence
DRB1_0802  206  INSGFILEKGHHEVG  ILEKGHHEV         0.2885        2203.7              50.00     Sequence
DRB1_0802  306  GGLLHHAPSLLAFTN  GGLLHHAPS         0.2884        2206.0              50.00     Sequence
DRB1_0802  207  NSGFILEKGHHEVGS  GFILEKGHH         0.2880        2216.6              50.00     Sequence
DRB1_0802   26  DLPGIMQHFTIPASA  GIMQHFTIP         0.2876        2226.4              50.00     Sequence
DRB1_0802   49  GLAFDGSSIRGFQSI  GSSIRGFQS         0.2865        2253.8              50.00     Sequence
DRB1_0802  297  LSDTARHYIGGLLHH  SDTARHYIG         0.2834        2329.7              50.00     Sequence
DRB1_0802  205  LINSGFILEKGHHEV  GFILEKGHH         0.2823        2357.0              50.00     Sequence
DRB1_0802  190  PNDQYVDLRDKMLTN  YVDLRDKML         0.2822        2360.0              50.00     Sequence
DRB1_0802  346  RSACVRIPITGSNPK  RSACVRIPI         0.2820        2364.5              50.00     Sequence
DRB1_0802  372  SGNPYLAFSAMLMAG  YLAFSAMLM         0.2816        2374.9              50.00     Sequence
DRB1_0802  179  VRHKGGYFPVAPNDQ  VRHKGGYFP         0.2805        2402.8              50.00     Sequence
DRB1_0802  103  YSRDPRNIARKAENY  YSRDPRNIA         0.2805        2403.9              50.00     Sequence
DRB1_0802  359  PKAKRLEFRSPDSSG  KAKRLEFRS         0.2796        2427.9              50.00     Sequence
DRB1_0802  156  AISGWWNTGAATEAD  GWWNTGAAT         0.2755        2538.0              50.00     Sequence
DRB1_0802   30  IMQHFTIPASAFDKS  IMQHFTIPA         0.2754        2540.4              50.00     Sequence
DRB1_0802  198  RDKMLTNLINSGFIL  RDKMLTNLI         0.2747        2559.2              50.00     Sequence
DRB1_0802  189  APNDQYVDLRDKMLT  YVDLRDKML         0.2737        2587.4              50.00     Sequence
DRB1_0802  331  PGYEAPINLVYSQRN  PINLVYSQR         0.2731        2603.5              50.00     Sequence
DRB1_0802   99  TLEPYSRDPRNIARK  YSRDPRNIA         0.2718        2640.4              50.00     Sequence
DRB1_0802  101  EPYSRDPRNIARKAE  YSRDPRNIA         0.2698        2699.5              50.00     Sequence
DRB1_0802  376  YLAFSAMLMAGLDGI  YLAFSAMLM         0.2684        2739.1              50.00     Sequence
DRB1_0802  149  GSFYEVDAISGWWNT  VDAISGWWN         0.2671        2780.3              50.00     Sequence
DRB1_0802   98  FTLEPYSRDPRNIAR  YSRDPRNIA         0.2663        2802.2              50.00     Sequence
DRB1_0802  222  GGQAEINYQFNSLLH  INYQFNSLL         0.2661        2807.9              50.00     Sequence
DRB1_0802  106  DPRNIARKAENYLIS  RNIARKAEN         0.2657        2820.6              50.00     Sequence
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DRB1_0802  107  PRNIARKAENYLIST  PRNIARKAE       0.2655      2826.4            50.00    Sequence
DRB1_0802  197  LRDKMLTNLINSGFI  RDKMLTNLI       0.2647      2851.0            50.00    Sequence
DRB1_0802  315  LLAFTNPTVNSYKRL  NPTVNSYKR       0.2645      2857.6            50.00    Sequence
DRB1_0802   73  DPETARIDPFRAAKT  RIDPFRAAK       0.2644      2860.4            50.00    Sequence
DRB1_0802  100  LEPYSRDPRNIARKA  YSRDPRNIA       0.2638      2880.5            50.00    Sequence
DRB1_0802  356  GSNPKAKRLEFRSPD  GSNPKAKRL       0.2627      2913.1            50.00    Sequence
DRB1_0802  349  CVRIPITGSNPKAKR  PITGSNPKA       0.2613      2958.9            50.00    Sequence
DRB1_0802   55  SSIRGFQSIHESDML  SIRGFQSIH       0.2611      2965.4            50.00    Sequence
DRB1_0802  341  YSQRNRSACVRIPIT  YSQRNRSAC       0.2611      2966.3            50.00    Sequence
DRB1_0802  342  SQRNRSACVRIPITG  RNRSACVRI       0.2604      2986.4            50.00    Sequence
DRB1_0802  361  AKRLEFRSPDSSGNP  RLEFRSPDS       0.2595      3017.3            50.00    Sequence
DRB1_0802  357  SNPKAKRLEFRSPDS  SNPKAKRLE       0.2591      3031.4            50.00    Sequence
DRB1_0802  348  ACVRIPITGSNPKAK  PITGSNPKA       0.2587      3042.9            50.00    Sequence
DRB1_0802   25  CDLPGIMQHFTIPAS  IMQHFTIPA       0.2579      3068.3            50.00    Sequence
DRB1_0802  270  NGSGMHCHQSLWKDG  GMHCHQSLW       0.2579      3069.7            50.00    Sequence
DRB1_0802  358  NPKAKRLEFRSPDSS  KAKRLEFRS       0.2569      3102.4            50.00    Sequence
DRB1_0802  201  MLTNLINSGFILEKG  MLTNLINSG       0.2566      3113.8            50.00    Sequence
DRB1_0802  105  RDPRNIARKAENYLI  RNIARKAEN       0.2559      3136.7            50.00    Sequence
DRB1_0802  278  QSLWKDGAPLMYDET  SLWKDGAPL       0.2553      3158.6            50.00    Sequence
DRB1_0802  148  NGSFYEVDAISGWWN  EVDAISGWW       0.2541      3199.9            50.00    Sequence
DRB1_0802   56  SIRGFQSIHESDMLL  SIRGFQSIH       0.2537      3210.8            50.00    Sequence
DRB1_0802  293  GYAGLSDTARHYIGG  GYAGLSDTA       0.2528      3243.5            50.00    Sequence
DRB1_0802  352  IPITGSNPKAKRLEF  PITGSNPKA       0.2509      3311.3            50.00    Sequence
DRB1_0802  258  TVTFMPKPLFGDNGS  VTFMPKPLF       0.2506      3323.1            50.00    Sequence
DRB1_0802  355  TGSNPKAKRLEFRSP  GSNPKAKRL       0.2504      3329.4            50.00    Sequence
DRB1_0802  199  DKMLTNLINSGFILE  MLTNLINSG       0.2504      3330.5            50.00    Sequence
DRB1_0802   97  PFTLEPYSRDPRNIA  YSRDPRNIA       0.2503      3331.7            50.00    Sequence
DRB1_0802  371  SSGNPYLAFSAMLMA  YLAFSAMLM       0.2494      3365.8            50.00    Sequence
DRB1_0802   48  DGLAFDGSSIRGFQS  GSSIRGFQS       0.2482      3408.9            50.00    Sequence
DRB1_0802  247  IIKNTAWQNGKTVTF  IIKNTAWQN       0.2478      3423.5            50.00    Sequence
DRB1_0802  328  RLVPGYEAPINLVYS  RLVPGYEAP       0.2469      3459.0            50.00    Sequence
DRB1_0802  347  SACVRIPITGSNPKA  ACVRIPITG       0.2467      3463.5            50.00    Sequence
DRB1_0802  327  KRLVPGYEAPINLVY  RLVPGYEAP       0.2449      3532.2            50.00    Sequence
DRB1_0802  362  KRLEFRSPDSSGNPY  RLEFRSPDS       0.2448      3538.5            50.00    Sequence
DRB1_0802  200  KMLTNLINSGFILEK  MLTNLINSG       0.2427      3617.3            50.00    Sequence
DRB1_0802  204  NLINSGFILEKGHHE  LINSGFILE       0.2417      3656.8            50.00    Sequence
DRB1_0802  326  YKRLVPGYEAPINLV  RLVPGYEAP       0.2411      3680.7            50.00    Sequence
DRB1_0802  159  GWWNTGAATEADGSP  GWWNTGAAT       0.2405      3705.3            50.00    Sequence
DRB1_0802  279  SLWKDGAPLMYDETG  SLWKDGAPL       0.2398      3732.4            50.00    Sequence
DRB1_0802  140  SVSFDSRANGSFYEV  SVSFDSRAN       0.2390      3764.8            50.00    Sequence
DRB1_0802   19  YVDVRFCDLPGIMQH  VDVRFCDLP       0.2365      3870.3            50.00    Sequence
DRB1_0802  292  TGYAGLSDTARHYIG  GYAGLSDTA       0.2353      3921.5            50.00    Sequence
DRB1_0802  196  DLRDKMLTNLINSGF  RDKMLTNLI       0.2351      3927.0            50.00    Sequence
DRB1_0802  104  SRDPRNIARKAENYL  RNIARKAEN       0.2351      3927.5            50.00    Sequence
DRB1_0802  370  DSSGNPYLAFSAMLM  YLAFSAMLM       0.2351      3929.6            50.00    Sequence
DRB1_0802  138  FDSVSFDSRANGSFY  SVSFDSRAN       0.2338      3983.2            50.00    Sequence
DRB1_0802  139  DSVSFDSRANGSFYE  SVSFDSRAN       0.2337      3987.1            50.00    Sequence
DRB1_0802  295  AGLSDTARHYIGGLL  GLSDTARHY       0.2330      4020.9            50.00    Sequence
DRB1_0802  354  ITGSNPKAKRLEFRS  GSNPKAKRL       0.2329      4023.4            50.00    Sequence
DRB1_0802  248  IKNTAWQNGKTVTFM  WQNGKTVTF       0.2321      4056.7            50.00    Sequence
DRB1_0802   18  EYVDVRFCDLPGIMQ  YVDVRFCDL       0.2313      4092.8            50.00    Sequence
DRB1_0802  314  SLLAFTNPTVNSYKR  LLAFTNPTV       0.2312      4098.0            50.00    Sequence
DRB1_0802  158  SGWWNTGAATEADGS  GWWNTGAAT       0.2301      4149.2            50.00    Sequence
DRB1_0802  231  FNSLLHAADDMQLYK  FNSLLHAAD       0.2298      4158.6            50.00    Sequence
DRB1_0802  249  KNTAWQNGKTVTFMP  TAWQNGKTV       0.2289      4200.1            50.00    Sequence
DRB1_0802  168  EADGSPNRGYKVRHK  PNRGYKVRH       0.2285      4217.7            50.00    Sequence
DRB1_0802  353  PITGSNPKAKRLEFR  PITGSNPKA       0.2279      4245.9            50.00    Sequence
DRB1_0802  294  YAGLSDTARHYIGGL  SDTARHYIG       0.2279      4249.2            50.00    Sequence
DRB1_0802   23  RFCDLPGIMQHFTIP  LPGIMQHFT       0.2273      4275.9            50.00    Sequence
DRB1_0802    4  TPDDVFKLAKDEKVE  FKLAKDEKV       0.2269      4291.8            50.00    Sequence
DRB1_0802  459  IEPVNIRPHPYEFAL  IEPVNIRPH       0.2269      4293.2            50.00    Sequence
DRB1_0802    8  VFKLAKDEKVEYVDV  FKLAKDEKV       0.2267      4301.5            50.00    Sequence
DRB1_0802  435  YLTEGGVFTNDLIET  YLTEGGVFT       0.2258      4343.0            50.00    Sequence
DRB1_0802  137  IFDSVSFDSRANGSF  SVSFDSRAN       0.2254      4362.4            50.00    Sequence
DRB1_0802  330  VPGYEAPINLVYSQR  YEAPINLVY       0.2242      4419.0            50.00    Sequence
DRB1_0802    3  KTPDDVFKLAKDEKV  FKLAKDEKV       0.2239      4436.4            50.00    Sequence
DRB1_0802  440  GVFTNDLIETWISFK  FTNDLIETW       0.2228      4489.6            50.00    Sequence
DRB1_0802  157  ISGWWNTGAATEADG  WWNTGAATE       0.2221      4524.1            50.00    Sequence
DRB1_0802    5  PDDVFKLAKDEKVEY  FKLAKDEKV       0.2213      4558.9            50.00    Sequence
DRB1_0802  203  TNLINSGFILEKGHH  GFILEKGHH       0.2208      4584.7            50.00    Sequence
DRB1_0802  458  EIEPVNIRPHPYEFA  IEPVNIRPH       0.2198      4637.2            50.00    Sequence
DRB1_0802   58  RGFQSIHESDMLLLP  RGFQSIHES       0.2193      4661.4            50.00    Sequence
DRB1_0802   31  MQHFTIPASAFDKSV  MQHFTIPAS       0.2178      4738.5            50.00    Sequence
DRB1_0802  383  LMAGLDGIKNKIEPQ  GIKNKIEPQ       0.2178      4739.1            50.00    Sequence
DRB1_0802  363  RLEFRSPDSSGNPYL  RLEFRSPDS       0.2169      4783.4            50.00    Sequence
DRB1_0802    7  DVFKLAKDEKVEYVD  FKLAKDEKV       0.2167      4795.7            50.00    Sequence
DRB1_0802   24  FCDLPGIMQHFTIPA  LPGIMQHFT       0.2157      4845.8            50.00    Sequence
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DRB1_0802   72  PDPETARIDPFRAAK  RIDPFRAAK        0.2156      4851.4          50.00    Sequence
DRB1_0802   57  IRGFQSIHESDMLLL  RGFQSIHES        0.2129      4997.4          50.00    Sequence
DRB1_0802  210  FILEKGHHEVGSGGQ  ILEKGHHEV        0.2106      5119.8          50.00    Sequence
DRB1_0802  236  HAADDMQLYKYIIKN  QLYKYIIKN        0.2105      5126.0          50.00    Sequence
DRB1_0802   20  VDVRFCDLPGIMQHF  VDVRFCDLP        0.2100      5156.8          50.00    Sequence
DRB1_0802  135  FYIFDSVSFDSRANG  SVSFDSRAN        0.2094      5186.7          50.00    Sequence
DRB1_0802    6  DDVFKLAKDEKVEYV  VFKLAKDEK        0.2090      5209.3          50.00    Sequence
DRB1_0802   17  VEYVDVRFCDLPGIM  VDVRFCDLP        0.2083      5252.5          50.00    Sequence
DRB1_0802  269  DNGSGMHCHQSLWKD  GSGMHCHQS        0.2073      5309.7          50.00    Sequence
DRB1_0802  377  LAFSAMLMAGLDGIK  AFSAMLMAG        0.2072      5311.1          50.00    Sequence
DRB1_0802  434  EYLTEGGVFTNDLIE  YLTEGGVFT        0.2067      5342.9          50.00    Sequence
DRB1_0802  439  GGVFTNDLIETWISF  FTNDLIETW        0.2063      5365.7          50.00    Sequence
DRB1_0802  108  RNIARKAENYLISTG  RNIARKAEN        0.2060      5381.3          50.00    Sequence
DRB1_0802  457  NEIEPVNIRPHPYEF  IEPVNIRPH        0.2058      5392.3          50.00    Sequence
DRB1_0802   22  VRFCDLPGIMQHFTI  RFCDLPGIM        0.2051      5433.3          50.00    Sequence
DRB1_0802  451  ISFKRENEIEPVNIR  FKRENEIEP        0.2048      5453.1          50.00    Sequence
DRB1_0802  307  GLLHHAPSLLAFTNP  GLLHHAPSL        0.2031      5551.8          50.00    Sequence
DRB1_0802  188  VAPNDQYVDLRDKML  YVDLRDKML        0.2020      5617.7          50.00    Sequence
DRB1_0802  313  PSLLAFTNPTVNSYK  LLAFTNPTV        0.2014      5657.0          50.00    Sequence
DRB1_0802  259  VTFMPKPLFGDNGSG  VTFMPKPLF        0.1998      5756.2          50.00    Sequence
DRB1_0802  136  YIFDSVSFDSRANGS  SVSFDSRAN        0.1986      5829.0          50.00    Sequence
DRB1_0802   89  NINFFVHDPFTLEPY  FFVHDPFTL        0.1982      5854.5          50.00    Sequence
DRB1_0802  460  EPVNIRPHPYEFALY  EPVNIRPHP        0.1982      5855.3          50.00    Sequence
DRB1_0802   21  DVRFCDLPGIMQHFT  RFCDLPGIM        0.1937      6145.3          50.00    Sequence
DRB1_0802  433  HEYLTEGGVFTNDLI  YLTEGGVFT        0.1936      6156.4          50.00    Sequence
DRB1_0802  438  EGGVFTNDLIETWIS  FTNDLIETW        0.1924      6239.1          50.00    Sequence
DRB1_0802  268  GDNGSGMHCHQSLWK  GMHCHQSLW        0.1917      6283.4          50.00    Sequence
DRB1_0802  378  AFSAMLMAGLDGIKN  AFSAMLMAG        0.1914      6303.6          50.00    Sequence
DRB1_0802  211  ILEKGHHEVGSGGQA  ILEKGHHEV        0.1891      6463.0          50.00    Sequence
DRB1_0802  369  PDSSGNPYLAFSAML  PDSSGNPYL        0.1849      6761.0          50.00    Sequence
DRB1_0802   32  QHFTIPASAFDKSVF  HFTIPASAF        0.1849      6765.6          50.00    Sequence
DRB1_0802  291  ETGYAGLSDTARHYI  GYAGLSDTA        0.1846      6787.0          50.00    Sequence
DRB1_0802  134  EFYIFDSVSFDSRAN  SVSFDSRAN        0.1844      6801.0          50.00    Sequence
DRB1_0802  430  EADHEYLTEGGVFTN  YLTEGGVFT        0.1831      6898.7          50.00    Sequence
DRB1_0802  116  NYLISTGIADTAYFG  NYLISTGIA        0.1830      6903.0          50.00    Sequence
DRB1_0802  429  LEADHEYLTEGGVFT  YLTEGGVFT        0.1824      6950.7          50.00    Sequence
DRB1_0802   88  LNINFFVHDPFTLEP  FFVHDPFTL        0.1822      6959.6          50.00    Sequence
DRB1_0802  329  LVPGYEAPINLVYSQ  YEAPINLVY        0.1815      7013.2          50.00    Sequence
DRB1_0802  312  APSLLAFTNPTVNSY  LLAFTNPTV        0.1810      7054.7          50.00    Sequence
DRB1_0802  431  ADHEYLTEGGVFTND  YLTEGGVFT        0.1805      7089.2          50.00    Sequence
DRB1_0802  309  LHHAPSLLAFTNPTV  LLAFTNPTV        0.1803      7107.3          50.00    Sequence
DRB1_0802  432  DHEYLTEGGVFTNDL  YLTEGGVFT        0.1798      7146.8          50.00    Sequence
DRB1_0802  160  WWNTGAATEADGSPN  WWNTGAATE        0.1797      7152.7          50.00    Sequence
DRB1_0802   96  DPFTLEPYSRDPRNI  LEPYSRDPR        0.1794      7177.5          50.00    Sequence
DRB1_0802  382  MLMAGLDGIKNKIEP  GLDGIKNKI        0.1793      7181.8          50.00    Sequence
DRB1_0802   86  KTLNINFFVHDPFTL  KTLNINFFV        0.1793      7184.0          50.00    Sequence
DRB1_0802  456  ENEIEPVNIRPHPYE  IEPVNIRPH        0.1789      7218.2          50.00    Sequence
DRB1_0802  147  ANGSFYEVDAISGWW  EVDAISGWW        0.1786      7243.0          50.00    Sequence
DRB1_0802  167  TEADGSPNRGYKVRH  SPNRGYKVR        0.1781      7278.2          50.00    Sequence
DRB1_0802  181  HKGGYFPVAPNDQYV  HKGGYFPVA        0.1779      7293.8          50.00    Sequence
DRB1_0802  180  RHKGGYFPVAPNDQY  HKGGYFPVA        0.1776      7317.7          50.00    Sequence
DRB1_0802  110  IARKAENYLISTGIA  IARKAENYL        0.1775      7326.7          50.00    Sequence
DRB1_0802   87  TLNINFFVHDPFTLE  TLNINFFVH        0.1768      7381.2          50.00    Sequence
DRB1_0802  112  RKAENYLISTGIADT  RKAENYLIS        0.1760      7443.7          50.00    Sequence
DRB1_0802  452  SFKRENEIEPVNIRP  FKRENEIEP        0.1753      7506.2          50.00    Sequence
DRB1_0802  221  SGGQAEINYQFNSLL  INYQFNSLL        0.1720      7773.5          50.00    Sequence
DRB1_0802  288  MYDETGYAGLSDTAR  MYDETGYAG        0.1720      7776.1          50.00    Sequence
DRB1_0802   33  HFTIPASAFDKSVFD  FTIPASAFD        0.1707      7887.6          50.00    Sequence
DRB1_0802  111  ARKAENYLISTGIAD  RKAENYLIS        0.1689      8038.6          50.00    Sequence
DRB1_0802   16  KVEYVDVRFCDLPGI  VDVRFCDLP        0.1678      8139.3          50.00    Sequence
DRB1_0802  115  ENYLISTGIADTAYF  NYLISTGIA        0.1674      8173.4          50.00    Sequence
DRB1_0802  311  HAPSLLAFTNPTVNS  LLAFTNPTV        0.1674      8174.7          50.00    Sequence
DRB1_0802   95  HDPFTLEPYSRDPRN  TLEPYSRDP        0.1659      8304.0          50.00    Sequence
DRB1_0802  280  LWKDGAPLMYDETGY  LWKDGAPLM        0.1659      8309.4          50.00    Sequence
DRB1_0802  381  AMLMAGLDGIKNKIE  MAGLDGIKN        0.1655      8338.4          50.00    Sequence
DRB1_0802  290  DETGYAGLSDTARHY  GYAGLSDTA        0.1655      8339.4          50.00    Sequence
DRB1_0802  114  AENYLISTGIADTAY  NYLISTGIA        0.1646      8422.4          50.00    Sequence
DRB1_0802  453  FKRENEIEPVNIRPH  FKRENEIEP        0.1639      8483.8          50.00    Sequence
DRB1_0802  113  KAENYLISTGIADTA  AENYLISTG        0.1633      8547.0          50.00    Sequence
DRB1_0802  109  NIARKAENYLISTGI  IARKAENYL        0.1626      8606.7          50.00    Sequence
DRB1_0802  117  YLISTGIADTAYFGA  YLISTGIAD        0.1622      8645.9          50.00    Sequence
DRB1_0802  461  PVNIRPHPYEFALYY  VNIRPHPYE        0.1618      8682.0          50.00    Sequence
DRB1_0802  235  LHAADDMQLYKYIIK  DMQLYKYII        0.1606      8798.1          50.00    Sequence
DRB1_0802  202  LTNLINSGFILEKGH  LINSGFILE        0.1605      8808.7          50.00    Sequence
DRB1_0802   90  INFFVHDPFTLEPYS  FFVHDPFTL        0.1587      8981.6          50.00    Sequence
DRB1_0802   94  VHDPFTLEPYSRDPR  TLEPYSRDP        0.1578      9067.8          50.00    Sequence
DRB1_0802   59  GFQSIHESDMLLLPD  GFQSIHESD        0.1572      9125.9          50.00    Sequence
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DRB1_0802   92  FFVHDPFTLEPYSRD  FFVHDPFTL         0.1561       9239.7                  50.00      Sequence
DRB1_0802  141  VSFDSRANGSFYEVD  FDSRANGSF         0.1559       9260.2                  50.00      Sequence
DRB1_0802   91  NFFVHDPFTLEPYSR  FFVHDPFTL         0.1556       9287.3                  50.00      Sequence
DRB1_0802  391  KNKIEPQAPVDKDLY  KNKIEPQAP         0.1556       9288.1                  50.00      Sequence
DRB1_0802    2  EKTPDDVFKLAKDEK  VFKLAKDEK         0.1543       9421.8                  50.00      Sequence
DRB1_0802   82  FRAAKTLNINFFVHD  FRAAKTLNI         0.1534       9504.7                  50.00      Sequence
DRB1_0802  308  LLHHAPSLLAFTNPT  LHHAPSLLA         0.1512       9741.0                  50.00      Sequence
DRB1_0802  310  HHAPSLLAFTNPTVN  LLAFTNPTV         0.1507       9792.2                  50.00      Sequence
DRB1_0802  267  FGDNGSGMHCHQSLW  GSGMHCHQS         0.1503       9829.5                  50.00      Sequence
DRB1_0802  380  SAMLMAGLDGIKNKI  MAGLDGIKN         0.1496       9909.5                  50.00      Sequence
DRB1_0802  287  LMYDETGYAGLSDTA  MYDETGYAG         0.1495       9915.5                  50.00      Sequence
DRB1_0802   34  FTIPASAFDKSVFDD  FTIPASAFD         0.1486      10019.0                  50.00      Sequence
DRB1_0802   15  EKVEYVDVRFCDLPG  VDVRFCDLP         0.1473      10160.3                  50.00      Sequence
DRB1_0802  368  SPDSSGNPYLAFSAM  PDSSGNPYL         0.1469      10200.2                  50.00      Sequence
DRB1_0802  462  VNIRPHPYEFALYYD  VNIRPHPYE         0.1459      10317.8                  50.00      Sequence
DRB1_0802    9  FKLAKDEKVEYVDVR  FKLAKDEKV         0.1445      10468.7                  50.00      Sequence
DRB1_0802  182  KGGYFPVAPNDQYVD  GGYFPVAPN         0.1443      10495.3                  50.00      Sequence
DRB1_0802   93  FVHDPFTLEPYSRDP  HDPFTLEPY         0.1435      10587.8                  50.00      Sequence
DRB1_0802   85  AKTLNINFFVHDPFT  NINFFVHDP         0.1432      10617.2                  50.00      Sequence
DRB1_0802  437  TEGGVFTNDLIETWI  FTNDLIETW         0.1427      10675.4                  50.00      Sequence
DRB1_0802  455  RENEIEPVNIRPHPY  IEPVNIRPH         0.1422      10733.6                  50.00      Sequence
DRB1_0802   71  LPDPETARIDPFRAA  TARIDPFRA         0.1416      10804.4                  50.00      Sequence
DRB1_0802  122  GIADTAYFGAEAEFY  GIADTAYFG         0.1412      10854.2                  50.00      Sequence
DRB1_0802   37  PASAFDKSVFDDGLA  PASAFDKSV         0.1402      10965.4                  50.00      Sequence
DRB1_0802  289  YDETGYAGLSDTARH  GYAGLSDTA         0.1399      11007.8                  50.00      Sequence
DRB1_0802  234  LLHAADDMQLYKYII  DMQLYKYII         0.1385      11172.7                  50.00      Sequence
DRB1_0802  367  RSPDSSGNPYLAFSA  PDSSGNPYL         0.1372      11325.9                  50.00      Sequence
DRB1_0802  125  DTAYFGAEAEFYIFD  YFGAEAEFY         0.1372      11326.1                  50.00      Sequence
DRB1_0802  166  ATEADGSPNRGYKVR  SPNRGYKVR         0.1370      11355.3                  50.00      Sequence
DRB1_0802  399  PVDKDLYELPPEEAA  PVDKDLYEL         0.1367      11390.3                  50.00      Sequence
DRB1_0802  364  LEFRSPDSSGNPYLA  PDSSGNPYL         0.1364      11433.2                  50.00      Sequence
DRB1_0802  286  PLMYDETGYAGLSDT  MYDETGYAG         0.1336      11777.8                  50.00      Sequence
DRB1_0802  133  AEFYIFDSVSFDSRA  FYIFDSVSF         0.1329      11869.4                  50.00      Sequence
DRB1_0802  128  YFGAEAEFYIFDSVS  YFGAEAEFY         0.1328      11881.6                  50.00      Sequence
DRB1_0802  412  AASIPQTPTQLSDVI  AASIPQTPT         0.1326      11904.8                  50.00      Sequence
DRB1_0802  119  ISTGIADTAYFGAEA  GIADTAYFG         0.1324      11937.3                  50.00      Sequence
DRB1_0802  118  LISTGIADTAYFGAE  LISTGIADT         0.1321      11969.8                  50.00      Sequence
DRB1_0802  124  ADTAYFGAEAEFYIF  YFGAEAEFY         0.1321      11977.4                  50.00      Sequence
DRB1_0802  379  FSAMLMAGLDGIKNK  FSAMLMAGL         0.1316      12034.3                  50.00      Sequence
DRB1_0802  417  QTPTQLSDVIDRLEA  SDVIDRLEA         0.1314      12067.0                  50.00      Sequence
DRB1_0802  418  TPTQLSDVIDRLEAD  SDVIDRLEA         0.1291      12373.4                  50.00      Sequence
DRB1_0802  415  IPQTPTQLSDVIDRL  IPQTPTQLS         0.1277      12556.0                  50.00      Sequence
DRB1_0802  436  LTEGGVFTNDLIETW  FTNDLIETW         0.1277      12562.8                  50.00      Sequence
DRB1_0802  454  KRENEIEPVNIRPHP  IEPVNIRPH         0.1275      12579.9                  50.00      Sequence
DRB1_0802  463  NIRPHPYEFALYYDV  HPYEFALYY         0.1274      12601.7                  50.00      Sequence
DRB1_0802   84  AAKTLNINFFVHDPF  KTLNINFFV         0.1273      12609.3                  50.00      Sequence
DRB1_0802  421  QLSDVIDRLEADHEY  QLSDVIDRL         0.1264      12738.7                  50.00      Sequence
DRB1_0802  161  WNTGAATEADGSPNR  WNTGAATEA         0.1258      12816.2                  50.00      Sequence
DRB1_0802  123  IADTAYFGAEAEFYI  YFGAEAEFY         0.1258      12824.4                  50.00      Sequence
DRB1_0802  411  EAASIPQTPTQLSDV  AASIPQTPT         0.1257      12836.6                  50.00      Sequence
DRB1_0802  183  GGYFPVAPNDQYVDL  GGYFPVAPN         0.1249      12942.6                  50.00      Sequence
DRB1_0802  409  PEEAASIPQTPTQLS  PEEAASIPQ         0.1248      12961.0                  50.00      Sequence
DRB1_0802  284  GAPLMYDETGYAGLS  MYDETGYAG         0.1242      13041.3                  50.00      Sequence
DRB1_0802   14  DEKVEYVDVRFCDLP  VDVRFCDLP         0.1236      13122.0                  50.00      Sequence
DRB1_0802  366  FRSPDSSGNPYLAFS  PDSSGNPYL         0.1236      13133.6                  50.00      Sequence
DRB1_0802   36  IPASAFDKSVFDDGL  PASAFDKSV         0.1230      13215.3                  50.00      Sequence
DRB1_0802  413  ASIPQTPTQLSDVID  IPQTPTQLS         0.1223      13310.3                  50.00      Sequence
DRB1_0802  285  APLMYDETGYAGLSD  LMYDETGYA         0.1219      13367.1                  50.00      Sequence
DRB1_0802  419  PTQLSDVIDRLEADH  QLSDVIDRL         0.1218      13389.7                  50.00      Sequence
DRB1_0802  126  TAYFGAEAEFYIFDS  YFGAEAEFY         0.1214      13442.0                  50.00      Sequence
DRB1_0802  132  EAEFYIFDSVSFDSR  FYIFDSVSF         0.1212      13466.3                  50.00      Sequence
DRB1_0802  146  RANGSFYEVDAISGW  FYEVDAISG         0.1211      13489.0                  50.00      Sequence
DRB1_0802  127  AYFGAEAEFYIFDSV  YFGAEAEFY         0.1209      13511.5                  50.00      Sequence
DRB1_0802  408  PPEEAASIPQTPTQL  PPEEAASIP         0.1201      13627.2                  50.00      Sequence
DRB1_0802   70  LLPDPETARIDPFRA  ETARIDPFR         0.1200      13651.3                  50.00      Sequence
DRB1_0802  410  EEAASIPQTPTQLSD  AASIPQTPT         0.1193      13759.8                  50.00      Sequence
DRB1_0802  215  GHHEVGSGGQAEINY  HEVGSGGQA         0.1192      13773.5                  50.00      Sequence
DRB1_0802  220  GSGGQAEINYQFNSL  GQAEINYQF         0.1191      13789.3                  50.00      Sequence
DRB1_0802  365  EFRSPDSSGNPYLAF  PDSSGNPYL         0.1183      13901.5                  50.00      Sequence
DRB1_0802  420  TQLSDVIDRLEADHE  SDVIDRLEA         0.1172      14070.0                  50.00      Sequence
DRB1_0802  422  LSDVIDRLEADHEYL  SDVIDRLEA         0.1171      14087.9                  50.00      Sequence
DRB1_0802  214  KGHHEVGSGGQAEIN  HEVGSGGQA         0.1167      14142.9                  50.00      Sequence
DRB1_0802  217  HEVGSGGQAEINYQF  HEVGSGGQA         0.1161      14244.4                  50.00      Sequence
DRB1_0802  212  LEKGHHEVGSGGQAE  HEVGSGGQA         0.1148      14434.0                  50.00      Sequence
DRB1_0802  423  SDVIDRLEADHEYLT  RLEADHEYL         0.1139      14579.5                  50.00      Sequence
DRB1_0802  400  VDKDLYELPPEEAAS  VDKDLYELP         0.1130      14722.2                  50.00      Sequence
DRB1_0802   45  VFDDGLAFDGSSIRG  GLAFDGSSI         0.1130      14723.6                  50.00      Sequence
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DRB1_0802  219  VGSGGQAEINYQFNS  GQAEINYQF        0.1129       14732.9              50.00      Sequence
DRB1_0802    1  TEKTPDDVFKLAKDE  PDDVFKLAK        0.1108       15077.3              50.00      Sequence
DRB1_0802   35  TIPASAFDKSVFDDG  PASAFDKSV        0.1107       15099.9              50.00      Sequence
DRB1_0802  216  HHEVGSGGQAEINYQ  HEVGSGGQA        0.1100       15211.5              50.00      Sequence
DRB1_0802  218  EVGSGGQAEINYQFN  GQAEINYQF        0.1095       15283.4              50.00      Sequence
DRB1_0802  414  SIPQTPTQLSDVIDR  IPQTPTQLS        0.1081       15523.6              50.00      Sequence
DRB1_0802  145  SRANGSFYEVDAISG  FYEVDAISG        0.1077       15595.8              50.00      Sequence
DRB1_0802  260  TFMPKPLFGDNGSGM  TFMPKPLFG        0.1077       15599.7              50.00      Sequence
DRB1_0802   47  DDGLAFDGSSIRGFQ  GLAFDGSSI        0.1076       15602.9              50.00      Sequence
DRB1_0802   83  RAAKTLNINFFVHDP  KTLNINFFV        0.1076       15613.9              50.00      Sequence
DRB1_0802  281  WKDGAPLMYDETGYA  WKDGAPLMY        0.1063       15827.9              50.00      Sequence
DRB1_0802   46  FDDGLAFDGSSIRGF  GLAFDGSSI        0.1060       15885.0              50.00      Sequence
DRB1_0802  165  AATEADGSPNRGYKV  GSPNRGYKV        0.1055       15974.5              50.00      Sequence
DRB1_0802  398  APVDKDLYELPPEEA  VDKDLYELP        0.1051       16036.5              50.00      Sequence
DRB1_0802  407  LPPEEAASIPQTPTQ  PPEEAASIP        0.1049       16065.6              50.00      Sequence
DRB1_0802  121  TGIADTAYFGAEAEF  GIADTAYFG        0.1042       16187.8              50.00      Sequence
DRB1_0802  213  EKGHHEVGSGGQAEI  HEVGSGGQA        0.1039       16245.3              50.00      Sequence
DRB1_0802  266  LFGDNGSGMHCHQSL  GSGMHCHQS        0.1029       16421.0              50.00      Sequence
DRB1_0802  187  PVAPNDQYVDLRDKM  QYVDLRDKM        0.1028       16448.5              50.00      Sequence
DRB1_0802  129  FGAEAEFYIFDSVSF  FGAEAEFYI        0.1027       16453.3              50.00      Sequence
DRB1_0802  283  DGAPLMYDETGYAGL  LMYDETGYA        0.1025       16500.9              50.00      Sequence
DRB1_0802   60  FQSIHESDMLLLPDP  FQSIHESDM        0.1022       16551.4              50.00      Sequence
DRB1_0802  416  PQTPTQLSDVIDRLE  TPTQLSDVI        0.1012       16732.7              50.00      Sequence
DRB1_0802  120  STGIADTAYFGAEAE  GIADTAYFG        0.1011       16748.3              50.00      Sequence
DRB1_0802  131  AEAEFYIFDSVSFDS  FYIFDSVSF        0.1007       16817.3              50.00      Sequence
DRB1_0802    0  VTEKTPDDVFKLAKD  PDDVFKLAK        0.1003       16893.7              50.00      Sequence
DRB1_0802  142  SFDSRANGSFYEVDA  FDSRANGSF        0.1002       16904.3              50.00      Sequence
DRB1_0802  265  PLFGDNGSGMHCHQS  GSGMHCHQS        0.0990       17134.3              50.00      Sequence
DRB1_0802   43  KSVFDDGLAFDGSSI  GLAFDGSSI        0.0984       17243.4              50.00      Sequence
DRB1_0802  397  QAPVDKDLYELPPEE  PVDKDLYEL        0.0974       17424.8              50.00      Sequence
DRB1_0802  282  KDGAPLMYDETGYAG  LMYDETGYA        0.0967       17564.5              50.00      Sequence
DRB1_0802   13  KDEKVEYVDVRFCDL  YVDVRFCDL        0.0951       17862.3              50.00      Sequence
DRB1_0802   62  SIHESDMLLLPDPET  SIHESDMLL        0.0943       18023.1              50.00      Sequence
DRB1_0802  392  NKIEPQAPVDKDLYE  NKIEPQAPV        0.0943       18023.9              50.00      Sequence
DRB1_0802   44  SVFDDGLAFDGSSIR  GLAFDGSSI        0.0942       18047.7              50.00      Sequence
DRB1_0802  143  FDSRANGSFYEVDAI  FDSRANGSF        0.0933       18222.1              50.00      Sequence
DRB1_0802   63  IHESDMLLLPDPETA  IHESDMLLL        0.0905       18778.5              50.00      Sequence
DRB1_0802  427  DRLEADHEYLTEGGV  RLEADHEYL        0.0902       18837.8              50.00      Sequence
DRB1_0802  233  SLLHAADDMQLYKYI  LLHAADDMQ        0.0901       18859.6              50.00      Sequence
DRB1_0802   10  KLAKDEKVEYVDVRF  KLAKDEKVE        0.0896       18965.2              50.00      Sequence
DRB1_0802  428  RLEADHEYLTEGGVF  RLEADHEYL        0.0896       18970.7              50.00      Sequence
DRB1_0802  405  YELPPEEAASIPQTP  YELPPEEAA        0.0894       19010.1              50.00      Sequence
DRB1_0802  396  PQAPVDKDLYELPPE  PVDKDLYEL        0.0888       19122.6              50.00      Sequence
DRB1_0802  186  FPVAPNDQYVDLRDK  FPVAPNDQY        0.0883       19227.6              50.00      Sequence
DRB1_0802  424  DVIDRLEADHEYLTE  RLEADHEYL        0.0882       19259.0              50.00      Sequence
DRB1_0802  425  VIDRLEADHEYLTEG  RLEADHEYL        0.0879       19313.5              50.00      Sequence
DRB1_0802  404  LYELPPEEAASIPQT  YELPPEEAA        0.0857       19780.2              50.00      Sequence
DRB1_0802   64  HESDMLLLPDPETAR  HESDMLLLP        0.0848       19968.6              50.00      Sequence
DRB1_0802  401  DKDLYELPPEEAASI  YELPPEEAA        0.0837       20210.5              50.00      Sequence
DRB1_0802  232  NSLLHAADDMQLYKY  LLHAADDMQ        0.0835       20252.5              50.00      Sequence
DRB1_0802  402  KDLYELPPEEAASIP  YELPPEEAA        0.0834       20277.1              50.00      Sequence
DRB1_0802   61  QSIHESDMLLLPDPE  QSIHESDML        0.0834       20277.5              50.00      Sequence
DRB1_0802   40  AFDKSVFDDGLAFDG  KSVFDDGLA        0.0824       20511.2              50.00      Sequence
DRB1_0802  406  ELPPEEAASIPQTPT  PPEEAASIP        0.0823       20528.1              50.00      Sequence
DRB1_0802  393  KIEPQAPVDKDLYEL  KIEPQAPVD        0.0822       20535.8              50.00      Sequence
DRB1_0802   41  FDKSVFDDGLAFDGS  KSVFDDGLA        0.0811       20801.7              50.00      Sequence
DRB1_0802   69  LLLPDPETARIDPFR  ETARIDPFR        0.0800       21041.9              50.00      Sequence
DRB1_0802  184  GYFPVAPNDQYVDLR  FPVAPNDQY        0.0799       21066.5              50.00      Sequence
DRB1_0802  185  YFPVAPNDQYVDLRD  YFPVAPNDQ        0.0799       21071.8              50.00      Sequence
DRB1_0802   66  SDMLLLPDPETARID  SDMLLLPDP        0.0795       21157.2              50.00      Sequence
DRB1_0802   65  ESDMLLLPDPETARI  SDMLLLPDP        0.0787       21349.2              50.00      Sequence
DRB1_0802  426  IDRLEADHEYLTEGG  RLEADHEYL        0.0786       21356.6              50.00      Sequence
DRB1_0802   38  ASAFDKSVFDDGLAF  KSVFDDGLA        0.0781       21466.4              50.00      Sequence
DRB1_0802  403  DLYELPPEEAASIPQ  YELPPEEAA        0.0774       21647.7              50.00      Sequence
DRB1_0802   12  AKDEKVEYVDVRFCD  KVEYVDVRF        0.0755       22086.5              50.00      Sequence
DRB1_0802   11  LAKDEKVEYVDVRFC  KVEYVDVRF        0.0750       22221.5              50.00      Sequence
DRB1_0802  395  EPQAPVDKDLYELPP  VDKDLYELP        0.0738       22490.9              50.00      Sequence
DRB1_0802  144  DSRANGSFYEVDAIS  SFYEVDAIS        0.0731       22660.0              50.00      Sequence
DRB1_0802   42  DKSVFDDGLAFDGSS  KSVFDDGLA        0.0708       23242.0              50.00      Sequence
DRB1_0802   39  SAFDKSVFDDGLAFD  KSVFDDGLA        0.0700       23433.9              50.00      Sequence
DRB1_0802  130  GAEAEFYIFDSVSFD  FYIFDSVSF        0.0696       23550.1              50.00      Sequence
DRB1_0802   68  MLLLPDPETARIDPF  MLLLPDPET        0.0664       24384.0              50.00      Sequence
DRB1_0802  164  GAATEADGSPNRGYK  DGSPNRGYK        0.0657       24565.6              50.00      Sequence
DRB1_0802   67  DMLLLPDPETARIDP  MLLLPDPET        0.0639       25053.1              50.00      Sequence
DRB1_0802  394  IEPQAPVDKDLYELP  PVDKDLYEL        0.0593       26313.9              50.00      Sequence
DRB1_0802  264  KPLFGDNGSGMHCHQ  FGDNGSGMH        0.0576       26823.0              50.00      Sequence
DRB1_0802  263  PKPLFGDNGSGMHCH  FGDNGSGMH        0.0553       27500.3              50.00      Sequence
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   DRB1_0802  262  MPKPLFGDNGSGMHC  FGDNGSGMH        0.0547      27662.4                50.00     Sequence
   DRB1_0802  261  FMPKPLFGDNGSGMH  FGDNGSGMH        0.0535      28023.3                50.00     Sequence
   DRB1_0802  163  TGAATEADGSPNRGY  AATEADGSP        0.0362      33780.4                50.00     Sequence
   DRB1_0802  162  NTGAATEADGSPNRG  ATEADGSPN        0.0354      34071.9                50.00     Sequence
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Allele: DRB1_0802. Number of high binders 12. Number of weak binders 40. Number of peptides 464

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0901  306  GGLLHHAPSLLAFTN  LLHHAPSLL        0.7453         15.7         SB     0.10     Sequence
   DRB1_0901  307  GLLHHAPSLLAFTNP  LLHHAPSLL        0.7318         18.2         SB     0.15     Sequence
   DRB1_0901  305  IGGLLHHAPSLLAFT  LLHHAPSLL        0.7300         18.6         SB     0.20     Sequence
   DRB1_0901  374  NPYLAFSAMLMAGLD  YLAFSAMLM        0.7207         20.5         SB     0.30     Sequence
   DRB1_0901  304  YIGGLLHHAPSLLAF  LLHHAPSLL        0.7180         21.1         SB     0.30     Sequence
   DRB1_0901  303  HYIGGLLHHAPSLLA  LLHHAPSLL        0.7170         21.4         SB     0.30     Sequence
   DRB1_0901  375  PYLAFSAMLMAGLDG  YLAFSAMLM        0.7129         22.3         SB     0.30     Sequence
   DRB1_0901  373  GNPYLAFSAMLMAGL  YLAFSAMLM        0.7065         23.9         SB     0.40     Sequence
   DRB1_0901  308  LLHHAPSLLAFTNPT  LLHHAPSLL        0.7043         24.5         SB     0.40     Sequence
   DRB1_0901  156  AISGWWNTGAATEAD  WNTGAATEA        0.6644         37.7         SB     1.00     Sequence
   DRB1_0901  158  SGWWNTGAATEADGS  WWNTGAATE        0.6586         40.2         SB     2.00     Sequence
   DRB1_0901  372  SGNPYLAFSAMLMAG  YLAFSAMLM        0.6576         40.7         SB     2.00     Sequence
   DRB1_0901  371  SSGNPYLAFSAMLMA  PYLAFSAML        0.6547         41.9         SB     2.00     Sequence
   DRB1_0901  157  ISGWWNTGAATEADG  WWNTGAATE        0.6531         42.7         SB     2.00     Sequence
   DRB1_0901  155  DAISGWWNTGAATEA  WWNTGAATE        0.6456         46.3         SB     2.00     Sequence
   DRB1_0901  376  YLAFSAMLMAGLDGI  YLAFSAMLM        0.6426         47.8         SB     2.00     Sequence
   DRB1_0901  326  YKRLVPGYEAPINLV  YKRLVPGYE        0.6418         48.2         SB     2.00     Sequence
   DRB1_0901  159  GWWNTGAATEADGSP  WNTGAATEA        0.6359         51.4         WB     2.00     Sequence
   DRB1_0901  160  WWNTGAATEADGSPN  WNTGAATEA        0.6325         53.3         WB     2.00     Sequence
   DRB1_0901  302  RHYIGGLLHHAPSLL  LLHHAPSLL        0.6136         65.4         WB     4.00     Sequence
   DRB1_0901   56  SIRGFQSIHESDMLL  RGFQSIHES        0.6074         70.0         WB     4.00     Sequence
   DRB1_0901   57  IRGFQSIHESDMLLL  RGFQSIHES        0.6055         71.4         WB     4.00     Sequence
   DRB1_0901  370  DSSGNPYLAFSAMLM  YLAFSAMLM        0.6040         72.6         WB     4.00     Sequence
   DRB1_0901   55  SSIRGFQSIHESDML  SSIRGFQSI        0.6003         75.5         WB     4.00     Sequence
   DRB1_0901   30  IMQHFTIPASAFDKS  FTIPASAFD        0.5992         76.5         WB     4.00     Sequence
   DRB1_0901  325  SYKRLVPGYEAPINL  YKRLVPGYE        0.5978         77.6         WB     4.00     Sequence
   DRB1_0901   31  MQHFTIPASAFDKSV  FTIPASAFD        0.5971         78.2         WB     4.00     Sequence
   DRB1_0901   54  GSSIRGFQSIHESDM  SSIRGFQSI        0.5938         81.0         WB     4.00     Sequence
   DRB1_0901   58  RGFQSIHESDMLLLP  RGFQSIHES        0.5923         82.3         WB     4.00     Sequence
   DRB1_0901  327  KRLVPGYEAPINLVY  LVPGYEAPI        0.5920         82.7         WB     8.00     Sequence
   DRB1_0901   32  QHFTIPASAFDKSVF  FTIPASAFD        0.5906         83.9         WB     8.00     Sequence
   DRB1_0901  115  ENYLISTGIADTAYF  NYLISTGIA        0.5896         84.9         WB     8.00     Sequence
   DRB1_0901  309  LHHAPSLLAFTNPTV  LHHAPSLLA        0.5782         95.9         WB     8.00     Sequence
   DRB1_0901  229  YQFNSLLHAADDMQL  LHAADDMQL        0.5761         98.1         WB     8.00     Sequence
   DRB1_0901  324  NSYKRLVPGYEAPIN  YKRLVPGYE        0.5761         98.2         WB     8.00     Sequence
   DRB1_0901  116  NYLISTGIADTAYFG  NYLISTGIA        0.5756         98.6         WB     8.00     Sequence
   DRB1_0901   29  GIMQHFTIPASAFDK  FTIPASAFD        0.5644        111.4         WB     8.00     Sequence
   DRB1_0901   33  HFTIPASAFDKSVFD  FTIPASAFD        0.5606        116.0         WB     8.00     Sequence
   DRB1_0901   28  PGIMQHFTIPASAFD  FTIPASAFD        0.5602        116.5         WB     8.00     Sequence
   DRB1_0901  114  AENYLISTGIADTAY  NYLISTGIA        0.5576        119.9         WB     8.00     Sequence
   DRB1_0901   77  ARIDPFRAAKTLNIN  FRAAKTLNI        0.5519        127.6         WB     8.00     Sequence
   DRB1_0901  154  VDAISGWWNTGAATE  WWNTGAATE        0.5489        131.7         WB     8.00     Sequence
   DRB1_0901  323  VNSYKRLVPGYEAPI  YKRLVPGYE        0.5362        151.1         WB    16.00     Sequence
   DRB1_0901  328  RLVPGYEAPINLVYS  LVPGYEAPI        0.5337        155.2         WB    16.00     Sequence
   DRB1_0901   59  GFQSIHESDMLLLPD  GFQSIHESD        0.5313        159.3         WB    16.00     Sequence
   DRB1_0901  113  KAENYLISTGIADTA  NYLISTGIA        0.5298        161.9         WB    16.00     Sequence
   DRB1_0901   78  RIDPFRAAKTLNINF  FRAAKTLNI        0.5255        169.7         WB    16.00     Sequence
   DRB1_0901  241  MQLYKYIIKNTAWQN  YKYIIKNTA        0.5237        173.1         WB    16.00     Sequence
   DRB1_0901   79  IDPFRAAKTLNINFF  FRAAKTLNI        0.5210        178.2         WB    16.00     Sequence
   DRB1_0901  240  DMQLYKYIIKNTAWQ  MQLYKYIIK        0.5207        178.7         WB    16.00     Sequence
   DRB1_0901   76  TARIDPFRAAKTLNI  FRAAKTLNI        0.5205        179.2         WB    16.00     Sequence
   DRB1_0901  258  TVTFMPKPLFGDNGS  VTFMPKPLF        0.5193        181.5         WB    16.00     Sequence
   DRB1_0901  256  GKTVTFMPKPLFGDN  VTFMPKPLF        0.5130        194.3         WB    16.00     Sequence
   DRB1_0901  230  QFNSLLHAADDMQLY  LHAADDMQL        0.5113        198.0         WB    16.00     Sequence
   DRB1_0901   80  DPFRAAKTLNINFFV  FRAAKTLNI        0.5112        198.2         WB    16.00     Sequence
   DRB1_0901  161  WNTGAATEADGSPNR  WNTGAATEA        0.5111        198.4         WB    16.00     Sequence
   DRB1_0901  377  LAFSAMLMAGLDGIK  LAFSAMLMA        0.5111        198.4         WB    16.00     Sequence
   DRB1_0901  343  QRNRSACVRIPITGS  QRNRSACVR        0.5045        212.9         WB    16.00     Sequence
   DRB1_0901  257  KTVTFMPKPLFGDNG  VTFMPKPLF        0.5043        213.4         WB    16.00     Sequence
   DRB1_0901   53  DGSSIRGFQSIHESD  SSIRGFQSI        0.5024        218.0         WB    16.00     Sequence
   DRB1_0901  231  FNSLLHAADDMQLYK  LHAADDMQL        0.5022        218.3         WB    16.00     Sequence
   DRB1_0901  390  IKNKIEPQAPVDKDL  NKIEPQAPV        0.5022        218.4         WB    16.00     Sequence
   DRB1_0901  259  VTFMPKPLFGDNGSG  VTFMPKPLF        0.5020        218.9         WB    16.00     Sequence
   DRB1_0901  342  SQRNRSACVRIPITG  RNRSACVRI        0.5013        220.4         WB    16.00     Sequence
   DRB1_0901  133  AEFYIFDSVSFDSRA  YIFDSVSFD        0.5010        221.1         WB    16.00     Sequence
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DRB1_0901    6  DDVFKLAKDEKVEYV  FKLAKDEKV         0.5008         221.7          WB    16.00      Sequence
DRB1_0901  112  RKAENYLISTGIADT  NYLISTGIA         0.4983         227.8          WB    16.00      Sequence
DRB1_0901    7  DVFKLAKDEKVEYVD  FKLAKDEKV         0.4983         227.8          WB    16.00      Sequence
DRB1_0901  322  TVNSYKRLVPGYEAP  YKRLVPGYE         0.4980         228.4          WB    16.00      Sequence
DRB1_0901  403  DLYELPPEEAASIPQ  LYELPPEEA         0.4973         230.3          WB    16.00      Sequence
DRB1_0901  132  EAEFYIFDSVSFDSR  YIFDSVSFD         0.4926         242.1          WB    32.00      Sequence
DRB1_0901  404  LYELPPEEAASIPQT  LYELPPEEA         0.4911         246.3          WB    32.00      Sequence
DRB1_0901  389  GIKNKIEPQAPVDKD  NKIEPQAPV         0.4908         247.1          WB    32.00      Sequence
DRB1_0901  126  TAYFGAEAEFYIFDS  AYFGAEAEF         0.4905         247.8          WB    32.00      Sequence
DRB1_0901  228  NYQFNSLLHAADDMQ  YQFNSLLHA         0.4905         247.8          WB    32.00      Sequence
DRB1_0901  255  NGKTVTFMPKPLFGD  VTFMPKPLF         0.4876         255.7          WB    32.00      Sequence
DRB1_0901  402  KDLYELPPEEAASIP  LYELPPEEA         0.4869         257.7          WB    32.00      Sequence
DRB1_0901  391  KNKIEPQAPVDKDLY  NKIEPQAPV         0.4859         260.6          WB    32.00      Sequence
DRB1_0901  125  DTAYFGAEAEFYIFD  AYFGAEAEF         0.4857         261.0          WB    32.00      Sequence
DRB1_0901  124  ADTAYFGAEAEFYIF  AYFGAEAEF         0.4849         263.2          WB    32.00      Sequence
DRB1_0901  392  NKIEPQAPVDKDLYE  NKIEPQAPV         0.4843         265.0          WB    32.00      Sequence
DRB1_0901   34  FTIPASAFDKSVFDD  FTIPASAFD         0.4838         266.4          WB    32.00      Sequence
DRB1_0901  278  QSLWKDGAPLMYDET  WKDGAPLMY         0.4823         270.8          WB    32.00      Sequence
DRB1_0901    5  PDDVFKLAKDEKVEY  FKLAKDEKV         0.4822         271.2          WB    32.00      Sequence
DRB1_0901  279  SLWKDGAPLMYDETG  WKDGAPLMY         0.4819         272.1          WB    32.00      Sequence
DRB1_0901  232  NSLLHAADDMQLYKY  LLHAADDMQ         0.4787         281.6          WB    32.00      Sequence
DRB1_0901  134  EFYIFDSVSFDSRAN  YIFDSVSFD         0.4763         289.0          WB    32.00      Sequence
DRB1_0901  123  IADTAYFGAEAEFYI  AYFGAEAEF         0.4753         292.2          WB    32.00      Sequence
DRB1_0901  131  AEAEFYIFDSVSFDS  YIFDSVSFD         0.4749         293.4          WB    32.00      Sequence
DRB1_0901  341  YSQRNRSACVRIPIT  QRNRSACVR         0.4741         295.8          WB    32.00      Sequence
DRB1_0901  301  ARHYIGGLLHHAPSL  ARHYIGGLL         0.4739         296.6          WB    32.00      Sequence
DRB1_0901  180  RHKGGYFPVAPNDQY  GYFPVAPND         0.4727         300.4          WB    32.00      Sequence
DRB1_0901  117  YLISTGIADTAYFGA  YLISTGIAD         0.4723         301.8          WB    32.00      Sequence
DRB1_0901  275  HCHQSLWKDGAPLMY  WKDGAPLMY         0.4712         305.4          WB    32.00      Sequence
DRB1_0901  111  ARKAENYLISTGIAD  NYLISTGIA         0.4701         309.0          WB    32.00      Sequence
DRB1_0901    4  TPDDVFKLAKDEKVE  FKLAKDEKV         0.4700         309.5          WB    32.00      Sequence
DRB1_0901  277  HQSLWKDGAPLMYDE  WKDGAPLMY         0.4699         309.6          WB    32.00      Sequence
DRB1_0901  227  INYQFNSLLHAADDM  YQFNSLLHA         0.4696         310.7          WB    32.00      Sequence
DRB1_0901  388  DGIKNKIEPQAPVDK  KIEPQAPVD         0.4694         311.5          WB    32.00      Sequence
DRB1_0901  337  INLVYSQRNRSACVR  INLVYSQRN         0.4676         317.5          WB    32.00      Sequence
DRB1_0901  338  NLVYSQRNRSACVRI  RNRSACVRI         0.4672         318.8          WB    32.00      Sequence
DRB1_0901  272  SGMHCHQSLWKDGAP  SGMHCHQSL         0.4672         319.0          WB    32.00      Sequence
DRB1_0901  178  KVRHKGGYFPVAPND  KVRHKGGYF         0.4666         321.0          WB    32.00      Sequence
DRB1_0901  462  VNIRPHPYEFALYYD  IRPHPYEFA         0.4665         321.4          WB    32.00      Sequence
DRB1_0901  276  CHQSLWKDGAPLMYD  WKDGAPLMY         0.4643         329.1          WB    32.00      Sequence
DRB1_0901  344  RNRSACVRIPITGSN  RNRSACVRI         0.4642         329.4          WB    32.00      Sequence
DRB1_0901  242  QLYKYIIKNTAWQNG  YKYIIKNTA         0.4639         330.3          WB    32.00      Sequence
DRB1_0901  369  PDSSGNPYLAFSAML  PYLAFSAML         0.4633         332.8          WB    32.00      Sequence
DRB1_0901  336  PINLVYSQRNRSACV  NLVYSQRNR         0.4624         335.7          WB    32.00      Sequence
DRB1_0901  271  GSGMHCHQSLWKDGA  SGMHCHQSL         0.4603         343.5          WB    32.00      Sequence
DRB1_0901    9  FKLAKDEKVEYVDVR  FKLAKDEKV         0.4600         344.6          WB    32.00      Sequence
DRB1_0901  181  HKGGYFPVAPNDQYV  GYFPVAPND         0.4597         345.7          WB    32.00      Sequence
DRB1_0901  461  PVNIRPHPYEFALYY  IRPHPYEFA         0.4589         348.9          WB    32.00      Sequence
DRB1_0901    8  VFKLAKDEKVEYVDV  FKLAKDEKV         0.4578         353.2          WB    32.00      Sequence
DRB1_0901  183  GGYFPVAPNDQYVDL  GYFPVAPND         0.4571         355.6          WB    32.00      Sequence
DRB1_0901  179  VRHKGGYFPVAPNDQ  RHKGGYFPV         0.4563         358.8          WB    32.00      Sequence
DRB1_0901  300  TARHYIGGLLHHAPS  ARHYIGGLL         0.4562         359.2          WB    32.00      Sequence
DRB1_0901   60  FQSIHESDMLLLPDP  QSIHESDML         0.4561         359.4          WB    32.00      Sequence
DRB1_0901  335  APINLVYSQRNRSAC  INLVYSQRN         0.4551         363.4          WB    32.00      Sequence
DRB1_0901  135  FYIFDSVSFDSRANG  YIFDSVSFD         0.4551         363.5          WB    32.00      Sequence
DRB1_0901  239  DDMQLYKYIIKNTAW  MQLYKYIIK         0.4550         363.9          WB    32.00      Sequence
DRB1_0901  233  SLLHAADDMQLYKYI  LHAADDMQL         0.4549         364.3          WB    32.00      Sequence
DRB1_0901  339  LVYSQRNRSACVRIP  QRNRSACVR         0.4539         368.4          WB    32.00      Sequence
DRB1_0901  321  PTVNSYKRLVPGYEA  YKRLVPGYE         0.4535         369.9          WB    32.00      Sequence
DRB1_0901  463  NIRPHPYEFALYYDV  IRPHPYEFA         0.4534         370.3          WB    32.00      Sequence
DRB1_0901  182  KGGYFPVAPNDQYVD  GYFPVAPND         0.4513         378.7          WB    32.00      Sequence
DRB1_0901   81  PFRAAKTLNINFFVH  FRAAKTLNI         0.4483         391.4          WB    32.00      Sequence
DRB1_0901  334  EAPINLVYSQRNRSA  INLVYSQRN         0.4469         397.1          WB    32.00      Sequence
DRB1_0901  270  NGSGMHCHQSLWKDG  SGMHCHQSL         0.4455         403.4          WB    32.00      Sequence
DRB1_0901  130  GAEAEFYIFDSVSFD  YIFDSVSFD         0.4446         407.3          WB    32.00      Sequence
DRB1_0901  280  LWKDGAPLMYDETGY  LWKDGAPLM         0.4412         422.3          WB    32.00      Sequence
DRB1_0901   88  LNINFFVHDPFTLEP  FVHDPFTLE         0.4411         422.9          WB    32.00      Sequence
DRB1_0901  387  LDGIKNKIEPQAPVD  KIEPQAPVD         0.4406         425.1          WB    32.00      Sequence
DRB1_0901   98  FTLEPYSRDPRNIAR  FTLEPYSRD         0.4406         425.1          WB    32.00      Sequence
DRB1_0901   52  FDGSSIRGFQSIHES  SSIRGFQSI         0.4392         431.6          WB    32.00      Sequence
DRB1_0901  401  DKDLYELPPEEAASI  LYELPPEEA         0.4367         443.5          WB    32.00      Sequence
DRB1_0901  329  LVPGYEAPINLVYSQ  LVPGYEAPI         0.4359         447.4          WB    32.00      Sequence
DRB1_0901   27  LPGIMQHFTIPASAF  HFTIPASAF         0.4356         448.9          WB    32.00      Sequence
DRB1_0901  340  VYSQRNRSACVRIPI  QRNRSACVR         0.4342         455.6          WB    32.00      Sequence
DRB1_0901  332  GYEAPINLVYSQRNR  GYEAPINLV         0.4342         455.7          WB    32.00      Sequence
DRB1_0901  460  EPVNIRPHPYEFALY  IRPHPYEFA         0.4337         457.9          WB    32.00      Sequence
DRB1_0901  127  AYFGAEAEFYIFDSV  YFGAEAEFY         0.4308         472.6          WB    32.00      Sequence
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DRB1_0901   97  PFTLEPYSRDPRNIA  FTLEPYSRD         0.4304         474.7          WB    32.00      Sequence
DRB1_0901  331  PGYEAPINLVYSQRN  GYEAPINLV         0.4303         475.6          WB    32.00      Sequence
DRB1_0901   89  NINFFVHDPFTLEPY  FVHDPFTLE         0.4291         481.3          WB    32.00      Sequence
DRB1_0901  333  YEAPINLVYSQRNRS  INLVYSQRN         0.4286         484.4          WB    32.00      Sequence
DRB1_0901  177  YKVRHKGGYFPVAPN  KVRHKGGYF         0.4279         488.0          WB    32.00      Sequence
DRB1_0901   75  ETARIDPFRAAKTLN  DPFRAAKTL         0.4274         490.7          WB    32.00      Sequence
DRB1_0901  226  EINYQFNSLLHAADD  INYQFNSLL         0.4270         492.8          WB    32.00      Sequence
DRB1_0901  269  DNGSGMHCHQSLWKD  MHCHQSLWK         0.4267         494.3          WB    32.00      Sequence
DRB1_0901  238  ADDMQLYKYIIKNTA  MQLYKYIIK         0.4253         502.0                50.00      Sequence
DRB1_0901  243  LYKYIIKNTAWQNGK  YKYIIKNTA         0.4243         507.0                50.00      Sequence
DRB1_0901  110  IARKAENYLISTGIA  NYLISTGIA         0.4221         519.7                50.00      Sequence
DRB1_0901   90  INFFVHDPFTLEPYS  FVHDPFTLE         0.4220         519.9                50.00      Sequence
DRB1_0901  122  GIADTAYFGAEAEFY  AYFGAEAEF         0.4216         522.3                50.00      Sequence
DRB1_0901  200  KMLTNLINSGFILEK  TNLINSGFI         0.4214         523.3                50.00      Sequence
DRB1_0901  400  VDKDLYELPPEEAAS  LYELPPEEA         0.4212         524.5                50.00      Sequence
DRB1_0901  199  DKMLTNLINSGFILE  MLTNLINSG         0.4204         529.3                50.00      Sequence
DRB1_0901   61  QSIHESDMLLLPDPE  QSIHESDML         0.4199         532.0                50.00      Sequence
DRB1_0901   87  TLNINFFVHDPFTLE  FVHDPFTLE         0.4159         555.3                50.00      Sequence
DRB1_0901  253  WQNGKTVTFMPKPLF  VTFMPKPLF         0.4137         568.6                50.00      Sequence
DRB1_0901  201  MLTNLINSGFILEKG  TNLINSGFI         0.4125         576.4                50.00      Sequence
DRB1_0901  405  YELPPEEAASIPQTP  YELPPEEAA         0.4122         577.9                50.00      Sequence
DRB1_0901  299  DTARHYIGGLLHHAP  ARHYIGGLL         0.4115         582.6                50.00      Sequence
DRB1_0901  274  MHCHQSLWKDGAPLM  LWKDGAPLM         0.4102         591.0                50.00      Sequence
DRB1_0901  184  GYFPVAPNDQYVDLR  GYFPVAPND         0.4097         594.0                50.00      Sequence
DRB1_0901  176  GYKVRHKGGYFPVAP  KVRHKGGYF         0.4085         601.6                50.00      Sequence
DRB1_0901  254  QNGKTVTFMPKPLFG  VTFMPKPLF         0.4075         608.1                50.00      Sequence
DRB1_0901  320  NPTVNSYKRLVPGYE  YKRLVPGYE         0.4065         615.1                50.00      Sequence
DRB1_0901  399  PVDKDLYELPPEEAA  LYELPPEEA         0.4059         619.0                50.00      Sequence
DRB1_0901  379  FSAMLMAGLDGIKNK  FSAMLMAGL         0.4049         625.4                50.00      Sequence
DRB1_0901  174  NRGYKVRHKGGYFPV  KVRHKGGYF         0.4037         634.2                50.00      Sequence
DRB1_0901  136  YIFDSVSFDSRANGS  YIFDSVSFD         0.4032         637.3                50.00      Sequence
DRB1_0901  172  SPNRGYKVRHKGGYF  SPNRGYKVR         0.4028         639.9                50.00      Sequence
DRB1_0901  175  RGYKVRHKGGYFPVA  KVRHKGGYF         0.4024         642.8                50.00      Sequence
DRB1_0901    3  KTPDDVFKLAKDEKV  FKLAKDEKV         0.4023         643.4                50.00      Sequence
DRB1_0901  459  IEPVNIRPHPYEFAL  IRPHPYEFA         0.4014         649.9                50.00      Sequence
DRB1_0901  449  TWISFKRENEIEPVN  TWISFKREN         0.4002         658.2                50.00      Sequence
DRB1_0901  298  SDTARHYIGGLLHHA  ARHYIGGLL         0.3984         671.5                50.00      Sequence
DRB1_0901  198  RDKMLTNLINSGFIL  KMLTNLINS         0.3962         687.7                50.00      Sequence
DRB1_0901  458  EIEPVNIRPHPYEFA  IRPHPYEFA         0.3951         695.9                50.00      Sequence
DRB1_0901  173  PNRGYKVRHKGGYFP  YKVRHKGGY         0.3938         705.9                50.00      Sequence
DRB1_0901  147  ANGSFYEVDAISGWW  SFYEVDAIS         0.3933         709.0                50.00      Sequence
DRB1_0901  273  GMHCHQSLWKDGAPL  GMHCHQSLW         0.3918         720.8                50.00      Sequence
DRB1_0901  148  NGSFYEVDAISGWWN  SFYEVDAIS         0.3917         722.1                50.00      Sequence
DRB1_0901   26  DLPGIMQHFTIPASA  QHFTIPASA         0.3906         730.3                50.00      Sequence
DRB1_0901  244  YKYIIKNTAWQNGKT  YKYIIKNTA         0.3875         755.2                50.00      Sequence
DRB1_0901  145  SRANGSFYEVDAISG  SFYEVDAIS         0.3868         761.4                50.00      Sequence
DRB1_0901  378  AFSAMLMAGLDGIKN  FSAMLMAGL         0.3866         762.8                50.00      Sequence
DRB1_0901   92  FFVHDPFTLEPYSRD  FVHDPFTLE         0.3865         763.8                50.00      Sequence
DRB1_0901  146  RANGSFYEVDAISGW  SFYEVDAIS         0.3858         769.4                50.00      Sequence
DRB1_0901  202  LTNLINSGFILEKGH  TNLINSGFI         0.3847         778.6                50.00      Sequence
DRB1_0901  330  VPGYEAPINLVYSQR  GYEAPINLV         0.3844         781.1                50.00      Sequence
DRB1_0901   19  YVDVRFCDLPGIMQH  YVDVRFCDL         0.3840         784.8                50.00      Sequence
DRB1_0901  448  ETWISFKRENEIEPV  SFKRENEIE         0.3834         789.7                50.00      Sequence
DRB1_0901  297  LSDTARHYIGGLLHH  ARHYIGGLL         0.3825         797.1                50.00      Sequence
DRB1_0901   51  AFDGSSIRGFQSIHE  SSIRGFQSI         0.3823         798.7                50.00      Sequence
DRB1_0901  450  WISFKRENEIEPVNI  SFKRENEIE         0.3819         802.3                50.00      Sequence
DRB1_0901   39  SAFDKSVFDDGLAFD  KSVFDDGLA         0.3815         806.0                50.00      Sequence
DRB1_0901  225  AEINYQFNSLLHAAD  INYQFNSLL         0.3815         806.4                50.00      Sequence
DRB1_0901  386  GLDGIKNKIEPQAPV  NKIEPQAPV         0.3812         808.9                50.00      Sequence
DRB1_0901  352  IPITGSNPKAKRLEF  TGSNPKAKR         0.3794         824.7                50.00      Sequence
DRB1_0901  197  LRDKMLTNLINSGFI  KMLTNLINS         0.3783         834.7                50.00      Sequence
DRB1_0901   91  NFFVHDPFTLEPYSR  FVHDPFTLE         0.3778         838.7                50.00      Sequence
DRB1_0901  268  GDNGSGMHCHQSLWK  SGMHCHQSL         0.3758         856.8                50.00      Sequence
DRB1_0901   24  FCDLPGIMQHFTIPA  FCDLPGIMQ         0.3754         861.2                50.00      Sequence
DRB1_0901  234  LLHAADDMQLYKYII  LLHAADDMQ         0.3752         862.9                50.00      Sequence
DRB1_0901  316  LAFTNPTVNSYKRLV  TVNSYKRLV         0.3750         864.9                50.00      Sequence
DRB1_0901  121  TGIADTAYFGAEAEF  AYFGAEAEF         0.3744         870.5                50.00      Sequence
DRB1_0901  118  LISTGIADTAYFGAE  LISTGIADT         0.3742         871.8                50.00      Sequence
DRB1_0901  434  EYLTEGGVFTNDLIE  YLTEGGVFT         0.3726         887.8                50.00      Sequence
DRB1_0901  291  ETGYAGLSDTARHYI  TGYAGLSDT         0.3717         895.9                50.00      Sequence
DRB1_0901   50  LAFDGSSIRGFQSIH  LAFDGSSIR         0.3708         904.7                50.00      Sequence
DRB1_0901  351  RIPITGSNPKAKRLE  TGSNPKAKR         0.3704         908.8                50.00      Sequence
DRB1_0901  149  GSFYEVDAISGWWNT  SFYEVDAIS         0.3702         910.5                50.00      Sequence
DRB1_0901  310  HHAPSLLAFTNPTVN  HHAPSLLAF         0.3696         916.6                50.00      Sequence
DRB1_0901  447  IETWISFKRENEIEP  SFKRENEIE         0.3685         927.7                50.00      Sequence
DRB1_0901  129  FGAEAEFYIFDSVSF  FYIFDSVSF         0.3677         935.4                50.00      Sequence
DRB1_0901  350  VRIPITGSNPKAKRL  TGSNPKAKR         0.3663         950.3                50.00      Sequence
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DRB1_0901  451  ISFKRENEIEPVNIR  SFKRENEIE         0.3662        951.2               50.00     Sequence
DRB1_0901  292  TGYAGLSDTARHYIG  TGYAGLSDT         0.3630        984.1               50.00     Sequence
DRB1_0901  203  TNLINSGFILEKGHH  TNLINSGFI         0.3625        989.4               50.00     Sequence
DRB1_0901  128  YFGAEAEFYIFDSVS  YFGAEAEFY         0.3625        990.3               50.00     Sequence
DRB1_0901   62  SIHESDMLLLPDPET  SIHESDMLL         0.3624        991.1               50.00     Sequence
DRB1_0901  144  DSRANGSFYEVDAIS  GSFYEVDAI         0.3607       1009.1               50.00     Sequence
DRB1_0901  452  SFKRENEIEPVNIRP  FKRENEIEP         0.3605       1011.4               50.00     Sequence
DRB1_0901  362  KRLEFRSPDSSGNPY  FRSPDSSGN         0.3598       1019.3               50.00     Sequence
DRB1_0901  109  NIARKAENYLISTGI  IARKAENYL         0.3594       1023.8               50.00     Sequence
DRB1_0901   40  AFDKSVFDDGLAFDG  KSVFDDGLA         0.3592       1026.0               50.00     Sequence
DRB1_0901  345  NRSACVRIPITGSNP  RSACVRIPI         0.3589       1028.7               50.00     Sequence
DRB1_0901   68  MLLLPDPETARIDPF  MLLLPDPET         0.3588       1030.4               50.00     Sequence
DRB1_0901  267  FGDNGSGMHCHQSLW  FGDNGSGMH         0.3577       1042.6               50.00     Sequence
DRB1_0901  295  AGLSDTARHYIGGLL  ARHYIGGLL         0.3572       1048.5               50.00     Sequence
DRB1_0901  433  HEYLTEGGVFTNDLI  YLTEGGVFT         0.3571       1049.2               50.00     Sequence
DRB1_0901   67  DMLLLPDPETARIDP  MLLLPDPET         0.3564       1057.2               50.00     Sequence
DRB1_0901  444  NDLIETWISFKRENE  WISFKRENE         0.3564       1057.4               50.00     Sequence
DRB1_0901  296  GLSDTARHYIGGLLH  ARHYIGGLL         0.3559       1063.0               50.00     Sequence
DRB1_0901  446  LIETWISFKRENEIE  SFKRENEIE         0.3545       1079.2               50.00     Sequence
DRB1_0901   41  FDKSVFDDGLAFDGS  KSVFDDGLA         0.3545       1079.4               50.00     Sequence
DRB1_0901  363  RLEFRSPDSSGNPYL  EFRSPDSSG         0.3540       1085.7               50.00     Sequence
DRB1_0901  453  FKRENEIEPVNIRPH  FKRENEIEP         0.3524       1103.7               50.00     Sequence
DRB1_0901  289  YDETGYAGLSDTARH  YDETGYAGL         0.3522       1107.1               50.00     Sequence
DRB1_0901  213  EKGHHEVGSGGQAEI  VGSGGQAEI         0.3515       1114.7               50.00     Sequence
DRB1_0901   18  EYVDVRFCDLPGIMQ  YVDVRFCDL         0.3509       1122.0               50.00     Sequence
DRB1_0901  353  PITGSNPKAKRLEFR  TGSNPKAKR         0.3504       1128.4               50.00     Sequence
DRB1_0901  435  YLTEGGVFTNDLIET  YLTEGGVFT         0.3503       1129.5               50.00     Sequence
DRB1_0901   93  FVHDPFTLEPYSRDP  FVHDPFTLE         0.3498       1135.4               50.00     Sequence
DRB1_0901  361  AKRLEFRSPDSSGNP  EFRSPDSSG         0.3482       1155.4               50.00     Sequence
DRB1_0901  317  AFTNPTVNSYKRLVP  AFTNPTVNS         0.3481       1157.3               50.00     Sequence
DRB1_0901  393  KIEPQAPVDKDLYEL  KIEPQAPVD         0.3478       1161.0               50.00     Sequence
DRB1_0901  214  KGHHEVGSGGQAEIN  VGSGGQAEI         0.3475       1164.8               50.00     Sequence
DRB1_0901  420  TQLSDVIDRLEADHE  QLSDVIDRL         0.3471       1169.1               50.00     Sequence
DRB1_0901  217  HEVGSGGQAEINYQF  VGSGGQAEI         0.3468       1172.9               50.00     Sequence
DRB1_0901  445  DLIETWISFKRENEI  WISFKRENE         0.3467       1175.0               50.00     Sequence
DRB1_0901  153  EVDAISGWWNTGAAT  EVDAISGWW         0.3465       1177.4               50.00     Sequence
DRB1_0901   74  PETARIDPFRAAKTL  DPFRAAKTL         0.3464       1178.4               50.00     Sequence
DRB1_0901  224  QAEINYQFNSLLHAA  INYQFNSLL         0.3459       1184.5               50.00     Sequence
DRB1_0901   96  DPFTLEPYSRDPRNI  FTLEPYSRD         0.3452       1193.8               50.00     Sequence
DRB1_0901   25  CDLPGIMQHFTIPAS  IMQHFTIPA         0.3451       1194.3               50.00     Sequence
DRB1_0901  261  FMPKPLFGDNGSGMH  FGDNGSGMH         0.3440       1208.9               50.00     Sequence
DRB1_0901   22  VRFCDLPGIMQHFTI  FCDLPGIMQ         0.3440       1208.9               50.00     Sequence
DRB1_0901  421  QLSDVIDRLEADHEY  QLSDVIDRL         0.3439       1211.2               50.00     Sequence
DRB1_0901  103  YSRDPRNIARKAENY  YSRDPRNIA         0.3426       1228.3               50.00     Sequence
DRB1_0901   42  DKSVFDDGLAFDGSS  VFDDGLAFD         0.3421       1234.8               50.00     Sequence
DRB1_0901  456  ENEIEPVNIRPHPYE  NEIEPVNIR         0.3419       1236.7               50.00     Sequence
DRB1_0901   23  RFCDLPGIMQHFTIP  FCDLPGIMQ         0.3403       1259.3               50.00     Sequence
DRB1_0901  281  WKDGAPLMYDETGYA  WKDGAPLMY         0.3401       1261.7               50.00     Sequence
DRB1_0901  415  IPQTPTQLSDVIDRL  IPQTPTQLS         0.3390       1276.7               50.00     Sequence
DRB1_0901  419  PTQLSDVIDRLEADH  QLSDVIDRL         0.3388       1279.0               50.00     Sequence
DRB1_0901  219  VGSGGQAEINYQFNS  VGSGGQAEI         0.3383       1286.7               50.00     Sequence
DRB1_0901  237  AADDMQLYKYIIKNT  MQLYKYIIK         0.3380       1289.9               50.00     Sequence
DRB1_0901  216  HHEVGSGGQAEINYQ  VGSGGQAEI         0.3378       1292.9               50.00     Sequence
DRB1_0901   86  KTLNINFFVHDPFTL  FFVHDPFTL         0.3373       1299.9               50.00     Sequence
DRB1_0901  406  ELPPEEAASIPQTPT  LPPEEAASI         0.3364       1312.2               50.00     Sequence
DRB1_0901  218  EVGSGGQAEINYQFN  VGSGGQAEI         0.3348       1336.1               50.00     Sequence
DRB1_0901  438  EGGVFTNDLIETWIS  GGVFTNDLI         0.3346       1338.9               50.00     Sequence
DRB1_0901  418  TPTQLSDVIDRLEAD  LSDVIDRLE         0.3330       1361.8               50.00     Sequence
DRB1_0901  171  GSPNRGYKVRHKGGY  SPNRGYKVR         0.3325       1369.6               50.00     Sequence
DRB1_0901  443  TNDLIETWISFKREN  TNDLIETWI         0.3324       1371.3               50.00     Sequence
DRB1_0901  106  DPRNIARKAENYLIS  IARKAENYL         0.3323       1371.8               50.00     Sequence
DRB1_0901  354  ITGSNPKAKRLEFRS  TGSNPKAKR         0.3316       1382.8               50.00     Sequence
DRB1_0901  457  NEIEPVNIRPHPYEF  NEIEPVNIR         0.3316       1382.9               50.00     Sequence
DRB1_0901  108  RNIARKAENYLISTG  IARKAENYL         0.3311       1390.2               50.00     Sequence
DRB1_0901  252  AWQNGKTVTFMPKPL  WQNGKTVTF         0.3308       1394.5               50.00     Sequence
DRB1_0901   66  SDMLLLPDPETARID  MLLLPDPET         0.3308       1395.3               50.00     Sequence
DRB1_0901  107  PRNIARKAENYLIST  IARKAENYL         0.3304       1401.1               50.00     Sequence
DRB1_0901   38  ASAFDKSVFDDGLAF  KSVFDDGLA         0.3299       1407.9               50.00     Sequence
DRB1_0901   21  DVRFCDLPGIMQHFT  FCDLPGIMQ         0.3294       1416.0               50.00     Sequence
DRB1_0901  360  KAKRLEFRSPDSSGN  EFRSPDSSG         0.3291       1420.5               50.00     Sequence
DRB1_0901  439  GGVFTNDLIETWISF  GGVFTNDLI         0.3290       1422.6               50.00     Sequence
DRB1_0901   37  PASAFDKSVFDDGLA  KSVFDDGLA         0.3286       1427.9               50.00     Sequence
DRB1_0901   49  GLAFDGSSIRGFQSI  AFDGSSIRG         0.3280       1438.6               50.00     Sequence
DRB1_0901  247  IIKNTAWQNGKTVTF  WQNGKTVTF         0.3271       1451.5               50.00     Sequence
DRB1_0901  315  LLAFTNPTVNSYKRL  LLAFTNPTV         0.3271       1451.7               50.00     Sequence
DRB1_0901  290  DETGYAGLSDTARHY  TGYAGLSDT         0.3271       1452.6               50.00     Sequence
DRB1_0901  311  HAPSLLAFTNPTVNS  LLAFTNPTV         0.3269       1455.8               50.00     Sequence
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    DRB1_0901  441  VFTNDLIETWISFKR  VFTNDLIET         0.3260       1468.7               50.00     Sequence
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    DRB1_0901  314  SLLAFTNPTVNSYKR  LLAFTNPTV         0.3254       1478.4               50.00     Sequence
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    DRB1_0901  432  DHEYLTEGGVFTNDL  YLTEGGVFT         0.3232       1514.9               50.00     Sequence
    DRB1_0901   10  KLAKDEKVEYVDVRF  KLAKDEKVE         0.3227       1523.3               50.00     Sequence
    DRB1_0901  440  GVFTNDLIETWISFK  VFTNDLIET         0.3218       1538.4               50.00     Sequence
    DRB1_0901  150  SFYEVDAISGWWNTG  SFYEVDAIS         0.3216       1541.0               50.00     Sequence
    DRB1_0901  143  FDSRANGSFYEVDAI  FDSRANGSF         0.3216       1541.5               50.00     Sequence
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    DRB1_0901  349  CVRIPITGSNPKAKR  ITGSNPKAK         0.3207       1556.5               50.00     Sequence
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    DRB1_0901  398  APVDKDLYELPPEEA  LYELPPEEA         0.3174       1613.1               50.00     Sequence
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    DRB1_0901  442  FTNDLIETWISFKRE  TNDLIETWI         0.3161       1636.3               50.00     Sequence
    DRB1_0901  119  ISTGIADTAYFGAEA  ISTGIADTA         0.3154       1647.4               50.00     Sequence
    DRB1_0901  152  YEVDAISGWWNTGAA  EVDAISGWW         0.3148       1658.5               50.00     Sequence
    DRB1_0901  382  MLMAGLDGIKNKIEP  MLMAGLDGI         0.3138       1675.7               50.00     Sequence
    DRB1_0901  318  FTNPTVNSYKRLVPG  TVNSYKRLV         0.3138       1677.5               50.00     Sequence
    DRB1_0901  190  PNDQYVDLRDKMLTN  YVDLRDKML         0.3123       1704.3               50.00     Sequence
    DRB1_0901  105  RDPRNIARKAENYLI  IARKAENYL         0.3115       1718.9               50.00     Sequence
    DRB1_0901  364  LEFRSPDSSGNPYLA  EFRSPDSSG         0.3114       1720.0               50.00     Sequence
    DRB1_0901   71  LPDPETARIDPFRAA  LPDPETARI         0.3109       1729.7               50.00     Sequence
    DRB1_0901  454  KRENEIEPVNIRPHP  NEIEPVNIR         0.3106       1736.0               50.00     Sequence
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    DRB1_0901  346  RSACVRIPITGSNPK  RSACVRIPI         0.3101       1745.8               50.00     Sequence
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    DRB1_0901  455  RENEIEPVNIRPHPY  NEIEPVNIR         0.3079       1786.3               50.00     Sequence
    DRB1_0901   48  DGLAFDGSSIRGFQS  AFDGSSIRG         0.3071       1802.3               50.00     Sequence
    DRB1_0901  417  QTPTQLSDVIDRLEA  QLSDVIDRL         0.3070       1805.0               50.00     Sequence
    DRB1_0901   43  KSVFDDGLAFDGSSI  VFDDGLAFD         0.3067       1810.6               50.00     Sequence
    DRB1_0901  422  LSDVIDRLEADHEYL  LSDVIDRLE         0.3063       1818.6               50.00     Sequence
    DRB1_0901  194  YVDLRDKMLTNLINS  YVDLRDKML         0.3055       1834.0               50.00     Sequence
    DRB1_0901  251  TAWQNGKTVTFMPKP  WQNGKTVTF         0.3053       1837.6               50.00     Sequence
    DRB1_0901  312  APSLLAFTNPTVNSY  LLAFTNPTV         0.3053       1838.6               50.00     Sequence
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    DRB1_0901  185  YFPVAPNDQYVDLRD  YFPVAPNDQ         0.3037       1871.0               50.00     Sequence
    DRB1_0901  437  TEGGVFTNDLIETWI  GGVFTNDLI         0.3036       1872.2               50.00     Sequence
    DRB1_0901  262  MPKPLFGDNGSGMHC  FGDNGSGMH         0.3035       1874.6               50.00     Sequence
    DRB1_0901  248  IKNTAWQNGKTVTFM  WQNGKTVTF         0.3034       1876.3               50.00     Sequence
    DRB1_0901  260  TFMPKPLFGDNGSGM  FMPKPLFGD         0.3034       1876.4               50.00     Sequence
    DRB1_0901  413  ASIPQTPTQLSDVID  IPQTPTQLS         0.3031       1881.9               50.00     Sequence
    DRB1_0901  246  YIIKNTAWQNGKTVT  YIIKNTAWQ         0.3031       1882.1               50.00     Sequence
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    DRB1_0901  384  MAGLDGIKNKIEPQA  GLDGIKNKI         0.3017       1912.1               50.00     Sequence
    DRB1_0901  101  EPYSRDPRNIARKAE  YSRDPRNIA         0.3014       1916.4               50.00     Sequence
    DRB1_0901   36  IPASAFDKSVFDDGL  IPASAFDKS         0.3012       1922.0               50.00     Sequence
    DRB1_0901  416  PQTPTQLSDVIDRLE  QLSDVIDRL         0.3009       1927.7               50.00     Sequence
    DRB1_0901   45  VFDDGLAFDGSSIRG  VFDDGLAFD         0.3003       1940.8               50.00     Sequence
    DRB1_0901  204  NLINSGFILEKGHHE  LINSGFILE         0.2996       1954.9               50.00     Sequence
    DRB1_0901  223  GQAEINYQFNSLLHA  INYQFNSLL         0.2991       1966.2               50.00     Sequence
    DRB1_0901  355  TGSNPKAKRLEFRSP  TGSNPKAKR         0.2985       1978.0               50.00     Sequence
    DRB1_0901  196  DLRDKMLTNLINSGF  DKMLTNLIN         0.2981       1986.3               50.00     Sequence
    DRB1_0901  407  LPPEEAASIPQTPTQ  LPPEEAASI         0.2971       2008.1               50.00     Sequence
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    DRB1_0901  205  LINSGFILEKGHHEV  LINSGFILE         0.2957       2040.1               50.00     Sequence
    DRB1_0901  193  QYVDLRDKMLTNLIN  YVDLRDKML         0.2948       2058.2               50.00     Sequence
    DRB1_0901  250  NTAWQNGKTVTFMPK  WQNGKTVTF         0.2942       2072.4               50.00     Sequence
    DRB1_0901  192  DQYVDLRDKMLTNLI  YVDLRDKML         0.2933       2094.1               50.00     Sequence
    DRB1_0901  245  KYIIKNTAWQNGKTV  KYIIKNTAW         0.2925       2110.8               50.00     Sequence
    DRB1_0901   15  EKVEYVDVRFCDLPG  KVEYVDVRF         0.2918       2128.0               50.00     Sequence
    DRB1_0901  100  LEPYSRDPRNIARKA  YSRDPRNIA         0.2911       2142.4               50.00     Sequence
    DRB1_0901   95  HDPFTLEPYSRDPRN  FTLEPYSRD         0.2904       2160.8               50.00     Sequence
    DRB1_0901  293  GYAGLSDTARHYIGG  GYAGLSDTA         0.2903       2162.2               50.00     Sequence
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DRB1_0901  436  LTEGGVFTNDLIETW  GGVFTNDLI        0.2903       2163.0              50.00     Sequence
DRB1_0901  142  SFDSRANGSFYEVDA  FDSRANGSF        0.2886       2202.8              50.00     Sequence
DRB1_0901  249  KNTAWQNGKTVTFMP  WQNGKTVTF        0.2883       2209.5              50.00     Sequence
DRB1_0901  430  EADHEYLTEGGVFTN  YLTEGGVFT        0.2874       2231.5              50.00     Sequence
DRB1_0901   94  VHDPFTLEPYSRDPR  FTLEPYSRD        0.2857       2273.1              50.00     Sequence
DRB1_0901   16  KVEYVDVRFCDLPGI  KVEYVDVRF        0.2857       2273.2              50.00     Sequence
DRB1_0901   14  DEKVEYVDVRFCDLP  KVEYVDVRF        0.2849       2292.2              50.00     Sequence
DRB1_0901   44  SVFDDGLAFDGSSIR  VFDDGLAFD        0.2848       2295.1              50.00     Sequence
DRB1_0901  412  AASIPQTPTQLSDVI  IPQTPTQLS        0.2841       2312.9              50.00     Sequence
DRB1_0901  235  LHAADDMQLYKYIIK  LHAADDMQL        0.2834       2328.4              50.00     Sequence
DRB1_0901   73  DPETARIDPFRAAKT  ARIDPFRAA        0.2832       2335.3              50.00     Sequence
DRB1_0901  170  DGSPNRGYKVRHKGG  SPNRGYKVR        0.2807       2397.7              50.00     Sequence
DRB1_0901  191  NDQYVDLRDKMLTNL  YVDLRDKML        0.2801       2413.8              50.00     Sequence
DRB1_0901  212  LEKGHHEVGSGGQAE  KGHHEVGSG        0.2796       2427.5              50.00     Sequence
DRB1_0901  211  ILEKGHHEVGSGGQA  KGHHEVGSG        0.2794       2432.1              50.00     Sequence
DRB1_0901  410  EEAASIPQTPTQLSD  IPQTPTQLS        0.2790       2443.7              50.00     Sequence
DRB1_0901  383  LMAGLDGIKNKIEPQ  GLDGIKNKI        0.2769       2498.4              50.00     Sequence
DRB1_0901  408  PPEEAASIPQTPTQL  EEAASIPQT        0.2767       2505.6              50.00     Sequence
DRB1_0901  294  YAGLSDTARHYIGGL  LSDTARHYI        0.2758       2528.6              50.00     Sequence
DRB1_0901  411  EAASIPQTPTQLSDV  IPQTPTQLS        0.2739       2580.7              50.00     Sequence
DRB1_0901  429  LEADHEYLTEGGVFT  YLTEGGVFT        0.2738       2584.0              50.00     Sequence
DRB1_0901   70  LLPDPETARIDPFRA  LPDPETARI        0.2729       2608.7              50.00     Sequence
DRB1_0901   47  DDGLAFDGSSIRGFQ  LAFDGSSIR        0.2716       2645.8              50.00     Sequence
DRB1_0901  348  ACVRIPITGSNPKAK  VRIPITGSN        0.2716       2646.1              50.00     Sequence
DRB1_0901   85  AKTLNINFFVHDPFT  INFFVHDPF        0.2716       2648.2              50.00     Sequence
DRB1_0901  365  EFRSPDSSGNPYLAF  EFRSPDSSG        0.2710       2662.9              50.00     Sequence
DRB1_0901   11  LAKDEKVEYVDVRFC  EKVEYVDVR        0.2694       2709.8              50.00     Sequence
DRB1_0901   17  VEYVDVRFCDLPGIM  YVDVRFCDL        0.2680       2753.3              50.00     Sequence
DRB1_0901   13  KDEKVEYVDVRFCDL  KVEYVDVRF        0.2673       2771.4              50.00     Sequence
DRB1_0901   46  FDDGLAFDGSSIRGF  LAFDGSSIR        0.2669       2785.8              50.00     Sequence
DRB1_0901  210  FILEKGHHEVGSGGQ  KGHHEVGSG        0.2651       2840.8              50.00     Sequence
DRB1_0901  195  VDLRDKMLTNLINSG  RDKMLTNLI        0.2647       2851.5              50.00     Sequence
DRB1_0901  359  PKAKRLEFRSPDSSG  EFRSPDSSG        0.2645       2859.1              50.00     Sequence
DRB1_0901   69  LLLPDPETARIDPFR  LPDPETARI        0.2630       2904.3              50.00     Sequence
DRB1_0901  423  SDVIDRLEADHEYLT  RLEADHEYL        0.2623       2927.8              50.00     Sequence
DRB1_0901  347  SACVRIPITGSNPKA  VRIPITGSN        0.2618       2941.5              50.00     Sequence
DRB1_0901  264  KPLFGDNGSGMHCHQ  FGDNGSGMH        0.2615       2953.5              50.00     Sequence
DRB1_0901  169  ADGSPNRGYKVRHKG  SPNRGYKVR        0.2604       2989.3              50.00     Sequence
DRB1_0901  236  HAADDMQLYKYIIKN  MQLYKYIIK        0.2603       2991.0              50.00     Sequence
DRB1_0901  368  SPDSSGNPYLAFSAM  NPYLAFSAM        0.2603       2991.9              50.00     Sequence
DRB1_0901  286  PLMYDETGYAGLSDT  YDETGYAGL        0.2594       3020.6              50.00     Sequence
DRB1_0901  151  FYEVDAISGWWNTGA  YEVDAISGW        0.2568       3107.1              50.00     Sequence
DRB1_0901  263  PKPLFGDNGSGMHCH  FGDNGSGMH        0.2563       3125.0              50.00     Sequence
DRB1_0901  141  VSFDSRANGSFYEVD  FDSRANGSF        0.2534       3224.4              50.00     Sequence
DRB1_0901   72  PDPETARIDPFRAAK  ARIDPFRAA        0.2516       3287.7              50.00     Sequence
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DRB1_0901  394  IEPQAPVDKDLYELP  EPQAPVDKD        0.2487       3390.0              50.00     Sequence
DRB1_0901  424  DVIDRLEADHEYLTE  DVIDRLEAD        0.2466       3470.3              50.00     Sequence
DRB1_0901  140  SVSFDSRANGSFYEV  FDSRANGSF        0.2424       3629.4              50.00     Sequence
DRB1_0901  137  IFDSVSFDSRANGSF  IFDSVSFDS        0.2384       3792.2              50.00     Sequence
DRB1_0901   12  AKDEKVEYVDVRFCD  KVEYVDVRF        0.2366       3867.0              50.00     Sequence
DRB1_0901  356  GSNPKAKRLEFRSPD  GSNPKAKRL        0.2353       3921.5              50.00     Sequence
DRB1_0901  167  TEADGSPNRGYKVRH  SPNRGYKVR        0.2349       3937.8              50.00     Sequence
DRB1_0901  208  SGFILEKGHHEVGSG  KGHHEVGSG        0.2343       3962.4              50.00     Sequence
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DRB1_0901  186  FPVAPNDQYVDLRDK  FPVAPNDQY        0.2293       4184.9              50.00     Sequence
DRB1_0901   84  AAKTLNINFFVHDPF  INFFVHDPF        0.2291       4194.0              50.00     Sequence
DRB1_0901  425  VIDRLEADHEYLTEG  VIDRLEADH        0.2262       4327.0              50.00     Sequence
DRB1_0901  358  NPKAKRLEFRSPDSS  RLEFRSPDS        0.2228       4486.6              50.00     Sequence
DRB1_0901    2  EKTPDDVFKLAKDEK  DVFKLAKDE        0.2211       4569.9              50.00     Sequence
DRB1_0901  426  IDRLEADHEYLTEGG  RLEADHEYL        0.2174       4755.7              50.00     Sequence
DRB1_0901  138  FDSVSFDSRANGSFY  FDSRANGSF        0.2157       4847.9              50.00     Sequence
DRB1_0901  395  EPQAPVDKDLYELPP  EPQAPVDKD        0.2148       4896.1              50.00     Sequence
DRB1_0901  221  SGGQAEINYQFNSLL  INYQFNSLL        0.2135       4960.7              50.00     Sequence
DRB1_0901  427  DRLEADHEYLTEGGV  RLEADHEYL        0.2118       5056.3              50.00     Sequence
DRB1_0901  187  PVAPNDQYVDLRDKM  QYVDLRDKM        0.2108       5111.1              50.00     Sequence
DRB1_0901  285  APLMYDETGYAGLSD  YDETGYAGL        0.2078       5279.7              50.00     Sequence
DRB1_0901  428  RLEADHEYLTEGGVF  RLEADHEYL        0.2071       5319.5              50.00     Sequence
DRB1_0901  222  GGQAEINYQFNSLLH  INYQFNSLL        0.2069       5328.0              50.00     Sequence
DRB1_0901  206  INSGFILEKGHHEVG  INSGFILEK        0.2046       5461.9              50.00     Sequence
DRB1_0901  366  FRSPDSSGNPYLAFS  FRSPDSSGN        0.2032       5549.4              50.00     Sequence
DRB1_0901  357  SNPKAKRLEFRSPDS  NPKAKRLEF        0.2005       5713.2              50.00     Sequence
DRB1_0901  162  NTGAATEADGSPNRG  NTGAATEAD        0.1997       5763.7              50.00     Sequence
DRB1_0901  220  GSGGQAEINYQFNSL  SGGQAEINY        0.1995       5776.0              50.00     Sequence
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   DRB1_0901  166  ATEADGSPNRGYKVR  SPNRGYKVR        0.1973        5915.0               50.00     Sequence
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   DRB1_0901  207  NSGFILEKGHHEVGS  FILEKGHHE        0.1924        6237.5               50.00     Sequence
   DRB1_0901  282  KDGAPLMYDETGYAG  KDGAPLMYD        0.1871        6605.2               50.00     Sequence
   DRB1_0901  284  GAPLMYDETGYAGLS  YDETGYAGL        0.1827        6924.3               50.00     Sequence
   DRB1_0901   83  RAAKTLNINFFVHDP  RAAKTLNIN        0.1771        7357.5               50.00     Sequence
   DRB1_0901    1  TEKTPDDVFKLAKDE  TEKTPDDVF        0.1736        7639.0               50.00     Sequence
   DRB1_0901  165  AATEADGSPNRGYKV  AATEADGSP        0.1732        7671.5               50.00     Sequence
   DRB1_0901  283  DGAPLMYDETGYAGL  LMYDETGYA        0.1711        7847.7               50.00     Sequence
   DRB1_0901  367  RSPDSSGNPYLAFSA  SGNPYLAFS        0.1658        8314.4               50.00     Sequence
   DRB1_0901  163  TGAATEADGSPNRGY  TGAATEADG        0.1618        8681.3               50.00     Sequence
   DRB1_0901  164  GAATEADGSPNRGYK  EADGSPNRG        0.1560        9247.9               50.00     Sequence
   DRB1_0901  397  QAPVDKDLYELPPEE  QAPVDKDLY        0.1538        9469.9               50.00     Sequence
   DRB1_0901  396  PQAPVDKDLYELPPE  PQAPVDKDL        0.1524        9609.4               50.00     Sequence
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Allele: DRB1_0901. Number of high binders 17. Number of weak binders 133. Number of peptides 464

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      Allele  pos          peptide      core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1101  241  MQLYKYIIKNTAWQN  YKYIIKNTA        0.8720           4.0          SB     0.05     Sequence
   DRB1_1101  242  QLYKYIIKNTAWQNG  YKYIIKNTA        0.8555           4.8          SB     0.10     Sequence
   DRB1_1101  243  LYKYIIKNTAWQNGK  YKYIIKNTA        0.8439           5.4          SB     0.15     Sequence
   DRB1_1101  240  DMQLYKYIIKNTAWQ  YKYIIKNTA        0.8302           6.3          SB     0.20     Sequence
   DRB1_1101  239  DDMQLYKYIIKNTAW  YKYIIKNTA        0.7829          10.5          SB     0.80     Sequence
   DRB1_1101  244  YKYIIKNTAWQNGKT  YKYIIKNTA        0.7717          11.8          SB     0.80     Sequence
   DRB1_1101  227  INYQFNSLLHAADDM  YQFNSLLHA        0.7157          21.7          SB     2.00     Sequence
   DRB1_1101  256  GKTVTFMPKPLFGDN  VTFMPKPLF        0.7093          23.2          SB     2.00     Sequence
   DRB1_1101  238  ADDMQLYKYIIKNTA  YKYIIKNTA        0.6997          25.8          SB     2.00     Sequence
   DRB1_1101  228  NYQFNSLLHAADDMQ  YQFNSLLHA        0.6989          26.0          SB     4.00     Sequence
   DRB1_1101  257  KTVTFMPKPLFGDNG  VTFMPKPLF        0.6965          26.7          SB     4.00     Sequence
   DRB1_1101  226  EINYQFNSLLHAADD  YQFNSLLHA        0.6958          26.9          SB     4.00     Sequence
   DRB1_1101  255  NGKTVTFMPKPLFGD  VTFMPKPLF        0.6845          30.4          SB     4.00     Sequence
   DRB1_1101  225  AEINYQFNSLLHAAD  YQFNSLLHA        0.6635          38.1          SB     4.00     Sequence
   DRB1_1101  229  YQFNSLLHAADDMQL  YQFNSLLHA        0.6535          42.5          SB     4.00     Sequence
   DRB1_1101  254  QNGKTVTFMPKPLFG  VTFMPKPLF        0.6422          48.0          SB     4.00     Sequence
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   DRB1_1101  305  IGGLLHHAPSLLAFT  LHHAPSLLA        0.6344          52.2          WB     8.00     Sequence
   DRB1_1101  258  TVTFMPKPLFGDNGS  VTFMPKPLF        0.6302          54.7          WB     8.00     Sequence
   DRB1_1101  304  YIGGLLHHAPSLLAF  LHHAPSLLA        0.6195          61.4          WB     8.00     Sequence
   DRB1_1101  198  RDKMLTNLINSGFIL  DKMLTNLIN        0.6186          62.0          WB     8.00     Sequence
   DRB1_1101  307  GLLHHAPSLLAFTNP  LHHAPSLLA        0.6128          66.0          WB     8.00     Sequence
   DRB1_1101  224  QAEINYQFNSLLHAA  YQFNSLLHA        0.6122          66.4          WB     8.00     Sequence
   DRB1_1101  197  LRDKMLTNLINSGFI  DKMLTNLIN        0.6048          71.9          WB     8.00     Sequence
   DRB1_1101   79  IDPFRAAKTLNINFF  PFRAAKTLN        0.6013          74.7          WB     8.00     Sequence
   DRB1_1101  199  DKMLTNLINSGFILE  DKMLTNLIN        0.6012          74.8          WB     8.00     Sequence
   DRB1_1101  303  HYIGGLLHHAPSLLA  LHHAPSLLA        0.5946          80.3          WB     8.00     Sequence
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   DRB1_1101  196  DLRDKMLTNLINSGF  DKMLTNLIN        0.5848          89.4          WB     8.00     Sequence
   DRB1_1101   80  DPFRAAKTLNINFFV  FRAAKTLNI        0.5642         111.6          WB    16.00     Sequence
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   DRB1_1101  302  RHYIGGLLHHAPSLL  RHYIGGLLH        0.5564         121.5          WB    16.00     Sequence
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   DRB1_1101  194  YVDLRDKMLTNLINS  VDLRDKMLT        0.5520         127.4          WB    16.00     Sequence
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   DRB1_1101  300  TARHYIGGLLHHAPS  RHYIGGLLH        0.5362         151.2          WB    16.00     Sequence
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   DRB1_1101  322  TVNSYKRLVPGYEAP  NSYKRLVPG        0.5241         172.4          WB    16.00     Sequence
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   DRB1_1101  174  NRGYKVRHKGGYFPV  YKVRHKGGY        0.5218         176.7          WB    16.00     Sequence
   DRB1_1101  337  INLVYSQRNRSACVR  LVYSQRNRS        0.5208         178.5          WB    16.00     Sequence
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   DRB1_1101  175  RGYKVRHKGGYFPVA  YKVRHKGGY        0.5168         186.5          WB    16.00     Sequence
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   DRB1_1101  299  DTARHYIGGLLHHAP  RHYIGGLLH        0.5129         194.5          WB    16.00     Sequence
   DRB1_1101  377  LAFSAMLMAGLDGIK  LAFSAMLMA        0.5127         194.9          WB    16.00     Sequence
   DRB1_1101  374  NPYLAFSAMLMAGLD  LAFSAMLMA        0.5099         200.9          WB    16.00     Sequence
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   DRB1_1101  336  PINLVYSQRNRSACV  INLVYSQRN        0.5016         219.8          WB    16.00     Sequence
   DRB1_1101  245  KYIIKNTAWQNGKTV  KYIIKNTAW        0.4998         224.2          WB    16.00     Sequence
   DRB1_1101  223  GQAEINYQFNSLLHA  YQFNSLLHA        0.4936         239.8          WB    16.00     Sequence
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DRB1_1101  173  PNRGYKVRHKGGYFP  YKVRHKGGY         0.4918         244.4         WB    16.00       Sequence
DRB1_1101  323  VNSYKRLVPGYEAPI  SYKRLVPGY         0.4878         255.0         WB    16.00       Sequence
DRB1_1101  320  NPTVNSYKRLVPGYE  TVNSYKRLV         0.4866         258.4         WB    16.00       Sequence
DRB1_1101  192  DQYVDLRDKMLTNLI  VDLRDKMLT         0.4845         264.4         WB    16.00       Sequence
DRB1_1101  335  APINLVYSQRNRSAC  INLVYSQRN         0.4807         275.5         WB    16.00       Sequence
DRB1_1101  373  GNPYLAFSAMLMAGL  LAFSAMLMA         0.4777         284.7         WB    16.00       Sequence
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DRB1_1101  448  ETWISFKRENEIEPV  TWISFKREN         0.4689         313.0         WB    32.00       Sequence
DRB1_1101  298  SDTARHYIGGLLHHA  RHYIGGLLH         0.4625         335.6         WB    32.00       Sequence
DRB1_1101  176  GYKVRHKGGYFPVAP  YKVRHKGGY         0.4618         338.1         WB    32.00       Sequence
DRB1_1101  259  VTFMPKPLFGDNGSG  VTFMPKPLF         0.4595         346.7         WB    32.00       Sequence
DRB1_1101  449  TWISFKRENEIEPVN  ISFKRENEI         0.4558         360.9         WB    32.00       Sequence
DRB1_1101  446  LIETWISFKRENEIE  TWISFKREN         0.4550         363.8         WB    32.00       Sequence
DRB1_1101  309  LHHAPSLLAFTNPTV  LHHAPSLLA         0.4477         393.7         WB    32.00       Sequence
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DRB1_1101  334  EAPINLVYSQRNRSA  INLVYSQRN         0.4382         436.6         WB    32.00       Sequence
DRB1_1101  230  QFNSLLHAADDMQLY  FNSLLHAAD         0.4364         445.2         WB    32.00       Sequence
DRB1_1101  319  TNPTVNSYKRLVPGY  TVNSYKRLV         0.4358         447.9         WB    32.00       Sequence
DRB1_1101  201  MLTNLINSGFILEKG  MLTNLINSG         0.4320         466.9         WB    32.00       Sequence
DRB1_1101  324  NSYKRLVPGYEAPIN  YKRLVPGYE         0.4318         467.7         WB    32.00       Sequence
DRB1_1101  338  NLVYSQRNRSACVRI  VYSQRNRSA         0.4310         471.8         WB    32.00       Sequence
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DRB1_1101   55  SSIRGFQSIHESDML  IRGFQSIHE         0.4181         542.2               32.00       Sequence
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DRB1_1101  171  GSPNRGYKVRHKGGY  YKVRHKGGY         0.3891         742.5               32.00       Sequence
DRB1_1101   22  VRFCDLPGIMQHFTI  FCDLPGIMQ         0.3885         747.0               32.00       Sequence
DRB1_1101  105  RDPRNIARKAENYLI  RNIARKAEN         0.3873         756.9               32.00       Sequence
DRB1_1101   82  FRAAKTLNINFFVHD  FRAAKTLNI         0.3867         762.2               32.00       Sequence
DRB1_1101  106  DPRNIARKAENYLIS  RNIARKAEN         0.3859         768.6               32.00       Sequence
DRB1_1101   31  MQHFTIPASAFDKSV  HFTIPASAF         0.3848         777.5               32.00       Sequence
DRB1_1101  325  SYKRLVPGYEAPINL  YKRLVPGYE         0.3809         811.1               32.00       Sequence
DRB1_1101  318  FTNPTVNSYKRLVPG  TVNSYKRLV         0.3752         862.4               32.00       Sequence
DRB1_1101  107  PRNIARKAENYLIST  RNIARKAEN         0.3749         865.7               32.00       Sequence
DRB1_1101  177  YKVRHKGGYFPVAPN  YKVRHKGGY         0.3738         875.9               32.00       Sequence
DRB1_1101  380  SAMLMAGLDGIKNKI  MAGLDGIKN         0.3735         879.1               32.00       Sequence
DRB1_1101   53  DGSSIRGFQSIHESD  SIRGFQSIH         0.3704         908.8               32.00       Sequence
DRB1_1101   19  YVDVRFCDLPGIMQH  FCDLPGIMQ         0.3692         920.3               32.00       Sequence
DRB1_1101  381  AMLMAGLDGIKNKIE  MAGLDGIKN         0.3682         930.4               32.00       Sequence
DRB1_1101  114  AENYLISTGIADTAY  YLISTGIAD         0.3671         941.7               32.00       Sequence
DRB1_1101  108  RNIARKAENYLISTG  RNIARKAEN         0.3667         945.7               32.00       Sequence
DRB1_1101  190  PNDQYVDLRDKMLTN  VDLRDKMLT         0.3662         951.0               32.00       Sequence
DRB1_1101  148  NGSFYEVDAISGWWN  FYEVDAISG         0.3659         953.8               32.00       Sequence
DRB1_1101   28  PGIMQHFTIPASAFD  HFTIPASAF         0.3624         991.2               32.00       Sequence
DRB1_1101  297  LSDTARHYIGGLLHH  RHYIGGLLH         0.3610        1006.0               32.00       Sequence
DRB1_1101  333  YEAPINLVYSQRNRS  INLVYSQRN         0.3604        1012.9               32.00       Sequence
DRB1_1101  115  ENYLISTGIADTAYF  YLISTGIAD         0.3576        1043.3               32.00       Sequence
DRB1_1101  246  YIIKNTAWQNGKTVT  IIKNTAWQN         0.3572        1048.4               32.00       Sequence
DRB1_1101  149  GSFYEVDAISGWWNT  FYEVDAISG         0.3569        1051.5               32.00       Sequence
DRB1_1101    6  DDVFKLAKDEKVEYV  VFKLAKDEK         0.3557        1065.0               32.00       Sequence
DRB1_1101  137  IFDSVSFDSRANGSF  VSFDSRANG         0.3483        1154.2               50.00       Sequence
DRB1_1101   23  RFCDLPGIMQHFTIP  FCDLPGIMQ         0.3465        1177.4               50.00       Sequence
DRB1_1101  113  KAENYLISTGIADTA  YLISTGIAD         0.3454        1191.5               50.00       Sequence
DRB1_1101  379  FSAMLMAGLDGIKNK  AMLMAGLDG         0.3444        1204.4               50.00       Sequence
DRB1_1101  317  AFTNPTVNSYKRLVP  AFTNPTVNS         0.3438        1212.4               50.00       Sequence
DRB1_1101  247  IIKNTAWQNGKTVTF  IIKNTAWQN         0.3416        1240.7               50.00       Sequence
DRB1_1101    7  DVFKLAKDEKVEYVD  FKLAKDEKV         0.3386        1281.7               50.00       Sequence
DRB1_1101   75  ETARIDPFRAAKTLN  PFRAAKTLN         0.3369        1305.4               50.00       Sequence
DRB1_1101  150  SFYEVDAISGWWNTG  FYEVDAISG         0.3355        1325.3               50.00       Sequence
DRB1_1101  312  APSLLAFTNPTVNSY  LLAFTNPTV         0.3350        1332.7               50.00       Sequence
DRB1_1101   52  FDGSSIRGFQSIHES  SIRGFQSIH         0.3340        1347.7               50.00       Sequence
DRB1_1101  116  NYLISTGIADTAYFG  YLISTGIAD         0.3336        1353.5               50.00       Sequence
DRB1_1101    5  PDDVFKLAKDEKVEY  VFKLAKDEK         0.3333        1357.7               50.00       Sequence
DRB1_1101  139  DSVSFDSRANGSFYE  VSFDSRANG         0.3332        1359.4               50.00       Sequence
DRB1_1101  340  VYSQRNRSACVRIPI  VYSQRNRSA         0.3325        1369.0               50.00       Sequence
DRB1_1101  147  ANGSFYEVDAISGWW  FYEVDAISG         0.3306        1397.9               50.00       Sequence
DRB1_1101  450  WISFKRENEIEPVNI  ISFKRENEI         0.3304        1400.7               50.00       Sequence
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DRB1_1101   18  EYVDVRFCDLPGIMQ  FCDLPGIMQ         0.3300       1406.6             50.00     Sequence
DRB1_1101  314  SLLAFTNPTVNSYKR  AFTNPTVNS         0.3299       1409.1             50.00     Sequence
DRB1_1101  138  FDSVSFDSRANGSFY  VSFDSRANG         0.3283       1433.2             50.00     Sequence
DRB1_1101  383  LMAGLDGIKNKIEPQ  MAGLDGIKN         0.3264       1463.1             50.00     Sequence
DRB1_1101  371  SSGNPYLAFSAMLMA  LAFSAMLMA         0.3245       1492.8             50.00     Sequence
DRB1_1101  104  SRDPRNIARKAENYL  RNIARKAEN         0.3244       1494.7             50.00     Sequence
DRB1_1101  382  MLMAGLDGIKNKIEP  MAGLDGIKN         0.3238       1505.4             50.00     Sequence
DRB1_1101   58  RGFQSIHESDMLLLP  GFQSIHESD         0.3237       1507.0             50.00     Sequence
DRB1_1101   51  AFDGSSIRGFQSIHE  IRGFQSIHE         0.3235       1509.4             50.00     Sequence
DRB1_1101  102  PYSRDPRNIARKAEN  RNIARKAEN         0.3230       1517.3             50.00     Sequence
DRB1_1101  384  MAGLDGIKNKIEPQA  MAGLDGIKN         0.3201       1565.9             50.00     Sequence
DRB1_1101  140  SVSFDSRANGSFYEV  VSFDSRANG         0.3188       1587.5             50.00     Sequence
DRB1_1101  296  GLSDTARHYIGGLLH  RHYIGGLLH         0.3180       1601.7             50.00     Sequence
DRB1_1101  252  AWQNGKTVTFMPKPL  TVTFMPKPL         0.3176       1608.5             50.00     Sequence
DRB1_1101  444  NDLIETWISFKRENE  IETWISFKR         0.3163       1632.1             50.00     Sequence
DRB1_1101  236  HAADDMQLYKYIIKN  DMQLYKYII         0.3138       1676.7             50.00     Sequence
DRB1_1101  311  HAPSLLAFTNPTVNS  LLAFTNPTV         0.3129       1692.7             50.00     Sequence
DRB1_1101  103  YSRDPRNIARKAENY  RNIARKAEN         0.3127       1697.0             50.00     Sequence
DRB1_1101  313  PSLLAFTNPTVNSYK  LLAFTNPTV         0.3126       1698.4             50.00     Sequence
DRB1_1101   27  LPGIMQHFTIPASAF  HFTIPASAF         0.3126       1699.4             50.00     Sequence
DRB1_1101  291  ETGYAGLSDTARHYI  YAGLSDTAR         0.3106       1735.3             50.00     Sequence
DRB1_1101  292  TGYAGLSDTARHYIG  YAGLSDTAR         0.3057       1829.9             50.00     Sequence
DRB1_1101  205  LINSGFILEKGHHEV  LINSGFILE         0.3027       1891.1             50.00     Sequence
DRB1_1101  136  YIFDSVSFDSRANGS  IFDSVSFDS         0.3019       1907.7             50.00     Sequence
DRB1_1101  112  RKAENYLISTGIADT  YLISTGIAD         0.3008       1930.2             50.00     Sequence
DRB1_1101  344  RNRSACVRIPITGSN  RSACVRIPI         0.2997       1952.5             50.00     Sequence
DRB1_1101   50  LAFDGSSIRGFQSIH  GSSIRGFQS         0.2991       1965.7             50.00     Sequence
DRB1_1101  343  QRNRSACVRIPITGS  RSACVRIPI         0.2980       1988.5             50.00     Sequence
DRB1_1101  135  FYIFDSVSFDSRANG  IFDSVSFDS         0.2964       2024.2             50.00     Sequence
DRB1_1101  332  GYEAPINLVYSQRNR  INLVYSQRN         0.2945       2067.0             50.00     Sequence
DRB1_1101    8  VFKLAKDEKVEYVDV  FKLAKDEKV         0.2942       2072.0             50.00     Sequence
DRB1_1101  189  APNDQYVDLRDKMLT  VDLRDKMLT         0.2938       2081.7             50.00     Sequence
DRB1_1101   32  QHFTIPASAFDKSVF  HFTIPASAF         0.2921       2120.2             50.00     Sequence
DRB1_1101  207  NSGFILEKGHHEVGS  GFILEKGHH         0.2906       2154.6             50.00     Sequence
DRB1_1101  204  NLINSGFILEKGHHE  LINSGFILE         0.2903       2161.5             50.00     Sequence
DRB1_1101  151  FYEVDAISGWWNTGA  FYEVDAISG         0.2874       2231.8             50.00     Sequence
DRB1_1101    4  TPDDVFKLAKDEKVE  VFKLAKDEK         0.2873       2233.8             50.00     Sequence
DRB1_1101  208  SGFILEKGHHEVGSG  GFILEKGHH         0.2871       2238.7             50.00     Sequence
DRB1_1101  134  EFYIFDSVSFDSRAN  IFDSVSFDS         0.2853       2283.2             50.00     Sequence
DRB1_1101  206  INSGFILEKGHHEVG  GFILEKGHH         0.2843       2308.1             50.00     Sequence
DRB1_1101  326  YKRLVPGYEAPINLV  YKRLVPGYE         0.2842       2309.0             50.00     Sequence
DRB1_1101  341  YSQRNRSACVRIPIT  RNRSACVRI         0.2836       2324.7             50.00     Sequence
DRB1_1101  342  SQRNRSACVRIPITG  RSACVRIPI         0.2811       2388.3             50.00     Sequence
DRB1_1101  202  LTNLINSGFILEKGH  LTNLINSGF         0.2803       2410.1             50.00     Sequence
DRB1_1101  156  AISGWWNTGAATEAD  WWNTGAATE         0.2792       2438.7             50.00     Sequence
DRB1_1101  315  LLAFTNPTVNSYKRL  AFTNPTVNS         0.2787       2450.8             50.00     Sequence
DRB1_1101  146  RANGSFYEVDAISGW  FYEVDAISG         0.2768       2502.2             50.00     Sequence
DRB1_1101   49  GLAFDGSSIRGFQSI  AFDGSSIRG         0.2754       2539.8             50.00     Sequence
DRB1_1101  157  ISGWWNTGAATEADG  WWNTGAATE         0.2751       2549.5             50.00     Sequence
DRB1_1101  360  KAKRLEFRSPDSSGN  RLEFRSPDS         0.2744       2568.4             50.00     Sequence
DRB1_1101  133  AEFYIFDSVSFDSRA  FYIFDSVSF         0.2738       2584.8             50.00     Sequence
DRB1_1101  293  GYAGLSDTARHYIGG  YAGLSDTAR         0.2733       2599.3             50.00     Sequence
DRB1_1101  100  LEPYSRDPRNIARKA  YSRDPRNIA         0.2731       2604.6             50.00     Sequence
DRB1_1101  290  DETGYAGLSDTARHY  YAGLSDTAR         0.2728       2612.4             50.00     Sequence
DRB1_1101  271  GSGMHCHQSLWKDGA  MHCHQSLWK         0.2720       2635.4             50.00     Sequence
DRB1_1101  316  LAFTNPTVNSYKRLV  AFTNPTVNS         0.2693       2712.2             50.00     Sequence
DRB1_1101  231  FNSLLHAADDMQLYK  FNSLLHAAD         0.2680       2751.6             50.00     Sequence
DRB1_1101  270  NGSGMHCHQSLWKDG  GMHCHQSLW         0.2665       2796.7             50.00     Sequence
DRB1_1101  345  NRSACVRIPITGSNP  RSACVRIPI         0.2644       2861.5             50.00     Sequence
DRB1_1101  141  VSFDSRANGSFYEVD  VSFDSRANG         0.2628       2910.9             50.00     Sequence
DRB1_1101  155  DAISGWWNTGAATEA  ISGWWNTGA         0.2628       2911.9             50.00     Sequence
DRB1_1101  170  DGSPNRGYKVRHKGG  PNRGYKVRH         0.2622       2931.4             50.00     Sequence
DRB1_1101  117  YLISTGIADTAYFGA  YLISTGIAD         0.2615       2951.2             50.00     Sequence
DRB1_1101  451  ISFKRENEIEPVNIR  ISFKRENEI         0.2580       3067.0             50.00     Sequence
DRB1_1101  386  GLDGIKNKIEPQAPV  GLDGIKNKI         0.2577       3078.0             50.00     Sequence
DRB1_1101  222  GGQAEINYQFNSLLH  NYQFNSLLH         0.2553       3156.0             50.00     Sequence
DRB1_1101  361  AKRLEFRSPDSSGNP  RLEFRSPDS         0.2551       3164.9             50.00     Sequence
DRB1_1101  101  EPYSRDPRNIARKAE  YSRDPRNIA         0.2549       3170.3             50.00     Sequence
DRB1_1101  385  AGLDGIKNKIEPQAP  GLDGIKNKI         0.2531       3232.4             50.00     Sequence
DRB1_1101  132  EAEFYIFDSVSFDSR  FYIFDSVSF         0.2530       3236.7             50.00     Sequence
DRB1_1101  362  KRLEFRSPDSSGNPY  RLEFRSPDS         0.2526       3249.5             50.00     Sequence
DRB1_1101  331  PGYEAPINLVYSQRN  INLVYSQRN         0.2524       3256.7             50.00     Sequence
DRB1_1101   17  VEYVDVRFCDLPGIM  YVDVRFCDL         0.2514       3292.8             50.00     Sequence
DRB1_1101   59  GFQSIHESDMLLLPD  FQSIHESDM         0.2502       3336.4             50.00     Sequence
DRB1_1101  111  ARKAENYLISTGIAD  YLISTGIAD         0.2498       3351.2             50.00     Sequence
DRB1_1101  277  HQSLWKDGAPLMYDE  LWKDGAPLM         0.2497       3356.2             50.00     Sequence
DRB1_1101  203  TNLINSGFILEKGHH  LINSGFILE         0.2476       3430.2             50.00     Sequence
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DRB1_1101  359  PKAKRLEFRSPDSSG  KAKRLEFRS        0.2471       3449.1              50.00     Sequence
DRB1_1101   99  TLEPYSRDPRNIARK  YSRDPRNIA        0.2463       3479.8              50.00     Sequence
DRB1_1101  346  RSACVRIPITGSNPK  RSACVRIPI        0.2451       3524.0              50.00     Sequence
DRB1_1101  209  GFILEKGHHEVGSGG  GFILEKGHH        0.2449       3532.2              50.00     Sequence
DRB1_1101  310  HHAPSLLAFTNPTVN  LLAFTNPTV        0.2411       3681.9              50.00     Sequence
DRB1_1101   48  DGLAFDGSSIRGFQS  LAFDGSSIR        0.2408       3694.1              50.00     Sequence
DRB1_1101    3  KTPDDVFKLAKDEKV  VFKLAKDEK        0.2386       3782.5              50.00     Sequence
DRB1_1101   33  HFTIPASAFDKSVFD  HFTIPASAF        0.2379       3813.3              50.00     Sequence
DRB1_1101  276  CHQSLWKDGAPLMYD  LWKDGAPLM        0.2372       3840.5              50.00     Sequence
DRB1_1101  272  SGMHCHQSLWKDGAP  MHCHQSLWK        0.2332       4010.8              50.00     Sequence
DRB1_1101  235  LHAADDMQLYKYIIK  DMQLYKYII        0.2328       4028.2              50.00     Sequence
DRB1_1101   84  AAKTLNINFFVHDPF  AAKTLNINF        0.2325       4040.5              50.00     Sequence
DRB1_1101  278  QSLWKDGAPLMYDET  LWKDGAPLM        0.2315       4083.9              50.00     Sequence
DRB1_1101  154  VDAISGWWNTGAATE  ISGWWNTGA        0.2306       4125.7              50.00     Sequence
DRB1_1101  443  TNDLIETWISFKREN  TWISFKREN        0.2304       4132.4              50.00     Sequence
DRB1_1101  269  DNGSGMHCHQSLWKD  GMHCHQSLW        0.2300       4153.4              50.00     Sequence
DRB1_1101  273  GMHCHQSLWKDGAPL  MHCHQSLWK        0.2299       4157.7              50.00     Sequence
DRB1_1101   98  FTLEPYSRDPRNIAR  YSRDPRNIA        0.2296       4168.0              50.00     Sequence
DRB1_1101  358  NPKAKRLEFRSPDSS  KAKRLEFRS        0.2288       4208.0              50.00     Sequence
DRB1_1101  289  YDETGYAGLSDTARH  YAGLSDTAR        0.2278       4252.6              50.00     Sequence
DRB1_1101   83  RAAKTLNINFFVHDP  AAKTLNINF        0.2274       4269.9              50.00     Sequence
DRB1_1101  251  TAWQNGKTVTFMPKP  WQNGKTVTF        0.2270       4288.6              50.00     Sequence
DRB1_1101  250  NTAWQNGKTVTFMPK  WQNGKTVTF        0.2263       4320.3              50.00     Sequence
DRB1_1101  145  SRANGSFYEVDAISG  FYEVDAISG        0.2236       4447.4              50.00     Sequence
DRB1_1101   24  FCDLPGIMQHFTIPA  FCDLPGIMQ        0.2234       4460.8              50.00     Sequence
DRB1_1101  249  KNTAWQNGKTVTFMP  AWQNGKTVT        0.2218       4535.6              50.00     Sequence
DRB1_1101  459  IEPVNIRPHPYEFAL  PVNIRPHPY        0.2212       4568.3              50.00     Sequence
DRB1_1101  275  HCHQSLWKDGAPLMY  LWKDGAPLM        0.2204       4608.3              50.00     Sequence
DRB1_1101  158  SGWWNTGAATEADGS  WWNTGAATE        0.2202       4616.7              50.00     Sequence
DRB1_1101   26  DLPGIMQHFTIPASA  IMQHFTIPA        0.2195       4652.8              50.00     Sequence
DRB1_1101  327  KRLVPGYEAPINLVY  KRLVPGYEA        0.2179       4732.7              50.00     Sequence
DRB1_1101  363  RLEFRSPDSSGNPYL  RLEFRSPDS        0.2177       4741.1              50.00     Sequence
DRB1_1101   97  PFTLEPYSRDPRNIA  YSRDPRNIA        0.2125       5018.8              50.00     Sequence
DRB1_1101  110  IARKAENYLISTGIA  NYLISTGIA        0.2101       5148.4              50.00     Sequence
DRB1_1101  274  MHCHQSLWKDGAPLM  HQSLWKDGA        0.2088       5219.8              50.00     Sequence
DRB1_1101  347  SACVRIPITGSNPKA  ACVRIPITG        0.2073       5307.6              50.00     Sequence
DRB1_1101  432  DHEYLTEGGVFTNDL  YLTEGGVFT        0.2063       5363.4              50.00     Sequence
DRB1_1101  458  EIEPVNIRPHPYEFA  PVNIRPHPY        0.2063       5365.3              50.00     Sequence
DRB1_1101  131  AEAEFYIFDSVSFDS  FYIFDSVSF        0.2050       5442.7              50.00     Sequence
DRB1_1101  279  SLWKDGAPLMYDETG  WKDGAPLMY        0.2047       5461.1              50.00     Sequence
DRB1_1101  387  LDGIKNKIEPQAPVD  GIKNKIEPQ        0.2033       5540.4              50.00     Sequence
DRB1_1101  433  HEYLTEGGVFTNDLI  YLTEGGVFT        0.2027       5579.5              50.00     Sequence
DRB1_1101  248  IKNTAWQNGKTVTFM  AWQNGKTVT        0.2014       5654.6              50.00     Sequence
DRB1_1101   88  LNINFFVHDPFTLEP  NFFVHDPFT        0.2011       5677.9              50.00     Sequence
DRB1_1101  370  DSSGNPYLAFSAMLM  YLAFSAMLM        0.1989       5809.7              50.00     Sequence
DRB1_1101   47  DDGLAFDGSSIRGFQ  LAFDGSSIR        0.1973       5912.5              50.00     Sequence
DRB1_1101  178  KVRHKGGYFPVAPND  KVRHKGGYF        0.1969       5941.2              50.00     Sequence
DRB1_1101  109  NIARKAENYLISTGI  RKAENYLIS        0.1967       5952.7              50.00     Sequence
DRB1_1101  268  GDNGSGMHCHQSLWK  GSGMHCHQS        0.1964       5970.6              50.00     Sequence
DRB1_1101   89  NINFFVHDPFTLEPY  NFFVHDPFT        0.1961       5991.0              50.00     Sequence
DRB1_1101   90  INFFVHDPFTLEPYS  NFFVHDPFT        0.1943       6110.8              50.00     Sequence
DRB1_1101  294  YAGLSDTARHYIGGL  YAGLSDTAR        0.1941       6120.3              50.00     Sequence
DRB1_1101  357  SNPKAKRLEFRSPDS  KAKRLEFRS        0.1931       6185.8              50.00     Sequence
DRB1_1101   16  KVEYVDVRFCDLPGI  YVDVRFCDL        0.1914       6302.5              50.00     Sequence
DRB1_1101  288  MYDETGYAGLSDTAR  YAGLSDTAR        0.1885       6507.5              50.00     Sequence
DRB1_1101  431  ADHEYLTEGGVFTND  YLTEGGVFT        0.1868       6625.3              50.00     Sequence
DRB1_1101   87  TLNINFFVHDPFTLE  INFFVHDPF        0.1865       6649.3              50.00     Sequence
DRB1_1101  460  EPVNIRPHPYEFALY  PVNIRPHPY        0.1858       6699.8              50.00     Sequence
DRB1_1101  348  ACVRIPITGSNPKAK  ACVRIPITG        0.1853       6730.7              50.00     Sequence
DRB1_1101  388  DGIKNKIEPQAPVDK  IKNKIEPQA        0.1843       6809.0              50.00     Sequence
DRB1_1101  183  GGYFPVAPNDQYVDL  FPVAPNDQY        0.1843       6810.2              50.00     Sequence
DRB1_1101  159  GWWNTGAATEADGSP  WWNTGAATE        0.1825       6941.8              50.00     Sequence
DRB1_1101  267  FGDNGSGMHCHQSLW  FGDNGSGMH        0.1787       7228.5              50.00     Sequence
DRB1_1101  430  EADHEYLTEGGVFTN  HEYLTEGGV        0.1784       7254.7              50.00     Sequence
DRB1_1101   25  CDLPGIMQHFTIPAS  IMQHFTIPA        0.1781       7280.9              50.00     Sequence
DRB1_1101  461  PVNIRPHPYEFALYY  PVNIRPHPY        0.1778       7306.3              50.00     Sequence
DRB1_1101   86  KTLNINFFVHDPFTL  TLNINFFVH        0.1757       7469.6              50.00     Sequence
DRB1_1101  330  VPGYEAPINLVYSQR  YEAPINLVY        0.1748       7541.8              50.00     Sequence
DRB1_1101   91  NFFVHDPFTLEPYSR  FFVHDPFTL        0.1747       7554.0              50.00     Sequence
DRB1_1101  349  CVRIPITGSNPKAKR  CVRIPITGS        0.1738       7626.4              50.00     Sequence
DRB1_1101   60  FQSIHESDMLLLPDP  FQSIHESDM        0.1735       7649.7              50.00     Sequence
DRB1_1101  264  KPLFGDNGSGMHCHQ  FGDNGSGMH        0.1733       7665.1              50.00     Sequence
DRB1_1101  169  ADGSPNRGYKVRHKG  PNRGYKVRH        0.1731       7686.7              50.00     Sequence
DRB1_1101  350  VRIPITGSNPKAKRL  PITGSNPKA        0.1719       7784.8              50.00     Sequence
DRB1_1101  188  VAPNDQYVDLRDKML  YVDLRDKML        0.1719       7786.9              50.00     Sequence
DRB1_1101  434  EYLTEGGVFTNDLIE  YLTEGGVFT        0.1718       7796.7              50.00     Sequence
DRB1_1101   85  AKTLNINFFVHDPFT  KTLNINFFV        0.1713       7832.5              50.00     Sequence
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DRB1_1101  457  NEIEPVNIRPHPYEF  PVNIRPHPY         0.1705       7899.0              50.00     Sequence
DRB1_1101   74  PETARIDPFRAAKTL  TARIDPFRA         0.1702       7932.3              50.00     Sequence
DRB1_1101  352  IPITGSNPKAKRLEF  PITGSNPKA         0.1700       7943.1              50.00     Sequence
DRB1_1101  125  DTAYFGAEAEFYIFD  YFGAEAEFY         0.1695       7984.9              50.00     Sequence
DRB1_1101  329  LVPGYEAPINLVYSQ  YEAPINLVY         0.1691       8023.5              50.00     Sequence
DRB1_1101  153  EVDAISGWWNTGAAT  VDAISGWWN         0.1679       8129.3              50.00     Sequence
DRB1_1101  265  PLFGDNGSGMHCHQS  FGDNGSGMH         0.1679       8131.4              50.00     Sequence
DRB1_1101  126  TAYFGAEAEFYIFDS  YFGAEAEFY         0.1666       8242.2              50.00     Sequence
DRB1_1101  182  KGGYFPVAPNDQYVD  FPVAPNDQY         0.1664       8265.6              50.00     Sequence
DRB1_1101  184  GYFPVAPNDQYVDLR  FPVAPNDQY         0.1656       8330.2              50.00     Sequence
DRB1_1101  124  ADTAYFGAEAEFYIF  YFGAEAEFY         0.1655       8338.3              50.00     Sequence
DRB1_1101   92  FFVHDPFTLEPYSRD  FFVHDPFTL         0.1643       8451.6              50.00     Sequence
DRB1_1101   66  SDMLLLPDPETARID  MLLLPDPET         0.1642       8458.5              50.00     Sequence
DRB1_1101   65  ESDMLLLPDPETARI  MLLLPDPET         0.1639       8490.7              50.00     Sequence
DRB1_1101  351  RIPITGSNPKAKRLE  PITGSNPKA         0.1634       8535.6              50.00     Sequence
DRB1_1101   46  FDDGLAFDGSSIRGF  LAFDGSSIR         0.1629       8584.6              50.00     Sequence
DRB1_1101  295  AGLSDTARHYIGGLL  AGLSDTARH         0.1610       8756.6              50.00     Sequence
DRB1_1101  435  YLTEGGVFTNDLIET  YLTEGGVFT         0.1609       8771.6              50.00     Sequence
DRB1_1101  266  LFGDNGSGMHCHQSL  FGDNGSGMH         0.1600       8850.1              50.00     Sequence
DRB1_1101    9  FKLAKDEKVEYVDVR  FKLAKDEKV         0.1579       9055.3              50.00     Sequence
DRB1_1101  353  PITGSNPKAKRLEFR  PITGSNPKA         0.1565       9191.4              50.00     Sequence
DRB1_1101   96  DPFTLEPYSRDPRNI  FTLEPYSRD         0.1560       9242.8              50.00     Sequence
DRB1_1101  452  SFKRENEIEPVNIRP  FKRENEIEP         0.1559       9252.1              50.00     Sequence
DRB1_1101  127  AYFGAEAEFYIFDSV  AYFGAEAEF         0.1517       9685.9              50.00     Sequence
DRB1_1101   15  EKVEYVDVRFCDLPG  VEYVDVRFC         0.1507       9790.2              50.00     Sequence
DRB1_1101  263  PKPLFGDNGSGMHCH  FGDNGSGMH         0.1507       9795.4              50.00     Sequence
DRB1_1101  130  GAEAEFYIFDSVSFD  FYIFDSVSF         0.1503       9833.3              50.00     Sequence
DRB1_1101  389  GIKNKIEPQAPVDKD  IKNKIEPQA         0.1494       9928.2              50.00     Sequence
DRB1_1101   67  DMLLLPDPETARIDP  MLLLPDPET         0.1490       9970.6              50.00     Sequence
DRB1_1101  420  TQLSDVIDRLEADHE  SDVIDRLEA         0.1482      10059.6              50.00     Sequence
DRB1_1101  328  RLVPGYEAPINLVYS  YEAPINLVY         0.1467      10226.7              50.00     Sequence
DRB1_1101   95  HDPFTLEPYSRDPRN  PFTLEPYSR         0.1464      10253.3              50.00     Sequence
DRB1_1101  354  ITGSNPKAKRLEFRS  NPKAKRLEF         0.1460      10301.6              50.00     Sequence
DRB1_1101  185  YFPVAPNDQYVDLRD  FPVAPNDQY         0.1460      10305.2              50.00     Sequence
DRB1_1101  355  TGSNPKAKRLEFRSP  NPKAKRLEF         0.1445      10466.8              50.00     Sequence
DRB1_1101  441  VFTNDLIETWISFKR  VFTNDLIET         0.1435      10580.7              50.00     Sequence
DRB1_1101  181  HKGGYFPVAPNDQYV  YFPVAPNDQ         0.1431      10631.4              50.00     Sequence
DRB1_1101  462  VNIRPHPYEFALYYD  VNIRPHPYE         0.1424      10709.5              50.00     Sequence
DRB1_1101  442  FTNDLIETWISFKRE  IETWISFKR         0.1419      10773.2              50.00     Sequence
DRB1_1101   62  SIHESDMLLLPDPET  MLLLPDPET         0.1404      10944.7              50.00     Sequence
DRB1_1101  262  MPKPLFGDNGSGMHC  FGDNGSGMH         0.1393      11081.0              50.00     Sequence
DRB1_1101  260  TFMPKPLFGDNGSGM  TFMPKPLFG         0.1382      11206.0              50.00     Sequence
DRB1_1101  422  LSDVIDRLEADHEYL  SDVIDRLEA         0.1381      11226.1              50.00     Sequence
DRB1_1101   94  VHDPFTLEPYSRDPR  PFTLEPYSR         0.1377      11268.1              50.00     Sequence
DRB1_1101  439  GGVFTNDLIETWISF  VFTNDLIET         0.1375      11299.5              50.00     Sequence
DRB1_1101  123  IADTAYFGAEAEFYI  YFGAEAEFY         0.1366      11409.4              50.00     Sequence
DRB1_1101  210  FILEKGHHEVGSGGQ  FILEKGHHE         0.1358      11505.9              50.00     Sequence
DRB1_1101  438  EGGVFTNDLIETWIS  VFTNDLIET         0.1355      11536.9              50.00     Sequence
DRB1_1101   64  HESDMLLLPDPETAR  MLLLPDPET         0.1353      11572.2              50.00     Sequence
DRB1_1101  168  EADGSPNRGYKVRHK  PNRGYKVRH         0.1352      11580.3              50.00     Sequence
DRB1_1101  221  SGGQAEINYQFNSLL  QAEINYQFN         0.1345      11666.2              50.00     Sequence
DRB1_1101    2  EKTPDDVFKLAKDEK  VFKLAKDEK         0.1343      11686.7              50.00     Sequence
DRB1_1101  440  GVFTNDLIETWISFK  VFTNDLIET         0.1335      11787.7              50.00     Sequence
DRB1_1101   73  DPETARIDPFRAAKT  TARIDPFRA         0.1334      11808.7              50.00     Sequence
DRB1_1101  419  PTQLSDVIDRLEADH  SDVIDRLEA         0.1329      11871.6              50.00     Sequence
DRB1_1101  180  RHKGGYFPVAPNDQY  FPVAPNDQY         0.1329      11874.4              50.00     Sequence
DRB1_1101  456  ENEIEPVNIRPHPYE  PVNIRPHPY         0.1328      11884.5              50.00     Sequence
DRB1_1101  356  GSNPKAKRLEFRSPD  KAKRLEFRS         0.1320      11984.5              50.00     Sequence
DRB1_1101   68  MLLLPDPETARIDPF  MLLLPDPET         0.1309      12131.2              50.00     Sequence
DRB1_1101  429  LEADHEYLTEGGVFT  YLTEGGVFT         0.1298      12281.1              50.00     Sequence
DRB1_1101   14  DEKVEYVDVRFCDLP  VEYVDVRFC         0.1291      12364.4              50.00     Sequence
DRB1_1101  287  LMYDETGYAGLSDTA  GYAGLSDTA         0.1291      12371.9              50.00     Sequence
DRB1_1101  280  LWKDGAPLMYDETGY  LWKDGAPLM         0.1283      12470.8              50.00     Sequence
DRB1_1101   61  QSIHESDMLLLPDPE  IHESDMLLL         0.1275      12581.0              50.00     Sequence
DRB1_1101   45  VFDDGLAFDGSSIRG  LAFDGSSIR         0.1275      12591.6              50.00     Sequence
DRB1_1101   93  FVHDPFTLEPYSRDP  FVHDPFTLE         0.1267      12700.8              50.00     Sequence
DRB1_1101  421  QLSDVIDRLEADHEY  SDVIDRLEA         0.1266      12701.6              50.00     Sequence
DRB1_1101  118  LISTGIADTAYFGAE  ISTGIADTA         0.1263      12751.1              50.00     Sequence
DRB1_1101  129  FGAEAEFYIFDSVSF  FYIFDSVSF         0.1243      13028.0              50.00     Sequence
DRB1_1101  179  VRHKGGYFPVAPNDQ  VRHKGGYFP         0.1241      13051.9              50.00     Sequence
DRB1_1101  261  FMPKPLFGDNGSGMH  FGDNGSGMH         0.1222      13329.5              50.00     Sequence
DRB1_1101  234  LLHAADDMQLYKYII  DMQLYKYII         0.1208      13532.2              50.00     Sequence
DRB1_1101  463  NIRPHPYEFALYYDV  HPYEFALYY         0.1191      13785.6              50.00     Sequence
DRB1_1101  152  YEVDAISGWWNTGAA  VDAISGWWN         0.1190      13803.8              50.00     Sequence
DRB1_1101  122  GIADTAYFGAEAEFY  YFGAEAEFY         0.1179      13969.2              50.00     Sequence
DRB1_1101   63  IHESDMLLLPDPETA  MLLLPDPET         0.1166      14166.4              50.00     Sequence
DRB1_1101  436  LTEGGVFTNDLIETW  VFTNDLIET         0.1153      14353.8              50.00     Sequence
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DRB1_1101  142  SFDSRANGSFYEVDA  FDSRANGSF        0.1146      14466.9                 50.00      Sequence
DRB1_1101  214  KGHHEVGSGGQAEIN  HEVGSGGQA        0.1131      14700.9                 50.00      Sequence
DRB1_1101   44  SVFDDGLAFDGSSIR  FDDGLAFDG        0.1117      14929.6                 50.00      Sequence
DRB1_1101  364  LEFRSPDSSGNPYLA  EFRSPDSSG        0.1113      15001.2                 50.00      Sequence
DRB1_1101  423  SDVIDRLEADHEYLT  SDVIDRLEA        0.1105      15129.1                 50.00      Sequence
DRB1_1101   35  TIPASAFDKSVFDDG  ASAFDKSVF        0.1104      15144.5                 50.00      Sequence
DRB1_1101   36  IPASAFDKSVFDDGL  ASAFDKSVF        0.1103      15156.6                 50.00      Sequence
DRB1_1101  418  TPTQLSDVIDRLEAD  SDVIDRLEA        0.1100      15205.4                 50.00      Sequence
DRB1_1101  213  EKGHHEVGSGGQAEI  HHEVGSGGQ        0.1082      15500.3                 50.00      Sequence
DRB1_1101  437  TEGGVFTNDLIETWI  VFTNDLIET        0.1082      15505.8                 50.00      Sequence
DRB1_1101  369  PDSSGNPYLAFSAML  PYLAFSAML        0.1080      15549.2                 50.00      Sequence
DRB1_1101   13  KDEKVEYVDVRFCDL  KVEYVDVRF        0.1072      15671.6                 50.00      Sequence
DRB1_1101  401  DKDLYELPPEEAASI  LYELPPEEA        0.1061      15856.1                 50.00      Sequence
DRB1_1101  160  WWNTGAATEADGSPN  WWNTGAATE        0.1053      16008.7                 50.00      Sequence
DRB1_1101  186  FPVAPNDQYVDLRDK  FPVAPNDQY        0.1044      16156.8                 50.00      Sequence
DRB1_1101   37  PASAFDKSVFDDGLA  SAFDKSVFD        0.1027      16454.2                 50.00      Sequence
DRB1_1101  119  ISTGIADTAYFGAEA  ISTGIADTA        0.1018      16616.9                 50.00      Sequence
DRB1_1101  128  YFGAEAEFYIFDSVS  YFGAEAEFY        0.1017      16629.1                 50.00      Sequence
DRB1_1101  167  TEADGSPNRGYKVRH  PNRGYKVRH        0.1016      16662.2                 50.00      Sequence
DRB1_1101  215  GHHEVGSGGQAEINY  HEVGSGGQA        0.1015      16675.0                 50.00      Sequence
DRB1_1101  212  LEKGHHEVGSGGQAE  KGHHEVGSG        0.1011      16750.6                 50.00      Sequence
DRB1_1101  399  PVDKDLYELPPEEAA  LYELPPEEA        0.1006      16845.0                 50.00      Sequence
DRB1_1101  211  ILEKGHHEVGSGGQA  ILEKGHHEV        0.0996      17021.9                 50.00      Sequence
DRB1_1101   34  FTIPASAFDKSVFDD  ASAFDKSVF        0.0982      17282.9                 50.00      Sequence
DRB1_1101  400  VDKDLYELPPEEAAS  LYELPPEEA        0.0970      17504.2                 50.00      Sequence
DRB1_1101  417  QTPTQLSDVIDRLEA  SDVIDRLEA        0.0970      17510.1                 50.00      Sequence
DRB1_1101   38  ASAFDKSVFDDGLAF  ASAFDKSVF        0.0968      17549.5                 50.00      Sequence
DRB1_1101  453  FKRENEIEPVNIRPH  FKRENEIEP        0.0967      17563.2                 50.00      Sequence
DRB1_1101  398  APVDKDLYELPPEEA  LYELPPEEA        0.0958      17726.0                 50.00      Sequence
DRB1_1101  402  KDLYELPPEEAASIP  LYELPPEEA        0.0952      17852.5                 50.00      Sequence
DRB1_1101  232  NSLLHAADDMQLYKY  NSLLHAADD        0.0951      17867.4                 50.00      Sequence
DRB1_1101  286  PLMYDETGYAGLSDT  MYDETGYAG        0.0946      17968.8                 50.00      Sequence
DRB1_1101  187  PVAPNDQYVDLRDKM  QYVDLRDKM        0.0915      18585.9                 50.00      Sequence
DRB1_1101   43  KSVFDDGLAFDGSSI  FDDGLAFDG        0.0910      18682.3                 50.00      Sequence
DRB1_1101   41  FDKSVFDDGLAFDGS  SVFDDGLAF        0.0900      18891.0                 50.00      Sequence
DRB1_1101  216  HHEVGSGGQAEINYQ  HEVGSGGQA        0.0888      19119.9                 50.00      Sequence
DRB1_1101  425  VIDRLEADHEYLTEG  VIDRLEADH        0.0853      19864.5                 50.00      Sequence
DRB1_1101  403  DLYELPPEEAASIPQ  LYELPPEEA        0.0851      19913.6                 50.00      Sequence
DRB1_1101  390  IKNKIEPQAPVDKDL  IKNKIEPQA        0.0843      20085.6                 50.00      Sequence
DRB1_1101   40  AFDKSVFDDGLAFDG  SVFDDGLAF        0.0842      20116.0                 50.00      Sequence
DRB1_1101  365  EFRSPDSSGNPYLAF  EFRSPDSSG        0.0839      20169.4                 50.00      Sequence
DRB1_1101  428  RLEADHEYLTEGGVF  HEYLTEGGV        0.0833      20292.7                 50.00      Sequence
DRB1_1101  455  RENEIEPVNIRPHPY  PVNIRPHPY        0.0830      20376.7                 50.00      Sequence
DRB1_1101  143  FDSRANGSFYEVDAI  FDSRANGSF        0.0827      20425.9                 50.00      Sequence
DRB1_1101  144  DSRANGSFYEVDAIS  SFYEVDAIS        0.0816      20679.9                 50.00      Sequence
DRB1_1101  424  DVIDRLEADHEYLTE  VIDRLEADH        0.0813      20739.3                 50.00      Sequence
DRB1_1101  285  APLMYDETGYAGLSD  MYDETGYAG        0.0798      21087.3                 50.00      Sequence
DRB1_1101   42  DKSVFDDGLAFDGSS  SVFDDGLAF        0.0797      21098.9                 50.00      Sequence
DRB1_1101  281  WKDGAPLMYDETGYA  WKDGAPLMY        0.0787      21336.8                 50.00      Sequence
DRB1_1101  233  SLLHAADDMQLYKYI  HAADDMQLY        0.0777      21564.2                 50.00      Sequence
DRB1_1101   39  SAFDKSVFDDGLAFD  SVFDDGLAF        0.0776      21602.0                 50.00      Sequence
DRB1_1101  404  LYELPPEEAASIPQT  LYELPPEEA        0.0771      21719.0                 50.00      Sequence
DRB1_1101  121  TGIADTAYFGAEAEF  IADTAYFGA        0.0762      21922.2                 50.00      Sequence
DRB1_1101  284  GAPLMYDETGYAGLS  LMYDETGYA        0.0745      22330.4                 50.00      Sequence
DRB1_1101   72  PDPETARIDPFRAAK  TARIDPFRA        0.0732      22637.2                 50.00      Sequence
DRB1_1101   11  LAKDEKVEYVDVRFC  KVEYVDVRF        0.0691      23680.1                 50.00      Sequence
DRB1_1101  415  IPQTPTQLSDVIDRL  IPQTPTQLS        0.0690      23708.3                 50.00      Sequence
DRB1_1101  166  ATEADGSPNRGYKVR  ADGSPNRGY        0.0672      24154.5                 50.00      Sequence
DRB1_1101  397  QAPVDKDLYELPPEE  VDKDLYELP        0.0669      24238.5                 50.00      Sequence
DRB1_1101   12  AKDEKVEYVDVRFCD  KVEYVDVRF        0.0661      24457.4                 50.00      Sequence
DRB1_1101  427  DRLEADHEYLTEGGV  HEYLTEGGV        0.0658      24523.9                 50.00      Sequence
DRB1_1101  220  GSGGQAEINYQFNSL  QAEINYQFN        0.0645      24885.3                 50.00      Sequence
DRB1_1101  368  SPDSSGNPYLAFSAM  SSGNPYLAF        0.0643      24939.7                 50.00      Sequence
DRB1_1101  120  STGIADTAYFGAEAE  GIADTAYFG        0.0640      25005.4                 50.00      Sequence
DRB1_1101   10  KLAKDEKVEYVDVRF  LAKDEKVEY        0.0616      25680.2                 50.00      Sequence
DRB1_1101  414  SIPQTPTQLSDVIDR  IPQTPTQLS        0.0613      25750.0                 50.00      Sequence
DRB1_1101  416  PQTPTQLSDVIDRLE  TQLSDVIDR        0.0607      25939.3                 50.00      Sequence
DRB1_1101  412  AASIPQTPTQLSDVI  IPQTPTQLS        0.0590      26417.4                 50.00      Sequence
DRB1_1101  411  EAASIPQTPTQLSDV  AASIPQTPT        0.0572      26934.9                 50.00      Sequence
DRB1_1101  410  EEAASIPQTPTQLSD  AASIPQTPT        0.0568      27040.6                 50.00      Sequence
DRB1_1101  283  DGAPLMYDETGYAGL  LMYDETGYA        0.0567      27061.4                 50.00      Sequence
DRB1_1101  396  PQAPVDKDLYELPPE  DKDLYELPP        0.0563      27196.7                 50.00      Sequence
DRB1_1101  409  PEEAASIPQTPTQLS  AASIPQTPT        0.0561      27258.3                 50.00      Sequence
DRB1_1101  165  AATEADGSPNRGYKV  ADGSPNRGY        0.0560      27282.2                 50.00      Sequence
DRB1_1101  217  HEVGSGGQAEINYQF  HEVGSGGQA        0.0551      27545.3                 50.00      Sequence
DRB1_1101  426  IDRLEADHEYLTEGG  RLEADHEYL        0.0529      28199.1                 50.00      Sequence
DRB1_1101  454  KRENEIEPVNIRPHP  IEPVNIRPH        0.0517      28574.4                 50.00      Sequence
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   DRB1_1101   71  LPDPETARIDPFRAA  TARIDPFRA         0.0507      28877.4             50.00     Sequence
   DRB1_1101  219  VGSGGQAEINYQFNS  QAEINYQFN         0.0484      29621.7             50.00     Sequence
   DRB1_1101  413  ASIPQTPTQLSDVID  IPQTPTQLS         0.0481      29712.3             50.00     Sequence
   DRB1_1101  161  WNTGAATEADGSPNR  WNTGAATEA         0.0475      29919.0             50.00     Sequence
   DRB1_1101  395  EPQAPVDKDLYELPP  DKDLYELPP         0.0460      30403.0             50.00     Sequence
   DRB1_1101  282  KDGAPLMYDETGYAG  LMYDETGYA         0.0427      31498.9             50.00     Sequence
   DRB1_1101  164  GAATEADGSPNRGYK  ATEADGSPN         0.0417      31835.1             50.00     Sequence
   DRB1_1101  391  KNKIEPQAPVDKDLY  NKIEPQAPV         0.0404      32279.7             50.00     Sequence
   DRB1_1101    1  TEKTPDDVFKLAKDE  PDDVFKLAK         0.0400      32434.5             50.00     Sequence
   DRB1_1101  408  PPEEAASIPQTPTQL  AASIPQTPT         0.0394      32656.3             50.00     Sequence
   DRB1_1101  367  RSPDSSGNPYLAFSA  SSGNPYLAF         0.0392      32699.4             50.00     Sequence
   DRB1_1101  366  FRSPDSSGNPYLAFS  FRSPDSSGN         0.0384      33010.5             50.00     Sequence
   DRB1_1101  218  EVGSGGQAEINYQFN  VGSGGQAEI         0.0363      33759.6             50.00     Sequence
   DRB1_1101  392  NKIEPQAPVDKDLYE  NKIEPQAPV         0.0362      33797.6             50.00     Sequence
   DRB1_1101   70  LLPDPETARIDPFRA  TARIDPFRA         0.0351      34183.0             50.00     Sequence
   DRB1_1101  163  TGAATEADGSPNRGY  ATEADGSPN         0.0347      34349.1             50.00     Sequence
   DRB1_1101  394  IEPQAPVDKDLYELP  QAPVDKDLY         0.0346      34403.1             50.00     Sequence
   DRB1_1101  407  LPPEEAASIPQTPTQ  AASIPQTPT         0.0303      36039.2             50.00     Sequence
   DRB1_1101  393  KIEPQAPVDKDLYEL  QAPVDKDLY         0.0294      36370.1             50.00     Sequence
   DRB1_1101   69  LLLPDPETARIDPFR  LLLPDPETA         0.0258      37829.5             50.00     Sequence
   DRB1_1101  162  NTGAATEADGSPNRG  ATEADGSPN         0.0242      38492.2             50.00     Sequence
   DRB1_1101    0  VTEKTPDDVFKLAKD  DDVFKLAKD         0.0218      39483.4             50.00     Sequence
   DRB1_1101  405  YELPPEEAASIPQTP  YELPPEEAA         0.0218      39498.4             50.00     Sequence
   DRB1_1101  406  ELPPEEAASIPQTPT  AASIPQTPT         0.0216      39564.7             50.00     Sequence
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Allele: DRB1_1101. Number of high binders 16. Number of weak binders 63. Number of peptides 464

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1302  304  YIGGLLHHAPSLLAF  LLHHAPSLL         0.6775         32.8         SB     2.00     Sequence
   DRB1_1302  305  IGGLLHHAPSLLAFT  LLHHAPSLL         0.6741         34.0         SB     2.00     Sequence
   DRB1_1302  306  GGLLHHAPSLLAFTN  LLHHAPSLL         0.6633         38.2         SB     2.00     Sequence
   DRB1_1302  303  HYIGGLLHHAPSLLA  LLHHAPSLL         0.6515         43.4         SB     4.00     Sequence
   DRB1_1302  307  GLLHHAPSLLAFTNP  LLHHAPSLL         0.6415         48.4         SB     4.00     Sequence
   DRB1_1302  241  MQLYKYIIKNTAWQN  KYIIKNTAW         0.6356         51.6         WB     4.00     Sequence
   DRB1_1302  242  QLYKYIIKNTAWQNG  KYIIKNTAW         0.6326         53.2         WB     4.00     Sequence
   DRB1_1302  243  LYKYIIKNTAWQNGK  KYIIKNTAW         0.6222         59.6         WB     4.00     Sequence
   DRB1_1302  244  YKYIIKNTAWQNGKT  KYIIKNTAW         0.6117         66.8         WB     4.00     Sequence
   DRB1_1302  245  KYIIKNTAWQNGKTV  KYIIKNTAW         0.5993         76.3         WB     8.00     Sequence
   DRB1_1302  308  LLHHAPSLLAFTNPT  LLHHAPSLL         0.5935         81.3         WB     8.00     Sequence
   DRB1_1302  240  DMQLYKYIIKNTAWQ  KYIIKNTAW         0.5714        103.2         WB     8.00     Sequence
   DRB1_1302  247  IIKNTAWQNGKTVTF  WQNGKTVTF         0.5664        109.0         WB     8.00     Sequence
   DRB1_1302  302  RHYIGGLLHHAPSLL  LLHHAPSLL         0.5629        113.2         WB     8.00     Sequence
   DRB1_1302  197  LRDKMLTNLINSGFI  LTNLINSGF         0.5617        114.7         WB     8.00     Sequence
   DRB1_1302  198  RDKMLTNLINSGFIL  LTNLINSGF         0.5612        115.3         WB     8.00     Sequence
   DRB1_1302  323  VNSYKRLVPGYEAPI  LVPGYEAPI         0.5492        131.3         WB     8.00     Sequence
   DRB1_1302  326  YKRLVPGYEAPINLV  LVPGYEAPI         0.5307        160.3         WB    16.00     Sequence
   DRB1_1302  239  DDMQLYKYIIKNTAW  KYIIKNTAW         0.5299        161.9         WB    16.00     Sequence
   DRB1_1302  248  IKNTAWQNGKTVTFM  WQNGKTVTF         0.5256        169.6         WB    16.00     Sequence
   DRB1_1302  324  NSYKRLVPGYEAPIN  LVPGYEAPI         0.5212        177.8         WB    16.00     Sequence
   DRB1_1302  199  DKMLTNLINSGFILE  LTNLINSGF         0.5196        180.8         WB    16.00     Sequence
   DRB1_1302  327  KRLVPGYEAPINLVY  LVPGYEAPI         0.5160        188.1         WB    16.00     Sequence
   DRB1_1302  200  KMLTNLINSGFILEK  LTNLINSGF         0.5081        204.9         WB    16.00     Sequence
   DRB1_1302  196  DLRDKMLTNLINSGF  RDKMLTNLI         0.5055        210.6         WB    16.00     Sequence
   DRB1_1302   79  IDPFRAAKTLNINFF  AKTLNINFF         0.4990        225.9         WB    16.00     Sequence
   DRB1_1302  325  SYKRLVPGYEAPINL  LVPGYEAPI         0.4975        229.6         WB    16.00     Sequence
   DRB1_1302  249  KNTAWQNGKTVTFMP  WQNGKTVTF         0.4957        234.2         WB    16.00     Sequence
   DRB1_1302   80  DPFRAAKTLNINFFV  AKTLNINFF         0.4909        246.7         WB    16.00     Sequence
   DRB1_1302  250  NTAWQNGKTVTFMPK  WQNGKTVTF         0.4820        271.8         WB    16.00     Sequence
   DRB1_1302  338  NLVYSQRNRSACVRI  RNRSACVRI         0.4776        284.9         WB    16.00     Sequence
   DRB1_1302  201  MLTNLINSGFILEKG  LTNLINSGF         0.4771        286.5         WB    16.00     Sequence
   DRB1_1302  328  RLVPGYEAPINLVYS  LVPGYEAPI         0.4748        293.7         WB    16.00     Sequence
   DRB1_1302   81  PFRAAKTLNINFFVH  AKTLNINFF         0.4695        311.1         WB    16.00     Sequence
   DRB1_1302  251  TAWQNGKTVTFMPKP  WQNGKTVTF         0.4651        326.3         WB    16.00     Sequence
   DRB1_1302  195  VDLRDKMLTNLINSG  RDKMLTNLI         0.4571        355.8         WB    16.00     Sequence
   DRB1_1302  339  LVYSQRNRSACVRIP  RNRSACVRI         0.4535        369.8         WB    16.00     Sequence
   DRB1_1302  309  LHHAPSLLAFTNPTV  LHHAPSLLA         0.4525        373.7         WB    16.00     Sequence
   DRB1_1302  202  LTNLINSGFILEKGH  LTNLINSGF         0.4520        375.9         WB    16.00     Sequence
   DRB1_1302  329  LVPGYEAPINLVYSQ  LVPGYEAPI         0.4508        380.7         WB    16.00     Sequence
   DRB1_1302   82  FRAAKTLNINFFVHD  FRAAKTLNI         0.4505        381.9         WB    16.00     Sequence
   DRB1_1302  252  AWQNGKTVTFMPKPL  WQNGKTVTF         0.4430        414.5         WB    32.00     Sequence
   DRB1_1302  340  VYSQRNRSACVRIPI  RNRSACVRI         0.4307        473.2         WB    32.00     Sequence
   DRB1_1302  222  GGQAEINYQFNSLLH  INYQFNSLL         0.4241        508.3               32.00     Sequence
   DRB1_1302  253  WQNGKTVTFMPKPLF  WQNGKTVTF         0.4219        520.6               32.00     Sequence
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DRB1_1302  107  PRNIARKAENYLIST  ARKAENYLI         0.4133         571.1                  32.00     Sequence
DRB1_1302  223  GQAEINYQFNSLLHA  INYQFNSLL         0.4131         572.5                  32.00     Sequence
DRB1_1302  193  QYVDLRDKMLTNLIN  RDKMLTNLI         0.4123         577.4                  32.00     Sequence
DRB1_1302  194  YVDLRDKMLTNLINS  RDKMLTNLI         0.4113         584.0                  32.00     Sequence
DRB1_1302  110  IARKAENYLISTGIA  ARKAENYLI         0.4090         598.3                  32.00     Sequence
DRB1_1302  106  DPRNIARKAENYLIS  ARKAENYLI         0.4067         613.8                  32.00     Sequence
DRB1_1302  221  SGGQAEINYQFNSLL  INYQFNSLL         0.4050         625.2                  32.00     Sequence
DRB1_1302  109  NIARKAENYLISTGI  ARKAENYLI         0.4031         637.7                  32.00     Sequence
DRB1_1302  174  NRGYKVRHKGGYFPV  KVRHKGGYF         0.4020         645.5                  32.00     Sequence
DRB1_1302  108  RNIARKAENYLISTG  ARKAENYLI         0.4018         647.3                  32.00     Sequence
DRB1_1302  192  DQYVDLRDKMLTNLI  RDKMLTNLI         0.3984         671.5                  32.00     Sequence
DRB1_1302  105  RDPRNIARKAENYLI  ARKAENYLI         0.3965         684.9                  32.00     Sequence
DRB1_1302  341  YSQRNRSACVRIPIT  RNRSACVRI         0.3933         709.6                  32.00     Sequence
DRB1_1302  224  QAEINYQFNSLLHAA  INYQFNSLL         0.3896         738.1                  32.00     Sequence
DRB1_1302   78  RIDPFRAAKTLNINF  FRAAKTLNI         0.3881         750.7                  32.00     Sequence
DRB1_1302  175  RGYKVRHKGGYFPVA  KVRHKGGYF         0.3872         758.0                  32.00     Sequence
DRB1_1302  111  ARKAENYLISTGIAD  ARKAENYLI         0.3869         759.9                  32.00     Sequence
DRB1_1302  173  PNRGYKVRHKGGYFP  KVRHKGGYF         0.3789         829.4                  32.00     Sequence
DRB1_1302  225  AEINYQFNSLLHAAD  INYQFNSLL         0.3745         869.7                  32.00     Sequence
DRB1_1302   83  RAAKTLNINFFVHDP  AKTLNINFF         0.3731         882.6                  32.00     Sequence
DRB1_1302   76  TARIDPFRAAKTLNI  FRAAKTLNI         0.3719         894.1                  32.00     Sequence
DRB1_1302  176  GYKVRHKGGYFPVAP  KVRHKGGYF         0.3713         899.7                  32.00     Sequence
DRB1_1302   77  ARIDPFRAAKTLNIN  FRAAKTLNI         0.3699         913.3                  32.00     Sequence
DRB1_1302   57  IRGFQSIHESDMLLL  IHESDMLLL         0.3699         914.1                  32.00     Sequence
DRB1_1302  246  YIIKNTAWQNGKTVT  IIKNTAWQN         0.3697         916.1                  32.00     Sequence
DRB1_1302  350  VRIPITGSNPKAKRL  GSNPKAKRL         0.3671         941.4                  32.00     Sequence
DRB1_1302  115  ENYLISTGIADTAYF  TGIADTAYF         0.3638         976.4                  32.00     Sequence
DRB1_1302  177  YKVRHKGGYFPVAPN  KVRHKGGYF         0.3620         995.2                  32.00     Sequence
DRB1_1302  172  SPNRGYKVRHKGGYF  KVRHKGGYF         0.3600        1016.5                  32.00     Sequence
DRB1_1302  337  INLVYSQRNRSACVR  SQRNRSACV         0.3599        1018.5                  32.00     Sequence
DRB1_1302  336  PINLVYSQRNRSACV  SQRNRSACV         0.3598        1018.7                  32.00     Sequence
DRB1_1302  342  SQRNRSACVRIPITG  RNRSACVRI         0.3597        1019.8                  32.00     Sequence
DRB1_1302  226  EINYQFNSLLHAADD  INYQFNSLL         0.3581        1037.9                  32.00     Sequence
DRB1_1302  203  TNLINSGFILEKGHH  TNLINSGFI         0.3567        1054.0                  32.00     Sequence
DRB1_1302   58  RGFQSIHESDMLLLP  IHESDMLLL         0.3511        1119.5                  32.00     Sequence
DRB1_1302  351  RIPITGSNPKAKRLE  GSNPKAKRL         0.3507        1124.2                  32.00     Sequence
DRB1_1302   84  AAKTLNINFFVHDPF  AKTLNINFF         0.3462        1180.2                  32.00     Sequence
DRB1_1302  227  INYQFNSLLHAADDM  INYQFNSLL         0.3435        1215.3                  32.00     Sequence
DRB1_1302  343  QRNRSACVRIPITGS  RNRSACVRI         0.3364        1312.4                  32.00     Sequence
DRB1_1302  332  GYEAPINLVYSQRNR  INLVYSQRN         0.3350        1332.8                  32.00     Sequence
DRB1_1302  373  GNPYLAFSAMLMAGL  FSAMLMAGL         0.3348        1335.3                  32.00     Sequence
DRB1_1302   59  GFQSIHESDMLLLPD  IHESDMLLL         0.3334        1355.9                  32.00     Sequence
DRB1_1302  334  EAPINLVYSQRNRSA  LVYSQRNRS         0.3327        1367.3                  32.00     Sequence
DRB1_1302  116  NYLISTGIADTAYFG  TGIADTAYF         0.3308        1394.5                  32.00     Sequence
DRB1_1302  335  APINLVYSQRNRSAC  LVYSQRNRS         0.3269        1454.7                  50.00     Sequence
DRB1_1302  344  RNRSACVRIPITGSN  RNRSACVRI         0.3269        1455.3                  50.00     Sequence
DRB1_1302  317  AFTNPTVNSYKRLVP  TVNSYKRLV         0.3265        1460.6                  50.00     Sequence
DRB1_1302   27  LPGIMQHFTIPASAF  HFTIPASAF         0.3261        1467.0                  50.00     Sequence
DRB1_1302  113  KAENYLISTGIADTA  ENYLISTGI         0.3224        1527.5                  50.00     Sequence
DRB1_1302  333  YEAPINLVYSQRNRS  INLVYSQRN         0.3217        1539.2                  50.00     Sequence
DRB1_1302  316  LAFTNPTVNSYKRLV  TVNSYKRLV         0.3210        1550.6                  50.00     Sequence
DRB1_1302  238  ADDMQLYKYIIKNTA  DMQLYKYII         0.3197        1572.9                  50.00     Sequence
DRB1_1302   28  PGIMQHFTIPASAFD  IMQHFTIPA         0.3190        1584.9                  50.00     Sequence
DRB1_1302  275  HCHQSLWKDGAPLMY  LWKDGAPLM         0.3171        1618.5                  50.00     Sequence
DRB1_1302  318  FTNPTVNSYKRLVPG  TVNSYKRLV         0.3154        1648.1                  50.00     Sequence
DRB1_1302  376  YLAFSAMLMAGLDGI  MLMAGLDGI         0.3146        1662.6                  50.00     Sequence
DRB1_1302   29  GIMQHFTIPASAFDK  IMQHFTIPA         0.3146        1662.7                  50.00     Sequence
DRB1_1302  262  MPKPLFGDNGSGMHC  LFGDNGSGM         0.3143        1668.1                  50.00     Sequence
DRB1_1302  331  PGYEAPINLVYSQRN  INLVYSQRN         0.3129        1693.9                  50.00     Sequence
DRB1_1302   60  FQSIHESDMLLLPDP  IHESDMLLL         0.3121        1708.0                  50.00     Sequence
DRB1_1302  374  NPYLAFSAMLMAGLD  FSAMLMAGL         0.3104        1738.8                  50.00     Sequence
DRB1_1302  263  PKPLFGDNGSGMHCH  LFGDNGSGM         0.3093        1761.1                  50.00     Sequence
DRB1_1302  114  AENYLISTGIADTAY  ENYLISTGI         0.3089        1768.5                  50.00     Sequence
DRB1_1302  112  RKAENYLISTGIADT  ENYLISTGI         0.3088        1770.3                  50.00     Sequence
DRB1_1302  178  KVRHKGGYFPVAPND  KVRHKGGYF         0.3085        1775.3                  50.00     Sequence
DRB1_1302  261  FMPKPLFGDNGSGMH  LFGDNGSGM         0.3076        1792.4                  50.00     Sequence
DRB1_1302  276  CHQSLWKDGAPLMYD  LWKDGAPLM         0.3072        1801.5                  50.00     Sequence
DRB1_1302  237  AADDMQLYKYIIKNT  DMQLYKYII         0.3067        1810.9                  50.00     Sequence
DRB1_1302  371  SSGNPYLAFSAMLMA  PYLAFSAML         0.3065        1813.6                  50.00     Sequence
DRB1_1302  348  ACVRIPITGSNPKAK  RIPITGSNP         0.3053        1838.4                  50.00     Sequence
DRB1_1302  321  PTVNSYKRLVPGYEA  TVNSYKRLV         0.3032        1880.9                  50.00     Sequence
DRB1_1302  117  YLISTGIADTAYFGA  TGIADTAYF         0.2989        1969.3                  50.00     Sequence
DRB1_1302  296  GLSDTARHYIGGLLH  ARHYIGGLL         0.2988        1973.0                  50.00     Sequence
DRB1_1302  347  SACVRIPITGSNPKA  RIPITGSNP         0.2983        1982.3                  50.00     Sequence
DRB1_1302  319  TNPTVNSYKRLVPGY  TVNSYKRLV         0.2982        1984.5                  50.00     Sequence
DRB1_1302   30  IMQHFTIPASAFDKS  HFTIPASAF         0.2981        1987.9                  50.00     Sequence
DRB1_1302  264  KPLFGDNGSGMHCHQ  LFGDNGSGM         0.2981        1987.9                  50.00     Sequence
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DRB1_1302  235  LHAADDMQLYKYIIK  DMQLYKYII         0.2961       2030.1                50.00      Sequence
DRB1_1302  370  DSSGNPYLAFSAMLM  PYLAFSAML         0.2959       2034.1                50.00      Sequence
DRB1_1302  277  HQSLWKDGAPLMYDE  LWKDGAPLM         0.2956       2040.6                50.00      Sequence
DRB1_1302  372  SGNPYLAFSAMLMAG  PYLAFSAML         0.2949       2056.6                50.00      Sequence
DRB1_1302  349  CVRIPITGSNPKAKR  RIPITGSNP         0.2939       2079.6                50.00      Sequence
DRB1_1302  265  PLFGDNGSGMHCHQS  LFGDNGSGM         0.2921       2119.3                50.00      Sequence
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DRB1_1302   24  FCDLPGIMQHFTIPA  IMQHFTIPA         0.2907       2152.0                50.00      Sequence
DRB1_1302   61  QSIHESDMLLLPDPE  IHESDMLLL         0.2893       2186.0                50.00      Sequence
DRB1_1302  375  PYLAFSAMLMAGLDG  FSAMLMAGL         0.2882       2210.9                50.00      Sequence
DRB1_1302  301  ARHYIGGLLHHAPSL  ARHYIGGLL         0.2877       2223.1                50.00      Sequence
DRB1_1302  352  IPITGSNPKAKRLEF  GSNPKAKRL         0.2876       2227.0                50.00      Sequence
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DRB1_1302  266  LFGDNGSGMHCHQSL  LFGDNGSGM         0.2842       2308.8                50.00      Sequence
DRB1_1302  274  MHCHQSLWKDGAPLM  LWKDGAPLM         0.2829       2343.3                50.00      Sequence
DRB1_1302  140  SVSFDSRANGSFYEV  DSRANGSFY         0.2818       2369.1                50.00      Sequence
DRB1_1302   25  CDLPGIMQHFTIPAS  IMQHFTIPA         0.2818       2369.3                50.00      Sequence
DRB1_1302  139  DSVSFDSRANGSFYE  DSRANGSFY         0.2817       2373.2                50.00      Sequence
DRB1_1302  260  TFMPKPLFGDNGSGM  LFGDNGSGM         0.2810       2390.8                50.00      Sequence
DRB1_1302  458  EIEPVNIRPHPYEFA  PVNIRPHPY         0.2808       2395.7                50.00      Sequence
DRB1_1302  295  AGLSDTARHYIGGLL  ARHYIGGLL         0.2806       2402.0                50.00      Sequence
DRB1_1302  236  HAADDMQLYKYIIKN  DMQLYKYII         0.2803       2410.1                50.00      Sequence
DRB1_1302  278  QSLWKDGAPLMYDET  LWKDGAPLM         0.2795       2429.9                50.00      Sequence
DRB1_1302  268  GDNGSGMHCHQSLWK  GMHCHQSLW         0.2786       2454.5                50.00      Sequence
DRB1_1302  171  GSPNRGYKVRHKGGY  GSPNRGYKV         0.2771       2494.3                50.00      Sequence
DRB1_1302  297  LSDTARHYIGGLLHH  ARHYIGGLL         0.2768       2501.7                50.00      Sequence
DRB1_1302  104  SRDPRNIARKAENYL  IARKAENYL         0.2744       2566.6                50.00      Sequence
DRB1_1302  381  AMLMAGLDGIKNKIE  MLMAGLDGI         0.2741       2576.0                50.00      Sequence
DRB1_1302  459  IEPVNIRPHPYEFAL  PVNIRPHPY         0.2731       2603.6                50.00      Sequence
DRB1_1302  322  TVNSYKRLVPGYEAP  TVNSYKRLV         0.2719       2637.3                50.00      Sequence
DRB1_1302  378  AFSAMLMAGLDGIKN  MLMAGLDGI         0.2709       2668.2                50.00      Sequence
DRB1_1302  141  VSFDSRANGSFYEVD  DSRANGSFY         0.2699       2697.4                50.00      Sequence
DRB1_1302  377  LAFSAMLMAGLDGIK  MLMAGLDGI         0.2688       2729.6                50.00      Sequence
DRB1_1302  457  NEIEPVNIRPHPYEF  PVNIRPHPY         0.2687       2732.3                50.00      Sequence
DRB1_1302   85  AKTLNINFFVHDPFT  AKTLNINFF         0.2683       2742.1                50.00      Sequence
DRB1_1302  118  LISTGIADTAYFGAE  TGIADTAYF         0.2675       2765.6                50.00      Sequence
DRB1_1302  166  ATEADGSPNRGYKVR  GSPNRGYKV         0.2670       2781.7                50.00      Sequence
DRB1_1302  386  GLDGIKNKIEPQAPV  NKIEPQAPV         0.2664       2800.7                50.00      Sequence
DRB1_1302  165  AATEADGSPNRGYKV  GSPNRGYKV         0.2662       2807.5                50.00      Sequence
DRB1_1302  269  DNGSGMHCHQSLWKD  GMHCHQSLW         0.2650       2844.2                50.00      Sequence
DRB1_1302  455  RENEIEPVNIRPHPY  PVNIRPHPY         0.2645       2858.8                50.00      Sequence
DRB1_1302  346  RSACVRIPITGSNPK  IPITGSNPK         0.2642       2868.1                50.00      Sequence
DRB1_1302  279  SLWKDGAPLMYDETG  LWKDGAPLM         0.2641       2869.4                50.00      Sequence
DRB1_1302   26  DLPGIMQHFTIPASA  IMQHFTIPA         0.2638       2880.1                50.00      Sequence
DRB1_1302   62  SIHESDMLLLPDPET  IHESDMLLL         0.2625       2919.2                50.00      Sequence
DRB1_1302  142  SFDSRANGSFYEVDA  DSRANGSFY         0.2619       2940.7                50.00      Sequence
DRB1_1302  234  LLHAADDMQLYKYII  DMQLYKYII         0.2610       2968.8                50.00      Sequence
DRB1_1302  138  FDSVSFDSRANGSFY  DSRANGSFY         0.2595       3016.3                50.00      Sequence
DRB1_1302  143  FDSRANGSFYEVDAI  DSRANGSFY         0.2576       3081.2                50.00      Sequence
DRB1_1302  435  YLTEGGVFTNDLIET  GGVFTNDLI         0.2550       3166.6                50.00      Sequence
DRB1_1302    6  DDVFKLAKDEKVEYV  LAKDEKVEY         0.2548       3175.7                50.00      Sequence
DRB1_1302  270  NGSGMHCHQSLWKDG  GMHCHQSLW         0.2546       3181.0                50.00      Sequence
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DRB1_1302  167  TEADGSPNRGYKVRH  GSPNRGYKV         0.2535       3218.5                50.00      Sequence
DRB1_1302  280  LWKDGAPLMYDETGY  LWKDGAPLM         0.2534       3224.6                50.00      Sequence
DRB1_1302  379  FSAMLMAGLDGIKNK  MLMAGLDGI         0.2529       3238.9                50.00      Sequence
DRB1_1302  298  SDTARHYIGGLLHHA  ARHYIGGLL         0.2504       3329.8                50.00      Sequence
DRB1_1302  168  EADGSPNRGYKVRHK  GSPNRGYKV         0.2490       3380.3                50.00      Sequence
DRB1_1302  436  LTEGGVFTNDLIETW  GGVFTNDLI         0.2451       3526.2                50.00      Sequence
DRB1_1302  353  PITGSNPKAKRLEFR  GSNPKAKRL         0.2443       3554.6                50.00      Sequence
DRB1_1302  217  HEVGSGGQAEINYQF  VGSGGQAEI         0.2435       3585.9                50.00      Sequence
DRB1_1302  299  DTARHYIGGLLHHAP  ARHYIGGLL         0.2414       3671.6                50.00      Sequence
DRB1_1302  218  EVGSGGQAEINYQFN  VGSGGQAEI         0.2411       3680.7                50.00      Sequence
DRB1_1302  300  TARHYIGGLLHHAPS  ARHYIGGLL         0.2403       3712.3                50.00      Sequence
DRB1_1302  271  GSGMHCHQSLWKDGA  GMHCHQSLW         0.2402       3716.8                50.00      Sequence
DRB1_1302  281  WKDGAPLMYDETGYA  LMYDETGYA         0.2396       3741.8                50.00      Sequence
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DRB1_1302  382  MLMAGLDGIKNKIEP  MLMAGLDGI         0.2378       3815.5                50.00      Sequence
DRB1_1302    5  PDDVFKLAKDEKVEY  LAKDEKVEY         0.2374       3832.0                50.00      Sequence
DRB1_1302  213  EKGHHEVGSGGQAEI  VGSGGQAEI         0.2372       3841.0                50.00      Sequence
DRB1_1302  369  PDSSGNPYLAFSAML  PYLAFSAML         0.2361       3887.3                50.00      Sequence
DRB1_1302  315  LLAFTNPTVNSYKRL  LAFTNPTVN         0.2352       3922.6                50.00      Sequence
DRB1_1302  460  EPVNIRPHPYEFALY  PVNIRPHPY         0.2348       3941.1                50.00      Sequence
DRB1_1302    7  DVFKLAKDEKVEYVD  LAKDEKVEY         0.2345       3954.4                50.00      Sequence
DRB1_1302  437  TEGGVFTNDLIETWI  GGVFTNDLI         0.2330       4020.5                50.00      Sequence
DRB1_1302  169  ADGSPNRGYKVRHKG  GSPNRGYKV         0.2320       4062.2                50.00      Sequence
DRB1_1302  291  ETGYAGLSDTARHYI  LSDTARHYI         0.2316       4079.4                50.00      Sequence
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DRB1_1302  273  GMHCHQSLWKDGAPL  GMHCHQSLW         0.2312        4096.2            50.00     Sequence
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DRB1_1302  409  PEEAASIPQTPTQLS  SIPQTPTQL         0.2295        4172.0            50.00     Sequence
DRB1_1302  453  FKRENEIEPVNIRPH  ENEIEPVNI         0.2288        4207.1            50.00     Sequence
DRB1_1302  267  FGDNGSGMHCHQSLW  GMHCHQSLW         0.2287        4212.1            50.00     Sequence
DRB1_1302    8  VFKLAKDEKVEYVDV  LAKDEKVEY         0.2256        4354.0            50.00     Sequence
DRB1_1302  433  HEYLTEGGVFTNDLI  GGVFTNDLI         0.2255        4358.4            50.00     Sequence
DRB1_1302  461  PVNIRPHPYEFALYY  PVNIRPHPY         0.2251        4379.5            50.00     Sequence
DRB1_1302  119  ISTGIADTAYFGAEA  TGIADTAYF         0.2234        4460.4            50.00     Sequence
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DRB1_1302  438  EGGVFTNDLIETWIS  GGVFTNDLI         0.2227        4494.9            50.00     Sequence
DRB1_1302  170  DGSPNRGYKVRHKGG  GSPNRGYKV         0.2225        4501.5            50.00     Sequence
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DRB1_1302  214  KGHHEVGSGGQAEIN  VGSGGQAEI         0.2219        4532.0            50.00     Sequence
DRB1_1302  219  VGSGGQAEINYQFNS  VGSGGQAEI         0.2218        4539.1            50.00     Sequence
DRB1_1302  388  DGIKNKIEPQAPVDK  NKIEPQAPV         0.2192        4665.0            50.00     Sequence
DRB1_1302  330  VPGYEAPINLVYSQR  GYEAPINLV         0.2190        4677.7            50.00     Sequence
DRB1_1302  272  SGMHCHQSLWKDGAP  GMHCHQSLW         0.2188        4688.0            50.00     Sequence
DRB1_1302  354  ITGSNPKAKRLEFRS  GSNPKAKRL         0.2187        4693.5            50.00     Sequence
DRB1_1302  310  HHAPSLLAFTNPTVN  LLAFTNPTV         0.2186        4695.1            50.00     Sequence
DRB1_1302  434  EYLTEGGVFTNDLIE  GGVFTNDLI         0.2172        4769.2            50.00     Sequence
DRB1_1302   65  ESDMLLLPDPETARI  LPDPETARI         0.2152        4871.6            50.00     Sequence
DRB1_1302  254  QNGKTVTFMPKPLFG  VTFMPKPLF         0.2150        4884.6            50.00     Sequence
DRB1_1302   56  SIRGFQSIHESDMLL  SIHESDMLL         0.2149        4890.0            50.00     Sequence
DRB1_1302  312  APSLLAFTNPTVNSY  LLAFTNPTV         0.2145        4908.1            50.00     Sequence
DRB1_1302  292  TGYAGLSDTARHYIG  LSDTARHYI         0.2144        4912.8            50.00     Sequence
DRB1_1302  204  NLINSGFILEKGHHE  NLINSGFIL         0.2143        4918.2            50.00     Sequence
DRB1_1302    9  FKLAKDEKVEYVDVR  LAKDEKVEY         0.2136        4955.7            50.00     Sequence
DRB1_1302   31  MQHFTIPASAFDKSV  HFTIPASAF         0.2136        4959.8            50.00     Sequence
DRB1_1302  345  NRSACVRIPITGSNP  RIPITGSNP         0.2133        4974.7            50.00     Sequence
DRB1_1302  410  EEAASIPQTPTQLSD  SIPQTPTQL         0.2131        4983.5            50.00     Sequence
DRB1_1302  181  HKGGYFPVAPNDQYV  FPVAPNDQY         0.2131        4986.5            50.00     Sequence
DRB1_1302  445  DLIETWISFKRENEI  ISFKRENEI         0.2124        5020.9            50.00     Sequence
DRB1_1302  182  KGGYFPVAPNDQYVD  FPVAPNDQY         0.2114        5078.0            50.00     Sequence
DRB1_1302  232  NSLLHAADDMQLYKY  LHAADDMQL         0.2107        5117.0            50.00     Sequence
DRB1_1302  412  AASIPQTPTQLSDVI  SIPQTPTQL         0.2106        5121.4            50.00     Sequence
DRB1_1302   71  LPDPETARIDPFRAA  LPDPETARI         0.2097        5171.3            50.00     Sequence
DRB1_1302   21  DVRFCDLPGIMQHFT  RFCDLPGIM         0.2097        5172.3            50.00     Sequence
DRB1_1302  454  KRENEIEPVNIRPHP  ENEIEPVNI         0.2083        5251.8            50.00     Sequence
DRB1_1302  294  YAGLSDTARHYIGGL  LSDTARHYI         0.2083        5252.7            50.00     Sequence
DRB1_1302   20  VDVRFCDLPGIMQHF  RFCDLPGIM         0.2078        5278.3            50.00     Sequence
DRB1_1302   32  QHFTIPASAFDKSVF  HFTIPASAF         0.2077        5281.9            50.00     Sequence
DRB1_1302   10  KLAKDEKVEYVDVRF  LAKDEKVEY         0.2074        5304.3            50.00     Sequence
DRB1_1302   22  VRFCDLPGIMQHFTI  RFCDLPGIM         0.2073        5307.9            50.00     Sequence
DRB1_1302  389  GIKNKIEPQAPVDKD  NKIEPQAPV         0.2064        5361.5            50.00     Sequence
DRB1_1302   66  SDMLLLPDPETARID  LPDPETARI         0.2057        5399.0            50.00     Sequence
DRB1_1302  120  STGIADTAYFGAEAE  TGIADTAYF         0.2043        5480.9            50.00     Sequence
DRB1_1302  401  DKDLYELPPEEAASI  LPPEEAASI         0.2033        5544.2            50.00     Sequence
DRB1_1302  411  EAASIPQTPTQLSDV  SIPQTPTQL         0.2032        5547.6            50.00     Sequence
DRB1_1302   48  DGLAFDGSSIRGFQS  GLAFDGSSI         0.2017        5641.0            50.00     Sequence
DRB1_1302  215  GHHEVGSGGQAEINY  VGSGGQAEI         0.2016        5644.2            50.00     Sequence
DRB1_1302  229  YQFNSLLHAADDMQL  LHAADDMQL         0.2011        5673.9            50.00     Sequence
DRB1_1302  230  QFNSLLHAADDMQLY  LHAADDMQL         0.2010        5683.3            50.00     Sequence
DRB1_1302  233  SLLHAADDMQLYKYI  LHAADDMQL         0.2004        5719.9            50.00     Sequence
DRB1_1302   68  MLLLPDPETARIDPF  LPDPETARI         0.2000        5744.5            50.00     Sequence
DRB1_1302   23  RFCDLPGIMQHFTIP  RFCDLPGIM         0.1995        5771.6            50.00     Sequence
DRB1_1302  383  LMAGLDGIKNKIEPQ  GLDGIKNKI         0.1994        5780.5            50.00     Sequence
DRB1_1302  183  GGYFPVAPNDQYVDL  FPVAPNDQY         0.1986        5830.6            50.00     Sequence
DRB1_1302  255  NGKTVTFMPKPLFGD  VTFMPKPLF         0.1981        5865.8            50.00     Sequence
DRB1_1302  216  HHEVGSGGQAEINYQ  VGSGGQAEI         0.1980        5872.2            50.00     Sequence
DRB1_1302   46  FDDGLAFDGSSIRGF  GLAFDGSSI         0.1977        5887.2            50.00     Sequence
DRB1_1302  313  PSLLAFTNPTVNSYK  LAFTNPTVN         0.1975        5899.5            50.00     Sequence
DRB1_1302   33  HFTIPASAFDKSVFD  HFTIPASAF         0.1965        5963.7            50.00     Sequence
DRB1_1302   70  LLPDPETARIDPFRA  LPDPETARI         0.1960        5997.7            50.00     Sequence
DRB1_1302  391  KNKIEPQAPVDKDLY  NKIEPQAPV         0.1957        6020.0            50.00     Sequence
DRB1_1302  293  GYAGLSDTARHYIGG  LSDTARHYI         0.1954        6038.8            50.00     Sequence
DRB1_1302  439  GGVFTNDLIETWISF  GGVFTNDLI         0.1951        6054.2            50.00     Sequence
DRB1_1302   49  GLAFDGSSIRGFQSI  GLAFDGSSI         0.1940        6131.0            50.00     Sequence
DRB1_1302   11  LAKDEKVEYVDVRFC  LAKDEKVEY         0.1939        6136.4            50.00     Sequence
DRB1_1302  205  LINSGFILEKGHHEV  ILEKGHHEV         0.1936        6156.4            50.00     Sequence
DRB1_1302  415  IPQTPTQLSDVIDRL  QLSDVIDRL         0.1936        6156.5            50.00     Sequence
DRB1_1302  155  DAISGWWNTGAATEA  WNTGAATEA         0.1935        6162.8            50.00     Sequence
DRB1_1302   67  DMLLLPDPETARIDP  LPDPETARI         0.1932        6184.8            50.00     Sequence
DRB1_1302  408  PPEEAASIPQTPTQL  SIPQTPTQL         0.1930        6197.3            50.00     Sequence
DRB1_1302   47  DDGLAFDGSSIRGFQ  GLAFDGSSI         0.1928        6210.4            50.00     Sequence
DRB1_1302  311  HAPSLLAFTNPTVNS  LLAFTNPTV         0.1920        6266.0            50.00     Sequence
DRB1_1302  231  FNSLLHAADDMQLYK  LHAADDMQL         0.1909        6339.1            50.00     Sequence
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DRB1_1302  404  LYELPPEEAASIPQT  LPPEEAASI      0.1909      6340.7          50.00     Sequence
DRB1_1302  384  MAGLDGIKNKIEPQA  GLDGIKNKI      0.1908      6347.6          50.00     Sequence
DRB1_1302  256  GKTVTFMPKPLFGDN  VTFMPKPLF      0.1907      6352.0          50.00     Sequence
DRB1_1302   45  VFDDGLAFDGSSIRG  GLAFDGSSI      0.1905      6365.8          50.00     Sequence
DRB1_1302  403  DLYELPPEEAASIPQ  LPPEEAASI      0.1899      6408.2          50.00     Sequence
DRB1_1302   69  LLLPDPETARIDPFR  LPDPETARI      0.1897      6422.7          50.00     Sequence
DRB1_1302   44  SVFDDGLAFDGSSIR  GLAFDGSSI      0.1890      6472.2          50.00     Sequence
DRB1_1302  191  NDQYVDLRDKMLTNL  LRDKMLTNL      0.1881      6535.4          50.00     Sequence
DRB1_1302  385  AGLDGIKNKIEPQAP  GLDGIKNKI      0.1879      6544.8          50.00     Sequence
DRB1_1302  402  KDLYELPPEEAASIP  LPPEEAASI      0.1879      6549.6          50.00     Sequence
DRB1_1302  414  SIPQTPTQLSDVIDR  SIPQTPTQL      0.1870      6608.9          50.00     Sequence
DRB1_1302  413  ASIPQTPTQLSDVID  SIPQTPTQL      0.1867      6629.5          50.00     Sequence
DRB1_1302  441  VFTNDLIETWISFKR  DLIETWISF      0.1855      6721.8          50.00     Sequence
DRB1_1302  121  TGIADTAYFGAEAEF  TGIADTAYF      0.1850      6753.6          50.00     Sequence
DRB1_1302  282  KDGAPLMYDETGYAG  LMYDETGYA      0.1836      6861.0          50.00     Sequence
DRB1_1302  390  IKNKIEPQAPVDKDL  NKIEPQAPV      0.1822      6966.8          50.00     Sequence
DRB1_1302  184  GYFPVAPNDQYVDLR  FPVAPNDQY      0.1818      6993.3          50.00     Sequence
DRB1_1302  355  TGSNPKAKRLEFRSP  GSNPKAKRL      0.1816      7005.5          50.00     Sequence
DRB1_1302  180  RHKGGYFPVAPNDQY  FPVAPNDQY      0.1815      7017.1          50.00     Sequence
DRB1_1302  406  ELPPEEAASIPQTPT  LPPEEAASI      0.1798      7145.3          50.00     Sequence
DRB1_1302  405  YELPPEEAASIPQTP  LPPEEAASI      0.1791      7198.8          50.00     Sequence
DRB1_1302  451  ISFKRENEIEPVNIR  ENEIEPVNI      0.1788      7223.9          50.00     Sequence
DRB1_1302  440  GVFTNDLIETWISFK  DLIETWISF      0.1783      7263.5          50.00     Sequence
DRB1_1302   19  YVDVRFCDLPGIMQH  RFCDLPGIM      0.1759      7455.8          50.00     Sequence
DRB1_1302  206  INSGFILEKGHHEVG  ILEKGHHEV      0.1739      7614.3          50.00     Sequence
DRB1_1302   86  KTLNINFFVHDPFTL  KTLNINFFV      0.1738      7625.1          50.00     Sequence
DRB1_1302  446  LIETWISFKRENEIE  ISFKRENEI      0.1729      7696.6          50.00     Sequence
DRB1_1302  356  GSNPKAKRLEFRSPD  GSNPKAKRL      0.1727      7717.9          50.00     Sequence
DRB1_1302  156  AISGWWNTGAATEAD  WNTGAATEA      0.1715      7821.4          50.00     Sequence
DRB1_1302  283  DGAPLMYDETGYAGL  LMYDETGYA      0.1710      7859.2          50.00     Sequence
DRB1_1302  452  SFKRENEIEPVNIRP  ENEIEPVNI      0.1701      7937.9          50.00     Sequence
DRB1_1302   73  DPETARIDPFRAAKT  IDPFRAAKT      0.1689      8037.9          50.00     Sequence
DRB1_1302  407  LPPEEAASIPQTPTQ  LPPEEAASI      0.1686      8066.5          50.00     Sequence
DRB1_1302  220  GSGGQAEINYQFNSL  GQAEINYQF      0.1680      8115.5          50.00     Sequence
DRB1_1302  257  KTVTFMPKPLFGDNG  VTFMPKPLF      0.1678      8137.1          50.00     Sequence
DRB1_1302  185  YFPVAPNDQYVDLRD  FPVAPNDQY      0.1671      8195.8          50.00     Sequence
DRB1_1302   74  PETARIDPFRAAKTL  IDPFRAAKT      0.1669      8216.2          50.00     Sequence
DRB1_1302  284  GAPLMYDETGYAGLS  LMYDETGYA      0.1636      8518.7          50.00     Sequence
DRB1_1302  416  PQTPTQLSDVIDRLE  QLSDVIDRL      0.1618      8686.6          50.00     Sequence
DRB1_1302   17  VEYVDVRFCDLPGIM  RFCDLPGIM      0.1612      8741.4          50.00     Sequence
DRB1_1302  207  NSGFILEKGHHEVGS  ILEKGHHEV      0.1594      8907.7          50.00     Sequence
DRB1_1302  147  ANGSFYEVDAISGWW  YEVDAISGW      0.1585      8999.6          50.00     Sequence
DRB1_1302   75  ETARIDPFRAAKTLN  IDPFRAAKT      0.1561      9233.3          50.00     Sequence
DRB1_1302  148  NGSFYEVDAISGWWN  YEVDAISGW      0.1554      9309.1          50.00     Sequence
DRB1_1302   18  EYVDVRFCDLPGIMQ  RFCDLPGIM      0.1554      9310.5          50.00     Sequence
DRB1_1302  450  WISFKRENEIEPVNI  KRENEIEPV      0.1551      9335.5          50.00     Sequence
DRB1_1302  432  DHEYLTEGGVFTNDL  EYLTEGGVF      0.1521      9646.2          50.00     Sequence
DRB1_1302  392  NKIEPQAPVDKDLYE  NKIEPQAPV      0.1520      9654.1          50.00     Sequence
DRB1_1302  442  FTNDLIETWISFKRE  DLIETWISF      0.1518      9674.4          50.00     Sequence
DRB1_1302  157  ISGWWNTGAATEADG  WNTGAATEA      0.1513      9731.2          50.00     Sequence
DRB1_1302  228  NYQFNSLLHAADDMQ  LLHAADDMQ      0.1511      9747.6          50.00     Sequence
DRB1_1302  417  QTPTQLSDVIDRLEA  QLSDVIDRL      0.1497      9898.8          50.00     Sequence
DRB1_1302  462  VNIRPHPYEFALYYD  RPHPYEFAL      0.1489      9985.6          50.00     Sequence
DRB1_1302  208  SGFILEKGHHEVGSG  ILEKGHHEV      0.1487     10002.8          50.00     Sequence
DRB1_1302    3  KTPDDVFKLAKDEKV  FKLAKDEKV      0.1486     10012.5          50.00     Sequence
DRB1_1302  179  VRHKGGYFPVAPNDQ  VRHKGGYFP      0.1475     10138.9          50.00     Sequence
DRB1_1302  258  TVTFMPKPLFGDNGS  VTFMPKPLF      0.1467     10222.1          50.00     Sequence
DRB1_1302   55  SSIRGFQSIHESDML  QSIHESDML      0.1465     10245.4          50.00     Sequence
DRB1_1302  149  GSFYEVDAISGWWNT  YEVDAISGW      0.1454     10369.5          50.00     Sequence
DRB1_1302  209  GFILEKGHHEVGSGG  ILEKGHHEV      0.1445     10474.2          50.00     Sequence
DRB1_1302   43  KSVFDDGLAFDGSSI  GLAFDGSSI      0.1428     10668.0          50.00     Sequence
DRB1_1302  285  APLMYDETGYAGLSD  LMYDETGYA      0.1427     10670.8          50.00     Sequence
DRB1_1302  463  NIRPHPYEFALYYDV  RPHPYEFAL      0.1427     10674.7          50.00     Sequence
DRB1_1302  153  EVDAISGWWNTGAAT  GWWNTGAAT      0.1407     10909.2          50.00     Sequence
DRB1_1302  443  TNDLIETWISFKREN  DLIETWISF      0.1403     10960.4          50.00     Sequence
DRB1_1302  290  DETGYAGLSDTARHY  GLSDTARHY      0.1367     11394.8          50.00     Sequence
DRB1_1302  186  FPVAPNDQYVDLRDK  FPVAPNDQY      0.1362     11460.3          50.00     Sequence
DRB1_1302  444  NDLIETWISFKRENE  DLIETWISF      0.1350     11603.5          50.00     Sequence
DRB1_1302   51  AFDGSSIRGFQSIHE  IRGFQSIHE      0.1343     11693.1          50.00     Sequence
DRB1_1302  447  IETWISFKRENEIEP  ISFKRENEI      0.1334     11808.8          50.00     Sequence
DRB1_1302  448  ETWISFKRENEIEPV  KRENEIEPV      0.1330     11856.1          50.00     Sequence
DRB1_1302  151  FYEVDAISGWWNTGA  YEVDAISGW      0.1330     11862.0          50.00     Sequence
DRB1_1302  286  PLMYDETGYAGLSDT  LMYDETGYA      0.1323     11950.7          50.00     Sequence
DRB1_1302  418  TPTQLSDVIDRLEAD  QLSDVIDRL      0.1316     12036.8          50.00     Sequence
DRB1_1302   50  LAFDGSSIRGFQSIH  LAFDGSSIR      0.1306     12170.0          50.00     Sequence
DRB1_1302  430  EADHEYLTEGGVFTN  EYLTEGGVF      0.1301     12238.1          50.00     Sequence
DRB1_1302  150  SFYEVDAISGWWNTG  YEVDAISGW      0.1300     12247.6          50.00     Sequence
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DRB1_1302  154  VDAISGWWNTGAATE  WWNTGAATE        0.1299     12264.9            50.00    Sequence
DRB1_1302  103  YSRDPRNIARKAENY  RNIARKAEN        0.1298     12281.3            50.00    Sequence
DRB1_1302  368  SPDSSGNPYLAFSAM  DSSGNPYLA        0.1285     12455.8            50.00    Sequence
DRB1_1302    4  TPDDVFKLAKDEKVE  FKLAKDEKV        0.1281     12508.8            50.00    Sequence
DRB1_1302   52  FDGSSIRGFQSIHES  IRGFQSIHE        0.1270     12647.7            50.00    Sequence
DRB1_1302  190  PNDQYVDLRDKMLTN  YVDLRDKML        0.1266     12714.1            50.00    Sequence
DRB1_1302  158  SGWWNTGAATEADGS  WNTGAATEA        0.1264     12732.5            50.00    Sequence
DRB1_1302  431  ADHEYLTEGGVFTND  EYLTEGGVF        0.1251     12915.9            50.00    Sequence
DRB1_1302  152  YEVDAISGWWNTGAA  YEVDAISGW        0.1248     12958.7            50.00    Sequence
DRB1_1302  259  VTFMPKPLFGDNGSG  VTFMPKPLF        0.1247     12971.5            50.00    Sequence
DRB1_1302  187  PVAPNDQYVDLRDKM  QYVDLRDKM        0.1243     13030.1            50.00    Sequence
DRB1_1302  449  TWISFKRENEIEPVN  KRENEIEPV        0.1232     13187.9            50.00    Sequence
DRB1_1302  287  LMYDETGYAGLSDTA  LMYDETGYA        0.1230     13214.9            50.00    Sequence
DRB1_1302  129  FGAEAEFYIFDSVSF  FYIFDSVSF        0.1220     13363.2            50.00    Sequence
DRB1_1302  188  VAPNDQYVDLRDKML  YVDLRDKML        0.1218     13388.3            50.00    Sequence
DRB1_1302  365  EFRSPDSSGNPYLAF  DSSGNPYLA        0.1218     13391.0            50.00    Sequence
DRB1_1302  210  FILEKGHHEVGSGGQ  ILEKGHHEV        0.1218     13392.2            50.00    Sequence
DRB1_1302  189  APNDQYVDLRDKMLT  YVDLRDKML        0.1211     13492.8            50.00    Sequence
DRB1_1302  102  PYSRDPRNIARKAEN  RNIARKAEN        0.1207     13551.2            50.00    Sequence
DRB1_1302  367  RSPDSSGNPYLAFSA  DSSGNPYLA        0.1199     13666.4            50.00    Sequence
DRB1_1302  130  GAEAEFYIFDSVSFD  FYIFDSVSF        0.1192     13762.1            50.00    Sequence
DRB1_1302   12  AKDEKVEYVDVRFCD  KVEYVDVRF        0.1191     13780.7            50.00    Sequence
DRB1_1302   54  GSSIRGFQSIHESDM  FQSIHESDM        0.1157     14294.0            50.00    Sequence
DRB1_1302  146  RANGSFYEVDAISGW  YEVDAISGW        0.1141     14549.1            50.00    Sequence
DRB1_1302   87  TLNINFFVHDPFTLE  FFVHDPFTL        0.1139     14576.4            50.00    Sequence
DRB1_1302  159  GWWNTGAATEADGSP  WNTGAATEA        0.1137     14606.4            50.00    Sequence
DRB1_1302  366  FRSPDSSGNPYLAFS  DSSGNPYLA        0.1135     14638.6            50.00    Sequence
DRB1_1302  364  LEFRSPDSSGNPYLA  DSSGNPYLA        0.1122     14848.7            50.00    Sequence
DRB1_1302   88  LNINFFVHDPFTLEP  FFVHDPFTL        0.1116     14948.2            50.00    Sequence
DRB1_1302  131  AEAEFYIFDSVSFDS  FYIFDSVSF        0.1111     15033.7            50.00    Sequence
DRB1_1302   38  ASAFDKSVFDDGLAF  SVFDDGLAF        0.1109     15059.6            50.00    Sequence
DRB1_1302   34  FTIPASAFDKSVFDD  FTIPASAFD        0.1077     15596.3            50.00    Sequence
DRB1_1302  132  EAEFYIFDSVSFDSR  FYIFDSVSF        0.1073     15655.2            50.00    Sequence
DRB1_1302  419  PTQLSDVIDRLEADH  QLSDVIDRL        0.1069     15722.7            50.00    Sequence
DRB1_1302  211  ILEKGHHEVGSGGQA  ILEKGHHEV        0.1067     15762.4            50.00    Sequence
DRB1_1302  100  LEPYSRDPRNIARKA  SRDPRNIAR        0.1051     16039.7            50.00    Sequence
DRB1_1302  133  AEFYIFDSVSFDSRA  FYIFDSVSF        0.1050     16051.6            50.00    Sequence
DRB1_1302  420  TQLSDVIDRLEADHE  QLSDVIDRL        0.1034     16334.9            50.00    Sequence
DRB1_1302   72  PDPETARIDPFRAAK  TARIDPFRA        0.1033     16343.2            50.00    Sequence
DRB1_1302   53  DGSSIRGFQSIHESD  IRGFQSIHE        0.1029     16420.8            50.00    Sequence
DRB1_1302  101  EPYSRDPRNIARKAE  YSRDPRNIA        0.1019     16599.4            50.00    Sequence
DRB1_1302   99  TLEPYSRDPRNIARK  SRDPRNIAR        0.1018     16622.6            50.00    Sequence
DRB1_1302   89  NINFFVHDPFTLEPY  FFVHDPFTL        0.1007     16827.3            50.00    Sequence
DRB1_1302  423  SDVIDRLEADHEYLT  RLEADHEYL        0.0989     17141.0            50.00    Sequence
DRB1_1302  428  RLEADHEYLTEGGVF  EYLTEGGVF        0.0987     17190.2            50.00    Sequence
DRB1_1302   39  SAFDKSVFDDGLAFD  SVFDDGLAF        0.0985     17217.4            50.00    Sequence
DRB1_1302   98  FTLEPYSRDPRNIAR  YSRDPRNIA        0.0985     17222.2            50.00    Sequence
DRB1_1302  134  EFYIFDSVSFDSRAN  FYIFDSVSF        0.0983     17256.5            50.00    Sequence
DRB1_1302  160  WWNTGAATEADGSPN  WNTGAATEA        0.0980     17308.1            50.00    Sequence
DRB1_1302   35  TIPASAFDKSVFDDG  ASAFDKSVF        0.0980     17308.9            50.00    Sequence
DRB1_1302  393  KIEPQAPVDKDLYEL  QAPVDKDLY        0.0968     17544.2            50.00    Sequence
DRB1_1302   16  KVEYVDVRFCDLPGI  KVEYVDVRF        0.0961     17678.3            50.00    Sequence
DRB1_1302  429  LEADHEYLTEGGVFT  EYLTEGGVF        0.0952     17845.3            50.00    Sequence
DRB1_1302   40  AFDKSVFDDGLAFDG  SVFDDGLAF        0.0952     17845.5            50.00    Sequence
DRB1_1302  421  QLSDVIDRLEADHEY  QLSDVIDRL        0.0951     17865.8            50.00    Sequence
DRB1_1302  135  FYIFDSVSFDSRANG  FYIFDSVSF        0.0947     17941.4            50.00    Sequence
DRB1_1302  422  LSDVIDRLEADHEYL  RLEADHEYL        0.0926     18357.9            50.00    Sequence
DRB1_1302   90  INFFVHDPFTLEPYS  FFVHDPFTL        0.0926     18368.4            50.00    Sequence
DRB1_1302  424  DVIDRLEADHEYLTE  RLEADHEYL        0.0904     18807.8            50.00    Sequence
DRB1_1302   13  KDEKVEYVDVRFCDL  KVEYVDVRF        0.0902     18839.2            50.00    Sequence
DRB1_1302   36  IPASAFDKSVFDDGL  DKSVFDDGL        0.0883     19232.6            50.00    Sequence
DRB1_1302  425  VIDRLEADHEYLTEG  RLEADHEYL        0.0875     19392.4            50.00    Sequence
DRB1_1302   37  PASAFDKSVFDDGLA  DKSVFDDGL        0.0873     19443.7            50.00    Sequence
DRB1_1302  394  IEPQAPVDKDLYELP  QAPVDKDLY        0.0847     19996.2            50.00    Sequence
DRB1_1302   14  DEKVEYVDVRFCDLP  KVEYVDVRF        0.0829     20393.7            50.00    Sequence
DRB1_1302  426  IDRLEADHEYLTEGG  RLEADHEYL        0.0824     20494.3            50.00    Sequence
DRB1_1302   41  FDKSVFDDGLAFDGS  SVFDDGLAF        0.0806     20908.5            50.00    Sequence
DRB1_1302   97  PFTLEPYSRDPRNIA  YSRDPRNIA        0.0804     20939.9            50.00    Sequence
DRB1_1302  145  SRANGSFYEVDAISG  RANGSFYEV        0.0800     21041.7            50.00    Sequence
DRB1_1302   91  NFFVHDPFTLEPYSR  FFVHDPFTL        0.0798     21091.6            50.00    Sequence
DRB1_1302  427  DRLEADHEYLTEGGV  RLEADHEYL        0.0785     21375.8            50.00    Sequence
DRB1_1302   64  HESDMLLLPDPETAR  LLLPDPETA        0.0777     21575.6            50.00    Sequence
DRB1_1302   15  EKVEYVDVRFCDLPG  KVEYVDVRF        0.0775     21619.1            50.00    Sequence
DRB1_1302  289  YDETGYAGLSDTARH  AGLSDTARH        0.0769     21767.0            50.00    Sequence
DRB1_1302  161  WNTGAATEADGSPNR  WNTGAATEA        0.0764     21865.9            50.00    Sequence
DRB1_1302  122  GIADTAYFGAEAEFY  AYFGAEAEF        0.0751     22197.0            50.00    Sequence
DRB1_1302   42  DKSVFDDGLAFDGSS  SVFDDGLAF        0.0742     22394.8            50.00    Sequence
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   DRB1_1302  395  EPQAPVDKDLYELPP  QAPVDKDLY        0.0738      22499.2                50.00     Sequence
   DRB1_1302   92  FFVHDPFTLEPYSRD  FFVHDPFTL        0.0706      23295.1                50.00     Sequence
   DRB1_1302    0  VTEKTPDDVFKLAKD  KTPDDVFKL        0.0698      23482.9                50.00     Sequence
   DRB1_1302  396  PQAPVDKDLYELPPE  QAPVDKDLY        0.0694      23592.7                50.00     Sequence
   DRB1_1302  397  QAPVDKDLYELPPEE  QAPVDKDLY        0.0675      24088.4                50.00     Sequence
   DRB1_1302    2  EKTPDDVFKLAKDEK  KTPDDVFKL        0.0653      24675.1                50.00     Sequence
   DRB1_1302    1  TEKTPDDVFKLAKDE  KTPDDVFKL        0.0626      25385.4                50.00     Sequence
   DRB1_1302  288  MYDETGYAGLSDTAR  DETGYAGLS        0.0618      25619.4                50.00     Sequence
   DRB1_1302  212  LEKGHHEVGSGGQAE  HEVGSGGQA        0.0602      26059.4                50.00     Sequence
   DRB1_1302  123  IADTAYFGAEAEFYI  AYFGAEAEF        0.0595      26266.7                50.00     Sequence
   DRB1_1302  137  IFDSVSFDSRANGSF  FDSRANGSF        0.0592      26364.6                50.00     Sequence
   DRB1_1302   96  DPFTLEPYSRDPRNI  PYSRDPRNI        0.0587      26485.8                50.00     Sequence
   DRB1_1302  124  ADTAYFGAEAEFYIF  GAEAEFYIF        0.0561      27254.8                50.00     Sequence
   DRB1_1302  363  RLEFRSPDSSGNPYL  RSPDSSGNP        0.0559      27318.2                50.00     Sequence
   DRB1_1302  362  KRLEFRSPDSSGNPY  RSPDSSGNP        0.0552      27519.4                50.00     Sequence
   DRB1_1302  398  APVDKDLYELPPEEA  LYELPPEEA        0.0533      28098.3                50.00     Sequence
   DRB1_1302   94  VHDPFTLEPYSRDPR  LEPYSRDPR        0.0523      28389.5                50.00     Sequence
   DRB1_1302   95  HDPFTLEPYSRDPRN  TLEPYSRDP        0.0505      28954.7                50.00     Sequence
   DRB1_1302  164  GAATEADGSPNRGYK  EADGSPNRG        0.0490      29417.3                50.00     Sequence
   DRB1_1302  399  PVDKDLYELPPEEAA  LYELPPEEA        0.0490      29435.8                50.00     Sequence
   DRB1_1302  125  DTAYFGAEAEFYIFD  GAEAEFYIF        0.0489      29456.8                50.00     Sequence
   DRB1_1302  128  YFGAEAEFYIFDSVS  EFYIFDSVS        0.0476      29883.4                50.00     Sequence
   DRB1_1302  163  TGAATEADGSPNRGY  ADGSPNRGY        0.0470      30071.9                50.00     Sequence
   DRB1_1302  136  YIFDSVSFDSRANGS  DSVSFDSRA        0.0463      30300.5                50.00     Sequence
   DRB1_1302  358  NPKAKRLEFRSPDSS  NPKAKRLEF        0.0457      30478.4                50.00     Sequence
   DRB1_1302  127  AYFGAEAEFYIFDSV  GAEAEFYIF        0.0457      30508.4                50.00     Sequence
   DRB1_1302  357  SNPKAKRLEFRSPDS  NPKAKRLEF        0.0456      30512.4                50.00     Sequence
   DRB1_1302  361  AKRLEFRSPDSSGNP  RSPDSSGNP        0.0448      30799.6                50.00     Sequence
   DRB1_1302  162  NTGAATEADGSPNRG  ATEADGSPN        0.0430      31402.6                50.00     Sequence
   DRB1_1302  126  TAYFGAEAEFYIFDS  GAEAEFYIF        0.0425      31564.8                50.00     Sequence
   DRB1_1302   93  FVHDPFTLEPYSRDP  FVHDPFTLE        0.0407      32173.4                50.00     Sequence
   DRB1_1302  360  KAKRLEFRSPDSSGN  FRSPDSSGN        0.0358      33947.9                50.00     Sequence
   DRB1_1302  359  PKAKRLEFRSPDSSG  RLEFRSPDS        0.0299      36193.5                50.00     Sequence
   DRB1_1302  400  VDKDLYELPPEEAAS  LYELPPEEA        0.0276      37089.4                50.00     Sequence
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Allele: DRB1_1302. Number of high binders 5. Number of weak binders 38. Number of peptides 464

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1501   27  LPGIMQHFTIPASAF  IMQHFTIPA        0.7790         10.9         SB     0.30     Sequence
   DRB1_1501   28  PGIMQHFTIPASAFD  IMQHFTIPA        0.7752         11.4         SB     0.30     Sequence
   DRB1_1501   26  DLPGIMQHFTIPASA  IMQHFTIPA        0.7633         12.9         SB     0.40     Sequence
   DRB1_1501   29  GIMQHFTIPASAFDK  IMQHFTIPA        0.7438         16.0         SB     0.80     Sequence
   DRB1_1501   25  CDLPGIMQHFTIPAS  IMQHFTIPA        0.7274         19.1         SB     1.00     Sequence
   DRB1_1501  311  HAPSLLAFTNPTVNS  SLLAFTNPT        0.7017         25.2         SB     2.00     Sequence
   DRB1_1501  310  HHAPSLLAFTNPTVN  SLLAFTNPT        0.6960         26.8         SB     2.00     Sequence
   DRB1_1501  312  APSLLAFTNPTVNSY  SLLAFTNPT        0.6910         28.3         SB     2.00     Sequence
   DRB1_1501  313  PSLLAFTNPTVNSYK  SLLAFTNPT        0.6777         32.7         SB     4.00     Sequence
   DRB1_1501  309  LHHAPSLLAFTNPTV  SLLAFTNPT        0.6631         38.3         SB     4.00     Sequence
   DRB1_1501   24  FCDLPGIMQHFTIPA  IMQHFTIPA        0.6545         42.0         SB     4.00     Sequence
   DRB1_1501   53  DGSSIRGFQSIHESD  SIRGFQSIH        0.6417         48.3         SB     4.00     Sequence
   DRB1_1501   52  FDGSSIRGFQSIHES  SIRGFQSIH        0.6415         48.4         SB     4.00     Sequence
   DRB1_1501   54  GSSIRGFQSIHESDM  SIRGFQSIH        0.6386         49.9         SB     4.00     Sequence
   DRB1_1501  153  EVDAISGWWNTGAAT  AISGWWNTG        0.6337         52.6         WB     4.00     Sequence
   DRB1_1501  154  VDAISGWWNTGAATE  AISGWWNTG        0.6231         59.0         WB     8.00     Sequence
   DRB1_1501  314  SLLAFTNPTVNSYKR  SLLAFTNPT        0.6222         59.6         WB     8.00     Sequence
   DRB1_1501   55  SSIRGFQSIHESDML  SIRGFQSIH        0.6218         59.9         WB     8.00     Sequence
   DRB1_1501  335  APINLVYSQRNRSAC  PINLVYSQR        0.6171         63.0         WB     8.00     Sequence
   DRB1_1501   51  AFDGSSIRGFQSIHE  SIRGFQSIH        0.6169         63.1         WB     8.00     Sequence
   DRB1_1501  334  EAPINLVYSQRNRSA  PINLVYSQR        0.6131         65.7         WB     8.00     Sequence
   DRB1_1501  152  YEVDAISGWWNTGAA  AISGWWNTG        0.6070         70.3         WB     8.00     Sequence
   DRB1_1501  336  PINLVYSQRNRSACV  PINLVYSQR        0.6043         72.4         WB     8.00     Sequence
   DRB1_1501  333  YEAPINLVYSQRNRS  PINLVYSQR        0.5877         86.6         WB     8.00     Sequence
   DRB1_1501   56  SIRGFQSIHESDMLL  SIRGFQSIH        0.5803         93.8         WB     8.00     Sequence
   DRB1_1501  155  DAISGWWNTGAATEA  AISGWWNTG        0.5789         95.2         WB     8.00     Sequence
   DRB1_1501   30  IMQHFTIPASAFDKS  IMQHFTIPA        0.5766         97.7         WB     8.00     Sequence
   DRB1_1501  151  FYEVDAISGWWNTGA  AISGWWNTG        0.5724        102.2         WB     8.00     Sequence
   DRB1_1501  337  INLVYSQRNRSACVR  LVYSQRNRS        0.5612        115.3         WB    16.00     Sequence
   DRB1_1501  443  TNDLIETWISFKREN  DLIETWISF        0.5597        117.2         WB    16.00     Sequence
   DRB1_1501  238  ADDMQLYKYIIKNTA  QLYKYIIKN        0.5582        119.2         WB    16.00     Sequence
   DRB1_1501  338  NLVYSQRNRSACVRI  LVYSQRNRS        0.5564        121.5         WB    16.00     Sequence
   DRB1_1501  237  AADDMQLYKYIIKNT  QLYKYIIKN        0.5552        123.1         WB    16.00     Sequence
   DRB1_1501  239  DDMQLYKYIIKNTAW  QLYKYIIKN        0.5523        127.0         WB    16.00     Sequence
   DRB1_1501  442  FTNDLIETWISFKRE  DLIETWISF        0.5517        127.8         WB    16.00     Sequence
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DRB1_1501  302  RHYIGGLLHHAPSLL  HYIGGLLHH        0.5503        129.7          WB    16.00      Sequence
DRB1_1501  372  SGNPYLAFSAMLMAG  PYLAFSAML        0.5481        132.9          WB    16.00      Sequence
DRB1_1501  441  VFTNDLIETWISFKR  DLIETWISF        0.5452        137.2          WB    16.00      Sequence
DRB1_1501  444  NDLIETWISFKRENE  LIETWISFK        0.5446        138.0          WB    16.00      Sequence
DRB1_1501  308  LLHHAPSLLAFTNPT  SLLAFTNPT        0.5435        139.6          WB    16.00      Sequence
DRB1_1501  240  DMQLYKYIIKNTAWQ  QLYKYIIKN        0.5407        144.0          WB    16.00      Sequence
DRB1_1501   50  LAFDGSSIRGFQSIH  SIRGFQSIH        0.5393        146.2          WB    16.00      Sequence
DRB1_1501  332  GYEAPINLVYSQRNR  PINLVYSQR        0.5391        146.5          WB    16.00      Sequence
DRB1_1501  373  GNPYLAFSAMLMAGL  PYLAFSAML        0.5380        148.3          WB    16.00      Sequence
DRB1_1501  327  KRLVPGYEAPINLVY  LVPGYEAPI        0.5364        150.9          WB    16.00      Sequence
DRB1_1501  236  HAADDMQLYKYIIKN  QLYKYIIKN        0.5319        158.4          WB    16.00      Sequence
DRB1_1501  326  YKRLVPGYEAPINLV  LVPGYEAPI        0.5292        163.0          WB    16.00      Sequence
DRB1_1501  303  HYIGGLLHHAPSLLA  LLHHAPSLL        0.5277        165.7          WB    16.00      Sequence
DRB1_1501  328  RLVPGYEAPINLVYS  LVPGYEAPI        0.5222        175.9          WB    16.00      Sequence
DRB1_1501  325  SYKRLVPGYEAPINL  LVPGYEAPI        0.5210        178.1          WB    16.00      Sequence
DRB1_1501  301  ARHYIGGLLHHAPSL  YIGGLLHHA        0.5201        180.0          WB    16.00      Sequence
DRB1_1501  241  MQLYKYIIKNTAWQN  QLYKYIIKN        0.5183        183.5          WB    16.00      Sequence
DRB1_1501  176  GYKVRHKGGYFPVAP  KVRHKGGYF        0.5045        212.9          WB    16.00      Sequence
DRB1_1501  175  RGYKVRHKGGYFPVA  KVRHKGGYF        0.5040        214.2          WB    16.00      Sequence
DRB1_1501   77  ARIDPFRAAKTLNIN  RIDPFRAAK        0.5030        216.5          WB    16.00      Sequence
DRB1_1501  177  YKVRHKGGYFPVAPN  KVRHKGGYF        0.5024        217.9          WB    16.00      Sequence
DRB1_1501   76  TARIDPFRAAKTLNI  RIDPFRAAK        0.5012        220.7          WB    16.00      Sequence
DRB1_1501  242  QLYKYIIKNTAWQNG  QLYKYIIKN        0.4993        225.3          WB    16.00      Sequence
DRB1_1501  150  SFYEVDAISGWWNTG  AISGWWNTG        0.4992        225.4          WB    16.00      Sequence
DRB1_1501  445  DLIETWISFKRENEI  DLIETWISF        0.4947        236.7          WB    16.00      Sequence
DRB1_1501  374  NPYLAFSAMLMAGLD  PYLAFSAML        0.4941        238.3          WB    16.00      Sequence
DRB1_1501   75  ETARIDPFRAAKTLN  RIDPFRAAK        0.4934        240.3          WB    16.00      Sequence
DRB1_1501  339  LVYSQRNRSACVRIP  LVYSQRNRS        0.4933        240.4          WB    16.00      Sequence
DRB1_1501  324  NSYKRLVPGYEAPIN  LVPGYEAPI        0.4932        240.6          WB    16.00      Sequence
DRB1_1501  198  RDKMLTNLINSGFIL  MLTNLINSG        0.4884        253.4          WB    32.00      Sequence
DRB1_1501  200  KMLTNLINSGFILEK  MLTNLINSG        0.4785        282.2          WB    32.00      Sequence
DRB1_1501  375  PYLAFSAMLMAGLDG  PYLAFSAML        0.4779        284.1          WB    32.00      Sequence
DRB1_1501  440  GVFTNDLIETWISFK  DLIETWISF        0.4775        285.3          WB    32.00      Sequence
DRB1_1501  199  DKMLTNLINSGFILE  MLTNLINSG        0.4762        289.3          WB    32.00      Sequence
DRB1_1501   78  RIDPFRAAKTLNINF  RIDPFRAAK        0.4757        290.8          WB    32.00      Sequence
DRB1_1501  174  NRGYKVRHKGGYFPV  KVRHKGGYF        0.4754        291.7          WB    32.00      Sequence
DRB1_1501  300  TARHYIGGLLHHAPS  HYIGGLLHH        0.4744        294.9          WB    32.00      Sequence
DRB1_1501  306  GGLLHHAPSLLAFTN  GLLHHAPSL        0.4718        303.5          WB    32.00      Sequence
DRB1_1501  304  YIGGLLHHAPSLLAF  GLLHHAPSL        0.4702        308.7          WB    32.00      Sequence
DRB1_1501  299  DTARHYIGGLLHHAP  HYIGGLLHH        0.4668        320.3          WB    32.00      Sequence
DRB1_1501  178  KVRHKGGYFPVAPND  KVRHKGGYF        0.4580        352.3          WB    32.00      Sequence
DRB1_1501  305  IGGLLHHAPSLLAFT  GLLHHAPSL        0.4578        353.1          WB    32.00      Sequence
DRB1_1501  173  PNRGYKVRHKGGYFP  KVRHKGGYF        0.4577        353.5          WB    32.00      Sequence
DRB1_1501  298  SDTARHYIGGLLHHA  HYIGGLLHH        0.4567        357.4          WB    32.00      Sequence
DRB1_1501  307  GLLHHAPSLLAFTNP  GLLHHAPSL        0.4530        371.8          WB    32.00      Sequence
DRB1_1501   74  PETARIDPFRAAKTL  RIDPFRAAK        0.4515        377.8          WB    32.00      Sequence
DRB1_1501  371  SSGNPYLAFSAMLMA  PYLAFSAML        0.4461        400.8          WB    32.00      Sequence
DRB1_1501  197  LRDKMLTNLINSGFI  MLTNLINSG        0.4445        407.8          WB    32.00      Sequence
DRB1_1501  156  AISGWWNTGAATEAD  AISGWWNTG        0.4404        426.4          WB    32.00      Sequence
DRB1_1501  323  VNSYKRLVPGYEAPI  LVPGYEAPI        0.4354        449.6          WB    32.00      Sequence
DRB1_1501  243  LYKYIIKNTAWQNGK  YIIKNTAWQ        0.4343        455.3          WB    32.00      Sequence
DRB1_1501  196  DLRDKMLTNLINSGF  MLTNLINSG        0.4301        476.6          WB    32.00      Sequence
DRB1_1501  244  YKYIIKNTAWQNGKT  YIIKNTAWQ        0.4211        525.2                32.00      Sequence
DRB1_1501  329  LVPGYEAPINLVYSQ  LVPGYEAPI        0.4189        537.5                32.00      Sequence
DRB1_1501  172  SPNRGYKVRHKGGYF  KVRHKGGYF        0.4154        558.3                32.00      Sequence
DRB1_1501  201  MLTNLINSGFILEKG  MLTNLINSG        0.4147        562.4                32.00      Sequence
DRB1_1501  195  VDLRDKMLTNLINSG  MLTNLINSG        0.4141        566.4                32.00      Sequence
DRB1_1501  225  AEINYQFNSLLHAAD  EINYQFNSL        0.4133        571.2                32.00      Sequence
DRB1_1501  331  PGYEAPINLVYSQRN  PINLVYSQR        0.4107        587.7                32.00      Sequence
DRB1_1501  224  QAEINYQFNSLLHAA  EINYQFNSL        0.4086        601.3                32.00      Sequence
DRB1_1501  370  DSSGNPYLAFSAMLM  PYLAFSAML        0.4084        602.7                32.00      Sequence
DRB1_1501  275  HCHQSLWKDGAPLMY  SLWKDGAPL        0.4082        603.7                32.00      Sequence
DRB1_1501  245  KYIIKNTAWQNGKTV  KYIIKNTAW        0.4050        624.9                32.00      Sequence
DRB1_1501  246  YIIKNTAWQNGKTVT  IIKNTAWQN        0.4049        625.5                32.00      Sequence
DRB1_1501  247  IIKNTAWQNGKTVTF  IIKNTAWQN        0.4036        634.2                32.00      Sequence
DRB1_1501   73  DPETARIDPFRAAKT  RIDPFRAAK        0.4020        645.5                32.00      Sequence
DRB1_1501  377  LAFSAMLMAGLDGIK  AFSAMLMAG        0.3967        683.4                32.00      Sequence
DRB1_1501  226  EINYQFNSLLHAADD  EINYQFNSL        0.3966        684.5                32.00      Sequence
DRB1_1501  378  AFSAMLMAGLDGIKN  AFSAMLMAG        0.3931        711.2                32.00      Sequence
DRB1_1501  112  RKAENYLISTGIADT  KAENYLIST        0.3895        739.5                32.00      Sequence
DRB1_1501  255  NGKTVTFMPKPLFGD  KTVTFMPKP        0.3888        744.4                32.00      Sequence
DRB1_1501  297  LSDTARHYIGGLLHH  HYIGGLLHH        0.3888        744.9                32.00      Sequence
DRB1_1501  360  KAKRLEFRSPDSSGN  KAKRLEFRS        0.3879        752.4                32.00      Sequence
DRB1_1501  254  QNGKTVTFMPKPLFG  KTVTFMPKP        0.3876        754.9                32.00      Sequence
DRB1_1501  110  IARKAENYLISTGIA  KAENYLIST        0.3874        756.0                32.00      Sequence
DRB1_1501  235  LHAADDMQLYKYIIK  DMQLYKYII        0.3866        763.0                32.00      Sequence
DRB1_1501  276  CHQSLWKDGAPLMYD  SLWKDGAPL        0.3860        767.5                32.00      Sequence
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DRB1_1501   23  RFCDLPGIMQHFTIP  GIMQHFTIP         0.3853         773.9                50.00      Sequence
DRB1_1501  358  NPKAKRLEFRSPDSS  KAKRLEFRS         0.3851         775.5                50.00      Sequence
DRB1_1501  111  ARKAENYLISTGIAD  KAENYLIST         0.3843         781.7                50.00      Sequence
DRB1_1501  359  PKAKRLEFRSPDSSG  KAKRLEFRS         0.3835         788.5                50.00      Sequence
DRB1_1501  113  KAENYLISTGIADTA  KAENYLIST         0.3832         791.4                50.00      Sequence
DRB1_1501  256  GKTVTFMPKPLFGDN  KTVTFMPKP         0.3797         822.2                50.00      Sequence
DRB1_1501  277  HQSLWKDGAPLMYDE  SLWKDGAPL         0.3794         824.3                50.00      Sequence
DRB1_1501  446  LIETWISFKRENEIE  LIETWISFK         0.3783         834.5                50.00      Sequence
DRB1_1501  253  WQNGKTVTFMPKPLF  KTVTFMPKP         0.3774         842.6                50.00      Sequence
DRB1_1501   57  IRGFQSIHESDMLLL  GFQSIHESD         0.3755         859.7                50.00      Sequence
DRB1_1501  149  GSFYEVDAISGWWNT  EVDAISGWW         0.3749         865.8                50.00      Sequence
DRB1_1501  376  YLAFSAMLMAGLDGI  AFSAMLMAG         0.3738         875.6                50.00      Sequence
DRB1_1501  274  MHCHQSLWKDGAPLM  SLWKDGAPL         0.3720         893.5                50.00      Sequence
DRB1_1501   49  GLAFDGSSIRGFQSI  LAFDGSSIR         0.3710         902.5                50.00      Sequence
DRB1_1501  252  AWQNGKTVTFMPKPL  AWQNGKTVT         0.3706         906.6                50.00      Sequence
DRB1_1501  223  GQAEINYQFNSLLHA  EINYQFNSL         0.3698         914.7                50.00      Sequence
DRB1_1501  369  PDSSGNPYLAFSAML  PYLAFSAML         0.3689         923.3                50.00      Sequence
DRB1_1501  439  GGVFTNDLIETWISF  DLIETWISF         0.3678         934.8                50.00      Sequence
DRB1_1501   47  DDGLAFDGSSIRGFQ  LAFDGSSIR         0.3669         943.5                50.00      Sequence
DRB1_1501  322  TVNSYKRLVPGYEAP  TVNSYKRLV         0.3655         958.5                50.00      Sequence
DRB1_1501   48  DGLAFDGSSIRGFQS  LAFDGSSIR         0.3654         959.3                50.00      Sequence
DRB1_1501  340  VYSQRNRSACVRIPI  VYSQRNRSA         0.3644         969.3                50.00      Sequence
DRB1_1501   15  EKVEYVDVRFCDLPG  KVEYVDVRF         0.3639         975.0                50.00      Sequence
DRB1_1501  357  SNPKAKRLEFRSPDS  KAKRLEFRS         0.3638         976.5                50.00      Sequence
DRB1_1501  278  QSLWKDGAPLMYDET  SLWKDGAPL         0.3611        1004.6                50.00      Sequence
DRB1_1501  249  KNTAWQNGKTVTFMP  AWQNGKTVT         0.3593        1024.9                50.00      Sequence
DRB1_1501   46  FDDGLAFDGSSIRGF  LAFDGSSIR         0.3577        1042.4                50.00      Sequence
DRB1_1501  257  KTVTFMPKPLFGDNG  KTVTFMPKP         0.3554        1068.5                50.00      Sequence
DRB1_1501  248  IKNTAWQNGKTVTFM  AWQNGKTVT         0.3526        1102.3                50.00      Sequence
DRB1_1501  227  INYQFNSLLHAADDM  QFNSLLHAA         0.3525        1102.8                50.00      Sequence
DRB1_1501   79  IDPFRAAKTLNINFF  AAKTLNINF         0.3500        1133.7                50.00      Sequence
DRB1_1501  381  AMLMAGLDGIKNKIE  LMAGLDGIK         0.3498        1135.6                50.00      Sequence
DRB1_1501   20  VDVRFCDLPGIMQHF  DVRFCDLPG         0.3481        1156.9                50.00      Sequence
DRB1_1501  457  NEIEPVNIRPHPYEF  EIEPVNIRP         0.3468        1172.9                50.00      Sequence
DRB1_1501  109  NIARKAENYLISTGI  KAENYLIST         0.3422        1232.5                50.00      Sequence
DRB1_1501  458  EIEPVNIRPHPYEFA  EIEPVNIRP         0.3400        1262.3                50.00      Sequence
DRB1_1501  251  TAWQNGKTVTFMPKP  AWQNGKTVT         0.3397        1266.9                50.00      Sequence
DRB1_1501   44  SVFDDGLAFDGSSIR  LAFDGSSIR         0.3385        1282.7                50.00      Sequence
DRB1_1501  273  GMHCHQSLWKDGAPL  SLWKDGAPL         0.3361        1317.1                50.00      Sequence
DRB1_1501  202  LTNLINSGFILEKGH  NLINSGFIL         0.3336        1352.9                50.00      Sequence
DRB1_1501  203  TNLINSGFILEKGHH  NLINSGFIL         0.3332        1359.1                50.00      Sequence
DRB1_1501  250  NTAWQNGKTVTFMPK  AWQNGKTVT         0.3313        1387.0                50.00      Sequence
DRB1_1501  321  PTVNSYKRLVPGYEA  TVNSYKRLV         0.3312        1389.2                50.00      Sequence
DRB1_1501   87  TLNINFFVHDPFTLE  NINFFVHDP         0.3305        1399.5                50.00      Sequence
DRB1_1501  315  LLAFTNPTVNSYKRL  LLAFTNPTV         0.3302        1404.1                50.00      Sequence
DRB1_1501  222  GGQAEINYQFNSLLH  EINYQFNSL         0.3287        1426.7                50.00      Sequence
DRB1_1501   45  VFDDGLAFDGSSIRG  LAFDGSSIR         0.3284        1431.1                50.00      Sequence
DRB1_1501   86  KTLNINFFVHDPFTL  NINFFVHDP         0.3276        1444.3                50.00      Sequence
DRB1_1501  330  VPGYEAPINLVYSQR  PINLVYSQR         0.3261        1467.3                50.00      Sequence
DRB1_1501   83  RAAKTLNINFFVHDP  KTLNINFFV         0.3254        1478.7                50.00      Sequence
DRB1_1501  455  RENEIEPVNIRPHPY  EIEPVNIRP         0.3231        1516.8                50.00      Sequence
DRB1_1501  320  NPTVNSYKRLVPGYE  TVNSYKRLV         0.3227        1523.2                50.00      Sequence
DRB1_1501  380  SAMLMAGLDGIKNKI  AMLMAGLDG         0.3216        1541.6                50.00      Sequence
DRB1_1501  456  ENEIEPVNIRPHPYE  EIEPVNIRP         0.3195        1576.9                50.00      Sequence
DRB1_1501  342  SQRNRSACVRIPITG  ACVRIPITG         0.3189        1587.3                50.00      Sequence
DRB1_1501   16  KVEYVDVRFCDLPGI  KVEYVDVRF         0.3186        1591.3                50.00      Sequence
DRB1_1501  279  SLWKDGAPLMYDETG  SLWKDGAPL         0.3182        1599.2                50.00      Sequence
DRB1_1501  382  MLMAGLDGIKNKIEP  LMAGLDGIK         0.3171        1617.5                50.00      Sequence
DRB1_1501  361  AKRLEFRSPDSSGNP  RLEFRSPDS         0.3171        1618.5                50.00      Sequence
DRB1_1501  108  RNIARKAENYLISTG  AENYLISTG         0.3169        1621.4                50.00      Sequence
DRB1_1501  383  LMAGLDGIKNKIEPQ  LMAGLDGIK         0.3147        1659.8                50.00      Sequence
DRB1_1501  343  QRNRSACVRIPITGS  ACVRIPITG         0.3131        1689.5                50.00      Sequence
DRB1_1501  379  FSAMLMAGLDGIKNK  LMAGLDGIK         0.3130        1691.3                50.00      Sequence
DRB1_1501   84  AAKTLNINFFVHDPF  KTLNINFFV         0.3126        1698.2                50.00      Sequence
DRB1_1501   88  LNINFFVHDPFTLEP  NINFFVHDP         0.3125        1700.9                50.00      Sequence
DRB1_1501   14  DEKVEYVDVRFCDLP  KVEYVDVRF         0.3106        1735.3                50.00      Sequence
DRB1_1501  114  AENYLISTGIADTAY  ENYLISTGI         0.3105        1737.3                50.00      Sequence
DRB1_1501  319  TNPTVNSYKRLVPGY  TVNSYKRLV         0.3096        1755.2                50.00      Sequence
DRB1_1501  194  YVDLRDKMLTNLINS  RDKMLTNLI         0.3095        1756.2                50.00      Sequence
DRB1_1501  454  KRENEIEPVNIRPHP  EIEPVNIRP         0.3088        1770.6                50.00      Sequence
DRB1_1501   19  YVDVRFCDLPGIMQH  DVRFCDLPG         0.3077        1790.5                50.00      Sequence
DRB1_1501  228  NYQFNSLLHAADDMQ  NYQFNSLLH         0.3073        1798.9                50.00      Sequence
DRB1_1501  341  YSQRNRSACVRIPIT  RNRSACVRI         0.3066        1813.4                50.00      Sequence
DRB1_1501   17  VEYVDVRFCDLPGIM  DVRFCDLPG         0.3065        1815.2                50.00      Sequence
DRB1_1501   18  EYVDVRFCDLPGIMQ  DVRFCDLPG         0.3056        1832.4                50.00      Sequence
DRB1_1501   81  PFRAAKTLNINFFVH  AAKTLNINF         0.2980        1988.9                50.00      Sequence
DRB1_1501  204  NLINSGFILEKGHHE  NLINSGFIL         0.2966        2018.7                50.00      Sequence
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DRB1_1501  207  NSGFILEKGHHEVGS  GFILEKGHH        0.2951       2052.0              50.00     Sequence
DRB1_1501  171  GSPNRGYKVRHKGGY  PNRGYKVRH        0.2951       2052.2              50.00     Sequence
DRB1_1501   13  KDEKVEYVDVRFCDL  KVEYVDVRF        0.2938       2082.2              50.00     Sequence
DRB1_1501   58  RGFQSIHESDMLLLP  GFQSIHESD        0.2931       2098.2              50.00     Sequence
DRB1_1501  344  RNRSACVRIPITGSN  ACVRIPITG        0.2928       2103.6              50.00     Sequence
DRB1_1501   85  AKTLNINFFVHDPFT  KTLNINFFV        0.2921       2120.5              50.00     Sequence
DRB1_1501   80  DPFRAAKTLNINFFV  AAKTLNINF        0.2915       2134.8              50.00     Sequence
DRB1_1501  234  LLHAADDMQLYKYII  DMQLYKYII        0.2914       2135.4              50.00     Sequence
DRB1_1501  453  FKRENEIEPVNIRPH  EIEPVNIRP        0.2910       2145.2              50.00     Sequence
DRB1_1501  208  SGFILEKGHHEVGSG  GFILEKGHH        0.2895       2180.2              50.00     Sequence
DRB1_1501   72  PDPETARIDPFRAAK  RIDPFRAAK        0.2894       2182.2              50.00     Sequence
DRB1_1501   82  FRAAKTLNINFFVHD  AAKTLNINF        0.2888       2197.3              50.00     Sequence
DRB1_1501  192  DQYVDLRDKMLTNLI  DLRDKMLTN        0.2886       2201.8              50.00     Sequence
DRB1_1501  131  AEAEFYIFDSVSFDS  EFYIFDSVS        0.2871       2238.0              50.00     Sequence
DRB1_1501  206  INSGFILEKGHHEVG  GFILEKGHH        0.2864       2254.4              50.00     Sequence
DRB1_1501  193  QYVDLRDKMLTNLIN  DLRDKMLTN        0.2864       2255.5              50.00     Sequence
DRB1_1501  356  GSNPKAKRLEFRSPD  KAKRLEFRS        0.2861       2262.5              50.00     Sequence
DRB1_1501  318  FTNPTVNSYKRLVPG  TVNSYKRLV        0.2848       2295.3              50.00     Sequence
DRB1_1501  130  GAEAEFYIFDSVSFD  EFYIFDSVS        0.2824       2355.9              50.00     Sequence
DRB1_1501  132  EAEFYIFDSVSFDSR  EFYIFDSVS        0.2805       2405.0              50.00     Sequence
DRB1_1501  205  LINSGFILEKGHHEV  GFILEKGHH        0.2795       2428.7              50.00     Sequence
DRB1_1501  384  MAGLDGIKNKIEPQA  GLDGIKNKI        0.2792       2437.2              50.00     Sequence
DRB1_1501  107  PRNIARKAENYLIST  IARKAENYL        0.2773       2489.6              50.00     Sequence
DRB1_1501   22  VRFCDLPGIMQHFTI  DLPGIMQHF        0.2771       2493.8              50.00     Sequence
DRB1_1501   12  AKDEKVEYVDVRFCD  KVEYVDVRF        0.2761       2522.3              50.00     Sequence
DRB1_1501   11  LAKDEKVEYVDVRFC  EKVEYVDVR        0.2748       2557.1              50.00     Sequence
DRB1_1501  191  NDQYVDLRDKMLTNL  DLRDKMLTN        0.2731       2604.5              50.00     Sequence
DRB1_1501  447  IETWISFKRENEIEP  IETWISFKR        0.2726       2617.3              50.00     Sequence
DRB1_1501   21  DVRFCDLPGIMQHFT  DVRFCDLPG        0.2709       2668.4              50.00     Sequence
DRB1_1501   89  NINFFVHDPFTLEPY  NINFFVHDP        0.2707       2671.9              50.00     Sequence
DRB1_1501  459  IEPVNIRPHPYEFAL  NIRPHPYEF        0.2706       2674.6              50.00     Sequence
DRB1_1501  129  FGAEAEFYIFDSVSF  EFYIFDSVS        0.2695       2708.5              50.00     Sequence
DRB1_1501  134  EFYIFDSVSFDSRAN  EFYIFDSVS        0.2683       2743.8              50.00     Sequence
DRB1_1501  115  ENYLISTGIADTAYF  ENYLISTGI        0.2666       2794.7              50.00     Sequence
DRB1_1501  284  GAPLMYDETGYAGLS  LMYDETGYA        0.2657       2822.1              50.00     Sequence
DRB1_1501  346  RSACVRIPITGSNPK  ACVRIPITG        0.2649       2844.6              50.00     Sequence
DRB1_1501  271  GSGMHCHQSLWKDGA  GMHCHQSLW        0.2648       2849.4              50.00     Sequence
DRB1_1501  348  ACVRIPITGSNPKAK  ACVRIPITG        0.2645       2858.7              50.00     Sequence
DRB1_1501  347  SACVRIPITGSNPKA  ACVRIPITG        0.2615       2951.1              50.00     Sequence
DRB1_1501  190  PNDQYVDLRDKMLTN  QYVDLRDKM        0.2595       3017.1              50.00     Sequence
DRB1_1501  272  SGMHCHQSLWKDGAP  GMHCHQSLW        0.2591       3030.6              50.00     Sequence
DRB1_1501  148  NGSFYEVDAISGWWN  EVDAISGWW        0.2584       3054.3              50.00     Sequence
DRB1_1501  179  VRHKGGYFPVAPNDQ  RHKGGYFPV        0.2575       3083.7              50.00     Sequence
DRB1_1501  355  TGSNPKAKRLEFRSP  KAKRLEFRS        0.2569       3103.2              50.00     Sequence
DRB1_1501  385  AGLDGIKNKIEPQAP  GLDGIKNKI        0.2545       3183.6              50.00     Sequence
DRB1_1501  460  EPVNIRPHPYEFALY  NIRPHPYEF        0.2538       3209.5              50.00     Sequence
DRB1_1501  317  AFTNPTVNSYKRLVP  TVNSYKRLV        0.2527       3247.2              50.00     Sequence
DRB1_1501  461  PVNIRPHPYEFALYY  NIRPHPYEF        0.2526       3249.7              50.00     Sequence
DRB1_1501  291  ETGYAGLSDTARHYI  GYAGLSDTA        0.2513       3297.0              50.00     Sequence
DRB1_1501  296  GLSDTARHYIGGLLH  TARHYIGGL        0.2512       3300.3              50.00     Sequence
DRB1_1501  283  DGAPLMYDETGYAGL  LMYDETGYA        0.2507       3317.4              50.00     Sequence
DRB1_1501  290  DETGYAGLSDTARHY  GYAGLSDTA        0.2502       3335.6              50.00     Sequence
DRB1_1501  133  AEFYIFDSVSFDSRA  EFYIFDSVS        0.2502       3336.8              50.00     Sequence
DRB1_1501  157  ISGWWNTGAATEADG  ISGWWNTGA        0.2496       3358.0              50.00     Sequence
DRB1_1501  345  NRSACVRIPITGSNP  ACVRIPITG        0.2494       3364.1              50.00     Sequence
DRB1_1501  170  DGSPNRGYKVRHKGG  PNRGYKVRH        0.2491       3377.8              50.00     Sequence
DRB1_1501  270  NGSGMHCHQSLWKDG  GMHCHQSLW        0.2490       3380.4              50.00     Sequence
DRB1_1501  292  TGYAGLSDTARHYIG  GYAGLSDTA        0.2455       3511.9              50.00     Sequence
DRB1_1501  349  CVRIPITGSNPKAKR  VRIPITGSN        0.2449       3534.7              50.00     Sequence
DRB1_1501   10  KLAKDEKVEYVDVRF  KVEYVDVRF        0.2431       3602.8              50.00     Sequence
DRB1_1501  350  VRIPITGSNPKAKRL  RIPITGSNP        0.2427       3616.7              50.00     Sequence
DRB1_1501  463  NIRPHPYEFALYYDV  NIRPHPYEF        0.2418       3653.9              50.00     Sequence
DRB1_1501  289  YDETGYAGLSDTARH  GYAGLSDTA        0.2396       3742.1              50.00     Sequence
DRB1_1501  221  SGGQAEINYQFNSLL  EINYQFNSL        0.2387       3777.2              50.00     Sequence
DRB1_1501  362  KRLEFRSPDSSGNPY  EFRSPDSSG        0.2386       3783.1              50.00     Sequence
DRB1_1501  462  VNIRPHPYEFALYYD  NIRPHPYEF        0.2363       3879.6              50.00     Sequence
DRB1_1501  262  MPKPLFGDNGSGMHC  LFGDNGSGM        0.2361       3885.1              50.00     Sequence
DRB1_1501  128  YFGAEAEFYIFDSVS  EFYIFDSVS        0.2357       3902.5              50.00     Sequence
DRB1_1501  263  PKPLFGDNGSGMHCH  LFGDNGSGM        0.2354       3915.9              50.00     Sequence
DRB1_1501  285  APLMYDETGYAGLSD  LMYDETGYA        0.2344       3959.0              50.00     Sequence
DRB1_1501  269  DNGSGMHCHQSLWKD  GMHCHQSLW        0.2343       3961.7              50.00     Sequence
DRB1_1501  281  WKDGAPLMYDETGYA  LMYDETGYA        0.2342       3964.9              50.00     Sequence
DRB1_1501  287  LMYDETGYAGLSDTA  LMYDETGYA        0.2340       3976.8              50.00     Sequence
DRB1_1501  286  PLMYDETGYAGLSDT  LMYDETGYA        0.2329       4022.3              50.00     Sequence
DRB1_1501  169  ADGSPNRGYKVRHKG  PNRGYKVRH        0.2327       4029.9              50.00     Sequence
DRB1_1501  209  GFILEKGHHEVGSGG  GFILEKGHH        0.2313       4094.4              50.00     Sequence
DRB1_1501   43  KSVFDDGLAFDGSSI  SVFDDGLAF        0.2302       4144.2              50.00     Sequence
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DRB1_1501  264  KPLFGDNGSGMHCHQ  LFGDNGSGM        0.2294       4178.0             50.00     Sequence
DRB1_1501  438  EGGVFTNDLIETWIS  NDLIETWIS        0.2293       4183.3             50.00     Sequence
DRB1_1501  430  EADHEYLTEGGVFTN  EYLTEGGVF        0.2283       4227.9             50.00     Sequence
DRB1_1501  282  KDGAPLMYDETGYAG  LMYDETGYA        0.2279       4245.2             50.00     Sequence
DRB1_1501  316  LAFTNPTVNSYKRLV  TVNSYKRLV        0.2278       4253.2             50.00     Sequence
DRB1_1501  295  AGLSDTARHYIGGLL  TARHYIGGL        0.2274       4267.7             50.00     Sequence
DRB1_1501  431  ADHEYLTEGGVFTND  EYLTEGGVF        0.2259       4341.3             50.00     Sequence
DRB1_1501  260  TFMPKPLFGDNGSGM  LFGDNGSGM        0.2241       4424.6             50.00     Sequence
DRB1_1501   59  GFQSIHESDMLLLPD  QSIHESDML        0.2234       4459.1             50.00     Sequence
DRB1_1501  180  RHKGGYFPVAPNDQY  RHKGGYFPV        0.2226       4498.7             50.00     Sequence
DRB1_1501  432  DHEYLTEGGVFTNDL  EYLTEGGVF        0.2225       4502.0             50.00     Sequence
DRB1_1501  135  FYIFDSVSFDSRANG  SVSFDSRAN        0.2222       4516.2             50.00     Sequence
DRB1_1501  258  TVTFMPKPLFGDNGS  TVTFMPKPL        0.2214       4557.0             50.00     Sequence
DRB1_1501  452  SFKRENEIEPVNIRP  EIEPVNIRP        0.2214       4557.0             50.00     Sequence
DRB1_1501  136  YIFDSVSFDSRANGS  SVSFDSRAN        0.2204       4604.7             50.00     Sequence
DRB1_1501  261  FMPKPLFGDNGSGMH  LFGDNGSGM        0.2195       4650.9             50.00     Sequence
DRB1_1501  168  EADGSPNRGYKVRHK  PNRGYKVRH        0.2187       4689.4             50.00     Sequence
DRB1_1501  106  DPRNIARKAENYLIS  IARKAENYL        0.2180       4728.9             50.00     Sequence
DRB1_1501  386  GLDGIKNKIEPQAPV  GLDGIKNKI        0.2146       4903.6             50.00     Sequence
DRB1_1501  265  PLFGDNGSGMHCHQS  LFGDNGSGM        0.2143       4918.5             50.00     Sequence
DRB1_1501  137  IFDSVSFDSRANGSF  SVSFDSRAN        0.2133       4975.7             50.00     Sequence
DRB1_1501  280  LWKDGAPLMYDETGY  LWKDGAPLM        0.2132       4980.7             50.00     Sequence
DRB1_1501  433  HEYLTEGGVFTNDLI  EYLTEGGVF        0.2105       5125.9             50.00     Sequence
DRB1_1501  189  APNDQYVDLRDKMLT  QYVDLRDKM        0.2093       5194.6             50.00     Sequence
DRB1_1501  351  RIPITGSNPKAKRLE  RIPITGSNP        0.2091       5204.7             50.00     Sequence
DRB1_1501  363  RLEFRSPDSSGNPYL  EFRSPDSSG        0.2088       5222.8             50.00     Sequence
DRB1_1501  293  GYAGLSDTARHYIGG  AGLSDTARH        0.2073       5305.9             50.00     Sequence
DRB1_1501  268  GDNGSGMHCHQSLWK  GMHCHQSLW        0.2062       5368.5             50.00     Sequence
DRB1_1501   64  HESDMLLLPDPETAR  DMLLLPDPE        0.2057       5402.5             50.00     Sequence
DRB1_1501   63  IHESDMLLLPDPETA  DMLLLPDPE        0.2043       5482.8             50.00     Sequence
DRB1_1501  423  SDVIDRLEADHEYLT  VIDRLEADH        0.2010       5681.4             50.00     Sequence
DRB1_1501  266  LFGDNGSGMHCHQSL  LFGDNGSGM        0.2006       5709.4             50.00     Sequence
DRB1_1501   61  QSIHESDMLLLPDPE  QSIHESDML        0.2002       5732.9             50.00     Sequence
DRB1_1501  138  FDSVSFDSRANGSFY  SVSFDSRAN        0.1987       5822.8             50.00     Sequence
DRB1_1501  229  YQFNSLLHAADDMQL  QFNSLLHAA        0.1982       5859.2             50.00     Sequence
DRB1_1501  105  RDPRNIARKAENYLI  IARKAENYL        0.1966       5958.6             50.00     Sequence
DRB1_1501  434  EYLTEGGVFTNDLIE  EYLTEGGVF        0.1954       6038.5             50.00     Sequence
DRB1_1501  294  YAGLSDTARHYIGGL  TARHYIGGL        0.1928       6207.4             50.00     Sequence
DRB1_1501  288  MYDETGYAGLSDTAR  GYAGLSDTA        0.1912       6313.9             50.00     Sequence
DRB1_1501  422  LSDVIDRLEADHEYL  VIDRLEADH        0.1900       6397.0             50.00     Sequence
DRB1_1501   62  SIHESDMLLLPDPET  DMLLLPDPE        0.1900       6401.9             50.00     Sequence
DRB1_1501  139  DSVSFDSRANGSFYE  SVSFDSRAN        0.1889       6475.9             50.00     Sequence
DRB1_1501   90  INFFVHDPFTLEPYS  INFFVHDPF        0.1879       6544.0             50.00     Sequence
DRB1_1501  424  DVIDRLEADHEYLTE  VIDRLEADH        0.1862       6667.5             50.00     Sequence
DRB1_1501  448  ETWISFKRENEIEPV  TWISFKREN        0.1853       6736.3             50.00     Sequence
DRB1_1501   40  AFDKSVFDDGLAFDG  KSVFDDGLA        0.1834       6874.8             50.00     Sequence
DRB1_1501  124  ADTAYFGAEAEFYIF  DTAYFGAEA        0.1829       6907.5             50.00     Sequence
DRB1_1501  167  TEADGSPNRGYKVRH  PNRGYKVRH        0.1827       6925.0             50.00     Sequence
DRB1_1501  116  NYLISTGIADTAYFG  NYLISTGIA        0.1820       6980.7             50.00     Sequence
DRB1_1501  387  LDGIKNKIEPQAPVD  GIKNKIEPQ        0.1813       7028.7             50.00     Sequence
DRB1_1501   42  DKSVFDDGLAFDGSS  SVFDDGLAF        0.1813       7030.0             50.00     Sequence
DRB1_1501  429  LEADHEYLTEGGVFT  EYLTEGGVF        0.1806       7083.9             50.00     Sequence
DRB1_1501  449  TWISFKRENEIEPVN  TWISFKREN        0.1803       7110.4             50.00     Sequence
DRB1_1501   65  ESDMLLLPDPETARI  LLLPDPETA        0.1797       7157.7             50.00     Sequence
DRB1_1501  352  IPITGSNPKAKRLEF  IPITGSNPK        0.1787       7231.7             50.00     Sequence
DRB1_1501   38  ASAFDKSVFDDGLAF  SVFDDGLAF        0.1784       7256.2             50.00     Sequence
DRB1_1501   39  SAFDKSVFDDGLAFD  SVFDDGLAF        0.1780       7285.8             50.00     Sequence
DRB1_1501  123  IADTAYFGAEAEFYI  DTAYFGAEA        0.1775       7323.2             50.00     Sequence
DRB1_1501   60  FQSIHESDMLLLPDP  QSIHESDML        0.1767       7391.8             50.00     Sequence
DRB1_1501  147  ANGSFYEVDAISGWW  EVDAISGWW        0.1764       7415.0             50.00     Sequence
DRB1_1501  122  GIADTAYFGAEAEFY  DTAYFGAEA        0.1759       7457.1             50.00     Sequence
DRB1_1501  259  VTFMPKPLFGDNGSG  VTFMPKPLF        0.1752       7509.1             50.00     Sequence
DRB1_1501  220  GSGGQAEINYQFNSL  EINYQFNSL        0.1752       7514.7             50.00     Sequence
DRB1_1501  233  SLLHAADDMQLYKYI  SLLHAADDM        0.1751       7521.8             50.00     Sequence
DRB1_1501  436  LTEGGVFTNDLIETW  LTEGGVFTN        0.1742       7595.5             50.00     Sequence
DRB1_1501  210  FILEKGHHEVGSGGQ  ILEKGHHEV        0.1741       7602.5             50.00     Sequence
DRB1_1501   71  LPDPETARIDPFRAA  ARIDPFRAA        0.1736       7639.7             50.00     Sequence
DRB1_1501   31  MQHFTIPASAFDKSV  HFTIPASAF        0.1720       7771.8             50.00     Sequence
DRB1_1501   66  SDMLLLPDPETARID  LLLPDPETA        0.1703       7922.9             50.00     Sequence
DRB1_1501  425  VIDRLEADHEYLTEG  VIDRLEADH        0.1696       7978.6             50.00     Sequence
DRB1_1501  421  QLSDVIDRLEADHEY  VIDRLEADH        0.1690       8032.5             50.00     Sequence
DRB1_1501  435  YLTEGGVFTNDLIET  LTEGGVFTN        0.1687       8060.0             50.00     Sequence
DRB1_1501  267  FGDNGSGMHCHQSLW  GMHCHQSLW        0.1679       8131.3             50.00     Sequence
DRB1_1501  389  GIKNKIEPQAPVDKD  KIEPQAPVD        0.1678       8133.1             50.00     Sequence
DRB1_1501   41  FDKSVFDDGLAFDGS  SVFDDGLAF        0.1673       8177.5             50.00     Sequence
DRB1_1501    9  FKLAKDEKVEYVDVR  EKVEYVDVR        0.1660       8300.3             50.00     Sequence
DRB1_1501  188  VAPNDQYVDLRDKML  QYVDLRDKM        0.1644       8439.7             50.00     Sequence
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    DRB1_1501  230  QFNSLLHAADDMQLY  QFNSLLHAA         0.1625       8614.5                  50.00     Sequence
    DRB1_1501  388  DGIKNKIEPQAPVDK  KIEPQAPVD         0.1622       8648.4                  50.00     Sequence
    DRB1_1501  420  TQLSDVIDRLEADHE  VIDRLEADH         0.1607       8786.1                  50.00     Sequence
    DRB1_1501  104  SRDPRNIARKAENYL  IARKAENYL         0.1603       8824.8                  50.00     Sequence
    DRB1_1501  146  RANGSFYEVDAISGW  RANGSFYEV         0.1592       8935.4                  50.00     Sequence
    DRB1_1501  211  ILEKGHHEVGSGGQA  ILEKGHHEV         0.1587       8976.4                  50.00     Sequence
    DRB1_1501  368  SPDSSGNPYLAFSAM  GNPYLAFSA         0.1586       8989.5                  50.00     Sequence
    DRB1_1501  354  ITGSNPKAKRLEFRS  KAKRLEFRS         0.1582       9030.4                  50.00     Sequence
    DRB1_1501  127  AYFGAEAEFYIFDSV  AEFYIFDSV         0.1575       9093.4                  50.00     Sequence
    DRB1_1501  451  ISFKRENEIEPVNIR  SFKRENEIE         0.1569       9152.3                  50.00     Sequence
    DRB1_1501    6  DDVFKLAKDEKVEYV  VFKLAKDEK         0.1555       9298.1                  50.00     Sequence
    DRB1_1501    5  PDDVFKLAKDEKVEY  VFKLAKDEK         0.1549       9351.4                  50.00     Sequence
    DRB1_1501  437  TEGGVFTNDLIETWI  GGVFTNDLI         0.1517       9681.1                  50.00     Sequence
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    DRB1_1501  181  HKGGYFPVAPNDQYV  HKGGYFPVA         0.1495       9916.5                  50.00     Sequence
    DRB1_1501   67  DMLLLPDPETARIDP  DMLLLPDPE         0.1495       9918.2                  50.00     Sequence
    DRB1_1501  212  LEKGHHEVGSGGQAE  EVGSGGQAE         0.1491       9958.9                  50.00     Sequence
    DRB1_1501  215  GHHEVGSGGQAEINY  HEVGSGGQA         0.1482      10056.8                  50.00     Sequence
    DRB1_1501   97  PFTLEPYSRDPRNIA  LEPYSRDPR         0.1480      10076.1                  50.00     Sequence
    DRB1_1501   37  PASAFDKSVFDDGLA  AFDKSVFDD         0.1480      10080.0                  50.00     Sequence
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    DRB1_1501  390  IKNKIEPQAPVDKDL  KIEPQAPVD         0.1470      10193.1                  50.00     Sequence
    DRB1_1501  391  KNKIEPQAPVDKDLY  KIEPQAPVD         0.1464      10256.0                  50.00     Sequence
    DRB1_1501  419  PTQLSDVIDRLEADH  VIDRLEADH         0.1461      10295.1                  50.00     Sequence
    DRB1_1501  125  DTAYFGAEAEFYIFD  DTAYFGAEA         0.1457      10330.7                  50.00     Sequence
    DRB1_1501  428  RLEADHEYLTEGGVF  EYLTEGGVF         0.1455      10355.2                  50.00     Sequence
    DRB1_1501  145  SRANGSFYEVDAISG  RANGSFYEV         0.1444      10484.8                  50.00     Sequence
    DRB1_1501    7  DVFKLAKDEKVEYVD  VFKLAKDEK         0.1439      10537.2                  50.00     Sequence
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    DRB1_1501   70  LLPDPETARIDPFRA  LLPDPETAR         0.1424      10705.8                  50.00     Sequence
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    DRB1_1501  213  EKGHHEVGSGGQAEI  HEVGSGGQA         0.1414      10822.8                  50.00     Sequence
    DRB1_1501   92  FFVHDPFTLEPYSRD  FFVHDPFTL         0.1396      11042.1                  50.00     Sequence
    DRB1_1501   98  FTLEPYSRDPRNIAR  TLEPYSRDP         0.1395      11049.0                  50.00     Sequence
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    DRB1_1501   36  IPASAFDKSVFDDGL  ASAFDKSVF         0.1375      11295.6                  50.00     Sequence
    DRB1_1501   94  VHDPFTLEPYSRDPR  LEPYSRDPR         0.1357      11517.4                  50.00     Sequence
    DRB1_1501  144  DSRANGSFYEVDAIS  SFYEVDAIS         0.1357      11522.0                  50.00     Sequence
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    DRB1_1501  450  WISFKRENEIEPVNI  ISFKRENEI         0.1335      11793.1                  50.00     Sequence
    DRB1_1501  217  HEVGSGGQAEINYQF  HEVGSGGQA         0.1332      11835.2                  50.00     Sequence
    DRB1_1501  117  YLISTGIADTAYFGA  YLISTGIAD         0.1329      11876.4                  50.00     Sequence
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    DRB1_1501  392  NKIEPQAPVDKDLYE  KIEPQAPVD         0.1312      12094.4                  50.00     Sequence
    DRB1_1501    4  TPDDVFKLAKDEKVE  VFKLAKDEK         0.1300      12253.6                  50.00     Sequence
    DRB1_1501   32  QHFTIPASAFDKSVF  HFTIPASAF         0.1284      12461.6                  50.00     Sequence
    DRB1_1501   68  MLLLPDPETARIDPF  LLLPDPETA         0.1279      12536.2                  50.00     Sequence
    DRB1_1501  103  YSRDPRNIARKAENY  RNIARKAEN         0.1270      12652.1                  50.00     Sequence
    DRB1_1501   93  FVHDPFTLEPYSRDP  FVHDPFTLE         0.1269      12667.7                  50.00     Sequence
    DRB1_1501  118  LISTGIADTAYFGAE  LISTGIADT         0.1267      12700.3                  50.00     Sequence
    DRB1_1501  120  STGIADTAYFGAEAE  DTAYFGAEA         0.1251      12909.0                  50.00     Sequence
    DRB1_1501    8  VFKLAKDEKVEYVDV  VFKLAKDEK         0.1245      12997.2                  50.00     Sequence
    DRB1_1501  158  SGWWNTGAATEADGS  GWWNTGAAT         0.1245      13000.0                  50.00     Sequence
    DRB1_1501   34  FTIPASAFDKSVFDD  ASAFDKSVF         0.1244      13013.9                  50.00     Sequence
    DRB1_1501  353  PITGSNPKAKRLEFR  PITGSNPKA         0.1222      13330.6                  50.00     Sequence
    DRB1_1501  187  PVAPNDQYVDLRDKM  QYVDLRDKM         0.1212      13471.4                  50.00     Sequence
    DRB1_1501  367  RSPDSSGNPYLAFSA  GNPYLAFSA         0.1207      13541.8                  50.00     Sequence
    DRB1_1501  418  TPTQLSDVIDRLEAD  QLSDVIDRL         0.1206      13562.4                  50.00     Sequence
    DRB1_1501    3  KTPDDVFKLAKDEKV  VFKLAKDEK         0.1188      13824.9                  50.00     Sequence
    DRB1_1501  364  LEFRSPDSSGNPYLA  EFRSPDSSG         0.1185      13869.2                  50.00     Sequence
    DRB1_1501  141  VSFDSRANGSFYEVD  SFDSRANGS         0.1181      13930.2                  50.00     Sequence
    DRB1_1501  166  ATEADGSPNRGYKVR  SPNRGYKVR         0.1161      14239.0                  50.00     Sequence
    DRB1_1501  100  LEPYSRDPRNIARKA  LEPYSRDPR         0.1140      14567.8                  50.00     Sequence
    DRB1_1501  143  FDSRANGSFYEVDAI  ANGSFYEVD         0.1140      14571.6                  50.00     Sequence
    DRB1_1501   69  LLLPDPETARIDPFR  LLPDPETAR         0.1137      14606.4                  50.00     Sequence
    DRB1_1501  417  QTPTQLSDVIDRLEA  QLSDVIDRL         0.1128      14762.4                  50.00     Sequence
    DRB1_1501   33  HFTIPASAFDKSVFD  HFTIPASAF         0.1117      14934.4                  50.00     Sequence
    DRB1_1501  416  PQTPTQLSDVIDRLE  TQLSDVIDR         0.1114      14975.1                  50.00     Sequence
    DRB1_1501  218  EVGSGGQAEINYQFN  EVGSGGQAE         0.1105      15129.3                  50.00     Sequence
    DRB1_1501  126  TAYFGAEAEFYIFDS  AYFGAEAEF         0.1105      15134.2                  50.00     Sequence
    DRB1_1501  142  SFDSRANGSFYEVDA  RANGSFYEV         0.1103      15161.7                  50.00     Sequence
    DRB1_1501  102  PYSRDPRNIARKAEN  RNIARKAEN         0.1079      15555.4                  50.00     Sequence
    DRB1_1501  101  EPYSRDPRNIARKAE  YSRDPRNIA         0.1032      16369.9                  50.00     Sequence
    DRB1_1501  415  IPQTPTQLSDVIDRL  TPTQLSDVI         0.1030      16397.7                  50.00     Sequence
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   DRB1_1501  119  ISTGIADTAYFGAEA  DTAYFGAEA        0.1015      16666.4                  50.00     Sequence
   DRB1_1501  365  EFRSPDSSGNPYLAF  EFRSPDSSG        0.1001      16934.3                  50.00     Sequence
   DRB1_1501  396  PQAPVDKDLYELPPE  VDKDLYELP        0.0986      17208.2                  50.00     Sequence
   DRB1_1501  219  VGSGGQAEINYQFNS  AEINYQFNS        0.0975      17407.3                  50.00     Sequence
   DRB1_1501  397  QAPVDKDLYELPPEE  VDKDLYELP        0.0964      17627.7                  50.00     Sequence
   DRB1_1501  231  FNSLLHAADDMQLYK  SLLHAADDM        0.0960      17690.0                  50.00     Sequence
   DRB1_1501  395  EPQAPVDKDLYELPP  VDKDLYELP        0.0948      17920.4                  50.00     Sequence
   DRB1_1501  398  APVDKDLYELPPEEA  VDKDLYELP        0.0943      18015.7                  50.00     Sequence
   DRB1_1501  393  KIEPQAPVDKDLYEL  KIEPQAPVD        0.0935      18179.0                  50.00     Sequence
   DRB1_1501  165  AATEADGSPNRGYKV  ATEADGSPN        0.0925      18386.9                  50.00     Sequence
   DRB1_1501  159  GWWNTGAATEADGSP  GWWNTGAAT        0.0917      18543.3                  50.00     Sequence
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   DRB1_1501  394  IEPQAPVDKDLYELP  VDKDLYELP        0.0894      18999.9                  50.00     Sequence
   DRB1_1501  400  VDKDLYELPPEEAAS  KDLYELPPE        0.0886      19171.7                  50.00     Sequence
   DRB1_1501  182  KGGYFPVAPNDQYVD  GGYFPVAPN        0.0878      19333.9                  50.00     Sequence
   DRB1_1501    2  EKTPDDVFKLAKDEK  VFKLAKDEK        0.0871      19474.8                  50.00     Sequence
   DRB1_1501  401  DKDLYELPPEEAASI  ELPPEEAAS        0.0853      19863.8                  50.00     Sequence
   DRB1_1501  402  KDLYELPPEEAASIP  ELPPEEAAS        0.0816      20674.7                  50.00     Sequence
   DRB1_1501  403  DLYELPPEEAASIPQ  ELPPEEAAS        0.0813      20744.0                  50.00     Sequence
   DRB1_1501  164  GAATEADGSPNRGYK  ATEADGSPN        0.0808      20866.7                  50.00     Sequence
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   DRB1_1501  404  LYELPPEEAASIPQT  ELPPEEAAS        0.0781      21483.8                  50.00     Sequence
   DRB1_1501  183  GGYFPVAPNDQYVDL  GGYFPVAPN        0.0775      21615.4                  50.00     Sequence
   DRB1_1501  186  FPVAPNDQYVDLRDK  PVAPNDQYV        0.0772      21688.4                  50.00     Sequence
   DRB1_1501  427  DRLEADHEYLTEGGV  RLEADHEYL        0.0766      21824.3                  50.00     Sequence
   DRB1_1501  405  YELPPEEAASIPQTP  ELPPEEAAS        0.0751      22194.8                  50.00     Sequence
   DRB1_1501  163  TGAATEADGSPNRGY  ATEADGSPN        0.0729      22719.1                  50.00     Sequence
   DRB1_1501  366  FRSPDSSGNPYLAFS  RSPDSSGNP        0.0694      23586.3                  50.00     Sequence
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   DRB1_1501  406  ELPPEEAASIPQTPT  ELPPEEAAS        0.0678      24012.7                  50.00     Sequence
   DRB1_1501  412  AASIPQTPTQLSDVI  ASIPQTPTQ        0.0670      24208.9                  50.00     Sequence
   DRB1_1501  184  GYFPVAPNDQYVDLR  PVAPNDQYV        0.0669      24251.1                  50.00     Sequence
   DRB1_1501  162  NTGAATEADGSPNRG  ATEADGSPN        0.0620      25556.8                  50.00     Sequence
   DRB1_1501  413  ASIPQTPTQLSDVID  ASIPQTPTQ        0.0620      25557.7                  50.00     Sequence
   DRB1_1501  411  EAASIPQTPTQLSDV  ASIPQTPTQ        0.0619      25598.9                  50.00     Sequence
   DRB1_1501  409  PEEAASIPQTPTQLS  ASIPQTPTQ        0.0615      25704.1                  50.00     Sequence
   DRB1_1501    1  TEKTPDDVFKLAKDE  DVFKLAKDE        0.0608      25908.2                  50.00     Sequence
   DRB1_1501  410  EEAASIPQTPTQLSD  ASIPQTPTQ        0.0596      26231.7                  50.00     Sequence
   DRB1_1501  161  WNTGAATEADGSPNR  ATEADGSPN        0.0580      26683.2                  50.00     Sequence
   DRB1_1501  408  PPEEAASIPQTPTQL  ASIPQTPTQ        0.0531      28153.3                  50.00     Sequence
   DRB1_1501  160  WWNTGAATEADGSPN  ATEADGSPN        0.0518      28550.9                  50.00     Sequence
   DRB1_1501  407  LPPEEAASIPQTPTQ  ASIPQTPTQ        0.0490      29438.3                  50.00     Sequence
   DRB1_1501    0  VTEKTPDDVFKLAKD  KTPDDVFKL        0.0443      30944.6                  50.00     Sequence
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Allele: DRB1_1501. Number of high binders 14. Number of weak binders 73. Number of peptides 464

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB3_0101  146  RANGSFYEVDAISGW  YEVDAISGW        0.6292         55.3          WB     0.80     Sequence
   DRB3_0101  147  ANGSFYEVDAISGWW  YEVDAISGW        0.6153         64.2          WB     0.80     Sequence
   DRB3_0101  423  SDVIDRLEADHEYLT  LEADHEYLT        0.6109         67.4          WB     1.00     Sequence
   DRB3_0101  148  NGSFYEVDAISGWWN  YEVDAISGW        0.6059         71.1          WB     1.00     Sequence
   DRB3_0101  424  DVIDRLEADHEYLTE  LEADHEYLT        0.6048         72.0          WB     1.00     Sequence
   DRB3_0101  425  VIDRLEADHEYLTEG  LEADHEYLT        0.5951         79.9          WB     1.00     Sequence
   DRB3_0101  232  NSLLHAADDMQLYKY  HAADDMQLY        0.5917         82.9          WB     2.00     Sequence
   DRB3_0101   97  PFTLEPYSRDPRNIA  YSRDPRNIA        0.5911         83.5          WB     2.00     Sequence
   DRB3_0101  231  FNSLLHAADDMQLYK  HAADDMQLY        0.5899         84.5          WB     2.00     Sequence
   DRB3_0101  230  QFNSLLHAADDMQLY  HAADDMQLY        0.5881         86.2          WB     2.00     Sequence
   DRB3_0101  233  SLLHAADDMQLYKYI  HAADDMQLY        0.5871         87.2          WB     2.00     Sequence
   DRB3_0101   98  FTLEPYSRDPRNIAR  YSRDPRNIA        0.5841         90.1          WB     2.00     Sequence
   DRB3_0101  149  GSFYEVDAISGWWNT  YEVDAISGW        0.5770         97.2          WB     2.00     Sequence
   DRB3_0101   87  TLNINFFVHDPFTLE  FVHDPFTLE        0.5715        103.2          WB     2.00     Sequence
   DRB3_0101  426  IDRLEADHEYLTEGG  LEADHEYLT        0.5703        104.5          WB     2.00     Sequence
   DRB3_0101   99  TLEPYSRDPRNIARK  YSRDPRNIA        0.5700        104.8          WB     2.00     Sequence
   DRB3_0101  234  LLHAADDMQLYKYII  HAADDMQLY        0.5669        108.4          WB     2.00     Sequence
   DRB3_0101  123  IADTAYFGAEAEFYI  FGAEAEFYI        0.5630        113.0          WB     2.00     Sequence
   DRB3_0101  436  LTEGGVFTNDLIETW  FTNDLIETW        0.5599        117.0          WB     2.00     Sequence
   DRB3_0101  437  TEGGVFTNDLIETWI  FTNDLIETW        0.5587        118.5          WB     2.00     Sequence
   DRB3_0101  124  ADTAYFGAEAEFYIF  FGAEAEFYI        0.5576        119.9          WB     2.00     Sequence
   DRB3_0101  235  LHAADDMQLYKYIIK  HAADDMQLY        0.5517        127.8          WB     2.00     Sequence
   DRB3_0101  438  EGGVFTNDLIETWIS  FTNDLIETW        0.5497        130.5          WB     2.00     Sequence
   DRB3_0101  100  LEPYSRDPRNIARKA  YSRDPRNIA        0.5489        131.7          WB     2.00     Sequence
   DRB3_0101   88  LNINFFVHDPFTLEP  FVHDPFTLE        0.5403        144.6          WB     2.00     Sequence
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DRB3_0101  427  DRLEADHEYLTEGGV  LEADHEYLT         0.5402         144.8          WB     2.00      Sequence
DRB3_0101  439  GGVFTNDLIETWISF  FTNDLIETW         0.5388         147.0          WB     2.00      Sequence
DRB3_0101  125  DTAYFGAEAEFYIFD  FGAEAEFYI         0.5381         148.1          WB     2.00      Sequence
DRB3_0101  150  SFYEVDAISGWWNTG  YEVDAISGW         0.5355         152.3          WB     2.00      Sequence
DRB3_0101   46  FDDGLAFDGSSIRGF  FDGSSIRGF         0.5260         168.8          WB     4.00      Sequence
DRB3_0101  101  EPYSRDPRNIARKAE  YSRDPRNIA         0.5246         171.4          WB     4.00      Sequence
DRB3_0101  428  RLEADHEYLTEGGVF  LEADHEYLT         0.5237         173.0          WB     4.00      Sequence
DRB3_0101  236  HAADDMQLYKYIIKN  HAADDMQLY         0.5230         174.3          WB     4.00      Sequence
DRB3_0101  151  FYEVDAISGWWNTGA  YEVDAISGW         0.5176         184.9          WB     4.00      Sequence
DRB3_0101  130  GAEAEFYIFDSVSFD  YIFDSVSFD         0.5154         189.2          WB     4.00      Sequence
DRB3_0101   47  DDGLAFDGSSIRGFQ  FDGSSIRGF         0.5145         191.0          WB     4.00      Sequence
DRB3_0101  440  GVFTNDLIETWISFK  FTNDLIETW         0.5104         199.9          WB     4.00      Sequence
DRB3_0101  102  PYSRDPRNIARKAEN  YSRDPRNIA         0.5099         201.0          WB     4.00      Sequence
DRB3_0101   89  NINFFVHDPFTLEPY  FVHDPFTLE         0.5028         217.0          WB     4.00      Sequence
DRB3_0101   48  DGLAFDGSSIRGFQS  FDGSSIRGF         0.5021         218.6          WB     4.00      Sequence
DRB3_0101  126  TAYFGAEAEFYIFDS  FGAEAEFYI         0.5002         223.2          WB     4.00      Sequence
DRB3_0101  441  VFTNDLIETWISFKR  FTNDLIETW         0.4908         247.1          WB     4.00      Sequence
DRB3_0101  429  LEADHEYLTEGGVFT  LEADHEYLT         0.4905         247.9          WB     4.00      Sequence
DRB3_0101   49  GLAFDGSSIRGFQSI  FDGSSIRGF         0.4884         253.5          WB     4.00      Sequence
DRB3_0101  131  AEAEFYIFDSVSFDS  YIFDSVSFD         0.4865         258.7          WB     4.00      Sequence
DRB3_0101  129  FGAEAEFYIFDSVSF  FGAEAEFYI         0.4832         268.1          WB     4.00      Sequence
DRB3_0101  127  AYFGAEAEFYIFDSV  FGAEAEFYI         0.4781         283.5          WB     4.00      Sequence
DRB3_0101  103  YSRDPRNIARKAENY  YSRDPRNIA         0.4748         293.7          WB     4.00      Sequence
DRB3_0101  152  YEVDAISGWWNTGAA  YEVDAISGW         0.4732         299.0          WB     4.00      Sequence
DRB3_0101   90  INFFVHDPFTLEPYS  FVHDPFTLE         0.4552         363.0          WB     8.00      Sequence
DRB3_0101   50  LAFDGSSIRGFQSIH  FDGSSIRGF         0.4547         364.9          WB     8.00      Sequence
DRB3_0101  442  FTNDLIETWISFKRE  FTNDLIETW         0.4532         371.2          WB     8.00      Sequence
DRB3_0101  132  EAEFYIFDSVSFDSR  YIFDSVSFD         0.4511         379.4          WB     8.00      Sequence
DRB3_0101  128  YFGAEAEFYIFDSVS  FGAEAEFYI         0.4422         417.9          WB     8.00      Sequence
DRB3_0101   86  KTLNINFFVHDPFTL  FFVHDPFTL         0.4210         525.5                 8.00      Sequence
DRB3_0101   91  NFFVHDPFTLEPYSR  FVHDPFTLE         0.4187         538.8                 8.00      Sequence
DRB3_0101   51  AFDGSSIRGFQSIHE  FDGSSIRGF         0.4165         551.8                 8.00      Sequence
DRB3_0101  276  CHQSLWKDGAPLMYD  WKDGAPLMY         0.4097         594.1                 8.00      Sequence
DRB3_0101  281  WKDGAPLMYDETGYA  LMYDETGYA         0.4090         598.8                 8.00      Sequence
DRB3_0101  275  HCHQSLWKDGAPLMY  WKDGAPLMY         0.4081         604.1                 8.00      Sequence
DRB3_0101  133  AEFYIFDSVSFDSRA  YIFDSVSFD         0.4046         627.5                 8.00      Sequence
DRB3_0101    5  PDDVFKLAKDEKVEY  FKLAKDEKV         0.4037         633.6                 8.00      Sequence
DRB3_0101   92  FFVHDPFTLEPYSRD  FVHDPFTLE         0.3998         661.0                 8.00      Sequence
DRB3_0101  277  HQSLWKDGAPLMYDE  WKDGAPLMY         0.3984         671.6                 8.00      Sequence
DRB3_0101    3  KTPDDVFKLAKDEKV  FKLAKDEKV         0.3970         681.2                 8.00      Sequence
DRB3_0101   52  FDGSSIRGFQSIHES  FDGSSIRGF         0.3905         731.6                 8.00      Sequence
DRB3_0101  278  QSLWKDGAPLMYDET  LWKDGAPLM         0.3855         771.8                 8.00      Sequence
DRB3_0101    6  DDVFKLAKDEKVEYV  FKLAKDEKV         0.3850         776.2                 8.00      Sequence
DRB3_0101  312  APSLLAFTNPTVNSY  FTNPTVNSY         0.3849         776.6                 8.00      Sequence
DRB3_0101   40  AFDKSVFDDGLAFDG  SVFDDGLAF         0.3824         798.0                 8.00      Sequence
DRB3_0101  313  PSLLAFTNPTVNSYK  FTNPTVNSY         0.3808         812.0                 8.00      Sequence
DRB3_0101    7  DVFKLAKDEKVEYVD  FKLAKDEKV         0.3805         815.2                 8.00      Sequence
DRB3_0101  279  SLWKDGAPLMYDETG  LWKDGAPLM         0.3793         825.2                 8.00      Sequence
DRB3_0101  134  EFYIFDSVSFDSRAN  YIFDSVSFD         0.3747         867.5                16.00      Sequence
DRB3_0101  316  LAFTNPTVNSYKRLV  FTNPTVNSY         0.3738         875.5                16.00      Sequence
DRB3_0101  282  KDGAPLMYDETGYAG  LMYDETGYA         0.3737         877.1                16.00      Sequence
DRB3_0101    4  TPDDVFKLAKDEKVE  FKLAKDEKV         0.3734         879.6                16.00      Sequence
DRB3_0101  314  SLLAFTNPTVNSYKR  FTNPTVNSY         0.3701         911.3                16.00      Sequence
DRB3_0101   57  IRGFQSIHESDMLLL  FQSIHESDM         0.3692         920.7                16.00      Sequence
DRB3_0101  283  DGAPLMYDETGYAGL  LMYDETGYA         0.3675         938.0                16.00      Sequence
DRB3_0101    8  VFKLAKDEKVEYVDV  FKLAKDEKV         0.3671         941.7                16.00      Sequence
DRB3_0101  315  LLAFTNPTVNSYKRL  FTNPTVNSY         0.3663         949.7                16.00      Sequence
DRB3_0101   38  ASAFDKSVFDDGLAF  SVFDDGLAF         0.3631         983.7                16.00      Sequence
DRB3_0101   58  RGFQSIHESDMLLLP  FQSIHESDM         0.3620         995.7                16.00      Sequence
DRB3_0101   41  FDKSVFDDGLAFDGS  SVFDDGLAF         0.3601        1016.5                16.00      Sequence
DRB3_0101   39  SAFDKSVFDDGLAFD  SVFDDGLAF         0.3598        1019.1                16.00      Sequence
DRB3_0101   44  SVFDDGLAFDGSSIR  LAFDGSSIR         0.3534        1092.8                16.00      Sequence
DRB3_0101  317  AFTNPTVNSYKRLVP  FTNPTVNSY         0.3527        1100.9                16.00      Sequence
DRB3_0101  303  HYIGGLLHHAPSLLA  LLHHAPSLL         0.3516        1113.8                16.00      Sequence
DRB3_0101  135  FYIFDSVSFDSRANG  YIFDSVSFD         0.3494        1140.9                16.00      Sequence
DRB3_0101  280  LWKDGAPLMYDETGY  LWKDGAPLM         0.3483        1153.9                16.00      Sequence
DRB3_0101  183  GGYFPVAPNDQYVDL  FPVAPNDQY         0.3458        1185.4                16.00      Sequence
DRB3_0101   59  GFQSIHESDMLLLPD  FQSIHESDM         0.3456        1188.0                16.00      Sequence
DRB3_0101  274  MHCHQSLWKDGAPLM  LWKDGAPLM         0.3452        1193.6                16.00      Sequence
DRB3_0101  284  GAPLMYDETGYAGLS  LMYDETGYA         0.3446        1201.9                16.00      Sequence
DRB3_0101  302  RHYIGGLLHHAPSLL  LLHHAPSLL         0.3432        1220.4                16.00      Sequence
DRB3_0101  182  KGGYFPVAPNDQYVD  FPVAPNDQY         0.3420        1235.9                16.00      Sequence
DRB3_0101  304  YIGGLLHHAPSLLAF  LLHHAPSLL         0.3404        1257.2                16.00      Sequence
DRB3_0101    9  FKLAKDEKVEYVDVR  FKLAKDEKV         0.3395        1270.2                16.00      Sequence
DRB3_0101  180  RHKGGYFPVAPNDQY  FPVAPNDQY         0.3385        1282.9                16.00      Sequence
DRB3_0101  122  GIADTAYFGAEAEFY  YFGAEAEFY         0.3357        1322.8                16.00      Sequence
DRB3_0101  181  HKGGYFPVAPNDQYV  FPVAPNDQY         0.3350        1332.5                16.00      Sequence
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DRB3_0101  184  GYFPVAPNDQYVDLR  FPVAPNDQY         0.3294        1416.7                 16.00      Sequence
DRB3_0101   56  SIRGFQSIHESDMLL  FQSIHESDM         0.3288        1424.9                 16.00      Sequence
DRB3_0101  318  FTNPTVNSYKRLVPG  FTNPTVNSY         0.3279        1438.8                 16.00      Sequence
DRB3_0101  261  FMPKPLFGDNGSGMH  FGDNGSGMH         0.3260        1469.1                 16.00      Sequence
DRB3_0101   60  FQSIHESDMLLLPDP  FQSIHESDM         0.3255        1476.5                 16.00      Sequence
DRB3_0101   93  FVHDPFTLEPYSRDP  FVHDPFTLE         0.3243        1496.2                 16.00      Sequence
DRB3_0101   42  DKSVFDDGLAFDGSS  SVFDDGLAF         0.3222        1530.5                 16.00      Sequence
DRB3_0101  285  APLMYDETGYAGLSD  LMYDETGYA         0.3222        1530.9                 16.00      Sequence
DRB3_0101   17  VEYVDVRFCDLPGIM  RFCDLPGIM         0.3159        1639.4                 16.00      Sequence
DRB3_0101  185  YFPVAPNDQYVDLRD  FPVAPNDQY         0.3153        1650.3                 16.00      Sequence
DRB3_0101  262  MPKPLFGDNGSGMHC  FGDNGSGMH         0.3148        1659.2                 16.00      Sequence
DRB3_0101  305  IGGLLHHAPSLLAFT  LLHHAPSLL         0.3145        1663.9                 16.00      Sequence
DRB3_0101   43  KSVFDDGLAFDGSSI  SVFDDGLAF         0.3140        1673.5                 16.00      Sequence
DRB3_0101  223  GQAEINYQFNSLLHA  INYQFNSLL         0.3136        1679.9                 16.00      Sequence
DRB3_0101   55  SSIRGFQSIHESDML  FQSIHESDM         0.3080        1784.9                 16.00      Sequence
DRB3_0101  186  FPVAPNDQYVDLRDK  FPVAPNDQY         0.3056        1832.0                 16.00      Sequence
DRB3_0101   76  TARIDPFRAAKTLNI  FRAAKTLNI         0.3048        1848.0                 16.00      Sequence
DRB3_0101  263  PKPLFGDNGSGMHCH  FGDNGSGMH         0.3036        1871.9                 16.00      Sequence
DRB3_0101   54  GSSIRGFQSIHESDM  FQSIHESDM         0.3031        1882.1                 16.00      Sequence
DRB3_0101  286  PLMYDETGYAGLSDT  LMYDETGYA         0.3003        1940.6                 16.00      Sequence
DRB3_0101   18  EYVDVRFCDLPGIMQ  RFCDLPGIM         0.2987        1973.6                 16.00      Sequence
DRB3_0101  222  GGQAEINYQFNSLLH  INYQFNSLL         0.2983        1982.6                 16.00      Sequence
DRB3_0101  306  GGLLHHAPSLLAFTN  LLHHAPSLL         0.2931        2097.9                 32.00      Sequence
DRB3_0101  463  NIRPHPYEFALYYDV  YEFALYYDV         0.2927        2107.3                 32.00      Sequence
DRB3_0101  136  YIFDSVSFDSRANGS  YIFDSVSFD         0.2918        2127.2                 32.00      Sequence
DRB3_0101   45  VFDDGLAFDGSSIRG  LAFDGSSIR         0.2916        2131.7                 32.00      Sequence
DRB3_0101   77  ARIDPFRAAKTLNIN  FRAAKTLNI         0.2894        2182.3                 32.00      Sequence
DRB3_0101  171  GSPNRGYKVRHKGGY  YKVRHKGGY         0.2893        2185.8                 32.00      Sequence
DRB3_0101  287  LMYDETGYAGLSDTA  LMYDETGYA         0.2876        2226.8                 32.00      Sequence
DRB3_0101  221  SGGQAEINYQFNSLL  INYQFNSLL         0.2851        2286.4                 32.00      Sequence
DRB3_0101  264  KPLFGDNGSGMHCHQ  FGDNGSGMH         0.2841        2311.8                 32.00      Sequence
DRB3_0101   19  YVDVRFCDLPGIMQH  RFCDLPGIM         0.2833        2332.2                 32.00      Sequence
DRB3_0101  172  SPNRGYKVRHKGGYF  YKVRHKGGY         0.2830        2338.9                 32.00      Sequence
DRB3_0101  307  GLLHHAPSLLAFTNP  LLHHAPSLL         0.2731        2603.7                 32.00      Sequence
DRB3_0101  265  PLFGDNGSGMHCHQS  FGDNGSGMH         0.2719        2638.5                 32.00      Sequence
DRB3_0101   10  KLAKDEKVEYVDVRF  LAKDEKVEY         0.2709        2667.1                 32.00      Sequence
DRB3_0101   64  HESDMLLLPDPETAR  LLPDPETAR         0.2701        2690.4                 32.00      Sequence
DRB3_0101   66  SDMLLLPDPETARID  LLPDPETAR         0.2692        2716.7                 32.00      Sequence
DRB3_0101   11  LAKDEKVEYVDVRFC  LAKDEKVEY         0.2687        2732.0                 32.00      Sequence
DRB3_0101   78  RIDPFRAAKTLNINF  FRAAKTLNI         0.2680        2750.6                 32.00      Sequence
DRB3_0101  173  PNRGYKVRHKGGYFP  YKVRHKGGY         0.2654        2829.1                 32.00      Sequence
DRB3_0101  189  APNDQYVDLRDKMLT  QYVDLRDKM         0.2636        2885.8                 32.00      Sequence
DRB3_0101   65  ESDMLLLPDPETARI  LLPDPETAR         0.2634        2892.8                 32.00      Sequence
DRB3_0101  188  VAPNDQYVDLRDKML  QYVDLRDKM         0.2619        2940.4                 32.00      Sequence
DRB3_0101  116  NYLISTGIADTAYFG  GIADTAYFG         0.2609        2973.3                 32.00      Sequence
DRB3_0101  224  QAEINYQFNSLLHAA  INYQFNSLL         0.2598        3006.1                 32.00      Sequence
DRB3_0101  137  IFDSVSFDSRANGSF  FDSRANGSF         0.2581        3063.7                 32.00      Sequence
DRB3_0101  308  LLHHAPSLLAFTNPT  LLHHAPSLL         0.2576        3079.3                 32.00      Sequence
DRB3_0101   67  DMLLLPDPETARIDP  LLPDPETAR         0.2541        3197.8                 32.00      Sequence
DRB3_0101  138  FDSVSFDSRANGSFY  FDSRANGSF         0.2528        3243.9                 32.00      Sequence
DRB3_0101  225  AEINYQFNSLLHAAD  INYQFNSLL         0.2510        3306.6                 32.00      Sequence
DRB3_0101  140  SVSFDSRANGSFYEV  FDSRANGSF         0.2494        3363.7                 32.00      Sequence
DRB3_0101   79  IDPFRAAKTLNINFF  FRAAKTLNI         0.2494        3366.4                 32.00      Sequence
DRB3_0101  174  NRGYKVRHKGGYFPV  YKVRHKGGY         0.2493        3369.5                 32.00      Sequence
DRB3_0101  111  ARKAENYLISTGIAD  ARKAENYLI         0.2455        3511.5                 32.00      Sequence
DRB3_0101  190  PNDQYVDLRDKMLTN  QYVDLRDKM         0.2445        3548.7                 32.00      Sequence
DRB3_0101   68  MLLLPDPETARIDPF  LLPDPETAR         0.2445        3550.3                 32.00      Sequence
DRB3_0101  117  YLISTGIADTAYFGA  GIADTAYFG         0.2441        3564.3                 32.00      Sequence
DRB3_0101  266  LFGDNGSGMHCHQSL  FGDNGSGMH         0.2439        3572.3                 32.00      Sequence
DRB3_0101   20  VDVRFCDLPGIMQHF  RFCDLPGIM         0.2435        3588.5                 32.00      Sequence
DRB3_0101  247  IIKNTAWQNGKTVTF  WQNGKTVTF         0.2421        3641.8                 32.00      Sequence
DRB3_0101  139  DSVSFDSRANGSFYE  FDSRANGSF         0.2409        3688.6                 32.00      Sequence
DRB3_0101  175  RGYKVRHKGGYFPVA  YKVRHKGGY         0.2404        3711.1                 32.00      Sequence
DRB3_0101   80  DPFRAAKTLNINFFV  FRAAKTLNI         0.2397        3738.6                 32.00      Sequence
DRB3_0101  327  KRLVPGYEAPINLVY  GYEAPINLV         0.2380        3806.3                 32.00      Sequence
DRB3_0101  226  EINYQFNSLLHAADD  INYQFNSLL         0.2371        3843.9                 32.00      Sequence
DRB3_0101  326  YKRLVPGYEAPINLV  GYEAPINLV         0.2369        3854.3                 32.00      Sequence
DRB3_0101  227  INYQFNSLLHAADDM  INYQFNSLL         0.2323        4048.4                 32.00      Sequence
DRB3_0101  248  IKNTAWQNGKTVTFM  WQNGKTVTF         0.2323        4051.4                 32.00      Sequence
DRB3_0101  118  LISTGIADTAYFGAE  GIADTAYFG         0.2310        4107.0                 32.00      Sequence
DRB3_0101   69  LLLPDPETARIDPFR  LLPDPETAR         0.2307        4118.8                 32.00      Sequence
DRB3_0101  192  DQYVDLRDKMLTNLI  QYVDLRDKM         0.2298        4161.3                 32.00      Sequence
DRB3_0101  191  NDQYVDLRDKMLTNL  QYVDLRDKM         0.2295        4174.3                 32.00      Sequence
DRB3_0101   82  FRAAKTLNINFFVHD  FRAAKTLNI         0.2291        4193.8                 32.00      Sequence
DRB3_0101   61  QSIHESDMLLLPDPE  IHESDMLLL         0.2282        4232.5                 32.00      Sequence
DRB3_0101  328  RLVPGYEAPINLVYS  GYEAPINLV         0.2274        4272.0                 32.00      Sequence
DRB3_0101   81  PFRAAKTLNINFFVH  FRAAKTLNI         0.2272        4280.6                 32.00      Sequence
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DRB3_0101  176  GYKVRHKGGYFPVAP  YKVRHKGGY        0.2261       4330.1                32.00     Sequence
DRB3_0101  177  YKVRHKGGYFPVAPN  YKVRHKGGY        0.2252       4372.2                32.00     Sequence
DRB3_0101  204  NLINSGFILEKGHHE  FILEKGHHE        0.2250       4381.3                32.00     Sequence
DRB3_0101  141  VSFDSRANGSFYEVD  FDSRANGSF        0.2243       4413.4                32.00     Sequence
DRB3_0101  205  LINSGFILEKGHHEV  FILEKGHHE        0.2234       4457.9                32.00     Sequence
DRB3_0101   62  SIHESDMLLLPDPET  IHESDMLLL        0.2216       4547.5                32.00     Sequence
DRB3_0101  143  FDSRANGSFYEVDAI  FDSRANGSF        0.2207       4593.0                32.00     Sequence
DRB3_0101  249  KNTAWQNGKTVTFMP  WQNGKTVTF        0.2197       4638.7                32.00     Sequence
DRB3_0101  447  IETWISFKRENEIEP  FKRENEIEP        0.2150       4885.2                32.00     Sequence
DRB3_0101  451  ISFKRENEIEPVNIR  ISFKRENEI        0.2145       4909.5                32.00     Sequence
DRB3_0101   35  TIPASAFDKSVFDDG  FDKSVFDDG        0.2139       4939.8                32.00     Sequence
DRB3_0101  119  ISTGIADTAYFGAEA  GIADTAYFG        0.2138       4948.0                32.00     Sequence
DRB3_0101  187  PVAPNDQYVDLRDKM  QYVDLRDKM        0.2135       4962.7                32.00     Sequence
DRB3_0101   36  IPASAFDKSVFDDGL  FDKSVFDDG        0.2131       4983.4                32.00     Sequence
DRB3_0101  267  FGDNGSGMHCHQSLW  FGDNGSGMH        0.2128       5002.8                32.00     Sequence
DRB3_0101  376  YLAFSAMLMAGLDGI  MLMAGLDGI        0.2126       5009.4                32.00     Sequence
DRB3_0101   21  DVRFCDLPGIMQHFT  RFCDLPGIM        0.2108       5107.7                32.00     Sequence
DRB3_0101  448  ETWISFKRENEIEPV  ISFKRENEI        0.2101       5151.0                32.00     Sequence
DRB3_0101  260  TFMPKPLFGDNGSGM  LFGDNGSGM        0.2097       5172.8                32.00     Sequence
DRB3_0101  142  SFDSRANGSFYEVDA  FDSRANGSF        0.2095       5181.5                32.00     Sequence
DRB3_0101  193  QYVDLRDKMLTNLIN  QYVDLRDKM        0.2082       5256.9                32.00     Sequence
DRB3_0101   70  LLPDPETARIDPFRA  LLPDPETAR        0.2080       5266.6                32.00     Sequence
DRB3_0101  371  SSGNPYLAFSAMLMA  YLAFSAMLM        0.2079       5271.1                32.00     Sequence
DRB3_0101  329  LVPGYEAPINLVYSQ  GYEAPINLV        0.2064       5358.2                50.00     Sequence
DRB3_0101  121  TGIADTAYFGAEAEF  GIADTAYFG        0.2057       5398.6                50.00     Sequence
DRB3_0101  449  TWISFKRENEIEPVN  ISFKRENEI        0.2043       5479.4                50.00     Sequence
DRB3_0101  206  INSGFILEKGHHEVG  FILEKGHHE        0.2041       5491.6                50.00     Sequence
DRB3_0101   63  IHESDMLLLPDPETA  IHESDMLLL        0.2040       5500.7                50.00     Sequence
DRB3_0101  145  SRANGSFYEVDAISG  FYEVDAISG        0.2039       5504.5                50.00     Sequence
DRB3_0101  217  HEVGSGGQAEINYQF  GQAEINYQF        0.2035       5528.1                50.00     Sequence
DRB3_0101  220  GSGGQAEINYQFNSL  GQAEINYQF        0.2027       5578.6                50.00     Sequence
DRB3_0101  250  NTAWQNGKTVTFMPK  WQNGKTVTF        0.2024       5595.8                50.00     Sequence
DRB3_0101   37  PASAFDKSVFDDGLA  FDKSVFDDG        0.2010       5680.3                50.00     Sequence
DRB3_0101  218  EVGSGGQAEINYQFN  GQAEINYQF        0.2008       5695.3                50.00     Sequence
DRB3_0101  450  WISFKRENEIEPVNI  ISFKRENEI        0.2000       5743.1                50.00     Sequence
DRB3_0101  107  PRNIARKAENYLIST  ARKAENYLI        0.1985       5836.8                50.00     Sequence
DRB3_0101  219  VGSGGQAEINYQFNS  GQAEINYQF        0.1984       5842.2                50.00     Sequence
DRB3_0101  115  ENYLISTGIADTAYF  TGIADTAYF        0.1981       5864.2                50.00     Sequence
DRB3_0101  330  VPGYEAPINLVYSQR  GYEAPINLV        0.1968       5947.6                50.00     Sequence
DRB3_0101  110  IARKAENYLISTGIA  ARKAENYLI        0.1952       6052.1                50.00     Sequence
DRB3_0101  105  RDPRNIARKAENYLI  ARKAENYLI        0.1950       6063.9                50.00     Sequence
DRB3_0101  370  DSSGNPYLAFSAMLM  YLAFSAMLM        0.1943       6108.8                50.00     Sequence
DRB3_0101  229  YQFNSLLHAADDMQL  LHAADDMQL        0.1942       6118.5                50.00     Sequence
DRB3_0101   16  KVEYVDVRFCDLPGI  VRFCDLPGI        0.1941       6123.2                50.00     Sequence
DRB3_0101   22  VRFCDLPGIMQHFTI  RFCDLPGIM        0.1935       6158.8                50.00     Sequence
DRB3_0101  255  NGKTVTFMPKPLFGD  FMPKPLFGD        0.1921       6259.3                50.00     Sequence
DRB3_0101  120  STGIADTAYFGAEAE  GIADTAYFG        0.1920       6262.0                50.00     Sequence
DRB3_0101  253  WQNGKTVTFMPKPLF  WQNGKTVTF        0.1912       6315.0                50.00     Sequence
DRB3_0101  106  DPRNIARKAENYLIS  ARKAENYLI        0.1912       6316.1                50.00     Sequence
DRB3_0101   28  PGIMQHFTIPASAFD  HFTIPASAF        0.1910       6333.5                50.00     Sequence
DRB3_0101  331  PGYEAPINLVYSQRN  GYEAPINLV        0.1908       6343.7                50.00     Sequence
DRB3_0101  251  TAWQNGKTVTFMPKP  WQNGKTVTF        0.1907       6352.8                50.00     Sequence
DRB3_0101   13  KDEKVEYVDVRFCDL  YVDVRFCDL        0.1891       6459.9                50.00     Sequence
DRB3_0101  198  RDKMLTNLINSGFIL  MLTNLINSG        0.1888       6480.5                50.00     Sequence
DRB3_0101  373  GNPYLAFSAMLMAGL  YLAFSAMLM        0.1887       6491.4                50.00     Sequence
DRB3_0101  377  LAFSAMLMAGLDGIK  MLMAGLDGI        0.1876       6564.9                50.00     Sequence
DRB3_0101  108  RNIARKAENYLISTG  ARKAENYLI        0.1866       6636.6                50.00     Sequence
DRB3_0101   27  LPGIMQHFTIPASAF  HFTIPASAF        0.1860       6679.7                50.00     Sequence
DRB3_0101  241  MQLYKYIIKNTAWQN  IIKNTAWQN        0.1851       6745.8                50.00     Sequence
DRB3_0101  207  NSGFILEKGHHEVGS  FILEKGHHE        0.1847       6777.7                50.00     Sequence
DRB3_0101  332  GYEAPINLVYSQRNR  GYEAPINLV        0.1846       6787.0                50.00     Sequence
DRB3_0101  421  QLSDVIDRLEADHEY  QLSDVIDRL        0.1838       6847.5                50.00     Sequence
DRB3_0101  252  AWQNGKTVTFMPKPL  WQNGKTVTF        0.1834       6870.5                50.00     Sequence
DRB3_0101  112  RKAENYLISTGIADT  YLISTGIAD        0.1834       6872.7                50.00     Sequence
DRB3_0101  109  NIARKAENYLISTGI  ARKAENYLI        0.1828       6920.2                50.00     Sequence
DRB3_0101   14  DEKVEYVDVRFCDLP  YVDVRFCDL        0.1807       7074.1                50.00     Sequence
DRB3_0101    0  VTEKTPDDVFKLAKD  TEKTPDDVF        0.1803       7111.6                50.00     Sequence
DRB3_0101  298  SDTARHYIGGLLHHA  YIGGLLHHA        0.1791       7201.7                50.00     Sequence
DRB3_0101  446  LIETWISFKRENEIE  ISFKRENEI        0.1784       7258.7                50.00     Sequence
DRB3_0101  291  ETGYAGLSDTARHYI  GLSDTARHY        0.1762       7427.7                50.00     Sequence
DRB3_0101  372  SGNPYLAFSAMLMAG  YLAFSAMLM        0.1754       7492.0                50.00     Sequence
DRB3_0101  242  QLYKYIIKNTAWQNG  IIKNTAWQN        0.1753       7502.1                50.00     Sequence
DRB3_0101  445  DLIETWISFKRENEI  ISFKRENEI        0.1751       7517.6                50.00     Sequence
DRB3_0101  194  YVDLRDKMLTNLINS  YVDLRDKML        0.1750       7524.4                50.00     Sequence
DRB3_0101  378  AFSAMLMAGLDGIKN  MLMAGLDGI        0.1737       7635.8                50.00     Sequence
DRB3_0101  422  LSDVIDRLEADHEYL  DRLEADHEY        0.1734       7657.6                50.00     Sequence
DRB3_0101  199  DKMLTNLINSGFILE  MLTNLINSG        0.1734       7661.2                50.00     Sequence
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DRB3_0101  195  VDLRDKMLTNLINSG  MLTNLINSG         0.1733       7664.6                 50.00     Sequence
DRB3_0101  374  NPYLAFSAMLMAGLD  YLAFSAMLM         0.1730       7692.2                 50.00     Sequence
DRB3_0101    1  TEKTPDDVFKLAKDE  KTPDDVFKL         0.1729       7701.6                 50.00     Sequence
DRB3_0101  292  TGYAGLSDTARHYIG  GLSDTARHY         0.1729       7704.1                 50.00     Sequence
DRB3_0101  113  KAENYLISTGIADTA  YLISTGIAD         0.1707       7882.3                 50.00     Sequence
DRB3_0101   29  GIMQHFTIPASAFDK  HFTIPASAF         0.1701       7936.8                 50.00     Sequence
DRB3_0101  256  GKTVTFMPKPLFGDN  FMPKPLFGD         0.1698       7964.6                 50.00     Sequence
DRB3_0101  452  SFKRENEIEPVNIRP  FKRENEIEP         0.1680       8115.6                 50.00     Sequence
DRB3_0101  299  DTARHYIGGLLHHAP  YIGGLLHHA         0.1680       8122.7                 50.00     Sequence
DRB3_0101   33  HFTIPASAFDKSVFD  HFTIPASAF         0.1673       8184.1                 50.00     Sequence
DRB3_0101  435  YLTEGGVFTNDLIET  VFTNDLIET         0.1654       8354.0                 50.00     Sequence
DRB3_0101   15  EKVEYVDVRFCDLPG  YVDVRFCDL         0.1654       8354.1                 50.00     Sequence
DRB3_0101  301  ARHYIGGLLHHAPSL  YIGGLLHHA         0.1641       8469.7                 50.00     Sequence
DRB3_0101   84  AAKTLNINFFVHDPF  AKTLNINFF         0.1639       8488.0                 50.00     Sequence
DRB3_0101   85  AKTLNINFFVHDPFT  AKTLNINFF         0.1633       8547.4                 50.00     Sequence
DRB3_0101  196  DLRDKMLTNLINSGF  MLTNLINSG         0.1630       8570.7                 50.00     Sequence
DRB3_0101  293  GYAGLSDTARHYIGG  GLSDTARHY         0.1626       8610.7                 50.00     Sequence
DRB3_0101  243  LYKYIIKNTAWQNGK  IIKNTAWQN         0.1625       8619.6                 50.00     Sequence
DRB3_0101  430  EADHEYLTEGGVFTN  YLTEGGVFT         0.1620       8666.3                 50.00     Sequence
DRB3_0101  375  PYLAFSAMLMAGLDG  YLAFSAMLM         0.1612       8744.3                 50.00     Sequence
DRB3_0101  415  IPQTPTQLSDVIDRL  QLSDVIDRL         0.1609       8766.8                 50.00     Sequence
DRB3_0101  294  YAGLSDTARHYIGGL  GLSDTARHY         0.1607       8784.5                 50.00     Sequence
DRB3_0101  416  PQTPTQLSDVIDRLE  QLSDVIDRL         0.1601       8848.9                 50.00     Sequence
DRB3_0101  197  LRDKMLTNLINSGFI  MLTNLINSG         0.1598       8877.5                 50.00     Sequence
DRB3_0101  379  FSAMLMAGLDGIKNK  MLMAGLDGI         0.1596       8887.8                 50.00     Sequence
DRB3_0101   83  RAAKTLNINFFVHDP  AKTLNINFF         0.1589       8963.2                 50.00     Sequence
DRB3_0101  200  KMLTNLINSGFILEK  MLTNLINSG         0.1586       8986.7                 50.00     Sequence
DRB3_0101  417  QTPTQLSDVIDRLEA  QLSDVIDRL         0.1582       9026.8                 50.00     Sequence
DRB3_0101   23  RFCDLPGIMQHFTIP  RFCDLPGIM         0.1580       9051.4                 50.00     Sequence
DRB3_0101  418  TPTQLSDVIDRLEAD  QLSDVIDRL         0.1574       9103.8                 50.00     Sequence
DRB3_0101  300  TARHYIGGLLHHAPS  YIGGLLHHA         0.1560       9244.6                 50.00     Sequence
DRB3_0101  208  SGFILEKGHHEVGSG  FILEKGHHE         0.1543       9415.1                 50.00     Sequence
DRB3_0101  257  KTVTFMPKPLFGDNG  FMPKPLFGD         0.1534       9511.5                 50.00     Sequence
DRB3_0101  295  AGLSDTARHYIGGLL  GLSDTARHY         0.1533       9516.9                 50.00     Sequence
DRB3_0101  431  ADHEYLTEGGVFTND  YLTEGGVFT         0.1528       9571.6                 50.00     Sequence
DRB3_0101   30  IMQHFTIPASAFDKS  HFTIPASAF         0.1524       9617.0                 50.00     Sequence
DRB3_0101  419  PTQLSDVIDRLEADH  QLSDVIDRL         0.1522       9629.8                 50.00     Sequence
DRB3_0101  461  PVNIRPHPYEFALYY  NIRPHPYEF         0.1519       9663.0                 50.00     Sequence
DRB3_0101  457  NEIEPVNIRPHPYEF  NIRPHPYEF         0.1519       9665.8                 50.00     Sequence
DRB3_0101  309  LHHAPSLLAFTNPTV  LHHAPSLLA         0.1515       9710.3                 50.00     Sequence
DRB3_0101  420  TQLSDVIDRLEADHE  QLSDVIDRL         0.1513       9725.5                 50.00     Sequence
DRB3_0101  462  VNIRPHPYEFALYYD  NIRPHPYEF         0.1504       9824.9                 50.00     Sequence
DRB3_0101  433  HEYLTEGGVFTNDLI  YLTEGGVFT         0.1482      10057.9                 50.00     Sequence
DRB3_0101  273  GMHCHQSLWKDGAPL  GMHCHQSLW         0.1479      10088.0                 50.00     Sequence
DRB3_0101  244  YKYIIKNTAWQNGKT  IIKNTAWQN         0.1476      10130.0                 50.00     Sequence
DRB3_0101   31  MQHFTIPASAFDKSV  HFTIPASAF         0.1470      10190.8                 50.00     Sequence
DRB3_0101  259  VTFMPKPLFGDNGSG  FMPKPLFGD         0.1468      10209.5                 50.00     Sequence
DRB3_0101  209  GFILEKGHHEVGSGG  FILEKGHHE         0.1457      10334.8                 50.00     Sequence
DRB3_0101  380  SAMLMAGLDGIKNKI  MLMAGLDGI         0.1456      10344.4                 50.00     Sequence
DRB3_0101  434  EYLTEGGVFTNDLIE  YLTEGGVFT         0.1453      10381.2                 50.00     Sequence
DRB3_0101  320  NPTVNSYKRLVPGYE  TVNSYKRLV         0.1440      10522.5                 50.00     Sequence
DRB3_0101   32  QHFTIPASAFDKSVF  HFTIPASAF         0.1434      10601.2                 50.00     Sequence
DRB3_0101  228  NYQFNSLLHAADDMQ  YQFNSLLHA         0.1417      10795.4                 50.00     Sequence
DRB3_0101  458  EIEPVNIRPHPYEFA  NIRPHPYEF         0.1410      10880.3                 50.00     Sequence
DRB3_0101  459  IEPVNIRPHPYEFAL  NIRPHPYEF         0.1409      10889.2                 50.00     Sequence
DRB3_0101  114  AENYLISTGIADTAY  YLISTGIAD         0.1407      10913.8                 50.00     Sequence
DRB3_0101  258  TVTFMPKPLFGDNGS  FMPKPLFGD         0.1405      10934.8                 50.00     Sequence
DRB3_0101  238  ADDMQLYKYIIKNTA  YKYIIKNTA         0.1405      10938.0                 50.00     Sequence
DRB3_0101  201  MLTNLINSGFILEKG  MLTNLINSG         0.1400      10993.0                 50.00     Sequence
DRB3_0101  269  DNGSGMHCHQSLWKD  GMHCHQSLW         0.1400      10993.3                 50.00     Sequence
DRB3_0101  268  GDNGSGMHCHQSLWK  GMHCHQSLW         0.1399      11010.0                 50.00     Sequence
DRB3_0101  290  DETGYAGLSDTARHY  GLSDTARHY         0.1392      11087.2                 50.00     Sequence
DRB3_0101  432  DHEYLTEGGVFTNDL  YLTEGGVFT         0.1386      11161.8                 50.00     Sequence
DRB3_0101  460  EPVNIRPHPYEFALY  NIRPHPYEF         0.1377      11275.9                 50.00     Sequence
DRB3_0101   71  LPDPETARIDPFRAA  ARIDPFRAA         0.1375      11296.3                 50.00     Sequence
DRB3_0101  381  AMLMAGLDGIKNKIE  MLMAGLDGI         0.1368      11378.1                 50.00     Sequence
DRB3_0101   12  AKDEKVEYVDVRFCD  EYVDVRFCD         0.1360      11473.9                 50.00     Sequence
DRB3_0101  321  PTVNSYKRLVPGYEA  TVNSYKRLV         0.1359      11491.5                 50.00     Sequence
DRB3_0101  144  DSRANGSFYEVDAIS  RANGSFYEV         0.1358      11505.6                 50.00     Sequence
DRB3_0101  296  GLSDTARHYIGGLLH  GLSDTARHY         0.1342      11701.1                 50.00     Sequence
DRB3_0101  270  NGSGMHCHQSLWKDG  GMHCHQSLW         0.1338      11749.3                 50.00     Sequence
DRB3_0101  319  TNPTVNSYKRLVPGY  TVNSYKRLV         0.1334      11807.3                 50.00     Sequence
DRB3_0101  271  GSGMHCHQSLWKDGA  GMHCHQSLW         0.1327      11897.1                 50.00     Sequence
DRB3_0101  272  SGMHCHQSLWKDGAP  GMHCHQSLW         0.1294      12323.4                 50.00     Sequence
DRB3_0101  240  DMQLYKYIIKNTAWQ  YKYIIKNTA         0.1292      12360.8                 50.00     Sequence
DRB3_0101  245  KYIIKNTAWQNGKTV  IIKNTAWQN         0.1286      12434.3                 50.00     Sequence
DRB3_0101  453  FKRENEIEPVNIRPH  NEIEPVNIR         0.1278      12538.6                 50.00     Sequence
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DRB3_0101  322  TVNSYKRLVPGYEAP  TVNSYKRLV         0.1268      12681.0             50.00     Sequence
DRB3_0101  338  NLVYSQRNRSACVRI  RNRSACVRI         0.1265      12721.6             50.00     Sequence
DRB3_0101  365  EFRSPDSSGNPYLAF  FRSPDSSGN         0.1263      12749.4             50.00     Sequence
DRB3_0101   72  PDPETARIDPFRAAK  ARIDPFRAA         0.1259      12810.3             50.00     Sequence
DRB3_0101  239  DDMQLYKYIIKNTAW  YKYIIKNTA         0.1250      12928.7             50.00     Sequence
DRB3_0101   73  DPETARIDPFRAAKT  ARIDPFRAA         0.1247      12966.3             50.00     Sequence
DRB3_0101   74  PETARIDPFRAAKTL  ARIDPFRAA         0.1240      13072.9             50.00     Sequence
DRB3_0101  336  PINLVYSQRNRSACV  SQRNRSACV         0.1231      13204.3             50.00     Sequence
DRB3_0101  399  PVDKDLYELPPEEAA  YELPPEEAA         0.1223      13318.6             50.00     Sequence
DRB3_0101   75  ETARIDPFRAAKTLN  ARIDPFRAA         0.1213      13454.9             50.00     Sequence
DRB3_0101  246  YIIKNTAWQNGKTVT  IIKNTAWQN         0.1206      13560.5             50.00     Sequence
DRB3_0101  333  YEAPINLVYSQRNRS  LVYSQRNRS         0.1204      13585.1             50.00     Sequence
DRB3_0101    2  EKTPDDVFKLAKDEK  KTPDDVFKL         0.1178      13970.3             50.00     Sequence
DRB3_0101  337  INLVYSQRNRSACVR  SQRNRSACV         0.1169      14109.6             50.00     Sequence
DRB3_0101   34  FTIPASAFDKSVFDD  SAFDKSVFD         0.1169      14117.5             50.00     Sequence
DRB3_0101  386  GLDGIKNKIEPQAPV  NKIEPQAPV         0.1168      14135.0             50.00     Sequence
DRB3_0101  210  FILEKGHHEVGSGGQ  FILEKGHHE         0.1166      14162.5             50.00     Sequence
DRB3_0101  202  LTNLINSGFILEKGH  NLINSGFIL         0.1160      14255.7             50.00     Sequence
DRB3_0101  364  LEFRSPDSSGNPYLA  FRSPDSSGN         0.1150      14410.0             50.00     Sequence
DRB3_0101  203  TNLINSGFILEKGHH  NLINSGFIL         0.1148      14443.6             50.00     Sequence
DRB3_0101  387  LDGIKNKIEPQAPVD  NKIEPQAPV         0.1134      14657.0             50.00     Sequence
DRB3_0101   94  VHDPFTLEPYSRDPR  FTLEPYSRD         0.1133      14680.0             50.00     Sequence
DRB3_0101  339  LVYSQRNRSACVRIP  SQRNRSACV         0.1126      14785.2             50.00     Sequence
DRB3_0101  362  KRLEFRSPDSSGNPY  FRSPDSSGN         0.1119      14895.4             50.00     Sequence
DRB3_0101  360  KAKRLEFRSPDSSGN  FRSPDSSGN         0.1115      14960.8             50.00     Sequence
DRB3_0101  297  LSDTARHYIGGLLHH  LSDTARHYI         0.1110      15042.9             50.00     Sequence
DRB3_0101  361  AKRLEFRSPDSSGNP  FRSPDSSGN         0.1108      15082.4             50.00     Sequence
DRB3_0101  366  FRSPDSSGNPYLAFS  FRSPDSSGN         0.1104      15150.1             50.00     Sequence
DRB3_0101  382  MLMAGLDGIKNKIEP  MLMAGLDGI         0.1099      15225.0             50.00     Sequence
DRB3_0101  363  RLEFRSPDSSGNPYL  FRSPDSSGN         0.1090      15369.3             50.00     Sequence
DRB3_0101  323  VNSYKRLVPGYEAPI  LVPGYEAPI         0.1087      15431.8             50.00     Sequence
DRB3_0101  369  PDSSGNPYLAFSAML  PYLAFSAML         0.1066      15783.4             50.00     Sequence
DRB3_0101  325  SYKRLVPGYEAPINL  LVPGYEAPI         0.1053      16003.2             50.00     Sequence
DRB3_0101  394  IEPQAPVDKDLYELP  QAPVDKDLY         0.1047      16108.3             50.00     Sequence
DRB3_0101  444  NDLIETWISFKRENE  LIETWISFK         0.1026      16474.4             50.00     Sequence
DRB3_0101  443  TNDLIETWISFKREN  LIETWISFK         0.1023      16531.3             50.00     Sequence
DRB3_0101  254  QNGKTVTFMPKPLFG  VTFMPKPLF         0.1021      16571.8             50.00     Sequence
DRB3_0101  324  NSYKRLVPGYEAPIN  LVPGYEAPI         0.1006      16839.3             50.00     Sequence
DRB3_0101  400  VDKDLYELPPEEAAS  YELPPEEAA         0.1004      16878.7             50.00     Sequence
DRB3_0101  401  DKDLYELPPEEAASI  YELPPEEAA         0.1003      16897.5             50.00     Sequence
DRB3_0101   96  DPFTLEPYSRDPRNI  FTLEPYSRD         0.0999      16959.8             50.00     Sequence
DRB3_0101  414  SIPQTPTQLSDVIDR  TQLSDVIDR         0.0998      16983.1             50.00     Sequence
DRB3_0101  395  EPQAPVDKDLYELPP  QAPVDKDLY         0.0995      17040.7             50.00     Sequence
DRB3_0101   95  HDPFTLEPYSRDPRN  FTLEPYSRD         0.0992      17088.7             50.00     Sequence
DRB3_0101  388  DGIKNKIEPQAPVDK  NKIEPQAPV         0.0983      17263.6             50.00     Sequence
DRB3_0101  392  NKIEPQAPVDKDLYE  NKIEPQAPV         0.0977      17380.8             50.00     Sequence
DRB3_0101  396  PQAPVDKDLYELPPE  QAPVDKDLY         0.0959      17715.9             50.00     Sequence
DRB3_0101  402  KDLYELPPEEAASIP  YELPPEEAA         0.0951      17873.5             50.00     Sequence
DRB3_0101  397  QAPVDKDLYELPPEE  QAPVDKDLY         0.0950      17892.5             50.00     Sequence
DRB3_0101  335  APINLVYSQRNRSAC  LVYSQRNRS         0.0946      17958.8             50.00     Sequence
DRB3_0101  310  HHAPSLLAFTNPTVN  HHAPSLLAF         0.0940      18086.2             50.00     Sequence
DRB3_0101  334  EAPINLVYSQRNRSA  LVYSQRNRS         0.0934      18195.5             50.00     Sequence
DRB3_0101  391  KNKIEPQAPVDKDLY  NKIEPQAPV         0.0926      18367.0             50.00     Sequence
DRB3_0101  393  KIEPQAPVDKDLYEL  QAPVDKDLY         0.0921      18463.8             50.00     Sequence
DRB3_0101  104  SRDPRNIARKAENYL  IARKAENYL         0.0912      18629.6             50.00     Sequence
DRB3_0101  455  RENEIEPVNIRPHPY  NEIEPVNIR         0.0907      18737.9             50.00     Sequence
DRB3_0101  403  DLYELPPEEAASIPQ  YELPPEEAA         0.0907      18747.5             50.00     Sequence
DRB3_0101  389  GIKNKIEPQAPVDKD  NKIEPQAPV         0.0904      18807.6             50.00     Sequence
DRB3_0101  390  IKNKIEPQAPVDKDL  NKIEPQAPV         0.0896      18973.6             50.00     Sequence
DRB3_0101  456  ENEIEPVNIRPHPYE  NEIEPVNIR         0.0894      18996.8             50.00     Sequence
DRB3_0101  398  APVDKDLYELPPEEA  LYELPPEEA         0.0890      19088.9             50.00     Sequence
DRB3_0101  404  LYELPPEEAASIPQT  YELPPEEAA         0.0863      19663.1             50.00     Sequence
DRB3_0101   25  CDLPGIMQHFTIPAS  IMQHFTIPA         0.0856      19796.7             50.00     Sequence
DRB3_0101  165  AATEADGSPNRGYKV  GSPNRGYKV         0.0853      19861.5             50.00     Sequence
DRB3_0101  340  VYSQRNRSACVRIPI  SQRNRSACV         0.0844      20051.9             50.00     Sequence
DRB3_0101  341  YSQRNRSACVRIPIT  SQRNRSACV         0.0842      20100.4             50.00     Sequence
DRB3_0101  153  EVDAISGWWNTGAAT  EVDAISGWW         0.0835      20262.8             50.00     Sequence
DRB3_0101  311  HAPSLLAFTNPTVNS  SLLAFTNPT         0.0816      20682.3             50.00     Sequence
DRB3_0101  179  VRHKGGYFPVAPNDQ  YFPVAPNDQ         0.0808      20850.4             50.00     Sequence
DRB3_0101  342  SQRNRSACVRIPITG  SQRNRSACV         0.0796      21142.1             50.00     Sequence
DRB3_0101  166  ATEADGSPNRGYKVR  GSPNRGYKV         0.0791      21234.9             50.00     Sequence
DRB3_0101  155  DAISGWWNTGAATEA  WNTGAATEA         0.0773      21672.7             50.00     Sequence
DRB3_0101   24  FCDLPGIMQHFTIPA  IMQHFTIPA         0.0766      21825.2             50.00     Sequence
DRB3_0101  454  KRENEIEPVNIRPHP  NEIEPVNIR         0.0762      21928.4             50.00     Sequence
DRB3_0101  288  MYDETGYAGLSDTAR  MYDETGYAG         0.0760      21972.1             50.00     Sequence
DRB3_0101  405  YELPPEEAASIPQTP  YELPPEEAA         0.0755      22088.7             50.00     Sequence
DRB3_0101  167  TEADGSPNRGYKVRH  GSPNRGYKV         0.0751      22184.5             50.00     Sequence
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   DRB3_0101  237  AADDMQLYKYIIKNT  ADDMQLYKY        0.0716      23030.7               50.00     Sequence
   DRB3_0101  154  VDAISGWWNTGAATE  GWWNTGAAT        0.0714      23081.6               50.00     Sequence
   DRB3_0101  178  KVRHKGGYFPVAPND  KVRHKGGYF        0.0701      23425.0               50.00     Sequence
   DRB3_0101  157  ISGWWNTGAATEADG  WNTGAATEA        0.0698      23495.3               50.00     Sequence
   DRB3_0101  168  EADGSPNRGYKVRHK  GSPNRGYKV        0.0697      23519.3               50.00     Sequence
   DRB3_0101  367  RSPDSSGNPYLAFSA  SSGNPYLAF        0.0688      23738.9               50.00     Sequence
   DRB3_0101   26  DLPGIMQHFTIPASA  IMQHFTIPA        0.0688      23759.2               50.00     Sequence
   DRB3_0101  169  ADGSPNRGYKVRHKG  GSPNRGYKV        0.0675      24088.2               50.00     Sequence
   DRB3_0101  344  RNRSACVRIPITGSN  RNRSACVRI        0.0673      24139.0               50.00     Sequence
   DRB3_0101  384  MAGLDGIKNKIEPQA  IKNKIEPQA        0.0667      24285.2               50.00     Sequence
   DRB3_0101  163  TGAATEADGSPNRGY  ADGSPNRGY        0.0651      24709.6               50.00     Sequence
   DRB3_0101  343  QRNRSACVRIPITGS  RNRSACVRI        0.0646      24855.7               50.00     Sequence
   DRB3_0101  413  ASIPQTPTQLSDVID  IPQTPTQLS        0.0635      25156.8               50.00     Sequence
   DRB3_0101  385  AGLDGIKNKIEPQAP  IKNKIEPQA        0.0620      25550.5               50.00     Sequence
   DRB3_0101  164  GAATEADGSPNRGYK  ADGSPNRGY        0.0608      25908.2               50.00     Sequence
   DRB3_0101  409  PEEAASIPQTPTQLS  IPQTPTQLS        0.0597      26203.6               50.00     Sequence
   DRB3_0101  412  AASIPQTPTQLSDVI  IPQTPTQLS        0.0595      26268.4               50.00     Sequence
   DRB3_0101  345  NRSACVRIPITGSNP  CVRIPITGS        0.0594      26290.5               50.00     Sequence
   DRB3_0101  158  SGWWNTGAATEADGS  WNTGAATEA        0.0592      26361.2               50.00     Sequence
   DRB3_0101  411  EAASIPQTPTQLSDV  IPQTPTQLS        0.0575      26838.0               50.00     Sequence
   DRB3_0101  410  EEAASIPQTPTQLSD  IPQTPTQLS        0.0568      27049.1               50.00     Sequence
   DRB3_0101  347  SACVRIPITGSNPKA  CVRIPITGS        0.0562      27207.3               50.00     Sequence
   DRB3_0101  346  RSACVRIPITGSNPK  CVRIPITGS        0.0562      27213.5               50.00     Sequence
   DRB3_0101  170  DGSPNRGYKVRHKGG  GSPNRGYKV        0.0561      27243.0               50.00     Sequence
   DRB3_0101  211  ILEKGHHEVGSGGQA  ILEKGHHEV        0.0545      27716.0               50.00     Sequence
   DRB3_0101  349  CVRIPITGSNPKAKR  CVRIPITGS        0.0544      27765.2               50.00     Sequence
   DRB3_0101  159  GWWNTGAATEADGSP  WNTGAATEA        0.0543      27791.4               50.00     Sequence
   DRB3_0101  289  YDETGYAGLSDTARH  YAGLSDTAR        0.0535      28029.0               50.00     Sequence
   DRB3_0101  348  ACVRIPITGSNPKAK  CVRIPITGS        0.0533      28094.6               50.00     Sequence
   DRB3_0101   53  DGSSIRGFQSIHESD  RGFQSIHES        0.0531      28135.1               50.00     Sequence
   DRB3_0101  359  PKAKRLEFRSPDSSG  LEFRSPDSS        0.0515      28632.9               50.00     Sequence
   DRB3_0101  358  NPKAKRLEFRSPDSS  LEFRSPDSS        0.0494      29299.8               50.00     Sequence
   DRB3_0101  350  VRIPITGSNPKAKRL  VRIPITGSN        0.0493      29328.6               50.00     Sequence
   DRB3_0101  408  PPEEAASIPQTPTQL  SIPQTPTQL        0.0487      29508.2               50.00     Sequence
   DRB3_0101  161  WNTGAATEADGSPNR  WNTGAATEA        0.0460      30400.3               50.00     Sequence
   DRB3_0101  383  LMAGLDGIKNKIEPQ  GLDGIKNKI        0.0447      30832.3               50.00     Sequence
   DRB3_0101  215  GHHEVGSGGQAEINY  SGGQAEINY        0.0444      30931.5               50.00     Sequence
   DRB3_0101  351  RIPITGSNPKAKRLE  ITGSNPKAK        0.0438      31123.9               50.00     Sequence
   DRB3_0101  216  HHEVGSGGQAEINYQ  SGGQAEINY        0.0432      31329.7               50.00     Sequence
   DRB3_0101  160  WWNTGAATEADGSPN  WNTGAATEA        0.0410      32086.5               50.00     Sequence
   DRB3_0101  406  ELPPEEAASIPQTPT  LPPEEAASI        0.0404      32311.2               50.00     Sequence
   DRB3_0101  213  EKGHHEVGSGGQAEI  VGSGGQAEI        0.0394      32644.3               50.00     Sequence
   DRB3_0101  407  LPPEEAASIPQTPTQ  LPPEEAASI        0.0393      32664.8               50.00     Sequence
   DRB3_0101  214  KGHHEVGSGGQAEIN  VGSGGQAEI        0.0388      32842.3               50.00     Sequence
   DRB3_0101  162  NTGAATEADGSPNRG  TEADGSPNR        0.0343      34491.8               50.00     Sequence
   DRB3_0101  356  GSNPKAKRLEFRSPD  KRLEFRSPD        0.0328      35058.4               50.00     Sequence
   DRB3_0101  212  LEKGHHEVGSGGQAE  HEVGSGGQA        0.0310      35758.3               50.00     Sequence
   DRB3_0101  357  SNPKAKRLEFRSPDS  KRLEFRSPD        0.0300      36122.7               50.00     Sequence
   DRB3_0101  352  IPITGSNPKAKRLEF  ITGSNPKAK        0.0268      37418.0               50.00     Sequence
   DRB3_0101  353  PITGSNPKAKRLEFR  ITGSNPKAK        0.0255      37931.6               50.00     Sequence
   DRB3_0101  354  ITGSNPKAKRLEFRS  NPKAKRLEF        0.0240      38563.0               50.00     Sequence
   DRB3_0101  355  TGSNPKAKRLEFRSP  TGSNPKAKR        0.0229      39010.0               50.00     Sequence
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Allele: DRB3_0101. Number of high binders 0. Number of weak binders 54. Number of peptides 464

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB4_0101  302  RHYIGGLLHHAPSLL  RHYIGGLLH        0.7363         17.3         SB     0.80     Sequence
   DRB4_0101  301  ARHYIGGLLHHAPSL  RHYIGGLLH        0.7221         20.2         SB     1.00     Sequence
   DRB4_0101  300  TARHYIGGLLHHAPS  RHYIGGLLH        0.6682         36.2         SB     4.00     Sequence
   DRB4_0101  223  GQAEINYQFNSLLHA  INYQFNSLL        0.6482         45.0         SB     4.00     Sequence
   DRB4_0101  303  HYIGGLLHHAPSLLA  IGGLLHHAP        0.6460         46.1         SB     4.00     Sequence
   DRB4_0101  222  GGQAEINYQFNSLLH  INYQFNSLL        0.6390         49.7         SB     4.00     Sequence
   DRB4_0101  299  DTARHYIGGLLHHAP  RHYIGGLLH        0.6342         52.4         WB     4.00     Sequence
   DRB4_0101  333  YEAPINLVYSQRNRS  INLVYSQRN        0.6341         52.4         WB     4.00     Sequence
   DRB4_0101  334  EAPINLVYSQRNRSA  INLVYSQRN        0.6332         52.9         WB     4.00     Sequence
   DRB4_0101  332  GYEAPINLVYSQRNR  INLVYSQRN        0.6281         55.9         WB     4.00     Sequence
   DRB4_0101  335  APINLVYSQRNRSAC  INLVYSQRN        0.6231         59.0         WB     8.00     Sequence
   DRB4_0101  221  SGGQAEINYQFNSLL  INYQFNSLL        0.6220         59.7         WB     8.00     Sequence
   DRB4_0101   84  AAKTLNINFFVHDPF  INFFVHDPF        0.6207         60.6         WB     8.00     Sequence
   DRB4_0101  224  QAEINYQFNSLLHAA  INYQFNSLL        0.6102         67.9         WB     8.00     Sequence
   DRB4_0101   85  AKTLNINFFVHDPFT  INFFVHDPF        0.6029         73.4         WB     8.00     Sequence
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DRB4_0101  331  PGYEAPINLVYSQRN  INLVYSQRN        0.6015         74.6        WB    8.00      Sequence
DRB4_0101   86  KTLNINFFVHDPFTL  INFFVHDPF        0.5998         76.0        WB    8.00      Sequence
DRB4_0101  298  SDTARHYIGGLLHHA  RHYIGGLLH        0.5914         83.2        WB    8.00      Sequence
DRB4_0101  305  IGGLLHHAPSLLAFT  GGLLHHAPS        0.5855         88.7        WB    8.00      Sequence
DRB4_0101  304  YIGGLLHHAPSLLAF  GGLLHHAPS        0.5764         97.8        WB    8.00      Sequence
DRB4_0101  336  PINLVYSQRNRSACV  INLVYSQRN        0.5752         99.2        WB    8.00      Sequence
DRB4_0101   87  TLNINFFVHDPFTLE  INFFVHDPF        0.5717        102.9        WB    8.00      Sequence
DRB4_0101  297  LSDTARHYIGGLLHH  RHYIGGLLH        0.5655        110.1        WB   16.00      Sequence
DRB4_0101   88  LNINFFVHDPFTLEP  INFFVHDPF        0.5642        111.6        WB   16.00      Sequence
DRB4_0101  337  INLVYSQRNRSACVR  INLVYSQRN        0.5550        123.3        WB   16.00      Sequence
DRB4_0101   54  GSSIRGFQSIHESDM  SSIRGFQSI        0.5497        130.6        WB   16.00      Sequence
DRB4_0101  306  GGLLHHAPSLLAFTN  GGLLHHAPS        0.5487        132.0        WB   16.00      Sequence
DRB4_0101   55  SSIRGFQSIHESDML  SSIRGFQSI        0.5481        132.9        WB   16.00      Sequence
DRB4_0101  225  AEINYQFNSLLHAAD  INYQFNSLL        0.5451        137.3        WB   16.00      Sequence
DRB4_0101   53  DGSSIRGFQSIHESD  SSIRGFQSI        0.5445        138.2        WB   16.00      Sequence
DRB4_0101  374  NPYLAFSAMLMAGLD  LAFSAMLMA        0.5438        139.2        WB   16.00      Sequence
DRB4_0101  373  GNPYLAFSAMLMAGL  PYLAFSAML        0.5393        146.1        WB   16.00      Sequence
DRB4_0101  372  SGNPYLAFSAMLMAG  LAFSAMLMA        0.5307        160.3        WB   16.00      Sequence
DRB4_0101   89  NINFFVHDPFTLEPY  INFFVHDPF        0.5257        169.4        WB   16.00      Sequence
DRB4_0101   52  FDGSSIRGFQSIHES  SIRGFQSIH        0.5205        179.2        WB   16.00      Sequence
DRB4_0101   56  SIRGFQSIHESDMLL  SIRGFQSIH        0.5137        192.7        WB   16.00      Sequence
DRB4_0101  360  KAKRLEFRSPDSSGN  LEFRSPDSS        0.5074        206.5        WB   16.00      Sequence
DRB4_0101   90  INFFVHDPFTLEPYS  INFFVHDPF        0.5073        206.6        WB   16.00      Sequence
DRB4_0101  359  PKAKRLEFRSPDSSG  LEFRSPDSS        0.5045        212.9        WB   16.00      Sequence
DRB4_0101  238  ADDMQLYKYIIKNTA  YKYIIKNTA        0.5016        219.8        WB   16.00      Sequence
DRB4_0101  371  SSGNPYLAFSAMLMA  PYLAFSAML        0.5012        220.8        WB   16.00      Sequence
DRB4_0101  375  PYLAFSAMLMAGLDG  LAFSAMLMA        0.5000        223.7        WB   16.00      Sequence
DRB4_0101  195  VDLRDKMLTNLINSG  VDLRDKMLT        0.4992        225.6        WB   16.00      Sequence
DRB4_0101  358  NPKAKRLEFRSPDSS  LEFRSPDSS        0.4979        228.8        WB   32.00      Sequence
DRB4_0101  227  INYQFNSLLHAADDM  INYQFNSLL        0.4960        233.6        WB   32.00      Sequence
DRB4_0101   25  CDLPGIMQHFTIPAS  LPGIMQHFT        0.4956        234.4        WB   32.00      Sequence
DRB4_0101   26  DLPGIMQHFTIPASA  LPGIMQHFT        0.4943        237.8        WB   32.00      Sequence
DRB4_0101  194  YVDLRDKMLTNLINS  VDLRDKMLT        0.4929        241.5        WB   32.00      Sequence
DRB4_0101  377  LAFSAMLMAGLDGIK  LAFSAMLMA        0.4898        249.7        WB   32.00      Sequence
DRB4_0101  226  EINYQFNSLLHAADD  INYQFNSLL        0.4892        251.4        WB   32.00      Sequence
DRB4_0101  361  AKRLEFRSPDSSGNP  LEFRSPDSS        0.4791        280.2        WB   32.00      Sequence
DRB4_0101   24  FCDLPGIMQHFTIPA  LPGIMQHFT        0.4748        293.8        WB   32.00      Sequence
DRB4_0101  376  YLAFSAMLMAGLDGI  LAFSAMLMA        0.4716        304.1        WB   32.00      Sequence
DRB4_0101   51  AFDGSSIRGFQSIHE  SSIRGFQSI        0.4676        317.4        WB   32.00      Sequence
DRB4_0101  255  NGKTVTFMPKPLFGD  VTFMPKPLF        0.4654        325.2        WB   32.00      Sequence
DRB4_0101  254  QNGKTVTFMPKPLFG  VTFMPKPLF        0.4633        332.6        WB   32.00      Sequence
DRB4_0101   23  RFCDLPGIMQHFTIP  LPGIMQHFT        0.4633        332.7        WB   32.00      Sequence
DRB4_0101  296  GLSDTARHYIGGLLH  RHYIGGLLH        0.4627        334.6        WB   32.00      Sequence
DRB4_0101  239  DDMQLYKYIIKNTAW  YKYIIKNTA        0.4616        339.0        WB   32.00      Sequence
DRB4_0101  233  SLLHAADDMQLYKYI  SLLHAADDM        0.4615        339.3        WB   32.00      Sequence
DRB4_0101  192  DQYVDLRDKMLTNLI  VDLRDKMLT        0.4611        340.5        WB   32.00      Sequence
DRB4_0101   21  DVRFCDLPGIMQHFT  LPGIMQHFT        0.4581        351.8        WB   32.00      Sequence
DRB4_0101  220  GSGGQAEINYQFNSL  QAEINYQFN        0.4579        352.6        WB   32.00      Sequence
DRB4_0101   16  KVEYVDVRFCDLPGI  VDVRFCDLP        0.4572        355.2        WB   32.00      Sequence
DRB4_0101   22  VRFCDLPGIMQHFTI  LPGIMQHFT        0.4559        360.4        WB   32.00      Sequence
DRB4_0101   15  EKVEYVDVRFCDLPG  VDVRFCDLP        0.4555        361.9        WB   32.00      Sequence
DRB4_0101  362  KRLEFRSPDSSGNPY  LEFRSPDSS        0.4536        369.5        WB   32.00      Sequence
DRB4_0101   57  IRGFQSIHESDMLLL  RGFQSIHES        0.4527        372.9        WB   32.00      Sequence
DRB4_0101  307  GLLHHAPSLLAFTNP  LHHAPSLLA        0.4505        382.1        WB   32.00      Sequence
DRB4_0101   14  DEKVEYVDVRFCDLP  VDVRFCDLP        0.4503        382.9        WB   32.00      Sequence
DRB4_0101   27  LPGIMQHFTIPASAF  LPGIMQHFT        0.4482        391.5        WB   32.00      Sequence
DRB4_0101  243  LYKYIIKNTAWQNGK  YKYIIKNTA        0.4477        393.6        WB   32.00      Sequence
DRB4_0101  253  WQNGKTVTFMPKPLF  VTFMPKPLF        0.4469        397.2        WB   32.00      Sequence
DRB4_0101  256  GKTVTFMPKPLFGDN  VTFMPKPLF        0.4455        403.2        WB   32.00      Sequence
DRB4_0101  193  QYVDLRDKMLTNLIN  VDLRDKMLT        0.4449        405.9        WB   32.00      Sequence
DRB4_0101  244  YKYIIKNTAWQNGKT  YKYIIKNTA        0.4448        406.2        WB   32.00      Sequence
DRB4_0101  232  NSLLHAADDMQLYKY  SLLHAADDM        0.4424        417.2        WB   32.00      Sequence
DRB4_0101  197  LRDKMLTNLINSGFI  LRDKMLTNL        0.4398        428.8        WB   32.00      Sequence
DRB4_0101  191  NDQYVDLRDKMLTNL  VDLRDKMLT        0.4392        431.8        WB   32.00      Sequence
DRB4_0101   20  VDVRFCDLPGIMQHF  VDVRFCDLP        0.4382        436.6        WB   32.00      Sequence
DRB4_0101  242  QLYKYIIKNTAWQNG  YKYIIKNTA        0.4309        472.0        WB   32.00      Sequence
DRB4_0101  459  IEPVNIRPHPYEFAL  IEPVNIRPH        0.4305        474.4        WB   32.00      Sequence
DRB4_0101  458  EIEPVNIRPHPYEFA  IEPVNIRPH        0.4302        475.9        WB   32.00      Sequence
DRB4_0101  234  LLHAADDMQLYKYII  DDMQLYKYI        0.4286        484.1        WB   32.00      Sequence
DRB4_0101   50  LAFDGSSIRGFQSIH  SSIRGFQSI        0.4283        485.7        WB   32.00      Sequence
DRB4_0101  422  LSDVIDRLEADHEYL  DVIDRLEAD        0.4277        489.1        WB   32.00      Sequence
DRB4_0101  423  SDVIDRLEADHEYLT  SDVIDRLEA        0.4276        489.4        WB   32.00      Sequence
DRB4_0101  378  AFSAMLMAGLDGIKN  MLMAGLDGI        0.4267        494.0        WB   32.00      Sequence
DRB4_0101   83  RAAKTLNINFFVHDP  AKTLNINFF        0.4261        497.7        WB   32.00      Sequence
DRB4_0101  229  YQFNSLLHAADDMQL  YQFNSLLHA        0.4258        499.3        WB   32.00      Sequence
DRB4_0101  228  NYQFNSLLHAADDMQ  YQFNSLLHA        0.4242        507.9             32.00      Sequence
DRB4_0101   82  FRAAKTLNINFFVHD  AKTLNINFF        0.4240        508.9             32.00      Sequence
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DRB4_0101   17  VEYVDVRFCDLPGIM  VDVRFCDLP         0.4235        511.9              32.00     Sequence
DRB4_0101  421  QLSDVIDRLEADHEY  DVIDRLEAD         0.4234        512.4              32.00     Sequence
DRB4_0101  196  DLRDKMLTNLINSGF  LRDKMLTNL         0.4214        523.4              32.00     Sequence
DRB4_0101  363  RLEFRSPDSSGNPYL  LEFRSPDSS         0.4201        530.9              32.00     Sequence
DRB4_0101  379  FSAMLMAGLDGIKNK  MLMAGLDGI         0.4180        543.1              32.00     Sequence
DRB4_0101   19  YVDVRFCDLPGIMQH  VDVRFCDLP         0.4154        558.6              32.00     Sequence
DRB4_0101   81  PFRAAKTLNINFFVH  AKTLNINFF         0.4153        558.9              32.00     Sequence
DRB4_0101  235  LHAADDMQLYKYIIK  DDMQLYKYI         0.4138        568.3              32.00     Sequence
DRB4_0101  257  KTVTFMPKPLFGDNG  VTFMPKPLF         0.4124        576.7              32.00     Sequence
DRB4_0101  380  SAMLMAGLDGIKNKI  AMLMAGLDG         0.4121        579.0              32.00     Sequence
DRB4_0101  230  QFNSLLHAADDMQLY  SLLHAADDM         0.4118        580.7              32.00     Sequence
DRB4_0101  231  FNSLLHAADDMQLYK  SLLHAADDM         0.4113        583.9              32.00     Sequence
DRB4_0101  237  AADDMQLYKYIIKNT  DDMQLYKYI         0.4095        595.3              32.00     Sequence
DRB4_0101  420  TQLSDVIDRLEADHE  VIDRLEADH         0.4093        596.4              32.00     Sequence
DRB4_0101  321  PTVNSYKRLVPGYEA  KRLVPGYEA         0.4089        599.4              32.00     Sequence
DRB4_0101   58  RGFQSIHESDMLLLP  FQSIHESDM         0.4088        599.9              32.00     Sequence
DRB4_0101  330  VPGYEAPINLVYSQR  APINLVYSQ         0.4036        634.8              32.00     Sequence
DRB4_0101  445  DLIETWISFKRENEI  ISFKRENEI         0.4036        634.8              32.00     Sequence
DRB4_0101  381  AMLMAGLDGIKNKIE  MLMAGLDGI         0.4026        641.5              32.00     Sequence
DRB4_0101  457  NEIEPVNIRPHPYEF  IEPVNIRPH         0.4017        647.5              50.00     Sequence
DRB4_0101  322  TVNSYKRLVPGYEAP  KRLVPGYEA         0.4016        648.1              50.00     Sequence
DRB4_0101  207  NSGFILEKGHHEVGS  SGFILEKGH         0.4014        649.8              50.00     Sequence
DRB4_0101  219  VGSGGQAEINYQFNS  QAEINYQFN         0.4004        657.1              50.00     Sequence
DRB4_0101  206  INSGFILEKGHHEVG  SGFILEKGH         0.3997        661.7              50.00     Sequence
DRB4_0101  370  DSSGNPYLAFSAMLM  NPYLAFSAM         0.3990        666.9              50.00     Sequence
DRB4_0101  190  PNDQYVDLRDKMLTN  VDLRDKMLT         0.3982        672.4              50.00     Sequence
DRB4_0101  424  DVIDRLEADHEYLTE  VIDRLEADH         0.3977        676.2              50.00     Sequence
DRB4_0101  236  HAADDMQLYKYIIKN  DDMQLYKYI         0.3966        684.5              50.00     Sequence
DRB4_0101  241  MQLYKYIIKNTAWQN  YKYIIKNTA         0.3962        687.1              50.00     Sequence
DRB4_0101  240  DMQLYKYIIKNTAWQ  YKYIIKNTA         0.3953        693.9              50.00     Sequence
DRB4_0101   79  IDPFRAAKTLNINFF  IDPFRAAKT         0.3942        702.4              50.00     Sequence
DRB4_0101   80  DPFRAAKTLNINFFV  AKTLNINFF         0.3925        715.6              50.00     Sequence
DRB4_0101  208  SGFILEKGHHEVGSG  SGFILEKGH         0.3918        721.2              50.00     Sequence
DRB4_0101  198  RDKMLTNLINSGFIL  KMLTNLINS         0.3911        726.8              50.00     Sequence
DRB4_0101  281  WKDGAPLMYDETGYA  PLMYDETGY         0.3898        736.8              50.00     Sequence
DRB4_0101   60  FQSIHESDMLLLPDP  FQSIHESDM         0.3898        737.0              50.00     Sequence
DRB4_0101  446  LIETWISFKRENEIE  ISFKRENEI         0.3864        764.5              50.00     Sequence
DRB4_0101   18  EYVDVRFCDLPGIMQ  VDVRFCDLP         0.3859        768.4              50.00     Sequence
DRB4_0101  308  LLHHAPSLLAFTNPT  LHHAPSLLA         0.3858        769.4              50.00     Sequence
DRB4_0101  447  IETWISFKRENEIEP  ISFKRENEI         0.3839        785.4              50.00     Sequence
DRB4_0101  444  NDLIETWISFKRENE  DLIETWISF         0.3825        797.3              50.00     Sequence
DRB4_0101   61  QSIHESDMLLLPDPE  IHESDMLLL         0.3814        806.4              50.00     Sequence
DRB4_0101  135  FYIFDSVSFDSRANG  VSFDSRANG         0.3799        819.9              50.00     Sequence
DRB4_0101  419  PTQLSDVIDRLEADH  VIDRLEADH         0.3793        825.0              50.00     Sequence
DRB4_0101   13  KDEKVEYVDVRFCDL  VEYVDVRFC         0.3793        825.7              50.00     Sequence
DRB4_0101  456  ENEIEPVNIRPHPYE  IEPVNIRPH         0.3787        830.4              50.00     Sequence
DRB4_0101   59  GFQSIHESDMLLLPD  FQSIHESDM         0.3779        838.3              50.00     Sequence
DRB4_0101  189  APNDQYVDLRDKMLT  VDLRDKMLT         0.3764        851.7              50.00     Sequence
DRB4_0101   62  SIHESDMLLLPDPET  DMLLLPDPE         0.3753        861.6              50.00     Sequence
DRB4_0101  460  EPVNIRPHPYEFALY  EPVNIRPHP         0.3743        871.3              50.00     Sequence
DRB4_0101  258  TVTFMPKPLFGDNGS  VTFMPKPLF         0.3731        882.6              50.00     Sequence
DRB4_0101   78  RIDPFRAAKTLNINF  IDPFRAAKT         0.3699        913.7              50.00     Sequence
DRB4_0101  280  LWKDGAPLMYDETGY  PLMYDETGY         0.3690        922.4              50.00     Sequence
DRB4_0101   63  IHESDMLLLPDPETA  SDMLLLPDP         0.3690        922.6              50.00     Sequence
DRB4_0101  323  VNSYKRLVPGYEAPI  KRLVPGYEA         0.3682        930.3              50.00     Sequence
DRB4_0101  338  NLVYSQRNRSACVRI  NLVYSQRNR         0.3679        933.7              50.00     Sequence
DRB4_0101  448  ETWISFKRENEIEPV  ISFKRENEI         0.3663        949.7              50.00     Sequence
DRB4_0101  199  DKMLTNLINSGFILE  KMLTNLINS         0.3647        966.4              50.00     Sequence
DRB4_0101  200  KMLTNLINSGFILEK  KMLTNLINS         0.3641        972.6              50.00     Sequence
DRB4_0101  136  YIFDSVSFDSRANGS  VSFDSRANG         0.3633        981.7              50.00     Sequence
DRB4_0101  324  NSYKRLVPGYEAPIN  KRLVPGYEA         0.3592       1026.1              50.00     Sequence
DRB4_0101  443  TNDLIETWISFKREN  ETWISFKRE         0.3591       1026.8              50.00     Sequence
DRB4_0101  325  SYKRLVPGYEAPINL  KRLVPGYEA         0.3582       1036.6              50.00     Sequence
DRB4_0101  205  LINSGFILEKGHHEV  SGFILEKGH         0.3552       1070.9              50.00     Sequence
DRB4_0101  284  GAPLMYDETGYAGLS  PLMYDETGY         0.3546       1078.2              50.00     Sequence
DRB4_0101   66  SDMLLLPDPETARID  SDMLLLPDP         0.3534       1092.7              50.00     Sequence
DRB4_0101   65  ESDMLLLPDPETARI  SDMLLLPDP         0.3525       1103.1              50.00     Sequence
DRB4_0101  283  DGAPLMYDETGYAGL  PLMYDETGY         0.3490       1145.7              50.00     Sequence
DRB4_0101  309  LHHAPSLLAFTNPTV  LHHAPSLLA         0.3484       1152.6              50.00     Sequence
DRB4_0101   64  HESDMLLLPDPETAR  SDMLLLPDP         0.3482       1155.7              50.00     Sequence
DRB4_0101  461  PVNIRPHPYEFALYY  PVNIRPHPY         0.3438       1211.4              50.00     Sequence
DRB4_0101   77  ARIDPFRAAKTLNIN  IDPFRAAKT         0.3438       1212.2              50.00     Sequence
DRB4_0101  455  RENEIEPVNIRPHPY  IEPVNIRPH         0.3434       1216.7              50.00     Sequence
DRB4_0101  369  PDSSGNPYLAFSAML  NPYLAFSAM         0.3429       1224.1              50.00     Sequence
DRB4_0101   12  AKDEKVEYVDVRFCD  VEYVDVRFC         0.3425       1229.3              50.00     Sequence
DRB4_0101   76  TARIDPFRAAKTLNI  DPFRAAKTL         0.3416       1240.6              50.00     Sequence
DRB4_0101  282  KDGAPLMYDETGYAG  PLMYDETGY         0.3388       1280.0              50.00     Sequence
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DRB4_0101  134  EFYIFDSVSFDSRAN  FDSVSFDSR         0.3369       1306.4              50.00      Sequence
DRB4_0101  271  GSGMHCHQSLWKDGA  SGMHCHQSL         0.3363       1314.0              50.00      Sequence
DRB4_0101   49  GLAFDGSSIRGFQSI  SSIRGFQSI         0.3363       1314.5              50.00      Sequence
DRB4_0101  270  NGSGMHCHQSLWKDG  SGMHCHQSL         0.3355       1326.4              50.00      Sequence
DRB4_0101  425  VIDRLEADHEYLTEG  VIDRLEADH         0.3342       1345.2              50.00      Sequence
DRB4_0101  382  MLMAGLDGIKNKIEP  MLMAGLDGI         0.3331       1361.1              50.00      Sequence
DRB4_0101  442  FTNDLIETWISFKRE  NDLIETWIS         0.3319       1378.6              50.00      Sequence
DRB4_0101  312  APSLLAFTNPTVNSY  LAFTNPTVN         0.3298       1409.5              50.00      Sequence
DRB4_0101  174  NRGYKVRHKGGYFPV  RGYKVRHKG         0.3292       1419.4              50.00      Sequence
DRB4_0101  311  HAPSLLAFTNPTVNS  LAFTNPTVN         0.3291       1420.8              50.00      Sequence
DRB4_0101  133  AEFYIFDSVSFDSRA  FYIFDSVSF         0.3289       1424.0              50.00      Sequence
DRB4_0101  252  AWQNGKTVTFMPKPL  GKTVTFMPK         0.3274       1447.6              50.00      Sequence
DRB4_0101  449  TWISFKRENEIEPVN  ISFKRENEI         0.3262       1465.5              50.00      Sequence
DRB4_0101  132  EAEFYIFDSVSFDSR  FYIFDSVSF         0.3262       1466.6              50.00      Sequence
DRB4_0101   94  VHDPFTLEPYSRDPR  DPFTLEPYS         0.3260       1469.4              50.00      Sequence
DRB4_0101  310  HHAPSLLAFTNPTVN  LAFTNPTVN         0.3257       1474.2              50.00      Sequence
DRB4_0101  414  SIPQTPTQLSDVIDR  IPQTPTQLS         0.3254       1479.3              50.00      Sequence
DRB4_0101   75  ETARIDPFRAAKTLN  IDPFRAAKT         0.3247       1489.9              50.00      Sequence
DRB4_0101  320  NPTVNSYKRLVPGYE  NPTVNSYKR         0.3241       1499.7              50.00      Sequence
DRB4_0101  203  TNLINSGFILEKGHH  SGFILEKGH         0.3235       1508.9              50.00      Sequence
DRB4_0101  413  ASIPQTPTQLSDVID  IPQTPTQLS         0.3229       1519.0              50.00      Sequence
DRB4_0101  390  IKNKIEPQAPVDKDL  NKIEPQAPV         0.3228       1520.8              50.00      Sequence
DRB4_0101  173  PNRGYKVRHKGGYFP  RGYKVRHKG         0.3216       1540.3              50.00      Sequence
DRB4_0101   95  HDPFTLEPYSRDPRN  DPFTLEPYS         0.3216       1540.6              50.00      Sequence
DRB4_0101  454  KRENEIEPVNIRPHP  IEPVNIRPH         0.3214       1544.2              50.00      Sequence
DRB4_0101  218  EVGSGGQAEINYQFN  QAEINYQFN         0.3199       1569.0              50.00      Sequence
DRB4_0101  137  IFDSVSFDSRANGSF  VSFDSRANG         0.3184       1595.9              50.00      Sequence
DRB4_0101  415  IPQTPTQLSDVIDRL  IPQTPTQLS         0.3182       1598.6              50.00      Sequence
DRB4_0101  313  PSLLAFTNPTVNSYK  LAFTNPTVN         0.3172       1615.3              50.00      Sequence
DRB4_0101  245  KYIIKNTAWQNGKTV  KYIIKNTAW         0.3166       1626.5              50.00      Sequence
DRB4_0101   11  LAKDEKVEYVDVRFC  VEYVDVRFC         0.3165       1628.1              50.00      Sequence
DRB4_0101   28  PGIMQHFTIPASAFD  QHFTIPASA         0.3162       1634.5              50.00      Sequence
DRB4_0101  327  KRLVPGYEAPINLVY  KRLVPGYEA         0.3160       1636.6              50.00      Sequence
DRB4_0101  462  VNIRPHPYEFALYYD  VNIRPHPYE         0.3160       1636.8              50.00      Sequence
DRB4_0101  175  RGYKVRHKGGYFPVA  RGYKVRHKG         0.3158       1640.6              50.00      Sequence
DRB4_0101  269  DNGSGMHCHQSLWKD  SGMHCHQSL         0.3146       1662.3              50.00      Sequence
DRB4_0101  202  LTNLINSGFILEKGH  LTNLINSGF         0.3145       1663.2              50.00      Sequence
DRB4_0101  204  NLINSGFILEKGHHE  SGFILEKGH         0.3143       1667.2              50.00      Sequence
DRB4_0101  201  MLTNLINSGFILEKG  LTNLINSGF         0.3143       1667.6              50.00      Sequence
DRB4_0101  259  VTFMPKPLFGDNGSG  VTFMPKPLF         0.3137       1679.3              50.00      Sequence
DRB4_0101  439  GGVFTNDLIETWISF  GGVFTNDLI         0.3136       1679.7              50.00      Sequence
DRB4_0101  389  GIKNKIEPQAPVDKD  KNKIEPQAP         0.3125       1700.4              50.00      Sequence
DRB4_0101  364  LEFRSPDSSGNPYLA  LEFRSPDSS         0.3108       1731.4              50.00      Sequence
DRB4_0101  391  KNKIEPQAPVDKDLY  NKIEPQAPV         0.3106       1736.6              50.00      Sequence
DRB4_0101  285  APLMYDETGYAGLSD  PLMYDETGY         0.3104       1738.8              50.00      Sequence
DRB4_0101  319  TNPTVNSYKRLVPGY  NPTVNSYKR         0.3088       1770.2              50.00      Sequence
DRB4_0101  412  AASIPQTPTQLSDVI  IPQTPTQLS         0.3083       1779.4              50.00      Sequence
DRB4_0101  209  GFILEKGHHEVGSGG  GFILEKGHH         0.3062       1819.5              50.00      Sequence
DRB4_0101  268  GDNGSGMHCHQSLWK  SGMHCHQSL         0.3057       1831.0              50.00      Sequence
DRB4_0101  418  TPTQLSDVIDRLEAD  DVIDRLEAD         0.3054       1836.5              50.00      Sequence
DRB4_0101  329  LVPGYEAPINLVYSQ  APINLVYSQ         0.3045       1855.1              50.00      Sequence
DRB4_0101  272  SGMHCHQSLWKDGAP  SGMHCHQSL         0.3040       1864.0              50.00      Sequence
DRB4_0101   30  IMQHFTIPASAFDKS  MQHFTIPAS         0.3037       1870.3              50.00      Sequence
DRB4_0101  326  YKRLVPGYEAPINLV  KRLVPGYEA         0.3027       1890.7              50.00      Sequence
DRB4_0101   96  DPFTLEPYSRDPRNI  DPFTLEPYS         0.3017       1911.4              50.00      Sequence
DRB4_0101  357  SNPKAKRLEFRSPDS  KRLEFRSPD         0.2982       1984.5              50.00      Sequence
DRB4_0101  388  DGIKNKIEPQAPVDK  KNKIEPQAP         0.2960       2033.4              50.00      Sequence
DRB4_0101  267  FGDNGSGMHCHQSLW  SGMHCHQSL         0.2956       2041.6              50.00      Sequence
DRB4_0101  172  SPNRGYKVRHKGGYF  RGYKVRHKG         0.2930       2098.8              50.00      Sequence
DRB4_0101  348  ACVRIPITGSNPKAK  VRIPITGSN         0.2926       2108.5              50.00      Sequence
DRB4_0101  279  SLWKDGAPLMYDETG  WKDGAPLMY         0.2925       2111.7              50.00      Sequence
DRB4_0101   29  GIMQHFTIPASAFDK  QHFTIPASA         0.2923       2115.6              50.00      Sequence
DRB4_0101  177  YKVRHKGGYFPVAPN  VRHKGGYFP         0.2916       2130.9              50.00      Sequence
DRB4_0101  115  ENYLISTGIADTAYF  ENYLISTGI         0.2910       2145.1              50.00      Sequence
DRB4_0101  386  GLDGIKNKIEPQAPV  KNKIEPQAP         0.2891       2189.1              50.00      Sequence
DRB4_0101  183  GGYFPVAPNDQYVDL  FPVAPNDQY         0.2887       2199.7              50.00      Sequence
DRB4_0101  349  CVRIPITGSNPKAKR  IPITGSNPK         0.2886       2202.2              50.00      Sequence
DRB4_0101  411  EAASIPQTPTQLSDV  IPQTPTQLS         0.2886       2202.3              50.00      Sequence
DRB4_0101   93  FVHDPFTLEPYSRDP  DPFTLEPYS         0.2877       2222.8              50.00      Sequence
DRB4_0101  182  KGGYFPVAPNDQYVD  FPVAPNDQY         0.2860       2265.2              50.00      Sequence
DRB4_0101  347  SACVRIPITGSNPKA  IPITGSNPK         0.2852       2284.1              50.00      Sequence
DRB4_0101  176  GYKVRHKGGYFPVAP  YKVRHKGGY         0.2846       2300.5              50.00      Sequence
DRB4_0101  114  AENYLISTGIADTAY  ENYLISTGI         0.2839       2317.2              50.00      Sequence
DRB4_0101  107  PRNIARKAENYLIST  RNIARKAEN         0.2837       2322.7              50.00      Sequence
DRB4_0101  441  VFTNDLIETWISFKR  NDLIETWIS         0.2830       2340.4              50.00      Sequence
DRB4_0101  350  VRIPITGSNPKAKRL  IPITGSNPK         0.2823       2357.0              50.00      Sequence
DRB4_0101  440  GVFTNDLIETWISFK  NDLIETWIS         0.2820       2364.9              50.00      Sequence
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DRB4_0101  131  AEAEFYIFDSVSFDS  AEFYIFDSV       0.2815      2378.3           50.00     Sequence
DRB4_0101  314  SLLAFTNPTVNSYKR  LAFTNPTVN       0.2815      2378.8           50.00     Sequence
DRB4_0101  106  DPRNIARKAENYLIS  RNIARKAEN       0.2812      2384.5           50.00     Sequence
DRB4_0101   92  FFVHDPFTLEPYSRD  DPFTLEPYS       0.2811      2387.8           50.00     Sequence
DRB4_0101  346  RSACVRIPITGSNPK  IPITGSNPK       0.2810      2390.3           50.00     Sequence
DRB4_0101  251  TAWQNGKTVTFMPKP  GKTVTFMPK       0.2805      2403.4           50.00     Sequence
DRB4_0101    3  KTPDDVFKLAKDEKV  FKLAKDEKV       0.2794      2432.7           50.00     Sequence
DRB4_0101  410  EEAASIPQTPTQLSD  IPQTPTQLS       0.2788      2447.7           50.00     Sequence
DRB4_0101   74  PETARIDPFRAAKTL  IDPFRAAKT       0.2785      2455.7           50.00     Sequence
DRB4_0101  266  LFGDNGSGMHCHQSL  SGMHCHQSL       0.2776      2479.8           50.00     Sequence
DRB4_0101  438  EGGVFTNDLIETWIS  GGVFTNDLI       0.2765      2509.6           50.00     Sequence
DRB4_0101  113  KAENYLISTGIADTA  ENYLISTGI       0.2764      2512.6           50.00     Sequence
DRB4_0101  463  NIRPHPYEFALYYDV  YEFALYYDV       0.2763      2516.0           50.00     Sequence
DRB4_0101    4  TPDDVFKLAKDEKVE  FKLAKDEKV       0.2761      2520.7           50.00     Sequence
DRB4_0101  339  LVYSQRNRSACVRIP  LVYSQRNRS       0.2757      2531.3           50.00     Sequence
DRB4_0101  450  WISFKRENEIEPVNI  ISFKRENEI       0.2750      2550.8           50.00     Sequence
DRB4_0101  180  RHKGGYFPVAPNDQY  GGYFPVAPN       0.2749      2554.9           50.00     Sequence
DRB4_0101  181  HKGGYFPVAPNDQYV  FPVAPNDQY       0.2747      2558.5           50.00     Sequence
DRB4_0101  108  RNIARKAENYLISTG  RNIARKAEN       0.2742      2572.7           50.00     Sequence
DRB4_0101  246  YIIKNTAWQNGKTVT  YIIKNTAWQ       0.2739      2580.8           50.00     Sequence
DRB4_0101  453  FKRENEIEPVNIRPH  IEPVNIRPH       0.2734      2597.0           50.00     Sequence
DRB4_0101  171  GSPNRGYKVRHKGGY  RGYKVRHKG       0.2716      2646.9           50.00     Sequence
DRB4_0101  178  KVRHKGGYFPVAPND  GGYFPVAPN       0.2716      2648.0           50.00     Sequence
DRB4_0101  105  RDPRNIARKAENYLI  RNIARKAEN       0.2713      2654.8           50.00     Sequence
DRB4_0101  387  LDGIKNKIEPQAPVD  KNKIEPQAP       0.2710      2664.9           50.00     Sequence
DRB4_0101  138  FDSVSFDSRANGSFY  FDSVSFDSR       0.2706      2675.0           50.00     Sequence
DRB4_0101   31  MQHFTIPASAFDKSV  MQHFTIPAS       0.2699      2697.4           50.00     Sequence
DRB4_0101  179  VRHKGGYFPVAPNDQ  GGYFPVAPN       0.2695      2708.3           50.00     Sequence
DRB4_0101  278  QSLWKDGAPLMYDET  WKDGAPLMY       0.2665      2797.2           50.00     Sequence
DRB4_0101    5  PDDVFKLAKDEKVEY  FKLAKDEKV       0.2649      2845.5           50.00     Sequence
DRB4_0101  417  QTPTQLSDVIDRLEA  QLSDVIDRL       0.2636      2886.2           50.00     Sequence
DRB4_0101  186  FPVAPNDQYVDLRDK  FPVAPNDQY       0.2613      2958.9           50.00     Sequence
DRB4_0101   67  DMLLLPDPETARIDP  DMLLLPDPE       0.2604      2989.0           50.00     Sequence
DRB4_0101  368  SPDSSGNPYLAFSAM  NPYLAFSAM       0.2580      3066.0           50.00     Sequence
DRB4_0101   48  DGLAFDGSSIRGFQS  LAFDGSSIR       0.2577      3075.6           50.00     Sequence
DRB4_0101   44  SVFDDGLAFDGSSIR  LAFDGSSIR       0.2576      3079.8           50.00     Sequence
DRB4_0101   91  NFFVHDPFTLEPYSR  DPFTLEPYS       0.2576      3080.6           50.00     Sequence
DRB4_0101  286  PLMYDETGYAGLSDT  PLMYDETGY       0.2568      3107.9           50.00     Sequence
DRB4_0101  184  GYFPVAPNDQYVDLR  FPVAPNDQY       0.2566      3112.5           50.00     Sequence
DRB4_0101  409  PEEAASIPQTPTQLS  IPQTPTQLS       0.2556      3148.8           50.00     Sequence
DRB4_0101  356  GSNPKAKRLEFRSPD  AKRLEFRSP       0.2549      3170.0           50.00     Sequence
DRB4_0101   46  FDDGLAFDGSSIRGF  LAFDGSSIR       0.2541      3198.6           50.00     Sequence
DRB4_0101  416  PQTPTQLSDVIDRLE  LSDVIDRLE       0.2533      3227.3           50.00     Sequence
DRB4_0101   45  VFDDGLAFDGSSIRG  LAFDGSSIR       0.2532      3229.6           50.00     Sequence
DRB4_0101  385  AGLDGIKNKIEPQAP  GLDGIKNKI       0.2526      3252.3           50.00     Sequence
DRB4_0101  188  VAPNDQYVDLRDKML  QYVDLRDKM       0.2520      3271.3           50.00     Sequence
DRB4_0101  295  AGLSDTARHYIGGLL  LSDTARHYI       0.2500      3343.1           50.00     Sequence
DRB4_0101  318  FTNPTVNSYKRLVPG  TVNSYKRLV       0.2492      3372.6           50.00     Sequence
DRB4_0101  116  NYLISTGIADTAYFG  ISTGIADTA       0.2483      3407.0           50.00     Sequence
DRB4_0101  345  NRSACVRIPITGSNP  VRIPITGSN       0.2476      3431.3           50.00     Sequence
DRB4_0101  250  NTAWQNGKTVTFMPK  GKTVTFMPK       0.2468      3460.1           50.00     Sequence
DRB4_0101  351  RIPITGSNPKAKRLE  IPITGSNPK       0.2466      3469.8           50.00     Sequence
DRB4_0101  104  SRDPRNIARKAENYL  RNIARKAEN       0.2465      3474.5           50.00     Sequence
DRB4_0101  451  ISFKRENEIEPVNIR  ISFKRENEI       0.2460      3491.4           50.00     Sequence
DRB4_0101   73  DPETARIDPFRAAKT  IDPFRAAKT       0.2457      3502.3           50.00     Sequence
DRB4_0101  152  YEVDAISGWWNTGAA  VDAISGWWN       0.2452      3521.2           50.00     Sequence
DRB4_0101  109  NIARKAENYLISTGI  ENYLISTGI       0.2436      3582.1           50.00     Sequence
DRB4_0101  130  GAEAEFYIFDSVSFD  AEFYIFDSV       0.2425      3627.1           50.00     Sequence
DRB4_0101  117  YLISTGIADTAYFGA  ISTGIADTA       0.2422      3636.2           50.00     Sequence
DRB4_0101  344  RNRSACVRIPITGSN  CVRIPITGS       0.2422      3639.9           50.00     Sequence
DRB4_0101  151  FYEVDAISGWWNTGA  VDAISGWWN       0.2415      3666.7           50.00     Sequence
DRB4_0101   32  QHFTIPASAFDKSVF  QHFTIPASA       0.2407      3696.4           50.00     Sequence
DRB4_0101  247  IIKNTAWQNGKTVTF  IIKNTAWQN       0.2407      3697.0           50.00     Sequence
DRB4_0101  170  DGSPNRGYKVRHKGG  RGYKVRHKG       0.2388      3774.7           50.00     Sequence
DRB4_0101   47  DDGLAFDGSSIRGFQ  LAFDGSSIR       0.2386      3781.9           50.00     Sequence
DRB4_0101  140  SVSFDSRANGSFYEV  VSFDSRANG       0.2378      3816.8           50.00     Sequence
DRB4_0101  316  LAFTNPTVNSYKRLV  LAFTNPTVN       0.2377      3817.6           50.00     Sequence
DRB4_0101  112  RKAENYLISTGIADT  ENYLISTGI       0.2355      3910.2           50.00     Sequence
DRB4_0101    2  EKTPDDVFKLAKDEK  VFKLAKDEK       0.2346      3948.1           50.00     Sequence
DRB4_0101  139  DSVSFDSRANGSFYE  VSFDSRANG       0.2335      3998.6           50.00     Sequence
DRB4_0101  328  RLVPGYEAPINLVYS  EAPINLVYS       0.2334      4001.2           50.00     Sequence
DRB4_0101    6  DDVFKLAKDEKVEYV  DVFKLAKDE       0.2332      4010.3           50.00     Sequence
DRB4_0101   10  KLAKDEKVEYVDVRF  EKVEYVDVR       0.2331      4015.7           50.00     Sequence
DRB4_0101   97  PFTLEPYSRDPRNIA  TLEPYSRDP       0.2325      4039.1           50.00     Sequence
DRB4_0101  153  EVDAISGWWNTGAAT  VDAISGWWN       0.2325      4041.7           50.00     Sequence
DRB4_0101   98  FTLEPYSRDPRNIAR  LEPYSRDPR       0.2319      4065.1           50.00     Sequence
DRB4_0101   99  TLEPYSRDPRNIARK  LEPYSRDPR       0.2280      4243.8           50.00     Sequence
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DRB4_0101  149  GSFYEVDAISGWWNT  VDAISGWWN         0.2276        4259.9              50.00     Sequence
DRB4_0101  111  ARKAENYLISTGIAD  ENYLISTGI         0.2259        4337.8              50.00     Sequence
DRB4_0101  392  NKIEPQAPVDKDLYE  NKIEPQAPV         0.2258        4343.3              50.00     Sequence
DRB4_0101  110  IARKAENYLISTGIA  ENYLISTGI         0.2239        4432.6              50.00     Sequence
DRB4_0101  150  SFYEVDAISGWWNTG  VDAISGWWN         0.2238        4437.7              50.00     Sequence
DRB4_0101    7  DVFKLAKDEKVEYVD  DVFKLAKDE         0.2236        4451.3              50.00     Sequence
DRB4_0101    0  VTEKTPDDVFKLAKD  VTEKTPDDV         0.2232        4466.4              50.00     Sequence
DRB4_0101  185  YFPVAPNDQYVDLRD  FPVAPNDQY         0.2227        4493.6              50.00     Sequence
DRB4_0101  275  HCHQSLWKDGAPLMY  CHQSLWKDG         0.2226        4497.8              50.00     Sequence
DRB4_0101  187  PVAPNDQYVDLRDKM  QYVDLRDKM         0.2191        4669.4              50.00     Sequence
DRB4_0101  276  CHQSLWKDGAPLMYD  CHQSLWKDG         0.2180        4729.1              50.00     Sequence
DRB4_0101  437  TEGGVFTNDLIETWI  GGVFTNDLI         0.2170        4777.2              50.00     Sequence
DRB4_0101  352  IPITGSNPKAKRLEF  IPITGSNPK         0.2164        4812.0              50.00     Sequence
DRB4_0101  343  QRNRSACVRIPITGS  CVRIPITGS         0.2155        4858.5              50.00     Sequence
DRB4_0101  383  LMAGLDGIKNKIEPQ  GLDGIKNKI         0.2151        4879.3              50.00     Sequence
DRB4_0101  129  FGAEAEFYIFDSVSF  AEFYIFDSV         0.2120        5045.8              50.00     Sequence
DRB4_0101  426  IDRLEADHEYLTEGG  IDRLEADHE         0.2109        5104.2              50.00     Sequence
DRB4_0101  169  ADGSPNRGYKVRHKG  RGYKVRHKG         0.2104        5132.5              50.00     Sequence
DRB4_0101  317  AFTNPTVNSYKRLVP  NPTVNSYKR         0.2102        5141.9              50.00     Sequence
DRB4_0101  315  LLAFTNPTVNSYKRL  LAFTNPTVN         0.2096        5175.1              50.00     Sequence
DRB4_0101  210  FILEKGHHEVGSGGQ  ILEKGHHEV         0.2096        5177.1              50.00     Sequence
DRB4_0101  100  LEPYSRDPRNIARKA  LEPYSRDPR         0.2075        5294.2              50.00     Sequence
DRB4_0101  103  YSRDPRNIARKAENY  RNIARKAEN         0.2056        5404.9              50.00     Sequence
DRB4_0101    8  VFKLAKDEKVEYVDV  FKLAKDEKV         0.2055        5409.0              50.00     Sequence
DRB4_0101  384  MAGLDGIKNKIEPQA  GLDGIKNKI         0.2053        5421.5              50.00     Sequence
DRB4_0101  154  VDAISGWWNTGAATE  VDAISGWWN         0.2051        5433.8              50.00     Sequence
DRB4_0101  355  TGSNPKAKRLEFRSP  AKRLEFRSP         0.2050        5443.5              50.00     Sequence
DRB4_0101  292  TGYAGLSDTARHYIG  GLSDTARHY         0.2046        5465.6              50.00     Sequence
DRB4_0101  436  LTEGGVFTNDLIETW  GGVFTNDLI         0.2042        5487.7              50.00     Sequence
DRB4_0101  148  NGSFYEVDAISGWWN  VDAISGWWN         0.2021        5615.6              50.00     Sequence
DRB4_0101  277  HQSLWKDGAPLMYDE  WKDGAPLMY         0.2016        5642.8              50.00     Sequence
DRB4_0101   68  MLLLPDPETARIDPF  MLLLPDPET         0.2003        5726.4              50.00     Sequence
DRB4_0101  118  LISTGIADTAYFGAE  LISTGIADT         0.2002        5730.8              50.00     Sequence
DRB4_0101  265  PLFGDNGSGMHCHQS  GSGMHCHQS         0.1998        5755.0              50.00     Sequence
DRB4_0101  102  PYSRDPRNIARKAEN  RNIARKAEN         0.1997        5761.9              50.00     Sequence
DRB4_0101    9  FKLAKDEKVEYVDVR  DEKVEYVDV         0.1993        5787.2              50.00     Sequence
DRB4_0101  294  YAGLSDTARHYIGGL  GLSDTARHY         0.1989        5815.2              50.00     Sequence
DRB4_0101  340  VYSQRNRSACVRIPI  VYSQRNRSA         0.1988        5818.4              50.00     Sequence
DRB4_0101  249  KNTAWQNGKTVTFMP  QNGKTVTFM         0.1986        5831.3              50.00     Sequence
DRB4_0101  399  PVDKDLYELPPEEAA  LYELPPEEA         0.1985        5838.7              50.00     Sequence
DRB4_0101  293  GYAGLSDTARHYIGG  GLSDTARHY         0.1965        5965.9              50.00     Sequence
DRB4_0101  248  IKNTAWQNGKTVTFM  IKNTAWQNG         0.1946        6088.1              50.00     Sequence
DRB4_0101  398  APVDKDLYELPPEEA  LYELPPEEA         0.1940        6130.6              50.00     Sequence
DRB4_0101  264  KPLFGDNGSGMHCHQ  KPLFGDNGS         0.1939        6133.9              50.00     Sequence
DRB4_0101  291  ETGYAGLSDTARHYI  GLSDTARHY         0.1937        6147.8              50.00     Sequence
DRB4_0101   43  KSVFDDGLAFDGSSI  GLAFDGSSI         0.1933        6172.6              50.00     Sequence
DRB4_0101   34  FTIPASAFDKSVFDD  IPASAFDKS         0.1916        6292.5              50.00     Sequence
DRB4_0101   33  HFTIPASAFDKSVFD  IPASAFDKS         0.1897        6422.8              50.00     Sequence
DRB4_0101  217  HEVGSGGQAEINYQF  GQAEINYQF         0.1884        6512.6              50.00     Sequence
DRB4_0101  393  KIEPQAPVDKDLYEL  IEPQAPVDK         0.1877        6561.3              50.00     Sequence
DRB4_0101  211  ILEKGHHEVGSGGQA  ILEKGHHEV         0.1863        6661.7              50.00     Sequence
DRB4_0101  141  VSFDSRANGSFYEVD  VSFDSRANG         0.1850        6752.9              50.00     Sequence
DRB4_0101    1  TEKTPDDVFKLAKDE  DVFKLAKDE         0.1836        6858.9              50.00     Sequence
DRB4_0101  435  YLTEGGVFTNDLIET  GGVFTNDLI         0.1836        6861.2              50.00     Sequence
DRB4_0101  119  ISTGIADTAYFGAEA  ISTGIADTA         0.1833        6879.4              50.00     Sequence
DRB4_0101  262  MPKPLFGDNGSGMHC  KPLFGDNGS         0.1823        6959.3              50.00     Sequence
DRB4_0101   72  PDPETARIDPFRAAK  ARIDPFRAA         0.1816        7012.0              50.00     Sequence
DRB4_0101  101  EPYSRDPRNIARKAE  EPYSRDPRN         0.1811        7049.2              50.00     Sequence
DRB4_0101  263  PKPLFGDNGSGMHCH  KPLFGDNGS         0.1795        7169.1              50.00     Sequence
DRB4_0101  400  VDKDLYELPPEEAAS  LYELPPEEA         0.1742        7595.9              50.00     Sequence
DRB4_0101  394  IEPQAPVDKDLYELP  PVDKDLYEL         0.1729        7700.1              50.00     Sequence
DRB4_0101  401  DKDLYELPPEEAASI  LYELPPEEA         0.1726        7722.3              50.00     Sequence
DRB4_0101  342  SQRNRSACVRIPITG  NRSACVRIP         0.1725        7733.8              50.00     Sequence
DRB4_0101  127  AYFGAEAEFYIFDSV  AEFYIFDSV         0.1718        7788.9              50.00     Sequence
DRB4_0101  260  TFMPKPLFGDNGSGM  KPLFGDNGS         0.1704        7908.4              50.00     Sequence
DRB4_0101   35  TIPASAFDKSVFDDG  IPASAFDKS         0.1701        7936.5              50.00     Sequence
DRB4_0101  261  FMPKPLFGDNGSGMH  KPLFGDNGS         0.1675        8163.3              50.00     Sequence
DRB4_0101  427  DRLEADHEYLTEGGV  DRLEADHEY         0.1673        8177.3              50.00     Sequence
DRB4_0101  434  EYLTEGGVFTNDLIE  GGVFTNDLI         0.1660        8297.0              50.00     Sequence
DRB4_0101  147  ANGSFYEVDAISGWW  GSFYEVDAI         0.1656        8332.9              50.00     Sequence
DRB4_0101  341  YSQRNRSACVRIPIT  NRSACVRIP         0.1652        8373.4              50.00     Sequence
DRB4_0101  128  YFGAEAEFYIFDSVS  AEFYIFDSV         0.1626        8607.6              50.00     Sequence
DRB4_0101  402  KDLYELPPEEAASIP  LYELPPEEA         0.1624        8624.8              50.00     Sequence
DRB4_0101   36  IPASAFDKSVFDDGL  IPASAFDKS         0.1620        8665.5              50.00     Sequence
DRB4_0101  408  PPEEAASIPQTPTQL  AASIPQTPT         0.1614        8722.8              50.00     Sequence
DRB4_0101   71  LPDPETARIDPFRAA  ARIDPFRAA         0.1598        8869.2              50.00     Sequence
DRB4_0101  397  QAPVDKDLYELPPEE  QAPVDKDLY         0.1591        8936.5              50.00     Sequence
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   DRB4_0101  168  EADGSPNRGYKVRHK  NRGYKVRHK        0.1584       9011.0                50.00     Sequence
   DRB4_0101  396  PQAPVDKDLYELPPE  VDKDLYELP        0.1583       9014.9                50.00     Sequence
   DRB4_0101  273  GMHCHQSLWKDGAPL  CHQSLWKDG        0.1556       9280.7                50.00     Sequence
   DRB4_0101  290  DETGYAGLSDTARHY  TGYAGLSDT        0.1525       9600.0                50.00     Sequence
   DRB4_0101  367  RSPDSSGNPYLAFSA  SPDSSGNPY        0.1520       9650.9                50.00     Sequence
   DRB4_0101   69  LLLPDPETARIDPFR  LLLPDPETA        0.1513       9725.3                50.00     Sequence
   DRB4_0101  155  DAISGWWNTGAATEA  DAISGWWNT        0.1512       9735.0                50.00     Sequence
   DRB4_0101  395  EPQAPVDKDLYELPP  VDKDLYELP        0.1507       9787.1                50.00     Sequence
   DRB4_0101  452  SFKRENEIEPVNIRP  KRENEIEPV        0.1507       9791.5                50.00     Sequence
   DRB4_0101  433  HEYLTEGGVFTNDLI  GGVFTNDLI        0.1502       9847.5                50.00     Sequence
   DRB4_0101   42  DKSVFDDGLAFDGSS  FDDGLAFDG        0.1487      10004.3                50.00     Sequence
   DRB4_0101  403  DLYELPPEEAASIPQ  LYELPPEEA        0.1445      10469.2                50.00     Sequence
   DRB4_0101   41  FDKSVFDDGLAFDGS  FDDGLAFDG        0.1435      10589.6                50.00     Sequence
   DRB4_0101  428  RLEADHEYLTEGGVF  RLEADHEYL        0.1429      10658.3                50.00     Sequence
   DRB4_0101  146  RANGSFYEVDAISGW  GSFYEVDAI        0.1411      10865.6                50.00     Sequence
   DRB4_0101  354  ITGSNPKAKRLEFRS  KAKRLEFRS        0.1397      11031.2                50.00     Sequence
   DRB4_0101  274  MHCHQSLWKDGAPLM  CHQSLWKDG        0.1395      11058.0                50.00     Sequence
   DRB4_0101  407  LPPEEAASIPQTPTQ  AASIPQTPT        0.1388      11132.2                50.00     Sequence
   DRB4_0101  404  LYELPPEEAASIPQT  LYELPPEEA        0.1323      11950.0                50.00     Sequence
   DRB4_0101  143  FDSRANGSFYEVDAI  GSFYEVDAI        0.1323      11953.1                50.00     Sequence
   DRB4_0101  353  PITGSNPKAKRLEFR  NPKAKRLEF        0.1304      12198.4                50.00     Sequence
   DRB4_0101   70  LLPDPETARIDPFRA  TARIDPFRA        0.1297      12285.2                50.00     Sequence
   DRB4_0101   40  AFDKSVFDDGLAFDG  FDDGLAFDG        0.1271      12643.8                50.00     Sequence
   DRB4_0101  287  LMYDETGYAGLSDTA  LMYDETGYA        0.1233      13169.5                50.00     Sequence
   DRB4_0101  145  SRANGSFYEVDAISG  GSFYEVDAI        0.1233      13169.6                50.00     Sequence
   DRB4_0101   37  PASAFDKSVFDDGLA  AFDKSVFDD        0.1232      13186.3                50.00     Sequence
   DRB4_0101  365  EFRSPDSSGNPYLAF  DSSGNPYLA        0.1231      13198.0                50.00     Sequence
   DRB4_0101  406  ELPPEEAASIPQTPT  AASIPQTPT        0.1228      13235.8                50.00     Sequence
   DRB4_0101  289  YDETGYAGLSDTARH  TGYAGLSDT        0.1212      13470.4                50.00     Sequence
   DRB4_0101  366  FRSPDSSGNPYLAFS  SPDSSGNPY        0.1206      13566.3                50.00     Sequence
   DRB4_0101  216  HHEVGSGGQAEINYQ  VGSGGQAEI        0.1195      13720.7                50.00     Sequence
   DRB4_0101  144  DSRANGSFYEVDAIS  GSFYEVDAI        0.1186      13850.3                50.00     Sequence
   DRB4_0101  167  TEADGSPNRGYKVRH  GSPNRGYKV        0.1184      13890.0                50.00     Sequence
   DRB4_0101  120  STGIADTAYFGAEAE  TGIADTAYF        0.1181      13939.8                50.00     Sequence
   DRB4_0101  212  LEKGHHEVGSGGQAE  LEKGHHEVG        0.1177      13998.0                50.00     Sequence
   DRB4_0101  121  TGIADTAYFGAEAEF  TGIADTAYF        0.1156      14317.1                50.00     Sequence
   DRB4_0101  215  GHHEVGSGGQAEINY  VGSGGQAEI        0.1147      14454.5                50.00     Sequence
   DRB4_0101   38  ASAFDKSVFDDGLAF  AFDKSVFDD        0.1112      15018.1                50.00     Sequence
   DRB4_0101  126  TAYFGAEAEFYIFDS  AYFGAEAEF        0.1080      15533.3                50.00     Sequence
   DRB4_0101   39  SAFDKSVFDDGLAFD  FDKSVFDDG        0.1064      15804.6                50.00     Sequence
   DRB4_0101  142  SFDSRANGSFYEVDA  FDSRANGSF        0.1047      16101.3                50.00     Sequence
   DRB4_0101  288  MYDETGYAGLSDTAR  TGYAGLSDT        0.1042      16201.4                50.00     Sequence
   DRB4_0101  429  LEADHEYLTEGGVFT  LEADHEYLT        0.1029      16430.0                50.00     Sequence
   DRB4_0101  214  KGHHEVGSGGQAEIN  VGSGGQAEI        0.0996      17021.2                50.00     Sequence
   DRB4_0101  166  ATEADGSPNRGYKVR  GSPNRGYKV        0.0973      17445.4                50.00     Sequence
   DRB4_0101  432  DHEYLTEGGVFTNDL  EGGVFTNDL        0.0973      17452.9                50.00     Sequence
   DRB4_0101  156  AISGWWNTGAATEAD  ISGWWNTGA        0.0972      17462.7                50.00     Sequence
   DRB4_0101  125  DTAYFGAEAEFYIFD  AYFGAEAEF        0.0953      17825.8                50.00     Sequence
   DRB4_0101  213  EKGHHEVGSGGQAEI  VGSGGQAEI        0.0943      18019.6                50.00     Sequence
   DRB4_0101  405  YELPPEEAASIPQTP  LPPEEAASI        0.0921      18462.2                50.00     Sequence
   DRB4_0101  124  ADTAYFGAEAEFYIF  AYFGAEAEF        0.0920      18486.4                50.00     Sequence
   DRB4_0101  123  IADTAYFGAEAEFYI  AYFGAEAEF        0.0886      19171.9                50.00     Sequence
   DRB4_0101  165  AATEADGSPNRGYKV  GSPNRGYKV        0.0853      19871.4                50.00     Sequence
   DRB4_0101  430  EADHEYLTEGGVFTN  HEYLTEGGV        0.0825      20480.6                50.00     Sequence
   DRB4_0101  431  ADHEYLTEGGVFTND  HEYLTEGGV        0.0824      20505.9                50.00     Sequence
   DRB4_0101  157  ISGWWNTGAATEADG  ISGWWNTGA        0.0778      21536.4                50.00     Sequence
   DRB4_0101  122  GIADTAYFGAEAEFY  AYFGAEAEF        0.0754      22109.5                50.00     Sequence
   DRB4_0101  158  SGWWNTGAATEADGS  SGWWNTGAA        0.0639      25056.6                50.00     Sequence
   DRB4_0101  164  GAATEADGSPNRGYK  ADGSPNRGY        0.0612      25798.8                50.00     Sequence
   DRB4_0101  161  WNTGAATEADGSPNR  WNTGAATEA        0.0595      26273.5                50.00     Sequence
   DRB4_0101  163  TGAATEADGSPNRGY  ADGSPNRGY        0.0581      26675.1                50.00     Sequence
   DRB4_0101  160  WWNTGAATEADGSPN  WNTGAATEA        0.0577      26783.5                50.00     Sequence
   DRB4_0101  159  GWWNTGAATEADGSP  WNTGAATEA        0.0538      27922.5                50.00     Sequence
   DRB4_0101  162  NTGAATEADGSPNRG  TGAATEADG        0.0475      29900.6                50.00     Sequence
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Allele: DRB4_0101. Number of high binders 6. Number of weak binders 84. Number of peptides 464

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB5_0101  335  APINLVYSQRNRSAC  INLVYSQRN        0.8085          7.9         SB     0.40     Sequence
   DRB5_0101  336  PINLVYSQRNRSACV  INLVYSQRN        0.8018          8.5         SB     0.80     Sequence
   DRB5_0101  334  EAPINLVYSQRNRSA  INLVYSQRN        0.7962          9.1         SB     0.80     Sequence
   DRB5_0101  337  INLVYSQRNRSACVR  INLVYSQRN        0.7936          9.3         SB     0.80     Sequence
   DRB5_0101  333  YEAPINLVYSQRNRS  INLVYSQRN        0.7541         14.3         SB     2.00     Sequence
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DRB5_0101  304  YIGGLLHHAPSLLAF  LHHAPSLLA         0.7373         17.2         SB     2.00      Sequence
DRB5_0101   78  RIDPFRAAKTLNINF  FRAAKTLNI         0.7363         17.3         SB     2.00      Sequence
DRB5_0101  303  HYIGGLLHHAPSLLA  LHHAPSLLA         0.7286         18.8         SB     2.00      Sequence
DRB5_0101   77  ARIDPFRAAKTLNIN  FRAAKTLNI         0.7250         19.6         SB     2.00      Sequence
DRB5_0101   79  IDPFRAAKTLNINFF  FRAAKTLNI         0.7194         20.8         SB     4.00      Sequence
DRB5_0101  306  GGLLHHAPSLLAFTN  LHHAPSLLA         0.7100         23.1         SB     4.00      Sequence
DRB5_0101  305  IGGLLHHAPSLLAFT  LHHAPSLLA         0.7073         23.7         SB     4.00      Sequence
DRB5_0101  338  NLVYSQRNRSACVRI  LVYSQRNRS         0.7047         24.4         SB     4.00      Sequence
DRB5_0101   76  TARIDPFRAAKTLNI  FRAAKTLNI         0.7003         25.6         SB     4.00      Sequence
DRB5_0101  302  RHYIGGLLHHAPSLL  RHYIGGLLH         0.6936         27.5         SB     4.00      Sequence
DRB5_0101   80  DPFRAAKTLNINFFV  FRAAKTLNI         0.6930         27.7         SB     4.00      Sequence
DRB5_0101  307  GLLHHAPSLLAFTNP  LHHAPSLLA         0.6896         28.7         SB     4.00      Sequence
DRB5_0101  197  LRDKMLTNLINSGFI  DKMLTNLIN         0.6763         33.2         SB     4.00      Sequence
DRB5_0101  196  DLRDKMLTNLINSGF  DKMLTNLIN         0.6672         36.6         SB     8.00      Sequence
DRB5_0101  207  NSGFILEKGHHEVGS  FILEKGHHE         0.6649         37.6         SB     8.00      Sequence
DRB5_0101  208  SGFILEKGHHEVGSG  FILEKGHHE         0.6580         40.5         SB     8.00      Sequence
DRB5_0101  206  INSGFILEKGHHEVG  GFILEKGHH         0.6531         42.7         SB     8.00      Sequence
DRB5_0101  332  GYEAPINLVYSQRNR  INLVYSQRN         0.6528         42.8         SB     8.00      Sequence
DRB5_0101  301  ARHYIGGLLHHAPSL  RHYIGGLLH         0.6512         43.5         SB     8.00      Sequence
DRB5_0101  198  RDKMLTNLINSGFIL  DKMLTNLIN         0.6495         44.4         SB     8.00      Sequence
DRB5_0101  241  MQLYKYIIKNTAWQN  YKYIIKNTA         0.6448         46.7         SB     8.00      Sequence
DRB5_0101  209  GFILEKGHHEVGSGG  FILEKGHHE         0.6360         51.3         WB     8.00      Sequence
DRB5_0101  205  LINSGFILEKGHHEV  GFILEKGHH         0.6315         53.9         WB     8.00      Sequence
DRB5_0101  195  VDLRDKMLTNLINSG  DKMLTNLIN         0.6303         54.6         WB     8.00      Sequence
DRB5_0101  300  TARHYIGGLLHHAPS  RHYIGGLLH         0.6287         55.5         WB     8.00      Sequence
DRB5_0101  242  QLYKYIIKNTAWQNG  YKYIIKNTA         0.6249         57.9         WB     8.00      Sequence
DRB5_0101  299  DTARHYIGGLLHHAP  RHYIGGLLH         0.6198         61.2         WB     8.00      Sequence
DRB5_0101  226  EINYQFNSLLHAADD  YQFNSLLHA         0.6178         62.5         WB     8.00      Sequence
DRB5_0101  240  DMQLYKYIIKNTAWQ  YKYIIKNTA         0.6147         64.6         WB     8.00      Sequence
DRB5_0101  227  INYQFNSLLHAADDM  YQFNSLLHA         0.6104         67.8         WB     8.00      Sequence
DRB5_0101  243  LYKYIIKNTAWQNGK  YKYIIKNTA         0.6080         69.5         WB     8.00      Sequence
DRB5_0101  225  AEINYQFNSLLHAAD  YQFNSLLHA         0.6064         70.7         WB     8.00      Sequence
DRB5_0101  339  LVYSQRNRSACVRIP  LVYSQRNRS         0.6043         72.4         WB    16.00      Sequence
DRB5_0101  298  SDTARHYIGGLLHHA  RHYIGGLLH         0.6023         73.9         WB    16.00      Sequence
DRB5_0101  194  YVDLRDKMLTNLINS  DKMLTNLIN         0.6003         75.6         WB    16.00      Sequence
DRB5_0101  204  NLINSGFILEKGHHE  FILEKGHHE         0.5912         83.4         WB    16.00      Sequence
DRB5_0101   81  PFRAAKTLNINFFVH  FRAAKTLNI         0.5909         83.6         WB    16.00      Sequence
DRB5_0101  199  DKMLTNLINSGFILE  KMLTNLINS         0.5847         89.5         WB    16.00      Sequence
DRB5_0101  224  QAEINYQFNSLLHAA  INYQFNSLL         0.5800         94.1         WB    16.00      Sequence
DRB5_0101  244  YKYIIKNTAWQNGKT  YIIKNTAWQ         0.5793         94.8         WB    16.00      Sequence
DRB5_0101  308  LLHHAPSLLAFTNPT  LHHAPSLLA         0.5760         98.3         WB    16.00      Sequence
DRB5_0101  228  NYQFNSLLHAADDMQ  YQFNSLLHA         0.5627        113.5         WB    16.00      Sequence
DRB5_0101  445  DLIETWISFKRENEI  IETWISFKR         0.5626        113.6         WB    16.00      Sequence
DRB5_0101  239  DDMQLYKYIIKNTAW  YKYIIKNTA         0.5546        123.9         WB    16.00      Sequence
DRB5_0101  378  AFSAMLMAGLDGIKN  FSAMLMAGL         0.5517        127.8         WB    16.00      Sequence
DRB5_0101  444  NDLIETWISFKRENE  IETWISFKR         0.5480        133.0         WB    16.00      Sequence
DRB5_0101  229  YQFNSLLHAADDMQL  YQFNSLLHA         0.5450        137.4         WB    16.00      Sequence
DRB5_0101   31  MQHFTIPASAFDKSV  FTIPASAFD         0.5445        138.1         WB    16.00      Sequence
DRB5_0101  446  LIETWISFKRENEIE  IETWISFKR         0.5414        142.8         WB    16.00      Sequence
DRB5_0101  443  TNDLIETWISFKREN  IETWISFKR         0.5383        147.8         WB    16.00      Sequence
DRB5_0101  193  QYVDLRDKMLTNLIN  DKMLTNLIN         0.5382        147.9         WB    16.00      Sequence
DRB5_0101  331  PGYEAPINLVYSQRN  INLVYSQRN         0.5356        152.1         WB    16.00      Sequence
DRB5_0101   30  IMQHFTIPASAFDKS  FTIPASAFD         0.5342        154.4         WB    16.00      Sequence
DRB5_0101  377  LAFSAMLMAGLDGIK  FSAMLMAGL         0.5338        155.2         WB    16.00      Sequence
DRB5_0101   32  QHFTIPASAFDKSVF  FTIPASAFD         0.5282        164.8         WB    16.00      Sequence
DRB5_0101  376  YLAFSAMLMAGLDGI  FSAMLMAGL         0.5233        173.9         WB    16.00      Sequence
DRB5_0101   29  GIMQHFTIPASAFDK  FTIPASAFD         0.5194        181.2         WB    32.00      Sequence
DRB5_0101   51  AFDGSSIRGFQSIHE  FDGSSIRGF         0.5185        183.0         WB    32.00      Sequence
DRB5_0101  447  IETWISFKRENEIEP  IETWISFKR         0.5172        185.6         WB    32.00      Sequence
DRB5_0101  375  PYLAFSAMLMAGLDG  FSAMLMAGL         0.5170        185.9         WB    32.00      Sequence
DRB5_0101  223  GQAEINYQFNSLLHA  YQFNSLLHA         0.5094        202.0         WB    32.00      Sequence
DRB5_0101  271  GSGMHCHQSLWKDGA  MHCHQSLWK         0.5024        217.8         WB    32.00      Sequence
DRB5_0101  245  KYIIKNTAWQNGKTV  YIIKNTAWQ         0.5013        220.5         WB    32.00      Sequence
DRB5_0101  297  LSDTARHYIGGLLHH  RHYIGGLLH         0.5002        223.1         WB    32.00      Sequence
DRB5_0101  379  FSAMLMAGLDGIKNK  FSAMLMAGL         0.4982        228.0         WB    32.00      Sequence
DRB5_0101  272  SGMHCHQSLWKDGAP  MHCHQSLWK         0.4956        234.4         WB    32.00      Sequence
DRB5_0101  316  LAFTNPTVNSYKRLV  LAFTNPTVN         0.4870        257.4         WB    32.00      Sequence
DRB5_0101  315  LLAFTNPTVNSYKRL  FTNPTVNSY         0.4866        258.4         WB    32.00      Sequence
DRB5_0101  270  NGSGMHCHQSLWKDG  MHCHQSLWK         0.4859        260.5         WB    32.00      Sequence
DRB5_0101   52  FDGSSIRGFQSIHES  FDGSSIRGF         0.4859        260.6         WB    32.00      Sequence
DRB5_0101  273  GMHCHQSLWKDGAPL  MHCHQSLWK         0.4835        267.3         WB    32.00      Sequence
DRB5_0101  442  FTNDLIETWISFKRE  IETWISFKR         0.4820        271.6         WB    32.00      Sequence
DRB5_0101  314  SLLAFTNPTVNSYKR  FTNPTVNSY         0.4817        272.6         WB    32.00      Sequence
DRB5_0101  374  NPYLAFSAMLMAGLD  FSAMLMAGL         0.4809        274.9         WB    32.00      Sequence
DRB5_0101    6  DDVFKLAKDEKVEYV  FKLAKDEKV         0.4778        284.3         WB    32.00      Sequence
DRB5_0101  238  ADDMQLYKYIIKNTA  YKYIIKNTA         0.4767        287.7         WB    32.00      Sequence
DRB5_0101   33  HFTIPASAFDKSVFD  FTIPASAFD         0.4751        292.7         WB    32.00      Sequence
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   DRB5_0101  325  SYKRLVPGYEAPINL  YKRLVPGYE        0.4749       293.3        WB   32.00      Sequence
   DRB5_0101   49  GLAFDGSSIRGFQSI  FDGSSIRGF        0.4722       302.0        WB   32.00      Sequence
   DRB5_0101  321  PTVNSYKRLVPGYEA  YKRLVPGYE        0.4722       302.1        WB   32.00      Sequence
   DRB5_0101  323  VNSYKRLVPGYEAPI  YKRLVPGYE        0.4721       302.5        WB   32.00      Sequence
   DRB5_0101   50  LAFDGSSIRGFQSIH  FDGSSIRGF        0.4693       311.7        WB   32.00      Sequence
   DRB5_0101  373  GNPYLAFSAMLMAGL  FSAMLMAGL        0.4663       322.0        WB   32.00      Sequence
   DRB5_0101  324  NSYKRLVPGYEAPIN  YKRLVPGYE        0.4660       323.1        WB   32.00      Sequence
   DRB5_0101    5  PDDVFKLAKDEKVEY  FKLAKDEKV        0.4646       327.9        WB   32.00      Sequence
   DRB5_0101  149  GSFYEVDAISGWWNT  FYEVDAISG        0.4623       336.2        WB   32.00      Sequence
   DRB5_0101  200  KMLTNLINSGFILEK  KMLTNLINS        0.4578       353.2        WB   32.00      Sequence
   DRB5_0101  309  LHHAPSLLAFTNPTV  LHHAPSLLA        0.4576       353.9        WB   32.00      Sequence
   DRB5_0101  340  VYSQRNRSACVRIPI  RNRSACVRI        0.4570       356.2        WB   32.00      Sequence
   DRB5_0101   75  ETARIDPFRAAKTLN  PFRAAKTLN        0.4566       357.5        WB   32.00      Sequence
   DRB5_0101  322  TVNSYKRLVPGYEAP  YKRLVPGYE        0.4559       360.2        WB   32.00      Sequence
   DRB5_0101   54  GSSIRGFQSIHESDM  IRGFQSIHE        0.4559       360.3        WB   32.00      Sequence
   DRB5_0101    7  DVFKLAKDEKVEYVD  FKLAKDEKV        0.4557       361.1        WB   32.00      Sequence
   DRB5_0101  313  PSLLAFTNPTVNSYK  LAFTNPTVN        0.4537       369.0        WB   32.00      Sequence
   DRB5_0101  269  DNGSGMHCHQSLWKD  MHCHQSLWK        0.4525       373.7        WB   32.00      Sequence
   DRB5_0101   48  DGLAFDGSSIRGFQS  FDGSSIRGF        0.4525       373.9        WB   32.00      Sequence
   DRB5_0101   28  PGIMQHFTIPASAFD  FTIPASAFD        0.4521       375.5        WB   32.00      Sequence
   DRB5_0101  246  YIIKNTAWQNGKTVT  YIIKNTAWQ        0.4501       383.6        WB   32.00      Sequence
   DRB5_0101  350  VRIPITGSNPKAKRL  ITGSNPKAK        0.4491       387.7        WB   32.00      Sequence
   DRB5_0101  125  DTAYFGAEAEFYIFD  YFGAEAEFY        0.4462       400.2        WB   32.00      Sequence
   DRB5_0101  124  ADTAYFGAEAEFYIF  YFGAEAEFY        0.4456       402.9        WB   32.00      Sequence
   DRB5_0101    4  TPDDVFKLAKDEKVE  FKLAKDEKV        0.4424       417.0        WB   32.00      Sequence
   DRB5_0101  174  NRGYKVRHKGGYFPV  YKVRHKGGY        0.4391       432.2        WB   32.00      Sequence
   DRB5_0101  175  RGYKVRHKGGYFPVA  YKVRHKGGY        0.4379       437.7        WB   32.00      Sequence
   DRB5_0101   53  DGSSIRGFQSIHESD  IRGFQSIHE        0.4379       437.9        WB   32.00      Sequence
   DRB5_0101    8  VFKLAKDEKVEYVDV  FKLAKDEKV        0.4377       438.6        WB   32.00      Sequence
   DRB5_0101  296  GLSDTARHYIGGLLH  RHYIGGLLH        0.4373       440.6        WB   32.00      Sequence
   DRB5_0101  320  NPTVNSYKRLVPGYE  YKRLVPGYE        0.4363       445.5        WB   32.00      Sequence
   DRB5_0101  126  TAYFGAEAEFYIFDS  YFGAEAEFY        0.4354       450.0        WB   32.00      Sequence
   DRB5_0101  150  SFYEVDAISGWWNTG  FYEVDAISG        0.4352       450.9        WB   32.00      Sequence
   DRB5_0101  351  RIPITGSNPKAKRLE  ITGSNPKAK        0.4344       454.6        WB   32.00      Sequence
   DRB5_0101  210  FILEKGHHEVGSGGQ  FILEKGHHE        0.4340       456.6        WB   32.00      Sequence
   DRB5_0101  148  NGSFYEVDAISGWWN  FYEVDAISG        0.4339       457.1        WB   32.00      Sequence
   DRB5_0101   55  SSIRGFQSIHESDML  IRGFQSIHE        0.4337       458.3        WB   32.00      Sequence
   DRB5_0101  203  TNLINSGFILEKGHH  GFILEKGHH        0.4275       490.1        WB   32.00      Sequence
   DRB5_0101  312  APSLLAFTNPTVNSY  LAFTNPTVN        0.4274       490.3        WB   32.00      Sequence
   DRB5_0101  381  AMLMAGLDGIKNKIE  LMAGLDGIK        0.4270       492.7        WB   32.00      Sequence
   DRB5_0101  147  ANGSFYEVDAISGWW  FYEVDAISG        0.4266       494.8        WB   32.00      Sequence
   DRB5_0101  326  YKRLVPGYEAPINLV  YKRLVPGYE        0.4265       495.5        WB   32.00      Sequence
   DRB5_0101  342  SQRNRSACVRIPITG  RNRSACVRI        0.4259       498.4        WB   32.00      Sequence
   DRB5_0101   47  DDGLAFDGSSIRGFQ  FDGSSIRGF        0.4246       505.6             32.00      Sequence
   DRB5_0101   82  FRAAKTLNINFFVHD  FRAAKTLNI        0.4235       511.8             32.00      Sequence
   DRB5_0101  441  VFTNDLIETWISFKR  IETWISFKR        0.4222       519.0             32.00      Sequence
   DRB5_0101    3  KTPDDVFKLAKDEKV  FKLAKDEKV        0.4221       519.2             32.00      Sequence
   DRB5_0101  274  MHCHQSLWKDGAPLM  MHCHQSLWK        0.4210       525.6             32.00      Sequence
   DRB5_0101  343  QRNRSACVRIPITGS  RNRSACVRI        0.4202       530.4             32.00      Sequence
   DRB5_0101  317  AFTNPTVNSYKRLVP  FTNPTVNSY        0.4193       535.3             32.00      Sequence
   DRB5_0101  349  CVRIPITGSNPKAKR  ITGSNPKAK        0.4185       540.2             32.00      Sequence
   DRB5_0101  382  MLMAGLDGIKNKIEP  MAGLDGIKN        0.4169       549.7             32.00      Sequence
   DRB5_0101  380  SAMLMAGLDGIKNKI  LMAGLDGIK        0.4162       553.8             32.00      Sequence
   DRB5_0101  127  AYFGAEAEFYIFDSV  YFGAEAEFY        0.4138       568.1             32.00      Sequence
   DRB5_0101  173  PNRGYKVRHKGGYFP  YKVRHKGGY        0.4138       568.4             32.00      Sequence
   DRB5_0101  344  RNRSACVRIPITGSN  RNRSACVRI        0.4136       569.6             32.00      Sequence
   DRB5_0101   95  HDPFTLEPYSRDPRN  PFTLEPYSR        0.4133       571.4             32.00      Sequence
   DRB5_0101  123  IADTAYFGAEAEFYI  YFGAEAEFY        0.4131       572.4             32.00      Sequence
   DRB5_0101   56  SIRGFQSIHESDMLL  IRGFQSIHE        0.4125       576.2             32.00      Sequence
   DRB5_0101  176  GYKVRHKGGYFPVAP  YKVRHKGGY        0.4118       580.6             50.00      Sequence
   DRB5_0101   94  VHDPFTLEPYSRDPR  PFTLEPYSR        0.4111       584.9             50.00      Sequence
   DRB5_0101  448  ETWISFKRENEIEPV  FKRENEIEP        0.4080       605.3             50.00      Sequence
   DRB5_0101   96  DPFTLEPYSRDPRNI  PFTLEPYSR        0.4071       611.2             50.00      Sequence
   DRB5_0101   92  FFVHDPFTLEPYSRD  PFTLEPYSR        0.4061       617.8             50.00      Sequence
   DRB5_0101  256  GKTVTFMPKPLFGDN  KTVTFMPKP        0.4008       653.8             50.00      Sequence
   DRB5_0101  352  IPITGSNPKAKRLEF  ITGSNPKAK        0.4006       655.3             50.00      Sequence
   DRB5_0101  230  QFNSLLHAADDMQLY  FNSLLHAAD        0.3989       667.4             50.00      Sequence
   DRB5_0101  341  YSQRNRSACVRIPIT  RNRSACVRI        0.3974       678.9             50.00      Sequence
   DRB5_0101  255  NGKTVTFMPKPLFGD  KTVTFMPKP        0.3972       680.0             50.00      Sequence
   DRB5_0101  268  GDNGSGMHCHQSLWK  MHCHQSLWK        0.3943       701.9             50.00      Sequence
   DRB5_0101  257  KTVTFMPKPLFGDNG  TFMPKPLFG        0.3927       713.6             50.00      Sequence
   DRB5_0101   97  PFTLEPYSRDPRNIA  PFTLEPYSR        0.3914       723.7             50.00      Sequence
   DRB5_0101   91  NFFVHDPFTLEPYSR  FFVHDPFTL        0.3913       725.0             50.00      Sequence
   DRB5_0101  146  RANGSFYEVDAISGW  FYEVDAISG        0.3901       734.5             50.00      Sequence
   DRB5_0101   46  FDDGLAFDGSSIRGF  LAFDGSSIR        0.3884       748.1             50.00      Sequence
   DRB5_0101  363  RLEFRSPDSSGNPYL  FRSPDSSGN        0.3880       751.3             50.00      Sequence
   DRB5_0101  348  ACVRIPITGSNPKAK  ITGSNPKAK        0.3875       755.1             50.00      Sequence
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DRB5_0101  192  DQYVDLRDKMLTNLI  YVDLRDKML        0.3865      763.2              50.00     Sequence
DRB5_0101  330  VPGYEAPINLVYSQR  YEAPINLVY        0.3849      777.2              50.00     Sequence
DRB5_0101   22  VRFCDLPGIMQHFTI  RFCDLPGIM        0.3844      781.0              50.00     Sequence
DRB5_0101   57  IRGFQSIHESDMLLL  IRGFQSIHE        0.3837      786.6              50.00     Sequence
DRB5_0101   23  RFCDLPGIMQHFTIP  FCDLPGIMQ        0.3826      796.8              50.00     Sequence
DRB5_0101  362  KRLEFRSPDSSGNPY  FRSPDSSGN        0.3824      797.9              50.00     Sequence
DRB5_0101  151  FYEVDAISGWWNTGA  FYEVDAISG        0.3794      824.5              50.00     Sequence
DRB5_0101  318  FTNPTVNSYKRLVPG  FTNPTVNSY        0.3775      841.5              50.00     Sequence
DRB5_0101   21  DVRFCDLPGIMQHFT  FCDLPGIMQ        0.3752      863.1              50.00     Sequence
DRB5_0101  254  QNGKTVTFMPKPLFG  KTVTFMPKP        0.3750      864.3              50.00     Sequence
DRB5_0101  177  YKVRHKGGYFPVAPN  YKVRHKGGY        0.3749      865.4              50.00     Sequence
DRB5_0101  449  TWISFKRENEIEPVN  FKRENEIEP        0.3746      868.2              50.00     Sequence
DRB5_0101   93  FVHDPFTLEPYSRDP  PFTLEPYSR        0.3744      870.2              50.00     Sequence
DRB5_0101  122  GIADTAYFGAEAEFY  YFGAEAEFY        0.3738      875.5              50.00     Sequence
DRB5_0101  383  LMAGLDGIKNKIEPQ  MAGLDGIKN        0.3727      886.0              50.00     Sequence
DRB5_0101  372  SGNPYLAFSAMLMAG  YLAFSAMLM        0.3659      953.9              50.00     Sequence
DRB5_0101  361  AKRLEFRSPDSSGNP  FRSPDSSGN        0.3646      967.8              50.00     Sequence
DRB5_0101  251  TAWQNGKTVTFMPKP  WQNGKTVTF        0.3627      987.4              50.00     Sequence
DRB5_0101  222  GGQAEINYQFNSLLH  INYQFNSLL        0.3598     1019.0              50.00     Sequence
DRB5_0101   74  PETARIDPFRAAKTL  RIDPFRAAK        0.3592     1025.8              50.00     Sequence
DRB5_0101  114  AENYLISTGIADTAY  YLISTGIAD        0.3583     1035.8              50.00     Sequence
DRB5_0101  250  NTAWQNGKTVTFMPK  TAWQNGKTV        0.3563     1058.7              50.00     Sequence
DRB5_0101  327  KRLVPGYEAPINLVY  PGYEAPINL        0.3556     1067.0              50.00     Sequence
DRB5_0101  111  ARKAENYLISTGIAD  YLISTGIAD        0.3537     1089.0              50.00     Sequence
DRB5_0101   20  VDVRFCDLPGIMQHF  RFCDLPGIM        0.3534     1092.0              50.00     Sequence
DRB5_0101  360  KAKRLEFRSPDSSGN  LEFRSPDSS        0.3522     1107.1              50.00     Sequence
DRB5_0101  364  LEFRSPDSSGNPYLA  FRSPDSSGN        0.3519     1110.4              50.00     Sequence
DRB5_0101  247  IIKNTAWQNGKTVTF  IIKNTAWQN        0.3507     1124.6              50.00     Sequence
DRB5_0101  172  SPNRGYKVRHKGGYF  YKVRHKGGY        0.3504     1128.6              50.00     Sequence
DRB5_0101  115  ENYLISTGIADTAYF  YLISTGIAD        0.3501     1131.8              50.00     Sequence
DRB5_0101  311  HAPSLLAFTNPTVNS  SLLAFTNPT        0.3496     1137.9              50.00     Sequence
DRB5_0101   87  TLNINFFVHDPFTLE  FFVHDPFTL        0.3489     1146.5              50.00     Sequence
DRB5_0101  128  YFGAEAEFYIFDSVS  YFGAEAEFY        0.3484     1152.9              50.00     Sequence
DRB5_0101  113  KAENYLISTGIADTA  YLISTGIAD        0.3462     1180.7              50.00     Sequence
DRB5_0101  329  LVPGYEAPINLVYSQ  PGYEAPINL        0.3457     1187.0              50.00     Sequence
DRB5_0101   88  LNINFFVHDPFTLEP  FFVHDPFTL        0.3448     1199.0              50.00     Sequence
DRB5_0101  112  RKAENYLISTGIADT  YLISTGIAD        0.3444     1203.9              50.00     Sequence
DRB5_0101  107  PRNIARKAENYLIST  IARKAENYL        0.3384     1285.0              50.00     Sequence
DRB5_0101  249  KNTAWQNGKTVTFMP  TAWQNGKTV        0.3370     1304.5              50.00     Sequence
DRB5_0101  145  SRANGSFYEVDAISG  FYEVDAISG        0.3365     1311.1              50.00     Sequence
DRB5_0101  463  NIRPHPYEFALYYDV  HPYEFALYY        0.3360     1318.9              50.00     Sequence
DRB5_0101  106  DPRNIARKAENYLIS  IARKAENYL        0.3353     1328.2              50.00     Sequence
DRB5_0101  108  RNIARKAENYLISTG  IARKAENYL        0.3342     1345.0              50.00     Sequence
DRB5_0101  183  GGYFPVAPNDQYVDL  YFPVAPNDQ        0.3341     1345.9              50.00     Sequence
DRB5_0101   27  LPGIMQHFTIPASAF  HFTIPASAF        0.3341     1346.7              50.00     Sequence
DRB5_0101  182  KGGYFPVAPNDQYVD  YFPVAPNDQ        0.3338     1350.4              50.00     Sequence
DRB5_0101   19  YVDVRFCDLPGIMQH  RFCDLPGIM        0.3336     1353.4              50.00     Sequence
DRB5_0101   86  KTLNINFFVHDPFTL  FFVHDPFTL        0.3325     1369.8              50.00     Sequence
DRB5_0101  201  MLTNLINSGFILEKG  MLTNLINSG        0.3305     1399.4              50.00     Sequence
DRB5_0101  248  IKNTAWQNGKTVTFM  TAWQNGKTV        0.3300     1406.7              50.00     Sequence
DRB5_0101  450  WISFKRENEIEPVNI  FKRENEIEP        0.3290     1423.1              50.00     Sequence
DRB5_0101  328  RLVPGYEAPINLVYS  PGYEAPINL        0.3266     1460.6              50.00     Sequence
DRB5_0101  191  NDQYVDLRDKMLTNL  YVDLRDKML        0.3258     1473.0              50.00     Sequence
DRB5_0101  258  TVTFMPKPLFGDNGS  TFMPKPLFG        0.3257     1473.4              50.00     Sequence
DRB5_0101   34  FTIPASAFDKSVFDD  FTIPASAFD        0.3255     1477.6              50.00     Sequence
DRB5_0101  231  FNSLLHAADDMQLYK  FNSLLHAAD        0.3253     1480.2              50.00     Sequence
DRB5_0101  237  AADDMQLYKYIIKNT  QLYKYIIKN        0.3241     1499.8              50.00     Sequence
DRB5_0101   89  NINFFVHDPFTLEPY  FFVHDPFTL        0.3239     1503.4              50.00     Sequence
DRB5_0101  461  PVNIRPHPYEFALYY  HPYEFALYY        0.3238     1505.4              50.00     Sequence
DRB5_0101  371  SSGNPYLAFSAMLMA  PYLAFSAML        0.3218     1537.5              50.00     Sequence
DRB5_0101  184  GYFPVAPNDQYVDLR  YFPVAPNDQ        0.3213     1546.0              50.00     Sequence
DRB5_0101  384  MAGLDGIKNKIEPQA  MAGLDGIKN        0.3205     1559.5              50.00     Sequence
DRB5_0101  155  DAISGWWNTGAATEA  WWNTGAATE        0.3202     1564.4              50.00     Sequence
DRB5_0101  287  LMYDETGYAGLSDTA  LMYDETGYA        0.3175     1610.1              50.00     Sequence
DRB5_0101  310  HHAPSLLAFTNPTVN  LAFTNPTVN        0.3175     1611.2              50.00     Sequence
DRB5_0101  286  PLMYDETGYAGLSDT  LMYDETGYA        0.3168     1623.9              50.00     Sequence
DRB5_0101  275  HCHQSLWKDGAPLMY  HCHQSLWKD        0.3167     1625.5              50.00     Sequence
DRB5_0101  181  HKGGYFPVAPNDQYV  YFPVAPNDQ        0.3162     1634.2              50.00     Sequence
DRB5_0101   90  INFFVHDPFTLEPYS  FFVHDPFTL        0.3159     1639.6              50.00     Sequence
DRB5_0101  116  NYLISTGIADTAYFG  YLISTGIAD        0.3145     1663.5              50.00     Sequence
DRB5_0101  319  TNPTVNSYKRLVPGY  NPTVNSYKR        0.3135     1682.2              50.00     Sequence
DRB5_0101  285  APLMYDETGYAGLSD  LMYDETGYA        0.3132     1686.7              50.00     Sequence
DRB5_0101  253  WQNGKTVTFMPKPLF  KTVTFMPKP        0.3132     1687.7              50.00     Sequence
DRB5_0101  462  VNIRPHPYEFALYYD  HPYEFALYY        0.3124     1701.7              50.00     Sequence
DRB5_0101    9  FKLAKDEKVEYVDVR  FKLAKDEKV        0.3124     1702.0              50.00     Sequence
DRB5_0101  451  ISFKRENEIEPVNIR  FKRENEIEP        0.3119     1711.2              50.00     Sequence
DRB5_0101  157  ISGWWNTGAATEADG  WWNTGAATE        0.3102     1743.6              50.00     Sequence
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DRB5_0101   24  FCDLPGIMQHFTIPA  FCDLPGIMQ        0.3100      1747.6              50.00     Sequence
DRB5_0101  105  RDPRNIARKAENYLI  RNIARKAEN        0.3097      1753.6              50.00     Sequence
DRB5_0101  346  RSACVRIPITGSNPK  VRIPITGSN        0.3087      1771.9              50.00     Sequence
DRB5_0101  353  PITGSNPKAKRLEFR  ITGSNPKAK        0.3073      1797.9              50.00     Sequence
DRB5_0101  284  GAPLMYDETGYAGLS  LMYDETGYA        0.3067      1809.6              50.00     Sequence
DRB5_0101  252  AWQNGKTVTFMPKPL  WQNGKTVTF        0.3053      1837.9              50.00     Sequence
DRB5_0101  156  AISGWWNTGAATEAD  WWNTGAATE        0.3053      1838.3              50.00     Sequence
DRB5_0101   58  RGFQSIHESDMLLLP  FQSIHESDM        0.3049      1846.6              50.00     Sequence
DRB5_0101  347  SACVRIPITGSNPKA  VRIPITGSN        0.3035      1873.5              50.00     Sequence
DRB5_0101  458  EIEPVNIRPHPYEFA  PVNIRPHPY        0.3034      1876.9              50.00     Sequence
DRB5_0101  292  TGYAGLSDTARHYIG  YAGLSDTAR        0.3015      1916.2              50.00     Sequence
DRB5_0101   18  EYVDVRFCDLPGIMQ  RFCDLPGIM        0.2998      1951.0              50.00     Sequence
DRB5_0101  110  IARKAENYLISTGIA  IARKAENYL        0.2998      1951.1              50.00     Sequence
DRB5_0101  354  ITGSNPKAKRLEFRS  ITGSNPKAK        0.2998      1951.7              50.00     Sequence
DRB5_0101  452  SFKRENEIEPVNIRP  FKRENEIEP        0.2991      1966.0              50.00     Sequence
DRB5_0101  137  IFDSVSFDSRANGSF  FDSVSFDSR        0.2989      1970.8              50.00     Sequence
DRB5_0101  293  GYAGLSDTARHYIGG  YAGLSDTAR        0.2986      1975.7              50.00     Sequence
DRB5_0101  154  VDAISGWWNTGAATE  WWNTGAATE        0.2973      2004.3              50.00     Sequence
DRB5_0101  109  NIARKAENYLISTGI  IARKAENYL        0.2971      2007.9              50.00     Sequence
DRB5_0101  294  YAGLSDTARHYIGGL  YAGLSDTAR        0.2965      2020.8              50.00     Sequence
DRB5_0101  135  FYIFDSVSFDSRANG  YIFDSVSFD        0.2958      2036.3              50.00     Sequence
DRB5_0101  459  IEPVNIRPHPYEFAL  PVNIRPHPY        0.2957      2039.1              50.00     Sequence
DRB5_0101  138  FDSVSFDSRANGSFY  FDSVSFDSR        0.2951      2051.6              50.00     Sequence
DRB5_0101  453  FKRENEIEPVNIRPH  FKRENEIEP        0.2946      2064.8              50.00     Sequence
DRB5_0101  370  DSSGNPYLAFSAMLM  YLAFSAMLM        0.2931      2096.7              50.00     Sequence
DRB5_0101  117  YLISTGIADTAYFGA  YLISTGIAD        0.2931      2098.4              50.00     Sequence
DRB5_0101  171  GSPNRGYKVRHKGGY  YKVRHKGGY        0.2926      2109.1              50.00     Sequence
DRB5_0101  185  YFPVAPNDQYVDLRD  YFPVAPNDQ        0.2921      2119.5              50.00     Sequence
DRB5_0101  179  VRHKGGYFPVAPNDQ  YFPVAPNDQ        0.2908      2151.4              50.00     Sequence
DRB5_0101  158  SGWWNTGAATEADGS  WWNTGAATE        0.2891      2189.9              50.00     Sequence
DRB5_0101  140  SVSFDSRANGSFYEV  FDSRANGSF        0.2861      2261.9              50.00     Sequence
DRB5_0101  291  ETGYAGLSDTARHYI  YAGLSDTAR        0.2858      2270.6              50.00     Sequence
DRB5_0101  276  CHQSLWKDGAPLMYD  SLWKDGAPL        0.2841      2313.2              50.00     Sequence
DRB5_0101  202  LTNLINSGFILEKGH  LTNLINSGF        0.2839      2316.3              50.00     Sequence
DRB5_0101  236  HAADDMQLYKYIIKN  QLYKYIIKN        0.2837      2321.6              50.00     Sequence
DRB5_0101  134  EFYIFDSVSFDSRAN  YIFDSVSFD        0.2828      2343.6              50.00     Sequence
DRB5_0101  365  EFRSPDSSGNPYLAF  FRSPDSSGN        0.2820      2365.2              50.00     Sequence
DRB5_0101  180  RHKGGYFPVAPNDQY  YFPVAPNDQ        0.2809      2394.4              50.00     Sequence
DRB5_0101  283  DGAPLMYDETGYAGL  LMYDETGYA        0.2782      2463.4              50.00     Sequence
DRB5_0101  136  YIFDSVSFDSRANGS  YIFDSVSFD        0.2772      2490.6              50.00     Sequence
DRB5_0101  133  AEFYIFDSVSFDSRA  YIFDSVSFD        0.2771      2495.0              50.00     Sequence
DRB5_0101  259  VTFMPKPLFGDNGSG  TFMPKPLFG        0.2736      2590.4              50.00     Sequence
DRB5_0101  440  GVFTNDLIETWISFK  DLIETWISF        0.2725      2621.0              50.00     Sequence
DRB5_0101  190  PNDQYVDLRDKMLTN  QYVDLRDKM        0.2719      2638.1              50.00     Sequence
DRB5_0101   26  DLPGIMQHFTIPASA  LPGIMQHFT        0.2718      2641.7              50.00     Sequence
DRB5_0101  159  GWWNTGAATEADGSP  WWNTGAATE        0.2714      2651.6              50.00     Sequence
DRB5_0101  139  DSVSFDSRANGSFYE  FDSRANGSF        0.2714      2653.4              50.00     Sequence
DRB5_0101  178  KVRHKGGYFPVAPND  VRHKGGYFP        0.2707      2673.7              50.00     Sequence
DRB5_0101  457  NEIEPVNIRPHPYEF  IEPVNIRPH        0.2706      2674.7              50.00     Sequence
DRB5_0101  277  HQSLWKDGAPLMYDE  WKDGAPLMY        0.2686      2734.8              50.00     Sequence
DRB5_0101  460  EPVNIRPHPYEFALY  PVNIRPHPY        0.2684      2741.3              50.00     Sequence
DRB5_0101  295  AGLSDTARHYIGGLL  GLSDTARHY        0.2681      2749.1              50.00     Sequence
DRB5_0101  132  EAEFYIFDSVSFDSR  FYIFDSVSF        0.2680      2753.1              50.00     Sequence
DRB5_0101   73  DPETARIDPFRAAKT  RIDPFRAAK        0.2677      2759.6              50.00     Sequence
DRB5_0101  432  DHEYLTEGGVFTNDL  YLTEGGVFT        0.2664      2800.9              50.00     Sequence
DRB5_0101   45  VFDDGLAFDGSSIRG  LAFDGSSIR        0.2647      2852.5              50.00     Sequence
DRB5_0101   25  CDLPGIMQHFTIPAS  LPGIMQHFT        0.2617      2947.4              50.00     Sequence
DRB5_0101  278  QSLWKDGAPLMYDET  WKDGAPLMY        0.2602      2994.5              50.00     Sequence
DRB5_0101   67  DMLLLPDPETARIDP  LLPDPETAR        0.2601      2997.8              50.00     Sequence
DRB5_0101  281  WKDGAPLMYDETGYA  LMYDETGYA        0.2582      3059.5              50.00     Sequence
DRB5_0101  433  HEYLTEGGVFTNDLI  YLTEGGVFT        0.2582      3061.3              50.00     Sequence
DRB5_0101  221  SGGQAEINYQFNSLL  INYQFNSLL        0.2580      3065.4              50.00     Sequence
DRB5_0101  456  ENEIEPVNIRPHPYE  EIEPVNIRP        0.2572      3091.6              50.00     Sequence
DRB5_0101  359  PKAKRLEFRSPDSSG  LEFRSPDSS        0.2558      3140.0              50.00     Sequence
DRB5_0101  431  ADHEYLTEGGVFTND  YLTEGGVFT        0.2556      3147.0              50.00     Sequence
DRB5_0101  430  EADHEYLTEGGVFTN  YLTEGGVFT        0.2491      3375.0              50.00     Sequence
DRB5_0101   66  SDMLLLPDPETARID  LLPDPETAR        0.2491      3375.4              50.00     Sequence
DRB5_0101   68  MLLLPDPETARIDPF  LPDPETARI        0.2491      3376.8              50.00     Sequence
DRB5_0101  279  SLWKDGAPLMYDETG  WKDGAPLMY        0.2477      3428.2              50.00     Sequence
DRB5_0101  455  RENEIEPVNIRPHPY  IEPVNIRPH        0.2466      3470.4              50.00     Sequence
DRB5_0101  141  VSFDSRANGSFYEVD  FDSRANGSF        0.2455      3510.9              50.00     Sequence
DRB5_0101  232  NSLLHAADDMQLYKY  LHAADDMQL        0.2430      3607.7              50.00     Sequence
DRB5_0101  345  NRSACVRIPITGSNP  ACVRIPITG        0.2425      3626.4              50.00     Sequence
DRB5_0101  290  DETGYAGLSDTARHY  YAGLSDTAR        0.2416      3661.4              50.00     Sequence
DRB5_0101  369  PDSSGNPYLAFSAML  PYLAFSAML        0.2405      3704.5              50.00     Sequence
DRB5_0101   59  GFQSIHESDMLLLPD  FQSIHESDM        0.2358      3898.0              50.00     Sequence
DRB5_0101  235  LHAADDMQLYKYIIK  MQLYKYIIK        0.2351      3928.1              50.00     Sequence
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DRB5_0101  189  APNDQYVDLRDKMLT  YVDLRDKML        0.2349       3936.6              50.00     Sequence
DRB5_0101   65  ESDMLLLPDPETARI  LLPDPETAR        0.2346       3952.0              50.00     Sequence
DRB5_0101  233  SLLHAADDMQLYKYI  LHAADDMQL        0.2342       3966.7              50.00     Sequence
DRB5_0101  282  KDGAPLMYDETGYAG  LMYDETGYA        0.2341       3972.5              50.00     Sequence
DRB5_0101  153  EVDAISGWWNTGAAT  VDAISGWWN        0.2334       4001.2              50.00     Sequence
DRB5_0101   98  FTLEPYSRDPRNIAR  FTLEPYSRD        0.2334       4003.7              50.00     Sequence
DRB5_0101  385  AGLDGIKNKIEPQAP  GLDGIKNKI        0.2324       4046.1              50.00     Sequence
DRB5_0101  131  AEAEFYIFDSVSFDS  FYIFDSVSF        0.2301       4147.1              50.00     Sequence
DRB5_0101   44  SVFDDGLAFDGSSIR  LAFDGSSIR        0.2265       4311.7              50.00     Sequence
DRB5_0101  434  EYLTEGGVFTNDLIE  YLTEGGVFT        0.2261       4332.4              50.00     Sequence
DRB5_0101  267  FGDNGSGMHCHQSLW  GMHCHQSLW        0.2227       4494.7              50.00     Sequence
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DRB5_0101  454  KRENEIEPVNIRPHP  EIEPVNIRP        0.2199       4630.9              50.00     Sequence
DRB5_0101  358  NPKAKRLEFRSPDSS  LEFRSPDSS        0.2197       4639.0              50.00     Sequence
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DRB5_0101  170  DGSPNRGYKVRHKGG  NRGYKVRHK        0.2148       4891.0              50.00     Sequence
DRB5_0101  435  YLTEGGVFTNDLIET  YLTEGGVFT        0.2140       4935.2              50.00     Sequence
DRB5_0101  429  LEADHEYLTEGGVFT  YLTEGGVFT        0.2120       5042.5              50.00     Sequence
DRB5_0101  234  LLHAADDMQLYKYII  LHAADDMQL        0.2111       5093.2              50.00     Sequence
DRB5_0101   60  FQSIHESDMLLLPDP  SIHESDMLL        0.2103       5137.8              50.00     Sequence
DRB5_0101  366  FRSPDSSGNPYLAFS  FRSPDSSGN        0.2100       5152.3              50.00     Sequence
DRB5_0101  104  SRDPRNIARKAENYL  RNIARKAEN        0.2091       5206.3              50.00     Sequence
DRB5_0101  142  SFDSRANGSFYEVDA  FDSRANGSF        0.2072       5314.3              50.00     Sequence
DRB5_0101  386  GLDGIKNKIEPQAPV  GLDGIKNKI        0.2061       5374.9              50.00     Sequence
DRB5_0101   70  LLPDPETARIDPFRA  LLPDPETAR        0.2054       5419.4              50.00     Sequence
DRB5_0101  188  VAPNDQYVDLRDKML  YVDLRDKML        0.2026       5586.4              50.00     Sequence
DRB5_0101  214  KGHHEVGSGGQAEIN  GHHEVGSGG        0.2023       5602.1              50.00     Sequence
DRB5_0101   72  PDPETARIDPFRAAK  TARIDPFRA        0.2019       5623.9              50.00     Sequence
DRB5_0101  213  EKGHHEVGSGGQAEI  GHHEVGSGG        0.2002       5728.5              50.00     Sequence
DRB5_0101   85  AKTLNINFFVHDPFT  LNINFFVHD        0.1990       5807.3              50.00     Sequence
DRB5_0101  215  GHHEVGSGGQAEINY  GHHEVGSGG        0.1985       5837.8              50.00     Sequence
DRB5_0101    2  EKTPDDVFKLAKDEK  VFKLAKDEK        0.1980       5870.3              50.00     Sequence
DRB5_0101  129  FGAEAEFYIFDSVSF  FYIFDSVSF        0.1975       5898.5              50.00     Sequence
DRB5_0101  130  GAEAEFYIFDSVSFD  FYIFDSVSF        0.1971       5927.0              50.00     Sequence
DRB5_0101  288  MYDETGYAGLSDTAR  YAGLSDTAR        0.1919       6267.1              50.00     Sequence
DRB5_0101   64  HESDMLLLPDPETAR  DMLLLPDPE        0.1918       6273.4              50.00     Sequence
DRB5_0101  439  GGVFTNDLIETWISF  DLIETWISF        0.1909       6339.8              50.00     Sequence
DRB5_0101  212  LEKGHHEVGSGGQAE  GHHEVGSGG        0.1892       6458.3              50.00     Sequence
DRB5_0101   69  LLLPDPETARIDPFR  LPDPETARI        0.1871       6605.8              50.00     Sequence
DRB5_0101  289  YDETGYAGLSDTARH  YAGLSDTAR        0.1867       6630.3              50.00     Sequence
DRB5_0101  169  ADGSPNRGYKVRHKG  NRGYKVRHK        0.1813       7033.5              50.00     Sequence
DRB5_0101   16  KVEYVDVRFCDLPGI  KVEYVDVRF        0.1801       7127.1              50.00     Sequence
DRB5_0101  401  DKDLYELPPEEAASI  DLYELPPEE        0.1784       7256.6              50.00     Sequence
DRB5_0101  211  ILEKGHHEVGSGGQA  GHHEVGSGG        0.1771       7359.0              50.00     Sequence
DRB5_0101  101  EPYSRDPRNIARKAE  EPYSRDPRN        0.1759       7453.8              50.00     Sequence
DRB5_0101  100  LEPYSRDPRNIARKA  EPYSRDPRN        0.1759       7454.3              50.00     Sequence
DRB5_0101  103  YSRDPRNIARKAENY  RNIARKAEN        0.1737       7636.6              50.00     Sequence
DRB5_0101  355  TGSNPKAKRLEFRSP  GSNPKAKRL        0.1736       7645.8              50.00     Sequence
DRB5_0101  160  WWNTGAATEADGSPN  WWNTGAATE        0.1731       7682.4              50.00     Sequence
DRB5_0101  280  LWKDGAPLMYDETGY  WKDGAPLMY        0.1723       7747.0              50.00     Sequence
DRB5_0101   15  EKVEYVDVRFCDLPG  KVEYVDVRF        0.1723       7752.8              50.00     Sequence
DRB5_0101   84  AAKTLNINFFVHDPF  LNINFFVHD        0.1716       7805.8              50.00     Sequence
DRB5_0101  402  KDLYELPPEEAASIP  DLYELPPEE        0.1706       7891.6              50.00     Sequence
DRB5_0101   83  RAAKTLNINFFVHDP  LNINFFVHD        0.1700       7945.1              50.00     Sequence
DRB5_0101  356  GSNPKAKRLEFRSPD  GSNPKAKRL        0.1697       7968.5              50.00     Sequence
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DRB5_0101   14  DEKVEYVDVRFCDLP  KVEYVDVRF        0.1685       8074.6              50.00     Sequence
DRB5_0101   99  TLEPYSRDPRNIARK  PYSRDPRNI        0.1682       8098.2              50.00     Sequence
DRB5_0101   62  SIHESDMLLLPDPET  SIHESDMLL        0.1680       8122.3              50.00     Sequence
DRB5_0101  261  FMPKPLFGDNGSGMH  LFGDNGSGM        0.1665       8251.6              50.00     Sequence
DRB5_0101  389  GIKNKIEPQAPVDKD  IEPQAPVDK        0.1663       8269.4              50.00     Sequence
DRB5_0101  403  DLYELPPEEAASIPQ  DLYELPPEE        0.1663       8274.0              50.00     Sequence
DRB5_0101  102  PYSRDPRNIARKAEN  RNIARKAEN        0.1655       8340.5              50.00     Sequence
DRB5_0101   63  IHESDMLLLPDPETA  MLLLPDPET        0.1650       8386.6              50.00     Sequence
DRB5_0101  390  IKNKIEPQAPVDKDL  IEPQAPVDK        0.1648       8408.1              50.00     Sequence
DRB5_0101   13  KDEKVEYVDVRFCDL  KVEYVDVRF        0.1638       8500.1              50.00     Sequence
DRB5_0101  411  EAASIPQTPTQLSDV  SIPQTPTQL        0.1634       8533.0              50.00     Sequence
DRB5_0101  388  DGIKNKIEPQAPVDK  IEPQAPVDK        0.1620       8660.5              50.00     Sequence
DRB5_0101   61  QSIHESDMLLLPDPE  SIHESDMLL        0.1616       8704.1              50.00     Sequence
DRB5_0101  266  LFGDNGSGMHCHQSL  LFGDNGSGM        0.1611       8752.6              50.00     Sequence
DRB5_0101   35  TIPASAFDKSVFDDG  TIPASAFDK        0.1593       8917.5              50.00     Sequence
DRB5_0101  265  PLFGDNGSGMHCHQS  LFGDNGSGM        0.1587       8976.3              50.00     Sequence
DRB5_0101  391  KNKIEPQAPVDKDLY  IEPQAPVDK        0.1585       8996.7              50.00     Sequence
DRB5_0101  412  AASIPQTPTQLSDVI  SIPQTPTQL        0.1577       9080.9              50.00     Sequence
DRB5_0101  357  SNPKAKRLEFRSPDS  PKAKRLEFR        0.1565       9197.5              50.00     Sequence
DRB5_0101  168  EADGSPNRGYKVRHK  NRGYKVRHK        0.1524       9611.9              50.00     Sequence
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   DRB5_0101  400  VDKDLYELPPEEAAS  DLYELPPEE        0.1490       9977.3                 50.00     Sequence
   DRB5_0101   43  KSVFDDGLAFDGSSI  FDDGLAFDG        0.1480      10084.4                 50.00     Sequence
   DRB5_0101  423  SDVIDRLEADHEYLT  IDRLEADHE        0.1465      10243.1                 50.00     Sequence
   DRB5_0101  422  LSDVIDRLEADHEYL  IDRLEADHE        0.1460      10298.2                 50.00     Sequence
   DRB5_0101  121  TGIADTAYFGAEAEF  GIADTAYFG        0.1457      10337.7                 50.00     Sequence
   DRB5_0101  392  NKIEPQAPVDKDLYE  IEPQAPVDK        0.1448      10433.0                 50.00     Sequence
   DRB5_0101  410  EEAASIPQTPTQLSD  SIPQTPTQL        0.1447      10453.0                 50.00     Sequence
   DRB5_0101  424  DVIDRLEADHEYLTE  IDRLEADHE        0.1435      10580.3                 50.00     Sequence
   DRB5_0101  264  KPLFGDNGSGMHCHQ  LFGDNGSGM        0.1435      10588.3                 50.00     Sequence
   DRB5_0101  438  EGGVFTNDLIETWIS  GVFTNDLIE        0.1432      10619.4                 50.00     Sequence
   DRB5_0101  368  SPDSSGNPYLAFSAM  PDSSGNPYL        0.1422      10735.9                 50.00     Sequence
   DRB5_0101  186  FPVAPNDQYVDLRDK  FPVAPNDQY        0.1420      10762.3                 50.00     Sequence
   DRB5_0101  263  PKPLFGDNGSGMHCH  LFGDNGSGM        0.1403      10957.1                 50.00     Sequence
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   DRB5_0101   42  DKSVFDDGLAFDGSS  VFDDGLAFD        0.1347      11641.3                 50.00     Sequence
   DRB5_0101   12  AKDEKVEYVDVRFCD  KVEYVDVRF        0.1344      11680.0                 50.00     Sequence
   DRB5_0101   39  SAFDKSVFDDGLAFD  SVFDDGLAF        0.1341      11719.7                 50.00     Sequence
   DRB5_0101  413  ASIPQTPTQLSDVID  SIPQTPTQL        0.1340      11732.7                 50.00     Sequence
   DRB5_0101   41  FDKSVFDDGLAFDGS  VFDDGLAFD        0.1335      11794.5                 50.00     Sequence
   DRB5_0101  421  QLSDVIDRLEADHEY  IDRLEADHE        0.1328      11886.8                 50.00     Sequence
   DRB5_0101  399  PVDKDLYELPPEEAA  DLYELPPEE        0.1327      11899.0                 50.00     Sequence
   DRB5_0101  409  PEEAASIPQTPTQLS  SIPQTPTQL        0.1327      11900.8                 50.00     Sequence
   DRB5_0101  387  LDGIKNKIEPQAPVD  LDGIKNKIE        0.1322      11964.2                 50.00     Sequence
   DRB5_0101   40  AFDKSVFDDGLAFDG  VFDDGLAFD        0.1320      11992.8                 50.00     Sequence
   DRB5_0101  405  YELPPEEAASIPQTP  LPPEEAASI        0.1280      12522.5                 50.00     Sequence
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   DRB5_0101  437  TEGGVFTNDLIETWI  GVFTNDLIE        0.1259      12801.9                 50.00     Sequence
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   DRB5_0101  220  GSGGQAEINYQFNSL  GQAEINYQF        0.1178      13972.0                 50.00     Sequence
   DRB5_0101  187  PVAPNDQYVDLRDKM  QYVDLRDKM        0.1177      13987.4                 50.00     Sequence
   DRB5_0101  398  APVDKDLYELPPEEA  DLYELPPEE        0.1163      14205.3                 50.00     Sequence
   DRB5_0101  406  ELPPEEAASIPQTPT  LPPEEAASI        0.1148      14446.0                 50.00     Sequence
   DRB5_0101  419  PTQLSDVIDRLEADH  TQLSDVIDR        0.1126      14793.6                 50.00     Sequence
   DRB5_0101   38  ASAFDKSVFDDGLAF  SAFDKSVFD        0.1095      15296.5                 50.00     Sequence
   DRB5_0101  367  RSPDSSGNPYLAFSA  PDSSGNPYL        0.1083      15495.9                 50.00     Sequence
   DRB5_0101  118  LISTGIADTAYFGAE  LISTGIADT        0.1078      15568.0                 50.00     Sequence
   DRB5_0101  418  TPTQLSDVIDRLEAD  TQLSDVIDR        0.1065      15791.6                 50.00     Sequence
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   DRB5_0101  428  RLEADHEYLTEGGVF  EYLTEGGVF        0.1008      16793.6                 50.00     Sequence
   DRB5_0101  417  QTPTQLSDVIDRLEA  TQLSDVIDR        0.1003      16899.0                 50.00     Sequence
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   DRB5_0101  394  IEPQAPVDKDLYELP  IEPQAPVDK        0.0962      17662.3                 50.00     Sequence
   DRB5_0101  166  ATEADGSPNRGYKVR  EADGSPNRG        0.0937      18141.6                 50.00     Sequence
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   DRB5_0101  161  WNTGAATEADGSPNR  WNTGAATEA        0.0893      19021.3                 50.00     Sequence
   DRB5_0101  416  PQTPTQLSDVIDRLE  TQLSDVIDR        0.0858      19760.3                 50.00     Sequence
   DRB5_0101  218  EVGSGGQAEINYQFN  GQAEINYQF        0.0845      20050.2                 50.00     Sequence
   DRB5_0101  427  DRLEADHEYLTEGGV  HEYLTEGGV        0.0838      20186.9                 50.00     Sequence
   DRB5_0101  217  HEVGSGGQAEINYQF  HEVGSGGQA        0.0824      20506.3                 50.00     Sequence
   DRB5_0101  397  QAPVDKDLYELPPEE  DLYELPPEE        0.0823      20523.4                 50.00     Sequence
   DRB5_0101    1  TEKTPDDVFKLAKDE  DVFKLAKDE        0.0814      20716.8                 50.00     Sequence
   DRB5_0101  165  AATEADGSPNRGYKV  EADGSPNRG        0.0803      20961.7                 50.00     Sequence
   DRB5_0101  164  GAATEADGSPNRGYK  TEADGSPNR        0.0800      21050.6                 50.00     Sequence
   DRB5_0101  163  TGAATEADGSPNRGY  EADGSPNRG        0.0743      22380.0                 50.00     Sequence
   DRB5_0101  162  NTGAATEADGSPNRG  EADGSPNRG        0.0659      24506.9                 50.00     Sequence
   DRB5_0101    0  VTEKTPDDVFKLAKD  VTEKTPDDV        0.0625      25429.4                 50.00     Sequence
   DRB5_0101  395  EPQAPVDKDLYELPP  PVDKDLYEL        0.0420      31728.8                 50.00     Sequence
   DRB5_0101  396  PQAPVDKDLYELPPE  PVDKDLYEL        0.0410      32079.5                 50.00     Sequence
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Allele: DRB5_0101. Number of high binders 26. Number of weak binders 99. Number of peptides 464
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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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         IAb  315  LLAFTNPTVNSYKRL  LAFTNPTVN        0.7748         11.4         SB     0.10     Sequence
         IAb  314  SLLAFTNPTVNSYKR  LAFTNPTVN        0.7717         11.8         SB     0.10     Sequence
         IAb  313  PSLLAFTNPTVNSYK  LAFTNPTVN        0.7622         13.1         SB     0.10     Sequence
         IAb  312  APSLLAFTNPTVNSY  LAFTNPTVN        0.7383         17.0         SB     0.20     Sequence
         IAb  316  LAFTNPTVNSYKRLV  LAFTNPTVN        0.6920         28.0         SB     0.40     Sequence
         IAb  311  HAPSLLAFTNPTVNS  LAFTNPTVN        0.6642         37.8         SB     0.80     Sequence
         IAb  157  ISGWWNTGAATEADG  GWWNTGAAT        0.6633         38.2         SB     0.80     Sequence
         IAb  156  AISGWWNTGAATEAD  GWWNTGAAT        0.6549         41.8         SB     0.80     Sequence
         IAb  158  SGWWNTGAATEADGS  GWWNTGAAT        0.6511         43.6         SB     0.80     Sequence
         IAb  155  DAISGWWNTGAATEA  GWWNTGAAT        0.6412         48.5         SB     1.00     Sequence
         IAb   79  IDPFRAAKTLNINFF  DPFRAAKTL        0.6334         52.8         WB     1.00     Sequence
         IAb   78  RIDPFRAAKTLNINF  DPFRAAKTL        0.6308         54.3         WB     1.00     Sequence
         IAb   77  ARIDPFRAAKTLNIN  DPFRAAKTL        0.6220         59.7         WB     2.00     Sequence
         IAb   76  TARIDPFRAAKTLNI  DPFRAAKTL        0.6111         67.2         WB     2.00     Sequence
         IAb  310  HHAPSLLAFTNPTVN  LAFTNPTVN        0.5992         76.4         WB     2.00     Sequence
         IAb  328  RLVPGYEAPINLVYS  PGYEAPINL        0.5920         82.6         WB     2.00     Sequence
         IAb  373  GNPYLAFSAMLMAGL  YLAFSAMLM        0.5903         84.1         WB     2.00     Sequence
         IAb  374  NPYLAFSAMLMAGLD  YLAFSAMLM        0.5870         87.3         WB     2.00     Sequence
         IAb  327  KRLVPGYEAPINLVY  PGYEAPINL        0.5864         87.8         WB     2.00     Sequence
         IAb  329  LVPGYEAPINLVYSQ  PGYEAPINL        0.5847         89.4         WB     2.00     Sequence
         IAb  226  EINYQFNSLLHAADD  YQFNSLLHA        0.5785         95.6         WB     2.00     Sequence
         IAb   30  IMQHFTIPASAFDKS  QHFTIPASA        0.5773         96.9         WB     2.00     Sequence
         IAb  225  AEINYQFNSLLHAAD  YQFNSLLHA        0.5763         97.9         WB     2.00     Sequence
         IAb  372  SGNPYLAFSAMLMAG  YLAFSAMLM        0.5759         98.3         WB     2.00     Sequence
         IAb   29  GIMQHFTIPASAFDK  QHFTIPASA        0.5750         99.3         WB     2.00     Sequence
         IAb  227  INYQFNSLLHAADDM  YQFNSLLHA        0.5729        101.6         WB     4.00     Sequence
         IAb  125  DTAYFGAEAEFYIFD  TAYFGAEAE        0.5702        104.6         WB     4.00     Sequence
         IAb  124  ADTAYFGAEAEFYIF  TAYFGAEAE        0.5669        108.4         WB     4.00     Sequence
         IAb   31  MQHFTIPASAFDKSV  QHFTIPASA        0.5662        109.2         WB     4.00     Sequence
         IAb  126  TAYFGAEAEFYIFDS  TAYFGAEAE        0.5611        115.5         WB     4.00     Sequence
         IAb  123  IADTAYFGAEAEFYI  TAYFGAEAE        0.5608        115.8         WB     4.00     Sequence
         IAb  371  SSGNPYLAFSAMLMA  YLAFSAMLM        0.5540        124.7         WB     4.00     Sequence
         IAb   28  PGIMQHFTIPASAFD  QHFTIPASA        0.5526        126.5         WB     4.00     Sequence
         IAb  159  GWWNTGAATEADGSP  GWWNTGAAT        0.5516        127.9         WB     4.00     Sequence
         IAb  306  GGLLHHAPSLLAFTN  LLHHAPSLL        0.5490        131.6         WB     4.00     Sequence
         IAb  305  IGGLLHHAPSLLAFT  LLHHAPSLL        0.5483        132.5         WB     4.00     Sequence
         IAb  326  YKRLVPGYEAPINLV  PGYEAPINL        0.5463        135.5         WB     4.00     Sequence
         IAb  224  QAEINYQFNSLLHAA  YQFNSLLHA        0.5459        136.1         WB     4.00     Sequence
         IAb  228  NYQFNSLLHAADDMQ  YQFNSLLHA        0.5429        140.6         WB     4.00     Sequence
         IAb  375  PYLAFSAMLMAGLDG  YLAFSAMLM        0.5407        144.0         WB     4.00     Sequence
         IAb  330  VPGYEAPINLVYSQR  PGYEAPINL        0.5334        155.8         WB     4.00     Sequence
         IAb  307  GLLHHAPSLLAFTNP  LLHHAPSLL        0.5323        157.7         WB     4.00     Sequence
         IAb   80  DPFRAAKTLNINFFV  DPFRAAKTL        0.5273        166.3         WB     4.00     Sequence
         IAb  122  GIADTAYFGAEAEFY  TAYFGAEAE        0.5238        172.9         WB     4.00     Sequence
         IAb  304  YIGGLLHHAPSLLAF  LLHHAPSLL        0.5169        186.3         WB     4.00     Sequence
         IAb   27  LPGIMQHFTIPASAF  QHFTIPASA        0.5129        194.5         WB     4.00     Sequence
         IAb  180  RHKGGYFPVAPNDQY  GGYFPVAPN        0.5025        217.6         WB     8.00     Sequence
         IAb  182  KGGYFPVAPNDQYVD  GGYFPVAPN        0.5022        218.3         WB     8.00     Sequence
         IAb  181  HKGGYFPVAPNDQYV  GGYFPVAPN        0.5017        219.5         WB     8.00     Sequence
         IAb  376  YLAFSAMLMAGLDGI  YLAFSAMLM        0.4983        227.9         WB     8.00     Sequence
         IAb  308  LLHHAPSLLAFTNPT  LLHHAPSLL        0.4911        246.2         WB     8.00     Sequence
         IAb  154  VDAISGWWNTGAATE  SGWWNTGAA        0.4910        246.4         WB     8.00     Sequence
         IAb   75  ETARIDPFRAAKTLN  IDPFRAAKT        0.4899        249.5         WB     8.00     Sequence
         IAb  179  VRHKGGYFPVAPNDQ  GGYFPVAPN        0.4860        260.3         WB     8.00     Sequence
         IAb  370  DSSGNPYLAFSAMLM  YLAFSAMLM        0.4858        260.9         WB     8.00     Sequence
         IAb  223  GQAEINYQFNSLLHA  YQFNSLLHA        0.4839        266.2         WB     8.00     Sequence
         IAb   32  QHFTIPASAFDKSVF  QHFTIPASA        0.4793        279.7         WB     8.00     Sequence
         IAb  302  RHYIGGLLHHAPSLL  RHYIGGLLH        0.4749        293.4         WB     8.00     Sequence
         IAb  303  HYIGGLLHHAPSLLA  LLHHAPSLL        0.4736        297.5         WB     8.00     Sequence
         IAb  121  TGIADTAYFGAEAEF  TAYFGAEAE        0.4714        304.6         WB     8.00     Sequence
         IAb  301  ARHYIGGLLHHAPSL  RHYIGGLLH        0.4686        314.0         WB     8.00     Sequence
         IAb  241  MQLYKYIIKNTAWQN  YKYIIKNTA        0.4650        326.4         WB     8.00     Sequence
         IAb  325  SYKRLVPGYEAPINL  PGYEAPINL        0.4556        361.7         WB     8.00     Sequence
         IAb  300  TARHYIGGLLHHAPS  RHYIGGLLH        0.4533        370.5         WB     8.00     Sequence
         IAb  351  RIPITGSNPKAKRLE  ITGSNPKAK        0.4521        375.6         WB     8.00     Sequence
         IAb  242  QLYKYIIKNTAWQNG  YKYIIKNTA        0.4473        395.3         WB     8.00     Sequence
         IAb   26  DLPGIMQHFTIPASA  QHFTIPASA        0.4417        420.0         WB     8.00     Sequence
         IAb  309  LHHAPSLLAFTNPTV  LHHAPSLLA        0.4400        427.8         WB     8.00     Sequence
         IAb  299  DTARHYIGGLLHHAP  RHYIGGLLH        0.4396        429.7         WB     8.00     Sequence
         IAb  153  EVDAISGWWNTGAAT  SGWWNTGAA        0.4374        440.1         WB     8.00     Sequence
         IAb  183  GGYFPVAPNDQYVDL  GGYFPVAPN        0.4366        443.9         WB     8.00     Sequence
         IAb  352  IPITGSNPKAKRLEF  ITGSNPKAK        0.4355        449.4         WB     8.00     Sequence
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IAb  229  YQFNSLLHAADDMQL  YQFNSLLHA         0.4340         456.7          WB    16.00      Sequence
IAb  350  VRIPITGSNPKAKRL  ITGSNPKAK         0.4318         467.8          WB    16.00      Sequence
IAb  178  KVRHKGGYFPVAPND  GGYFPVAPN         0.4317         468.3          WB    16.00      Sequence
IAb  240  DMQLYKYIIKNTAWQ  YKYIIKNTA         0.4300         476.6          WB    16.00      Sequence
IAb   49  GLAFDGSSIRGFQSI  LAFDGSSIR         0.4275         490.0          WB    16.00      Sequence
IAb  402  KDLYELPPEEAASIP  YELPPEEAA         0.4181         542.4                16.00      Sequence
IAb   48  DGLAFDGSSIRGFQS  LAFDGSSIR         0.4171         548.3                16.00      Sequence
IAb  250  NTAWQNGKTVTFMPK  TAWQNGKTV         0.4170         548.9                16.00      Sequence
IAb   74  PETARIDPFRAAKTL  IDPFRAAKT         0.4144         564.6                16.00      Sequence
IAb  249  KNTAWQNGKTVTFMP  TAWQNGKTV         0.4136         569.6                16.00      Sequence
IAb  401  DKDLYELPPEEAASI  LYELPPEEA         0.4094         596.0                16.00      Sequence
IAb  362  KRLEFRSPDSSGNPY  LEFRSPDSS         0.4088         599.7                16.00      Sequence
IAb  363  RLEFRSPDSSGNPYL  LEFRSPDSS         0.4087         600.8                16.00      Sequence
IAb  298  SDTARHYIGGLLHHA  RHYIGGLLH         0.4082         603.5                16.00      Sequence
IAb  239  DDMQLYKYIIKNTAW  YKYIIKNTA         0.4072         610.0                16.00      Sequence
IAb  120  STGIADTAYFGAEAE  TAYFGAEAE         0.4072         610.0                16.00      Sequence
IAb  251  TAWQNGKTVTFMPKP  TAWQNGKTV         0.4061         617.7                16.00      Sequence
IAb  247  IIKNTAWQNGKTVTF  TAWQNGKTV         0.4054         622.3                16.00      Sequence
IAb  248  IKNTAWQNGKTVTFM  TAWQNGKTV         0.4053         622.9                16.00      Sequence
IAb  243  LYKYIIKNTAWQNGK  YKYIIKNTA         0.4050         625.3                16.00      Sequence
IAb  361  AKRLEFRSPDSSGNP  LEFRSPDSS         0.4016         648.3                16.00      Sequence
IAb  177  YKVRHKGGYFPVAPN  GGYFPVAPN         0.3981         673.2                16.00      Sequence
IAb   47  DDGLAFDGSSIRGFQ  LAFDGSSIR         0.3980         674.0                16.00      Sequence
IAb  349  CVRIPITGSNPKAKR  ITGSNPKAK         0.3959         689.6                16.00      Sequence
IAb  404  LYELPPEEAASIPQT  LYELPPEEA         0.3932         710.1                16.00      Sequence
IAb  403  DLYELPPEEAASIPQ  LYELPPEEA         0.3856         771.2                16.00      Sequence
IAb  278  QSLWKDGAPLMYDET  WKDGAPLMY         0.3842         782.9                16.00      Sequence
IAb  257  KTVTFMPKPLFGDNG  TVTFMPKPL         0.3826         796.1                16.00      Sequence
IAb  256  GKTVTFMPKPLFGDN  TVTFMPKPL         0.3804         815.6                16.00      Sequence
IAb  400  VDKDLYELPPEEAAS  YELPPEEAA         0.3804         815.8                16.00      Sequence
IAb  331  PGYEAPINLVYSQRN  PGYEAPINL         0.3799         819.8                16.00      Sequence
IAb  258  TVTFMPKPLFGDNGS  TVTFMPKPL         0.3765         850.4                16.00      Sequence
IAb  360  KAKRLEFRSPDSSGN  LEFRSPDSS         0.3759         856.3                16.00      Sequence
IAb  277  HQSLWKDGAPLMYDE  WKDGAPLMY         0.3726         887.5                16.00      Sequence
IAb  364  LEFRSPDSSGNPYLA  LEFRSPDSS         0.3726         887.8                16.00      Sequence
IAb  255  NGKTVTFMPKPLFGD  TVTFMPKPL         0.3717         895.8                16.00      Sequence
IAb  160  WWNTGAATEADGSPN  WNTGAATEA         0.3708         904.7                16.00      Sequence
IAb  115  ENYLISTGIADTAYF  YLISTGIAD         0.3704         908.5                16.00      Sequence
IAb  353  PITGSNPKAKRLEFR  ITGSNPKAK         0.3697         915.8                16.00      Sequence
IAb  409  PEEAASIPQTPTQLS  EAASIPQTP         0.3695         918.0                16.00      Sequence
IAb  238  ADDMQLYKYIIKNTA  YKYIIKNTA         0.3691         922.0                16.00      Sequence
IAb   46  FDDGLAFDGSSIRGF  LAFDGSSIR         0.3691         922.1                16.00      Sequence
IAb  114  AENYLISTGIADTAY  YLISTGIAD         0.3675         937.7                16.00      Sequence
IAb  161  WNTGAATEADGSPNR  WNTGAATEA         0.3657         955.9                16.00      Sequence
IAb  408  PPEEAASIPQTPTQL  EAASIPQTP         0.3634         980.2                16.00      Sequence
IAb  348  ACVRIPITGSNPKAK  ITGSNPKAK         0.3619         996.2                16.00      Sequence
IAb  116  NYLISTGIADTAYFG  YLISTGIAD         0.3606        1010.9                16.00      Sequence
IAb  276  CHQSLWKDGAPLMYD  WKDGAPLMY         0.3602        1015.0                16.00      Sequence
IAb  279  SLWKDGAPLMYDETG  SLWKDGAPL         0.3597        1019.8                16.00      Sequence
IAb  377  LAFSAMLMAGLDGIK  LAFSAMLMA         0.3590        1028.3                16.00      Sequence
IAb  246  YIIKNTAWQNGKTVT  TAWQNGKTV         0.3575        1044.6                16.00      Sequence
IAb  244  YKYIIKNTAWQNGKT  YKYIIKNTA         0.3572        1048.1                16.00      Sequence
IAb  369  PDSSGNPYLAFSAML  NPYLAFSAM         0.3546        1078.4                16.00      Sequence
IAb  399  PVDKDLYELPPEEAA  LYELPPEEA         0.3530        1096.5                16.00      Sequence
IAb   81  PFRAAKTLNINFFVH  FRAAKTLNI         0.3510        1120.8                16.00      Sequence
IAb  411  EAASIPQTPTQLSDV  SIPQTPTQL         0.3498        1135.2                16.00      Sequence
IAb  410  EEAASIPQTPTQLSD  EAASIPQTP         0.3487        1149.6                16.00      Sequence
IAb  113  KAENYLISTGIADTA  YLISTGIAD         0.3461        1182.2                16.00      Sequence
IAb  405  YELPPEEAASIPQTP  YELPPEEAA         0.3457        1187.6                32.00      Sequence
IAb  275  HCHQSLWKDGAPLMY  SLWKDGAPL         0.3436        1214.6                32.00      Sequence
IAb  254  QNGKTVTFMPKPLFG  TVTFMPKPL         0.3432        1220.3                32.00      Sequence
IAb  407  LPPEEAASIPQTPTQ  EAASIPQTP         0.3371        1303.1                32.00      Sequence
IAb   50  LAFDGSSIRGFQSIH  LAFDGSSIR         0.3365        1311.5                32.00      Sequence
IAb  324  NSYKRLVPGYEAPIN  VPGYEAPIN         0.3340        1347.0                32.00      Sequence
IAb  245  KYIIKNTAWQNGKTV  TAWQNGKTV         0.3330        1361.8                32.00      Sequence
IAb  317  AFTNPTVNSYKRLVP  AFTNPTVNS         0.3240        1500.8                32.00      Sequence
IAb  406  ELPPEEAASIPQTPT  EAASIPQTP         0.3163        1632.2                32.00      Sequence
IAb  291  ETGYAGLSDTARHYI  YAGLSDTAR         0.3112        1723.9                32.00      Sequence
IAb  152  YEVDAISGWWNTGAA  SGWWNTGAA         0.3108        1731.2                32.00      Sequence
IAb  359  PKAKRLEFRSPDSSG  LEFRSPDSS         0.3071        1803.1                32.00      Sequence
IAb  184  GYFPVAPNDQYVDLR  YFPVAPNDQ         0.3052        1839.4                32.00      Sequence
IAb  412  AASIPQTPTQLSDVI  SIPQTPTQL         0.3051        1842.5                32.00      Sequence
IAb  117  YLISTGIADTAYFGA  YLISTGIAD         0.3037        1870.9                32.00      Sequence
IAb  347  SACVRIPITGSNPKA  IPITGSNPK         0.2995        1957.3                32.00      Sequence
IAb  112  RKAENYLISTGIADT  YLISTGIAD         0.2959        2033.8                32.00      Sequence
IAb  290  DETGYAGLSDTARHY  YAGLSDTAR         0.2937        2084.9                32.00      Sequence
IAb  292  TGYAGLSDTARHYIG  TGYAGLSDT         0.2900        2169.7                32.00      Sequence
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IAb  297  LSDTARHYIGGLLHH  RHYIGGLLH         0.2899       2171.5              32.00      Sequence
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IAb   57  IRGFQSIHESDMLLL  RGFQSIHES         0.2843       2306.9              32.00      Sequence
IAb  354  ITGSNPKAKRLEFRS  ITGSNPKAK         0.2842       2309.8              32.00      Sequence
IAb   56  SIRGFQSIHESDMLL  RGFQSIHES         0.2833       2333.0              32.00      Sequence
IAb   67  DMLLLPDPETARIDP  LLLPDPETA         0.2830       2339.6              32.00      Sequence
IAb  413  ASIPQTPTQLSDVID  SIPQTPTQL         0.2830       2340.8              32.00      Sequence
IAb   73  DPETARIDPFRAAKT  IDPFRAAKT         0.2818       2369.8              32.00      Sequence
IAb  289  YDETGYAGLSDTARH  TGYAGLSDT         0.2763       2516.3              32.00      Sequence
IAb  358  NPKAKRLEFRSPDSS  LEFRSPDSS         0.2760       2523.6              32.00      Sequence
IAb  111  ARKAENYLISTGIAD  YLISTGIAD         0.2750       2552.5              32.00      Sequence
IAb  337  INLVYSQRNRSACVR  INLVYSQRN         0.2747       2559.5              32.00      Sequence
IAb   55  SSIRGFQSIHESDML  RGFQSIHES         0.2744       2566.8              32.00      Sequence
IAb   66  SDMLLLPDPETARID  LLLPDPETA         0.2735       2593.6              32.00      Sequence
IAb  414  SIPQTPTQLSDVIDR  SIPQTPTQL         0.2714       2652.7              32.00      Sequence
IAb   33  HFTIPASAFDKSVFD  FTIPASAFD         0.2713       2654.0              32.00      Sequence
IAb  336  PINLVYSQRNRSACV  INLVYSQRN         0.2704       2681.3              32.00      Sequence
IAb   68  MLLLPDPETARIDPF  LLLPDPETA         0.2682       2745.8              32.00      Sequence
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IAb  368  SPDSSGNPYLAFSAM  NPYLAFSAM         0.2670       2783.0              32.00      Sequence
IAb   91  NFFVHDPFTLEPYSR  FFVHDPFTL         0.2659       2816.3              32.00      Sequence
IAb  252  AWQNGKTVTFMPKPL  TVTFMPKPL         0.2647       2852.5              32.00      Sequence
IAb  323  VNSYKRLVPGYEAPI  YKRLVPGYE         0.2641       2872.1              32.00      Sequence
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IAb   90  INFFVHDPFTLEPYS  FFVHDPFTL         0.2569       3104.2              32.00      Sequence
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IAb  259  VTFMPKPLFGDNGSG  VTFMPKPLF         0.2459       3497.0              32.00      Sequence
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IAb  334  EAPINLVYSQRNRSA  INLVYSQRN         0.2406       3702.0              50.00      Sequence
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IAb  287  LMYDETGYAGLSDTA  TGYAGLSDT         0.2144       4914.6              50.00      Sequence
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IAb  388  DGIKNKIEPQAPVDK  KNKIEPQAP         0.2014       5660.0              50.00      Sequence
IAb  318  FTNPTVNSYKRLVPG  FTNPTVNSY         0.2012       5671.2              50.00      Sequence
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IAb  127  AYFGAEAEFYIFDSV  AYFGAEAEF         0.2003       5724.0              50.00      Sequence
IAb  458  EIEPVNIRPHPYEFA  IEPVNIRPH         0.2003       5726.1              50.00      Sequence
IAb  218  EVGSGGQAEINYQFN  EVGSGGQAE         0.1999       5749.1              50.00      Sequence
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IAb  237  AADDMQLYKYIIKNT  QLYKYIIKN        0.1997      5765.2            50.00     Sequence
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IAb   53  DGSSIRGFQSIHESD  RGFQSIHES        0.1989      5811.7            50.00     Sequence
IAb  110  IARKAENYLISTGIA  ENYLISTGI        0.1979      5877.5            50.00     Sequence
IAb   40  AFDKSVFDDGLAFDG  SVFDDGLAF        0.1946      6088.8            50.00     Sequence
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IAb  321  PTVNSYKRLVPGYEA  YKRLVPGYE        0.1935      6163.7            50.00     Sequence
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IAb   14  DEKVEYVDVRFCDLP  VEYVDVRFC         0.0391       32757.2              50.00     Sequence
IAb  426  IDRLEADHEYLTEGG  IDRLEADHE         0.0374       33355.1              50.00     Sequence
IAb  417  QTPTQLSDVIDRLEA  QTPTQLSDV         0.0359       33892.8              50.00     Sequence
IAb  190  PNDQYVDLRDKMLTN  YVDLRDKML         0.0351       34208.6              50.00     Sequence
IAb  424  DVIDRLEADHEYLTE  IDRLEADHE         0.0345       34432.1              50.00     Sequence
IAb  395  EPQAPVDKDLYELPP  EPQAPVDKD         0.0337       34709.7              50.00     Sequence
IAb   11  LAKDEKVEYVDVRFC  VEYVDVRFC         0.0335       34787.1              50.00     Sequence
IAb  425  VIDRLEADHEYLTEG  IDRLEADHE         0.0334       34848.5              50.00     Sequence
IAb  423  SDVIDRLEADHEYLT  IDRLEADHE         0.0331       34949.3              50.00     Sequence
IAb   13  KDEKVEYVDVRFCDL  VEYVDVRFC         0.0325       35167.4              50.00     Sequence
IAb  189  APNDQYVDLRDKMLT  DQYVDLRDK         0.0324       35221.1              50.00     Sequence
IAb  418  TPTQLSDVIDRLEAD  TPTQLSDVI         0.0316       35527.7              50.00     Sequence
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         IAb   12  AKDEKVEYVDVRFCD  VEYVDVRFC        0.0315      35560.0                50.00     Sequence
         IAb  422  LSDVIDRLEADHEYL  IDRLEADHE        0.0314      35592.7                50.00     Sequence
         IAb  419  PTQLSDVIDRLEADH  PTQLSDVID        0.0312      35687.2                50.00     Sequence
         IAb    0  VTEKTPDDVFKLAKD  VTEKTPDDV        0.0307      35886.2                50.00     Sequence
         IAb  420  TQLSDVIDRLEADHE  IDRLEADHE        0.0285      36728.4                50.00     Sequence
         IAb   10  KLAKDEKVEYVDVRF  KLAKDEKVE        0.0259      37798.4                50.00     Sequence
         IAb  421  QLSDVIDRLEADHEY  DVIDRLEAD        0.0248      38225.7                50.00     Sequence
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Allele: IAb. Number of high binders 10. Number of weak binders 67. Number of peptides 464

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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         IAd  342  SQRNRSACVRIPITG  RNRSACVRI        0.3780        836.8                 4.00     Sequence
         IAd  343  QRNRSACVRIPITGS  RSACVRIPI        0.3769        847.1                 4.00     Sequence
         IAd  341  YSQRNRSACVRIPIT  RSACVRIPI        0.3655        958.3                 4.00     Sequence
         IAd   73  DPETARIDPFRAAKT  TARIDPFRA        0.3620        995.2                 4.00     Sequence
         IAd  378  AFSAMLMAGLDGIKN  FSAMLMAGL        0.3493       1142.2                 8.00     Sequence
         IAd   74  PETARIDPFRAAKTL  TARIDPFRA        0.3478       1160.5                 8.00     Sequence
         IAd   26  DLPGIMQHFTIPASA  IMQHFTIPA        0.3474       1165.3                 8.00     Sequence
         IAd  340  VYSQRNRSACVRIPI  RSACVRIPI        0.3418       1238.3                 8.00     Sequence
         IAd   28  PGIMQHFTIPASAFD  IMQHFTIPA        0.3399       1264.4                 8.00     Sequence
         IAd   27  LPGIMQHFTIPASAF  IMQHFTIPA        0.3367       1308.4                 8.00     Sequence
         IAd  344  RNRSACVRIPITGSN  RSACVRIPI        0.3366       1309.9                 8.00     Sequence
         IAd   30  IMQHFTIPASAFDKS  MQHFTIPAS        0.3334       1356.6                 8.00     Sequence
         IAd  379  FSAMLMAGLDGIKNK  FSAMLMAGL        0.3164       1630.4                 8.00     Sequence
         IAd   29  GIMQHFTIPASAFDK  IMQHFTIPA        0.3143       1666.8                 8.00     Sequence
         IAd   25  CDLPGIMQHFTIPAS  IMQHFTIPA        0.3142       1669.2                 8.00     Sequence
         IAd  406  ELPPEEAASIPQTPT  PEEAASIPQ        0.2944       2068.9                16.00     Sequence
         IAd   72  PDPETARIDPFRAAK  TARIDPFRA        0.2927       2106.0                16.00     Sequence
         IAd   75  ETARIDPFRAAKTLN  TARIDPFRA        0.2921       2121.1                16.00     Sequence
         IAd  404  LYELPPEEAASIPQT  PEEAASIPQ        0.2918       2127.6                16.00     Sequence
         IAd  233  SLLHAADDMQLYKYI  LHAADDMQL        0.2915       2133.0                16.00     Sequence
         IAd  232  NSLLHAADDMQLYKY  LHAADDMQL        0.2889       2194.9                16.00     Sequence
         IAd  235  LHAADDMQLYKYIIK  LHAADDMQL        0.2888       2196.4                16.00     Sequence
         IAd  234  LLHAADDMQLYKYII  LHAADDMQL        0.2874       2230.2                16.00     Sequence
         IAd  376  YLAFSAMLMAGLDGI  FSAMLMAGL        0.2859       2267.1                16.00     Sequence
         IAd  407  LPPEEAASIPQTPTQ  PEEAASIPQ        0.2835       2327.7                16.00     Sequence
         IAd  377  LAFSAMLMAGLDGIK  FSAMLMAGL        0.2795       2428.9                16.00     Sequence
         IAd  405  YELPPEEAASIPQTP  PEEAASIPQ        0.2790       2444.1                16.00     Sequence
         IAd   71  LPDPETARIDPFRAA  TARIDPFRA        0.2755       2537.2                16.00     Sequence
         IAd  409  PEEAASIPQTPTQLS  PEEAASIPQ        0.2715       2650.7                16.00     Sequence
         IAd  345  NRSACVRIPITGSNP  RSACVRIPI        0.2710       2663.4                16.00     Sequence
         IAd  149  GSFYEVDAISGWWNT  FYEVDAISG        0.2695       2706.6                16.00     Sequence
         IAd  309  LHHAPSLLAFTNPTV  LHHAPSLLA        0.2688       2729.7                16.00     Sequence
         IAd   76  TARIDPFRAAKTLNI  TARIDPFRA        0.2674       2770.4                16.00     Sequence
         IAd  408  PPEEAASIPQTPTQL  PEEAASIPQ        0.2652       2837.6                16.00     Sequence
         IAd  307  GLLHHAPSLLAFTNP  LHHAPSLLA        0.2635       2889.5                16.00     Sequence
         IAd  375  PYLAFSAMLMAGLDG  FSAMLMAGL        0.2634       2891.4                16.00     Sequence
         IAd  308  LLHHAPSLLAFTNPT  LHHAPSLLA        0.2632       2898.0                16.00     Sequence
         IAd  148  NGSFYEVDAISGWWN  FYEVDAISG        0.2628       2909.7                16.00     Sequence
         IAd  146  RANGSFYEVDAISGW  FYEVDAISG        0.2615       2951.4                16.00     Sequence
         IAd  306  GGLLHHAPSLLAFTN  LHHAPSLLA        0.2611       2964.7                16.00     Sequence
         IAd  112  RKAENYLISTGIADT  RKAENYLIS        0.2564       3118.4                16.00     Sequence
         IAd  346  RSACVRIPITGSNPK  RSACVRIPI        0.2564       3120.9                16.00     Sequence
         IAd  147  ANGSFYEVDAISGWW  FYEVDAISG        0.2494       3367.2                16.00     Sequence
         IAd  305  IGGLLHHAPSLLAFT  LHHAPSLLA        0.2485       3399.0                16.00     Sequence
         IAd  230  QFNSLLHAADDMQLY  LHAADDMQL        0.2481       3414.2                16.00     Sequence
         IAd  111  ARKAENYLISTGIAD  RKAENYLIS        0.2474       3438.9                16.00     Sequence
         IAd  110  IARKAENYLISTGIA  RKAENYLIS        0.2473       3444.1                16.00     Sequence
         IAd  339  LVYSQRNRSACVRIP  NRSACVRIP        0.2468       3461.5                16.00     Sequence
         IAd  145  SRANGSFYEVDAISG  FYEVDAISG        0.2378       3816.7                32.00     Sequence
         IAd   31  MQHFTIPASAFDKSV  MQHFTIPAS        0.2353       3921.5                32.00     Sequence
         IAd  158  SGWWNTGAATEADGS  WNTGAATEA        0.2335       3998.9                32.00     Sequence
         IAd  109  NIARKAENYLISTGI  RKAENYLIS        0.2330       4018.9                32.00     Sequence
         IAd  374  NPYLAFSAMLMAGLD  FSAMLMAGL        0.2329       4025.3                32.00     Sequence
         IAd  108  RNIARKAENYLISTG  ARKAENYLI        0.2308       4114.9                32.00     Sequence
         IAd  373  GNPYLAFSAMLMAGL  FSAMLMAGL        0.2282       4232.4                32.00     Sequence
         IAd  231  FNSLLHAADDMQLYK  LHAADDMQL        0.2282       4234.9                32.00     Sequence
         IAd  229  YQFNSLLHAADDMQL  QFNSLLHAA        0.2263       4321.4                32.00     Sequence
         IAd  304  YIGGLLHHAPSLLAF  LHHAPSLLA        0.2243       4416.7                32.00     Sequence
         IAd  113  KAENYLISTGIADTA  ISTGIADTA        0.2234       4460.3                32.00     Sequence
         IAd  380  SAMLMAGLDGIKNKI  MAGLDGIKN        0.2224       4509.8                32.00     Sequence
         IAd  157  ISGWWNTGAATEADG  WNTGAATEA        0.2204       4604.1                32.00     Sequence
         IAd  403  DLYELPPEEAASIPQ  PEEAASIPQ        0.2203       4608.5                32.00     Sequence
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IAd  415  IPQTPTQLSDVIDRL  TQLSDVIDR         0.2189        4683.5              32.00      Sequence
IAd  251  TAWQNGKTVTFMPKP  GKTVTFMPK         0.2119        5050.5              32.00      Sequence
IAd  156  AISGWWNTGAATEAD  WNTGAATEA         0.2116        5063.5              32.00      Sequence
IAd   24  FCDLPGIMQHFTIPA  IMQHFTIPA         0.2104        5132.7              32.00      Sequence
IAd  275  HCHQSLWKDGAPLMY  WKDGAPLMY         0.2101        5146.3              32.00      Sequence
IAd  114  AENYLISTGIADTAY  ISTGIADTA         0.2064        5360.7              32.00      Sequence
IAd  381  AMLMAGLDGIKNKIE  MAGLDGIKN         0.2054        5415.5              32.00      Sequence
IAd  236  HAADDMQLYKYIIKN  ADDMQLYKY         0.2050        5440.3              32.00      Sequence
IAd  303  HYIGGLLHHAPSLLA  LHHAPSLLA         0.2040        5499.1              32.00      Sequence
IAd  155  DAISGWWNTGAATEA  WNTGAATEA         0.2038        5514.2              32.00      Sequence
IAd   70  LLPDPETARIDPFRA  TARIDPFRA         0.2030        5560.2              32.00      Sequence
IAd   77  ARIDPFRAAKTLNIN  FRAAKTLNI         0.2024        5595.9              32.00      Sequence
IAd  238  ADDMQLYKYIIKNTA  YKYIIKNTA         0.1990        5805.1              32.00      Sequence
IAd  417  QTPTQLSDVIDRLEA  TQLSDVIDR         0.1967        5952.8              32.00      Sequence
IAd  150  SFYEVDAISGWWNTG  FYEVDAISG         0.1951        6054.4              32.00      Sequence
IAd  243  LYKYIIKNTAWQNGK  YKYIIKNTA         0.1942        6116.1              32.00      Sequence
IAd  416  PQTPTQLSDVIDRLE  TQLSDVIDR         0.1931        6188.4              32.00      Sequence
IAd  237  AADDMQLYKYIIKNT  ADDMQLYKY         0.1922        6247.8              32.00      Sequence
IAd  276  CHQSLWKDGAPLMYD  WKDGAPLMY         0.1896        6426.3              32.00      Sequence
IAd  299  DTARHYIGGLLHHAP  RHYIGGLLH         0.1877        6562.8              32.00      Sequence
IAd  431  ADHEYLTEGGVFTND  YLTEGGVFT         0.1875        6578.8              32.00      Sequence
IAd  242  QLYKYIIKNTAWQNG  YKYIIKNTA         0.1864        6651.4              32.00      Sequence
IAd  300  TARHYIGGLLHHAPS  RHYIGGLLH         0.1858        6694.6              32.00      Sequence
IAd  382  MLMAGLDGIKNKIEP  MAGLDGIKN         0.1855        6721.1              32.00      Sequence
IAd  414  SIPQTPTQLSDVIDR  QTPTQLSDV         0.1845        6791.0              32.00      Sequence
IAd  298  SDTARHYIGGLLHHA  RHYIGGLLH         0.1835        6862.7              32.00      Sequence
IAd  430  EADHEYLTEGGVFTN  YLTEGGVFT         0.1830        6904.1              32.00      Sequence
IAd  159  GWWNTGAATEADGSP  WNTGAATEA         0.1818        6992.4              32.00      Sequence
IAd  107  PRNIARKAENYLIST  ARKAENYLI         0.1812        7040.0              32.00      Sequence
IAd  324  NSYKRLVPGYEAPIN  KRLVPGYEA         0.1803        7105.1              32.00      Sequence
IAd  442  FTNDLIETWISFKRE  IETWISFKR         0.1796        7159.5              32.00      Sequence
IAd  252  AWQNGKTVTFMPKPL  GKTVTFMPK         0.1795        7170.2              32.00      Sequence
IAd  321  PTVNSYKRLVPGYEA  KRLVPGYEA         0.1780        7286.6              50.00      Sequence
IAd  244  YKYIIKNTAWQNGKT  YKYIIKNTA         0.1770        7365.7              50.00      Sequence
IAd  161  WNTGAATEADGSPNR  WNTGAATEA         0.1766        7398.8              50.00      Sequence
IAd  310  HHAPSLLAFTNPTVN  APSLLAFTN         0.1756        7476.5              50.00      Sequence
IAd  338  NLVYSQRNRSACVRI  RNRSACVRI         0.1753        7500.5              50.00      Sequence
IAd  432  DHEYLTEGGVFTNDL  YLTEGGVFT         0.1745        7564.4              50.00      Sequence
IAd  372  SGNPYLAFSAMLMAG  LAFSAMLMA         0.1740        7610.9              50.00      Sequence
IAd  250  NTAWQNGKTVTFMPK  GKTVTFMPK         0.1733        7665.0              50.00      Sequence
IAd  160  WWNTGAATEADGSPN  WNTGAATEA         0.1728        7709.2              50.00      Sequence
IAd  323  VNSYKRLVPGYEAPI  KRLVPGYEA         0.1728        7710.5              50.00      Sequence
IAd  447  IETWISFKRENEIEP  IETWISFKR         0.1715        7818.4              50.00      Sequence
IAd  441  VFTNDLIETWISFKR  IETWISFKR         0.1705        7900.7              50.00      Sequence
IAd  322  TVNSYKRLVPGYEAP  KRLVPGYEA         0.1705        7903.3              50.00      Sequence
IAd  151  FYEVDAISGWWNTGA  FYEVDAISG         0.1681        8110.5              50.00      Sequence
IAd  391  KNKIEPQAPVDKDLY  IEPQAPVDK         0.1675        8167.4              50.00      Sequence
IAd  384  MAGLDGIKNKIEPQA  MAGLDGIKN         0.1674        8171.7              50.00      Sequence
IAd  443  TNDLIETWISFKREN  IETWISFKR         0.1674        8176.1              50.00      Sequence
IAd  410  EEAASIPQTPTQLSD  EEAASIPQT         0.1670        8205.4              50.00      Sequence
IAd  253  WQNGKTVTFMPKPLF  GKTVTFMPK         0.1662        8279.4              50.00      Sequence
IAd  297  LSDTARHYIGGLLHH  RHYIGGLLH         0.1659        8310.3              50.00      Sequence
IAd  175  RGYKVRHKGGYFPVA  VRHKGGYFP         0.1653        8358.0              50.00      Sequence
IAd  446  LIETWISFKRENEIE  IETWISFKR         0.1648        8402.4              50.00      Sequence
IAd  411  EAASIPQTPTQLSDV  AASIPQTPT         0.1648        8402.5              50.00      Sequence
IAd  144  DSRANGSFYEVDAIS  RANGSFYEV         0.1645        8430.1              50.00      Sequence
IAd  392  NKIEPQAPVDKDLYE  IEPQAPVDK         0.1645        8432.0              50.00      Sequence
IAd  177  YKVRHKGGYFPVAPN  RHKGGYFPV         0.1642        8458.6              50.00      Sequence
IAd  433  HEYLTEGGVFTNDLI  YLTEGGVFT         0.1640        8478.6              50.00      Sequence
IAd  448  ETWISFKRENEIEPV  KRENEIEPV         0.1640        8479.6              50.00      Sequence
IAd  371  SSGNPYLAFSAMLMA  LAFSAMLMA         0.1639        8487.3              50.00      Sequence
IAd  176  GYKVRHKGGYFPVAP  RHKGGYFPV         0.1637        8505.3              50.00      Sequence
IAd  325  SYKRLVPGYEAPINL  KRLVPGYEA         0.1632        8556.3              50.00      Sequence
IAd  389  GIKNKIEPQAPVDKD  IEPQAPVDK         0.1614        8721.5              50.00      Sequence
IAd  247  IIKNTAWQNGKTVTF  IKNTAWQNG         0.1613        8728.3              50.00      Sequence
IAd  106  DPRNIARKAENYLIS  ARKAENYLI         0.1605        8804.2              50.00      Sequence
IAd   32  QHFTIPASAFDKSVF  IPASAFDKS         0.1589        8955.6              50.00      Sequence
IAd  277  HQSLWKDGAPLMYDE  WKDGAPLMY         0.1583        9020.0              50.00      Sequence
IAd  453  FKRENEIEPVNIRPH  KRENEIEPV         0.1582        9025.6              50.00      Sequence
IAd  278  QSLWKDGAPLMYDET  WKDGAPLMY         0.1578        9068.1              50.00      Sequence
IAd   79  IDPFRAAKTLNINFF  FRAAKTLNI         0.1577        9072.1              50.00      Sequence
IAd  452  SFKRENEIEPVNIRP  KRENEIEPV         0.1575        9092.8              50.00      Sequence
IAd  296  GLSDTARHYIGGLLH  RHYIGGLLH         0.1560        9247.6              50.00      Sequence
IAd  383  LMAGLDGIKNKIEPQ  MAGLDGIKN         0.1557        9279.3              50.00      Sequence
IAd  450  WISFKRENEIEPVNI  KRENEIEPV         0.1540        9452.3              50.00      Sequence
IAd  393  KIEPQAPVDKDLYEL  IEPQAPVDK         0.1536        9491.8              50.00      Sequence
IAd  241  MQLYKYIIKNTAWQN  YKYIIKNTA         0.1535        9498.6              50.00      Sequence
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IAd  412  AASIPQTPTQLSDVI  AASIPQTPT        0.1514      9718.2              50.00     Sequence
IAd  294  YAGLSDTARHYIGGL  YAGLSDTAR        0.1513      9728.1              50.00     Sequence
IAd  394  IEPQAPVDKDLYELP  IEPQAPVDK        0.1513      9731.5              50.00     Sequence
IAd  143  FDSRANGSFYEVDAI  SRANGSFYE        0.1508      9777.1              50.00     Sequence
IAd  444  NDLIETWISFKRENE  IETWISFKR        0.1505      9807.3              50.00     Sequence
IAd  449  TWISFKRENEIEPVN  KRENEIEPV        0.1501      9857.3              50.00     Sequence
IAd  451  ISFKRENEIEPVNIR  KRENEIEPV        0.1485     10025.4              50.00     Sequence
IAd    9  FKLAKDEKVEYVDVR  FKLAKDEKV        0.1485     10030.6              50.00     Sequence
IAd  413  ASIPQTPTQLSDVID  IPQTPTQLS        0.1482     10055.6              50.00     Sequence
IAd  245  KYIIKNTAWQNGKTV  IKNTAWQNG        0.1477     10109.5              50.00     Sequence
IAd  390  IKNKIEPQAPVDKDL  IEPQAPVDK        0.1474     10146.9              50.00     Sequence
IAd   60  FQSIHESDMLLLPDP  IHESDMLLL        0.1470     10189.3              50.00     Sequence
IAd  401  DKDLYELPPEEAASI  KDLYELPPE        0.1467     10226.2              50.00     Sequence
IAd  347  SACVRIPITGSNPKA  ACVRIPITG        0.1462     10276.0              50.00     Sequence
IAd  445  DLIETWISFKRENEI  IETWISFKR        0.1454     10365.4              50.00     Sequence
IAd  402  KDLYELPPEEAASIP  KDLYELPPE        0.1452     10393.2              50.00     Sequence
IAd    8  VFKLAKDEKVEYVDV  FKLAKDEKV        0.1443     10487.7              50.00     Sequence
IAd    6  DDVFKLAKDEKVEYV  FKLAKDEKV        0.1442     10499.4              50.00     Sequence
IAd    7  DVFKLAKDEKVEYVD  FKLAKDEKV        0.1442     10502.9              50.00     Sequence
IAd   81  PFRAAKTLNINFFVH  FRAAKTLNI        0.1439     10544.1              50.00     Sequence
IAd  224  QAEINYQFNSLLHAA  YQFNSLLHA        0.1438     10545.5              50.00     Sequence
IAd  429  LEADHEYLTEGGVFT  YLTEGGVFT        0.1438     10548.5              50.00     Sequence
IAd   82  FRAAKTLNINFFVHD  FRAAKTLNI        0.1437     10558.6              50.00     Sequence
IAd   78  RIDPFRAAKTLNINF  FRAAKTLNI        0.1436     10573.3              50.00     Sequence
IAd  248  IKNTAWQNGKTVTFM  IKNTAWQNG        0.1434     10591.5              50.00     Sequence
IAd  178  KVRHKGGYFPVAPND  RHKGGYFPV        0.1431     10627.4              50.00     Sequence
IAd  254  QNGKTVTFMPKPLFG  GKTVTFMPK        0.1429     10657.5              50.00     Sequence
IAd  115  ENYLISTGIADTAYF  ISTGIADTA        0.1417     10793.7              50.00     Sequence
IAd  174  NRGYKVRHKGGYFPV  RHKGGYFPV        0.1415     10821.7              50.00     Sequence
IAd  274  MHCHQSLWKDGAPLM  MHCHQSLWK        0.1409     10889.7              50.00     Sequence
IAd  246  YIIKNTAWQNGKTVT  IKNTAWQNG        0.1403     10957.9              50.00     Sequence
IAd   52  FDGSSIRGFQSIHES  RGFQSIHES        0.1402     10968.8              50.00     Sequence
IAd  195  VDLRDKMLTNLINSG  LRDKMLTNL        0.1393     11075.7              50.00     Sequence
IAd  180  RHKGGYFPVAPNDQY  RHKGGYFPV        0.1386     11155.4              50.00     Sequence
IAd  118  LISTGIADTAYFGAE  IADTAYFGA        0.1372     11336.8              50.00     Sequence
IAd  454  KRENEIEPVNIRPHP  KRENEIEPV        0.1371     11337.7              50.00     Sequence
IAd  388  DGIKNKIEPQAPVDK  IEPQAPVDK        0.1371     11344.9              50.00     Sequence
IAd  311  HAPSLLAFTNPTVNS  APSLLAFTN        0.1370     11350.1              50.00     Sequence
IAd  255  NGKTVTFMPKPLFGD  GKTVTFMPK        0.1355     11540.7              50.00     Sequence
IAd  194  YVDLRDKMLTNLINS  KMLTNLINS        0.1352     11578.9              50.00     Sequence
IAd   57  IRGFQSIHESDMLLL  IHESDMLLL        0.1350     11601.5              50.00     Sequence
IAd  179  VRHKGGYFPVAPNDQ  RHKGGYFPV        0.1347     11636.1              50.00     Sequence
IAd   61  QSIHESDMLLLPDPE  IHESDMLLL        0.1346     11652.1              50.00     Sequence
IAd  140  SVSFDSRANGSFYEV  RANGSFYEV        0.1339     11739.5              50.00     Sequence
IAd  256  GKTVTFMPKPLFGDN  GKTVTFMPK        0.1326     11908.5              50.00     Sequence
IAd   80  DPFRAAKTLNINFFV  FRAAKTLNI        0.1322     11961.5              50.00     Sequence
IAd   63  IHESDMLLLPDPETA  IHESDMLLL        0.1289     12392.9              50.00     Sequence
IAd   62  SIHESDMLLLPDPET  IHESDMLLL        0.1288     12403.4              50.00     Sequence
IAd  295  AGLSDTARHYIGGLL  AGLSDTARH        0.1288     12411.2              50.00     Sequence
IAd  279  SLWKDGAPLMYDETG  WKDGAPLMY        0.1264     12735.8              50.00     Sequence
IAd  119  ISTGIADTAYFGAEA  ISTGIADTA        0.1260     12787.7              50.00     Sequence
IAd  239  DDMQLYKYIIKNTAW  YKYIIKNTA        0.1258     12818.7              50.00     Sequence
IAd  434  EYLTEGGVFTNDLIE  YLTEGGVFT        0.1254     12868.3              50.00     Sequence
IAd  117  YLISTGIADTAYFGA  IADTAYFGA        0.1239     13087.9              50.00     Sequence
IAd    5  PDDVFKLAKDEKVEY  FKLAKDEKV        0.1231     13196.6              50.00     Sequence
IAd  399  PVDKDLYELPPEEAA  LYELPPEEA        0.1223     13306.1              50.00     Sequence
IAd  196  DLRDKMLTNLINSGF  LRDKMLTNL        0.1223     13311.4              50.00     Sequence
IAd  129  FGAEAEFYIFDSVSF  AEFYIFDSV        0.1215     13431.8              50.00     Sequence
IAd  152  YEVDAISGWWNTGAA  YEVDAISGW        0.1212     13466.7              50.00     Sequence
IAd   33  HFTIPASAFDKSVFD  IPASAFDKS        0.1209     13515.9              50.00     Sequence
IAd  420  TQLSDVIDRLEADHE  TQLSDVIDR        0.1202     13615.6              50.00     Sequence
IAd  193  QYVDLRDKMLTNLIN  LRDKMLTNL        0.1201     13637.3              50.00     Sequence
IAd  225  AEINYQFNSLLHAAD  YQFNSLLHA        0.1196     13714.2              50.00     Sequence
IAd  326  YKRLVPGYEAPINLV  KRLVPGYEA        0.1193     13756.3              50.00     Sequence
IAd  240  DMQLYKYIIKNTAWQ  YKYIIKNTA        0.1192     13760.0              50.00     Sequence
IAd  281  WKDGAPLMYDETGYA  WKDGAPLMY        0.1191     13780.8              50.00     Sequence
IAd  132  EAEFYIFDSVSFDSR  AEFYIFDSV        0.1190     13797.7              50.00     Sequence
IAd   11  LAKDEKVEYVDVRFC  VEYVDVRFC        0.1186     13857.5              50.00     Sequence
IAd  400  VDKDLYELPPEEAAS  LYELPPEEA        0.1170     14094.3              50.00     Sequence
IAd  273  GMHCHQSLWKDGAPL  MHCHQSLWK        0.1156     14315.7              50.00     Sequence
IAd   58  RGFQSIHESDMLLLP  IHESDMLLL        0.1149     14424.0              50.00     Sequence
IAd  370  DSSGNPYLAFSAMLM  YLAFSAMLM        0.1142     14538.1              50.00     Sequence
IAd  141  VSFDSRANGSFYEVD  RANGSFYEV        0.1135     14647.7              50.00     Sequence
IAd  435  YLTEGGVFTNDLIET  YLTEGGVFT        0.1131     14699.7              50.00     Sequence
IAd   51  AFDGSSIRGFQSIHE  GSSIRGFQS        0.1129     14743.9              50.00     Sequence
IAd  197  LRDKMLTNLINSGFI  LRDKMLTNL        0.1128     14756.8              50.00     Sequence
IAd  226  EINYQFNSLLHAADD  YQFNSLLHA        0.1128     14758.1              50.00     Sequence
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IAd  127  AYFGAEAEFYIFDSV  FGAEAEFYI         0.1125       14795.0                 50.00     Sequence
IAd  130  GAEAEFYIFDSVSFD  GAEAEFYIF         0.1125       14804.0                 50.00     Sequence
IAd  249  KNTAWQNGKTVTFMP  WQNGKTVTF         0.1125       14809.9                 50.00     Sequence
IAd  120  STGIADTAYFGAEAE  IADTAYFGA         0.1121       14873.5                 50.00     Sequence
IAd  192  DQYVDLRDKMLTNLI  VDLRDKMLT         0.1113       15001.8                 50.00     Sequence
IAd  189  APNDQYVDLRDKMLT  DQYVDLRDK         0.1105       15120.6                 50.00     Sequence
IAd  131  AEAEFYIFDSVSFDS  AEFYIFDSV         0.1105       15129.4                 50.00     Sequence
IAd  280  LWKDGAPLMYDETGY  WKDGAPLMY         0.1101       15193.8                 50.00     Sequence
IAd  320  NPTVNSYKRLVPGYE  NPTVNSYKR         0.1100       15216.5                 50.00     Sequence
IAd  421  QLSDVIDRLEADHEY  QLSDVIDRL         0.1094       15299.5                 50.00     Sequence
IAd  331  PGYEAPINLVYSQRN  EAPINLVYS         0.1086       15446.2                 50.00     Sequence
IAd  418  TPTQLSDVIDRLEAD  QLSDVIDRL         0.1084       15476.1                 50.00     Sequence
IAd  355  TGSNPKAKRLEFRSP  KAKRLEFRS         0.1083       15491.2                 50.00     Sequence
IAd  356  GSNPKAKRLEFRSPD  AKRLEFRSP         0.1080       15540.1                 50.00     Sequence
IAd  398  APVDKDLYELPPEEA  LYELPPEEA         0.1078       15572.9                 50.00     Sequence
IAd  301  ARHYIGGLLHHAPSL  RHYIGGLLH         0.1068       15747.2                 50.00     Sequence
IAd  327  KRLVPGYEAPINLVY  KRLVPGYEA         0.1058       15919.8                 50.00     Sequence
IAd   53  DGSSIRGFQSIHESD  RGFQSIHES         0.1057       15934.6                 50.00     Sequence
IAd  142  SFDSRANGSFYEVDA  RANGSFYEV         0.1051       16032.5                 50.00     Sequence
IAd   35  TIPASAFDKSVFDDG  IPASAFDKS         0.1049       16063.9                 50.00     Sequence
IAd  228  NYQFNSLLHAADDMQ  YQFNSLLHA         0.1047       16103.4                 50.00     Sequence
IAd  128  YFGAEAEFYIFDSVS  FGAEAEFYI         0.1042       16199.7                 50.00     Sequence
IAd  227  INYQFNSLLHAADDM  QFNSLLHAA         0.1036       16298.7                 50.00     Sequence
IAd  223  GQAEINYQFNSLLHA  YQFNSLLHA         0.1036       16307.5                 50.00     Sequence
IAd  319  TNPTVNSYKRLVPGY  NPTVNSYKR         0.1031       16395.2                 50.00     Sequence
IAd  358  NPKAKRLEFRSPDSS  AKRLEFRSP         0.1029       16417.2                 50.00     Sequence
IAd    3  KTPDDVFKLAKDEKV  FKLAKDEKV         0.1025       16489.2                 50.00     Sequence
IAd  332  GYEAPINLVYSQRNR  APINLVYSQ         0.1025       16494.9                 50.00     Sequence
IAd  133  AEFYIFDSVSFDSRA  AEFYIFDSV         0.1025       16496.1                 50.00     Sequence
IAd  395  EPQAPVDKDLYELPP  EPQAPVDKD         0.1024       16509.9                 50.00     Sequence
IAd   34  FTIPASAFDKSVFDD  IPASAFDKS         0.1019       16598.5                 50.00     Sequence
IAd  397  QAPVDKDLYELPPEE  KDLYELPPE         0.1018       16625.7                 50.00     Sequence
IAd  357  SNPKAKRLEFRSPDS  AKRLEFRSP         0.1017       16642.2                 50.00     Sequence
IAd  190  PNDQYVDLRDKMLTN  VDLRDKMLT         0.1015       16674.1                 50.00     Sequence
IAd  123  IADTAYFGAEAEFYI  IADTAYFGA         0.1013       16703.9                 50.00     Sequence
IAd   59  GFQSIHESDMLLLPD  IHESDMLLL         0.1012       16735.2                 50.00     Sequence
IAd   36  IPASAFDKSVFDDGL  IPASAFDKS         0.1008       16798.4                 50.00     Sequence
IAd  348  ACVRIPITGSNPKAK  ACVRIPITG         0.1005       16850.4                 50.00     Sequence
IAd  334  EAPINLVYSQRNRSA  VYSQRNRSA         0.1005       16851.9                 50.00     Sequence
IAd  419  PTQLSDVIDRLEADH  TQLSDVIDR         0.1000       16951.2                 50.00     Sequence
IAd   12  AKDEKVEYVDVRFCD  VEYVDVRFC         0.0995       17030.8                 50.00     Sequence
IAd  121  TGIADTAYFGAEAEF  IADTAYFGA         0.0995       17042.2                 50.00     Sequence
IAd    4  TPDDVFKLAKDEKVE  FKLAKDEKV         0.0990       17139.1                 50.00     Sequence
IAd  292  TGYAGLSDTARHYIG  YAGLSDTAR         0.0989       17156.2                 50.00     Sequence
IAd  359  PKAKRLEFRSPDSSG  AKRLEFRSP         0.0981       17289.6                 50.00     Sequence
IAd   83  RAAKTLNINFFVHDP  RAAKTLNIN         0.0977       17371.9                 50.00     Sequence
IAd  191  NDQYVDLRDKMLTNL  VDLRDKMLT         0.0977       17372.5                 50.00     Sequence
IAd  396  PQAPVDKDLYELPPE  KDLYELPPE         0.0973       17442.2                 50.00     Sequence
IAd  272  SGMHCHQSLWKDGAP  MHCHQSLWK         0.0973       17442.9                 50.00     Sequence
IAd   10  KLAKDEKVEYVDVRF  AKDEKVEYV         0.0973       17445.0                 50.00     Sequence
IAd  423  SDVIDRLEADHEYLT  SDVIDRLEA         0.0972       17468.4                 50.00     Sequence
IAd  291  ETGYAGLSDTARHYI  YAGLSDTAR         0.0971       17484.5                 50.00     Sequence
IAd  422  LSDVIDRLEADHEYL  SDVIDRLEA         0.0965       17600.7                 50.00     Sequence
IAd  221  SGGQAEINYQFNSLL  GGQAEINYQ         0.0964       17613.6                 50.00     Sequence
IAd   22  VRFCDLPGIMQHFTI  VRFCDLPGI         0.0958       17732.5                 50.00     Sequence
IAd   54  GSSIRGFQSIHESDM  RGFQSIHES         0.0947       17943.3                 50.00     Sequence
IAd  290  DETGYAGLSDTARHY  YAGLSDTAR         0.0941       18064.3                 50.00     Sequence
IAd  116  NYLISTGIADTAYFG  ISTGIADTA         0.0937       18136.9                 50.00     Sequence
IAd  330  VPGYEAPINLVYSQR  EAPINLVYS         0.0936       18161.7                 50.00     Sequence
IAd  126  TAYFGAEAEFYIFDS  EAEFYIFDS         0.0936       18162.7                 50.00     Sequence
IAd   23  RFCDLPGIMQHFTIP  FCDLPGIMQ         0.0913       18629.0                 50.00     Sequence
IAd  222  GGQAEINYQFNSLLH  GQAEINYQF         0.0898       18919.4                 50.00     Sequence
IAd  293  GYAGLSDTARHYIGG  YAGLSDTAR         0.0893       19028.5                 50.00     Sequence
IAd  198  RDKMLTNLINSGFIL  RDKMLTNLI         0.0887       19144.5                 50.00     Sequence
IAd  289  YDETGYAGLSDTARH  YAGLSDTAR         0.0883       19224.0                 50.00     Sequence
IAd  337  INLVYSQRNRSACVR  QRNRSACVR         0.0882       19252.1                 50.00     Sequence
IAd  135  FYIFDSVSFDSRANG  FDSVSFDSR         0.0881       19283.0                 50.00     Sequence
IAd  329  LVPGYEAPINLVYSQ  EAPINLVYS         0.0875       19394.9                 50.00     Sequence
IAd  134  EFYIFDSVSFDSRAN  FDSVSFDSR         0.0867       19572.4                 50.00     Sequence
IAd   55  SSIRGFQSIHESDML  IRGFQSIHE         0.0867       19578.1                 50.00     Sequence
IAd  220  GSGGQAEINYQFNSL  GQAEINYQF         0.0864       19623.5                 50.00     Sequence
IAd   16  KVEYVDVRFCDLPGI  VEYVDVRFC         0.0864       19638.8                 50.00     Sequence
IAd  213  EKGHHEVGSGGQAEI  HEVGSGGQA         0.0860       19708.2                 50.00     Sequence
IAd   21  DVRFCDLPGIMQHFT  VRFCDLPGI         0.0859       19749.6                 50.00     Sequence
IAd  219  VGSGGQAEINYQFNS  GGQAEINYQ         0.0858       19756.7                 50.00     Sequence
IAd   50  LAFDGSSIRGFQSIH  GSSIRGFQS         0.0855       19820.9                 50.00     Sequence
IAd  218  EVGSGGQAEINYQFN  GQAEINYQF         0.0850       19928.4                 50.00     Sequence
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IAd  302  RHYIGGLLHHAPSLL  RHYIGGLLH         0.0849      19944.2              50.00      Sequence
IAd   37  PASAFDKSVFDDGLA  PASAFDKSV         0.0849      19961.9              50.00      Sequence
IAd  122  GIADTAYFGAEAEFY  IADTAYFGA         0.0848      19982.8              50.00      Sequence
IAd  217  HEVGSGGQAEINYQF  HEVGSGGQA         0.0847      19986.9              50.00      Sequence
IAd  424  DVIDRLEADHEYLTE  IDRLEADHE         0.0845      20049.3              50.00      Sequence
IAd  105  RDPRNIARKAENYLI  ARKAENYLI         0.0836      20229.1              50.00      Sequence
IAd  312  APSLLAFTNPTVNSY  APSLLAFTN         0.0833      20310.9              50.00      Sequence
IAd   69  LLLPDPETARIDPFR  PETARIDPF         0.0828      20422.2              50.00      Sequence
IAd   49  GLAFDGSSIRGFQSI  GSSIRGFQS         0.0826      20449.2              50.00      Sequence
IAd  318  FTNPTVNSYKRLVPG  NPTVNSYKR         0.0825      20477.3              50.00      Sequence
IAd  214  KGHHEVGSGGQAEIN  KGHHEVGSG         0.0818      20644.1              50.00      Sequence
IAd  181  HKGGYFPVAPNDQYV  HKGGYFPVA         0.0806      20905.3              50.00      Sequence
IAd  369  PDSSGNPYLAFSAML  GNPYLAFSA         0.0802      20983.9              50.00      Sequence
IAd   15  EKVEYVDVRFCDLPG  VEYVDVRFC         0.0802      20993.9              50.00      Sequence
IAd   91  NFFVHDPFTLEPYSR  HDPFTLEPY         0.0802      20999.8              50.00      Sequence
IAd   92  FFVHDPFTLEPYSRD  HDPFTLEPY         0.0800      21034.0              50.00      Sequence
IAd   20  VDVRFCDLPGIMQHF  VRFCDLPGI         0.0797      21117.4              50.00      Sequence
IAd   94  VHDPFTLEPYSRDPR  PFTLEPYSR         0.0796      21125.2              50.00      Sequence
IAd   95  HDPFTLEPYSRDPRN  PFTLEPYSR         0.0796      21134.3              50.00      Sequence
IAd  101  EPYSRDPRNIARKAE  DPRNIARKA         0.0793      21199.6              50.00      Sequence
IAd  455  RENEIEPVNIRPHPY  IEPVNIRPH         0.0793      21207.6              50.00      Sequence
IAd  328  RLVPGYEAPINLVYS  EAPINLVYS         0.0788      21309.8              50.00      Sequence
IAd   48  DGLAFDGSSIRGFQS  GSSIRGFQS         0.0786      21370.2              50.00      Sequence
IAd  333  YEAPINLVYSQRNRS  EAPINLVYS         0.0784      21410.3              50.00      Sequence
IAd   64  HESDMLLLPDPETAR  SDMLLLPDP         0.0782      21449.7              50.00      Sequence
IAd   13  KDEKVEYVDVRFCDL  VEYVDVRFC         0.0778      21555.1              50.00      Sequence
IAd  456  ENEIEPVNIRPHPYE  IEPVNIRPH         0.0777      21570.3              50.00      Sequence
IAd   45  VFDDGLAFDGSSIRG  AFDGSSIRG         0.0776      21602.3              50.00      Sequence
IAd   93  FVHDPFTLEPYSRDP  PFTLEPYSR         0.0774      21639.5              50.00      Sequence
IAd  368  SPDSSGNPYLAFSAM  GNPYLAFSA         0.0771      21716.2              50.00      Sequence
IAd  186  FPVAPNDQYVDLRDK  DQYVDLRDK         0.0766      21831.1              50.00      Sequence
IAd   56  SIRGFQSIHESDMLL  RGFQSIHES         0.0761      21942.2              50.00      Sequence
IAd  212  LEKGHHEVGSGGQAE  HEVGSGGQA         0.0761      21952.9              50.00      Sequence
IAd  271  GSGMHCHQSLWKDGA  MHCHQSLWK         0.0761      21953.3              50.00      Sequence
IAd   14  DEKVEYVDVRFCDLP  VEYVDVRFC         0.0759      21983.3              50.00      Sequence
IAd  136  YIFDSVSFDSRANGS  FDSVSFDSR         0.0757      22034.2              50.00      Sequence
IAd  137  IFDSVSFDSRANGSF  FDSVSFDSR         0.0757      22036.6              50.00      Sequence
IAd   46  FDDGLAFDGSSIRGF  LAFDGSSIR         0.0755      22102.1              50.00      Sequence
IAd  124  ADTAYFGAEAEFYIF  GAEAEFYIF         0.0752      22173.0              50.00      Sequence
IAd  102  PYSRDPRNIARKAEN  DPRNIARKA         0.0751      22181.1              50.00      Sequence
IAd  188  VAPNDQYVDLRDKML  DQYVDLRDK         0.0748      22255.9              50.00      Sequence
IAd  426  IDRLEADHEYLTEGG  IDRLEADHE         0.0746      22305.3              50.00      Sequence
IAd  335  APINLVYSQRNRSAC  APINLVYSQ         0.0743      22373.7              50.00      Sequence
IAd  427  DRLEADHEYLTEGGV  HEYLTEGGV         0.0738      22510.2              50.00      Sequence
IAd  257  KTVTFMPKPLFGDNG  KTVTFMPKP         0.0731      22663.2              50.00      Sequence
IAd  425  VIDRLEADHEYLTEG  RLEADHEYL         0.0729      22712.2              50.00      Sequence
IAd   65  ESDMLLLPDPETARI  ESDMLLLPD         0.0724      22845.3              50.00      Sequence
IAd  187  PVAPNDQYVDLRDKM  DQYVDLRDK         0.0724      22850.5              50.00      Sequence
IAd  288  MYDETGYAGLSDTAR  YAGLSDTAR         0.0719      22964.3              50.00      Sequence
IAd   41  FDKSVFDDGLAFDGS  KSVFDDGLA         0.0719      22978.7              50.00      Sequence
IAd  315  LLAFTNPTVNSYKRL  NPTVNSYKR         0.0718      22982.7              50.00      Sequence
IAd  103  YSRDPRNIARKAENY  DPRNIARKA         0.0716      23032.0              50.00      Sequence
IAd  428  RLEADHEYLTEGGVF  HEYLTEGGV         0.0714      23090.4              50.00      Sequence
IAd  387  LDGIKNKIEPQAPVD  KNKIEPQAP         0.0714      23090.9              50.00      Sequence
IAd  354  ITGSNPKAKRLEFRS  KAKRLEFRS         0.0711      23162.7              50.00      Sequence
IAd   42  DKSVFDDGLAFDGSS  FDDGLAFDG         0.0704      23337.2              50.00      Sequence
IAd  104  SRDPRNIARKAENYL  DPRNIARKA         0.0694      23589.9              50.00      Sequence
IAd   17  VEYVDVRFCDLPGIM  VEYVDVRFC         0.0694      23605.7              50.00      Sequence
IAd   43  KSVFDDGLAFDGSSI  KSVFDDGLA         0.0690      23693.2              50.00      Sequence
IAd   40  AFDKSVFDDGLAFDG  KSVFDDGLA         0.0689      23730.9              50.00      Sequence
IAd  316  LAFTNPTVNSYKRLV  NPTVNSYKR         0.0688      23762.3              50.00      Sequence
IAd  349  CVRIPITGSNPKAKR  CVRIPITGS         0.0686      23796.0              50.00      Sequence
IAd  216  HHEVGSGGQAEINYQ  HEVGSGGQA         0.0686      23796.5              50.00      Sequence
IAd   68  MLLLPDPETARIDPF  PETARIDPF         0.0686      23798.5              50.00      Sequence
IAd  211  ILEKGHHEVGSGGQA  HEVGSGGQA         0.0684      23846.0              50.00      Sequence
IAd    0  VTEKTPDDVFKLAKD  KTPDDVFKL         0.0681      23931.0              50.00      Sequence
IAd   38  ASAFDKSVFDDGLAF  FDKSVFDDG         0.0673      24145.8              50.00      Sequence
IAd  162  NTGAATEADGSPNRG  GAATEADGS         0.0672      24172.8              50.00      Sequence
IAd  317  AFTNPTVNSYKRLVP  NPTVNSYKR         0.0669      24246.1              50.00      Sequence
IAd    1  TEKTPDDVFKLAKDE  KTPDDVFKL         0.0668      24279.4              50.00      Sequence
IAd   19  YVDVRFCDLPGIMQH  VRFCDLPGI         0.0665      24343.6              50.00      Sequence
IAd  436  LTEGGVFTNDLIETW  VFTNDLIET         0.0653      24659.4              50.00      Sequence
IAd  153  EVDAISGWWNTGAAT  SGWWNTGAA         0.0649      24762.0              50.00      Sequence
IAd  270  NGSGMHCHQSLWKDG  CHQSLWKDG         0.0649      24770.6              50.00      Sequence
IAd  154  VDAISGWWNTGAATE  SGWWNTGAA         0.0649      24778.1              50.00      Sequence
IAd    2  EKTPDDVFKLAKDEK  KTPDDVFKL         0.0649      24786.4              50.00      Sequence
IAd  139  DSVSFDSRANGSFYE  SRANGSFYE         0.0644      24903.6              50.00      Sequence
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IAd  459  IEPVNIRPHPYEFAL  IEPVNIRPH         0.0644       24913.8                50.00      Sequence
IAd  458  EIEPVNIRPHPYEFA  IEPVNIRPH         0.0643       24948.4                50.00      Sequence
IAd   84  AAKTLNINFFVHDPF  AAKTLNINF         0.0640       25007.0                50.00      Sequence
IAd  100  LEPYSRDPRNIARKA  DPRNIARKA         0.0636       25133.4                50.00      Sequence
IAd  314  SLLAFTNPTVNSYKR  NPTVNSYKR         0.0633       25202.9                50.00      Sequence
IAd  457  NEIEPVNIRPHPYEF  IEPVNIRPH         0.0633       25213.2                50.00      Sequence
IAd   18  EYVDVRFCDLPGIMQ  VRFCDLPGI         0.0614       25718.3                50.00      Sequence
IAd  138  FDSVSFDSRANGSFY  FDSVSFDSR         0.0611       25819.5                50.00      Sequence
IAd  215  GHHEVGSGGQAEINY  HEVGSGGQA         0.0602       26076.9                50.00      Sequence
IAd   66  SDMLLLPDPETARID  SDMLLLPDP         0.0595       26260.7                50.00      Sequence
IAd  284  GAPLMYDETGYAGLS  MYDETGYAG         0.0594       26305.3                50.00      Sequence
IAd  360  KAKRLEFRSPDSSGN  AKRLEFRSP         0.0590       26402.9                50.00      Sequence
IAd  367  RSPDSSGNPYLAFSA  GNPYLAFSA         0.0589       26434.3                50.00      Sequence
IAd   44  SVFDDGLAFDGSSIR  LAFDGSSIR         0.0580       26694.7                50.00      Sequence
IAd  283  DGAPLMYDETGYAGL  LMYDETGYA         0.0577       26788.4                50.00      Sequence
IAd  163  TGAATEADGSPNRGY  GAATEADGS         0.0571       26964.7                50.00      Sequence
IAd  282  KDGAPLMYDETGYAG  LMYDETGYA         0.0570       26974.0                50.00      Sequence
IAd   47  DDGLAFDGSSIRGFQ  FDGSSIRGF         0.0569       27000.3                50.00      Sequence
IAd  269  DNGSGMHCHQSLWKD  HCHQSLWKD         0.0564       27166.4                50.00      Sequence
IAd  336  PINLVYSQRNRSACV  VYSQRNRSA         0.0558       27327.1                50.00      Sequence
IAd  386  GLDGIKNKIEPQAPV  KNKIEPQAP         0.0552       27501.8                50.00      Sequence
IAd  361  AKRLEFRSPDSSGNP  AKRLEFRSP         0.0551       27537.5                50.00      Sequence
IAd  173  PNRGYKVRHKGGYFP  VRHKGGYFP         0.0551       27540.2                50.00      Sequence
IAd  125  DTAYFGAEAEFYIFD  GAEAEFYIF         0.0550       27573.9                50.00      Sequence
IAd  440  GVFTNDLIETWISFK  VFTNDLIET         0.0543       27798.6                50.00      Sequence
IAd   90  INFFVHDPFTLEPYS  HDPFTLEPY         0.0542       27804.3                50.00      Sequence
IAd  353  PITGSNPKAKRLEFR  PITGSNPKA         0.0532       28129.3                50.00      Sequence
IAd   89  NINFFVHDPFTLEPY  HDPFTLEPY         0.0526       28289.5                50.00      Sequence
IAd  385  AGLDGIKNKIEPQAP  KNKIEPQAP         0.0523       28403.9                50.00      Sequence
IAd   39  SAFDKSVFDDGLAFD  KSVFDDGLA         0.0514       28672.2                50.00      Sequence
IAd  200  KMLTNLINSGFILEK  INSGFILEK         0.0503       29000.8                50.00      Sequence
IAd  199  DKMLTNLINSGFILE  KMLTNLINS         0.0503       29011.1                50.00      Sequence
IAd  438  EGGVFTNDLIETWIS  VFTNDLIET         0.0497       29203.9                50.00      Sequence
IAd  169  ADGSPNRGYKVRHKG  GSPNRGYKV         0.0497       29213.4                50.00      Sequence
IAd   85  AKTLNINFFVHDPFT  AKTLNINFF         0.0485       29571.8                50.00      Sequence
IAd  171  GSPNRGYKVRHKGGY  GSPNRGYKV         0.0473       29976.4                50.00      Sequence
IAd  439  GGVFTNDLIETWISF  VFTNDLIET         0.0468       30136.1                50.00      Sequence
IAd  170  DGSPNRGYKVRHKGG  GSPNRGYKV         0.0459       30430.6                50.00      Sequence
IAd  172  SPNRGYKVRHKGGYF  RGYKVRHKG         0.0456       30518.0                50.00      Sequence
IAd  185  YFPVAPNDQYVDLRD  APNDQYVDL         0.0450       30731.7                50.00      Sequence
IAd  313  PSLLAFTNPTVNSYK  PSLLAFTNP         0.0450       30740.7                50.00      Sequence
IAd  287  LMYDETGYAGLSDTA  MYDETGYAG         0.0449       30751.0                50.00      Sequence
IAd  164  GAATEADGSPNRGYK  GAATEADGS         0.0439       31081.5                50.00      Sequence
IAd  165  AATEADGSPNRGYKV  AATEADGSP         0.0436       31187.3                50.00      Sequence
IAd  463  NIRPHPYEFALYYDV  YEFALYYDV         0.0436       31201.1                50.00      Sequence
IAd   97  PFTLEPYSRDPRNIA  PFTLEPYSR         0.0435       31227.8                50.00      Sequence
IAd  184  GYFPVAPNDQYVDLR  APNDQYVDL         0.0422       31685.9                50.00      Sequence
IAd  437  TEGGVFTNDLIETWI  VFTNDLIET         0.0421       31710.9                50.00      Sequence
IAd  286  PLMYDETGYAGLSDT  MYDETGYAG         0.0417       31829.9                50.00      Sequence
IAd   96  DPFTLEPYSRDPRNI  PFTLEPYSR         0.0388       32849.4                50.00      Sequence
IAd  166  ATEADGSPNRGYKVR  GSPNRGYKV         0.0381       33121.0                50.00      Sequence
IAd  268  GDNGSGMHCHQSLWK  MHCHQSLWK         0.0380       33159.4                50.00      Sequence
IAd  210  FILEKGHHEVGSGGQ  KGHHEVGSG         0.0378       33232.3                50.00      Sequence
IAd  201  MLTNLINSGFILEKG  INSGFILEK         0.0373       33398.8                50.00      Sequence
IAd  285  APLMYDETGYAGLSD  MYDETGYAG         0.0372       33417.3                50.00      Sequence
IAd  183  GGYFPVAPNDQYVDL  GGYFPVAPN         0.0360       33856.9                50.00      Sequence
IAd   99  TLEPYSRDPRNIARK  RDPRNIARK         0.0336       34758.9                50.00      Sequence
IAd  461  PVNIRPHPYEFALYY  IRPHPYEFA         0.0329       35012.5                50.00      Sequence
IAd  460  EPVNIRPHPYEFALY  IRPHPYEFA         0.0323       35266.5                50.00      Sequence
IAd  182  KGGYFPVAPNDQYVD  GGYFPVAPN         0.0320       35363.6                50.00      Sequence
IAd  365  EFRSPDSSGNPYLAF  DSSGNPYLA         0.0318       35444.4                50.00      Sequence
IAd  364  LEFRSPDSSGNPYLA  DSSGNPYLA         0.0315       35569.6                50.00      Sequence
IAd  350  VRIPITGSNPKAKRL  VRIPITGSN         0.0315       35573.5                50.00      Sequence
IAd  202  LTNLINSGFILEKGH  INSGFILEK         0.0305       35934.4                50.00      Sequence
IAd  168  EADGSPNRGYKVRHK  GSPNRGYKV         0.0293       36434.3                50.00      Sequence
IAd  366  FRSPDSSGNPYLAFS  DSSGNPYLA         0.0291       36499.1                50.00      Sequence
IAd  208  SGFILEKGHHEVGSG  KGHHEVGSG         0.0284       36760.6                50.00      Sequence
IAd  209  GFILEKGHHEVGSGG  KGHHEVGSG         0.0283       36792.9                50.00      Sequence
IAd   98  FTLEPYSRDPRNIAR  EPYSRDPRN         0.0272       37271.3                50.00      Sequence
IAd   86  KTLNINFFVHDPFTL  KTLNINFFV         0.0255       37952.5                50.00      Sequence
IAd  351  RIPITGSNPKAKRLE  GSNPKAKRL         0.0247       38267.9                50.00      Sequence
IAd  462  VNIRPHPYEFALYYD  IRPHPYEFA         0.0244       38378.2                50.00      Sequence
IAd   67  DMLLLPDPETARIDP  MLLLPDPET         0.0243       38459.7                50.00      Sequence
IAd  266  LFGDNGSGMHCHQSL  SGMHCHQSL         0.0242       38494.3                50.00      Sequence
IAd  205  LINSGFILEKGHHEV  NSGFILEKG         0.0241       38536.3                50.00      Sequence
IAd  167  TEADGSPNRGYKVRH  GSPNRGYKV         0.0240       38583.5                50.00      Sequence
IAd  267  FGDNGSGMHCHQSLW  SGMHCHQSL         0.0237       38680.1                50.00      Sequence
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         IAd  206  INSGFILEKGHHEVG  NSGFILEKG        0.0228      39082.2                50.00     Sequence
         IAd  363  RLEFRSPDSSGNPYL  FRSPDSSGN        0.0223      39262.3                50.00     Sequence
         IAd  362  KRLEFRSPDSSGNPY  FRSPDSSGN        0.0223      39290.8                50.00     Sequence
         IAd  203  TNLINSGFILEKGHH  INSGFILEK        0.0222      39323.1                50.00     Sequence
         IAd  204  NLINSGFILEKGHHE  NSGFILEKG        0.0219      39462.5                50.00     Sequence
         IAd  352  IPITGSNPKAKRLEF  GSNPKAKRL        0.0197      40400.9                50.00     Sequence
         IAd   87  TLNINFFVHDPFTLE  INFFVHDPF        0.0175      41355.3                50.00     Sequence
         IAd  258  TVTFMPKPLFGDNGS  TFMPKPLFG        0.0175      41382.6                50.00     Sequence
         IAd  265  PLFGDNGSGMHCHQS  GSGMHCHQS        0.0174      41433.7                50.00     Sequence
         IAd   88  LNINFFVHDPFTLEP  INFFVHDPF        0.0154      42330.9                50.00     Sequence
         IAd  207  NSGFILEKGHHEVGS  NSGFILEKG        0.0150      42531.1                50.00     Sequence
         IAd  262  MPKPLFGDNGSGMHC  GDNGSGMHC        0.0132      43339.8                50.00     Sequence
         IAd  259  VTFMPKPLFGDNGSG  MPKPLFGDN        0.0130      43446.9                50.00     Sequence
         IAd  263  PKPLFGDNGSGMHCH  GDNGSGMHC        0.0113      44242.9                50.00     Sequence
         IAd  260  TFMPKPLFGDNGSGM  MPKPLFGDN        0.0105      44649.3                50.00     Sequence
         IAd  264  KPLFGDNGSGMHCHQ  GDNGSGMHC        0.0103      44724.7                50.00     Sequence
         IAd  261  FMPKPLFGDNGSGMH  FMPKPLFGD        0.0100      44855.0                50.00     Sequence
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Allele: IAd. Number of high binders 0. Number of weak binders 0. Number of peptides 464

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
-----------------------------------------------------------------------------------------------
         IAs  252  AWQNGKTVTFMPKPL  KTVTFMPKP        0.4325        464.4          WB     0.40     Sequence
         IAs  256  GKTVTFMPKPLFGDN  KTVTFMPKP        0.4292        481.2          WB     0.40     Sequence
         IAs  254  QNGKTVTFMPKPLFG  KTVTFMPKP        0.4272        491.3          WB     0.40     Sequence
         IAs  255  NGKTVTFMPKPLFGD  KTVTFMPKP        0.4265        495.5          WB     0.40     Sequence
         IAs  253  WQNGKTVTFMPKPLF  KTVTFMPKP        0.4227        516.3                 0.80     Sequence
         IAs   17  VEYVDVRFCDLPGIM  RFCDLPGIM        0.4081        604.5                 0.80     Sequence
         IAs   18  EYVDVRFCDLPGIMQ  RFCDLPGIM        0.3898        736.6                 0.80     Sequence
         IAs  342  SQRNRSACVRIPITG  NRSACVRIP        0.3871        758.4                 0.80     Sequence
         IAs  345  NRSACVRIPITGSNP  NRSACVRIP        0.3810        810.6                 0.80     Sequence
         IAs  343  QRNRSACVRIPITGS  NRSACVRIP        0.3777        839.8                 0.80     Sequence
         IAs  344  RNRSACVRIPITGSN  NRSACVRIP        0.3762        853.9                 1.00     Sequence
         IAs  251  TAWQNGKTVTFMPKP  KTVTFMPKP        0.3735        878.7                 1.00     Sequence
         IAs   19  YVDVRFCDLPGIMQH  RFCDLPGIM        0.3729        885.0                 1.00     Sequence
         IAs   20  VDVRFCDLPGIMQHF  RFCDLPGIM        0.3605       1011.6                 2.00     Sequence
         IAs   22  VRFCDLPGIMQHFTI  RFCDLPGIM        0.3485       1151.7                 2.00     Sequence
         IAs   21  DVRFCDLPGIMQHFT  RFCDLPGIM        0.3427       1227.0                 2.00     Sequence
         IAs  341  YSQRNRSACVRIPIT  NRSACVRIP        0.3394       1270.5                 2.00     Sequence
         IAs  257  KTVTFMPKPLFGDNG  KTVTFMPKP        0.3334       1355.6                 2.00     Sequence
         IAs  340  VYSQRNRSACVRIPI  RSACVRIPI        0.3285       1430.1                 2.00     Sequence
         IAs  411  EAASIPQTPTQLSDV  EAASIPQTP        0.2998       1951.0                 4.00     Sequence
         IAs  410  EEAASIPQTPTQLSD  EAASIPQTP        0.2983       1983.6                 4.00     Sequence
         IAs  406  ELPPEEAASIPQTPT  EAASIPQTP        0.2950       2055.5                 4.00     Sequence
         IAs  409  PEEAASIPQTPTQLS  EAASIPQTP        0.2940       2077.0                 4.00     Sequence
         IAs  407  LPPEEAASIPQTPTQ  EAASIPQTP        0.2938       2081.0                 4.00     Sequence
         IAs  408  PPEEAASIPQTPTQL  EAASIPQTP        0.2938       2081.9                 4.00     Sequence
         IAs   61  QSIHESDMLLLPDPE  SDMLLLPDP        0.2681       2748.5                 4.00     Sequence
         IAs  405  YELPPEEAASIPQTP  EAASIPQTP        0.2470       3453.0                 8.00     Sequence
         IAs   63  IHESDMLLLPDPETA  SDMLLLPDP        0.2395       3745.3                 8.00     Sequence
         IAs  346  RSACVRIPITGSNPK  RSACVRIPI        0.2392       3757.9                 8.00     Sequence
         IAs   64  HESDMLLLPDPETAR  SDMLLLPDP        0.2368       3858.0                 8.00     Sequence
         IAs   23  RFCDLPGIMQHFTIP  RFCDLPGIM        0.2329       4023.9                 8.00     Sequence
         IAs   62  SIHESDMLLLPDPET  DMLLLPDPE        0.2321       4060.4                 8.00     Sequence
         IAs  250  NTAWQNGKTVTFMPK  QNGKTVTFM        0.2228       4487.4                 8.00     Sequence
         IAs   66  SDMLLLPDPETARID  SDMLLLPDP        0.2217       4540.3                 8.00     Sequence
         IAs   16  KVEYVDVRFCDLPGI  VDVRFCDLP        0.2173       4760.8                 8.00     Sequence
         IAs   65  ESDMLLLPDPETARI  SDMLLLPDP        0.2162       4818.7                 8.00     Sequence
         IAs  347  SACVRIPITGSNPKA  SACVRIPIT        0.1930       6194.3                16.00     Sequence
         IAs   60  FQSIHESDMLLLPDP  QSIHESDML        0.1921       6257.8                16.00     Sequence
         IAs  181  HKGGYFPVAPNDQYV  FPVAPNDQY        0.1907       6349.9                16.00     Sequence
         IAs  180  RHKGGYFPVAPNDQY  FPVAPNDQY        0.1884       6511.8                16.00     Sequence
         IAs  339  LVYSQRNRSACVRIP  NRSACVRIP        0.1856       6712.6                16.00     Sequence
         IAs  396  PQAPVDKDLYELPPE  KDLYELPPE        0.1806       7085.6                16.00     Sequence
         IAs  456  ENEIEPVNIRPHPYE  EPVNIRPHP        0.1785       7244.5                16.00     Sequence
         IAs  179  VRHKGGYFPVAPNDQ  KGGYFPVAP        0.1762       7428.9                16.00     Sequence
         IAs  178  KVRHKGGYFPVAPND  KGGYFPVAP        0.1760       7444.5                16.00     Sequence
         IAs   55  SSIRGFQSIHESDML  QSIHESDML        0.1758       7460.5                16.00     Sequence
         IAs  397  QAPVDKDLYELPPEE  KDLYELPPE        0.1749       7533.9                16.00     Sequence
         IAs  455  RENEIEPVNIRPHPY  EPVNIRPHP        0.1710       7864.3                16.00     Sequence
         IAs  324  NSYKRLVPGYEAPIN  VPGYEAPIN        0.1695       7986.8                16.00     Sequence
         IAs  457  NEIEPVNIRPHPYEF  EPVNIRPHP        0.1683       8095.6                16.00     Sequence
         IAs  177  YKVRHKGGYFPVAPN  KGGYFPVAP        0.1664       8266.0                16.00     Sequence
         IAs  412  AASIPQTPTQLSDVI  AASIPQTPT        0.1654       8355.4                16.00     Sequence
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IAs  459  IEPVNIRPHPYEFAL  EPVNIRPHP        0.1653       8360.6                16.00     Sequence
IAs  390  IKNKIEPQAPVDKDL  NKIEPQAPV        0.1628       8586.0                16.00     Sequence
IAs  398  APVDKDLYELPPEEA  KDLYELPPE        0.1627       8596.8                16.00     Sequence
IAs  454  KRENEIEPVNIRPHP  EPVNIRPHP        0.1616       8704.2                16.00     Sequence
IAs  458  EIEPVNIRPHPYEFA  EPVNIRPHP        0.1609       8769.8                16.00     Sequence
IAs   77  ARIDPFRAAKTLNIN  RAAKTLNIN        0.1603       8822.6                16.00     Sequence
IAs   56  SIRGFQSIHESDMLL  QSIHESDML        0.1599       8867.8                32.00     Sequence
IAs  389  GIKNKIEPQAPVDKD  KNKIEPQAP        0.1585       8994.7                32.00     Sequence
IAs  387  LDGIKNKIEPQAPVD  NKIEPQAPV        0.1585       8995.6                32.00     Sequence
IAs  386  GLDGIKNKIEPQAPV  NKIEPQAPV        0.1574       9108.7                32.00     Sequence
IAs  400  VDKDLYELPPEEAAS  KDLYELPPE        0.1554       9307.2                32.00     Sequence
IAs  402  KDLYELPPEEAASIP  KDLYELPPE        0.1546       9385.8                32.00     Sequence
IAs  388  DGIKNKIEPQAPVDK  KNKIEPQAP        0.1541       9437.5                32.00     Sequence
IAs  399  PVDKDLYELPPEEAA  KDLYELPPE        0.1521       9640.6                32.00     Sequence
IAs   79  IDPFRAAKTLNINFF  RAAKTLNIN        0.1507       9795.9                32.00     Sequence
IAs  401  DKDLYELPPEEAASI  KDLYELPPE        0.1506       9802.5                32.00     Sequence
IAs   78  RIDPFRAAKTLNINF  RAAKTLNIN        0.1504       9822.4                32.00     Sequence
IAs  258  TVTFMPKPLFGDNGS  TVTFMPKPL        0.1498       9885.6                32.00     Sequence
IAs  182  KGGYFPVAPNDQYVD  KGGYFPVAP        0.1497       9898.9                32.00     Sequence
IAs   83  RAAKTLNINFFVHDP  RAAKTLNIN        0.1467      10228.7                32.00     Sequence
IAs   59  GFQSIHESDMLLLPD  QSIHESDML        0.1466      10231.2                32.00     Sequence
IAs   82  FRAAKTLNINFFVHD  RAAKTLNIN        0.1465      10249.5                32.00     Sequence
IAs   57  IRGFQSIHESDMLLL  QSIHESDML        0.1464      10252.5                32.00     Sequence
IAs   80  DPFRAAKTLNINFFV  RAAKTLNIN        0.1457      10337.9                32.00     Sequence
IAs  391  KNKIEPQAPVDKDLY  KNKIEPQAP        0.1447      10449.3                32.00     Sequence
IAs  325  SYKRLVPGYEAPINL  RLVPGYEAP        0.1441      10518.6                32.00     Sequence
IAs   81  PFRAAKTLNINFFVH  RAAKTLNIN        0.1440      10530.9                32.00     Sequence
IAs   58  RGFQSIHESDMLLLP  QSIHESDML        0.1415      10817.8                32.00     Sequence
IAs  361  AKRLEFRSPDSSGNP  AKRLEFRSP        0.1410      10875.5                32.00     Sequence
IAs  326  YKRLVPGYEAPINLV  RLVPGYEAP        0.1407      10910.5                32.00     Sequence
IAs  460  EPVNIRPHPYEFALY  EPVNIRPHP        0.1396      11036.3                32.00     Sequence
IAs  176  GYKVRHKGGYFPVAP  KGGYFPVAP        0.1383      11196.8                32.00     Sequence
IAs  328  RLVPGYEAPINLVYS  RLVPGYEAP        0.1381      11220.9                32.00     Sequence
IAs  230  QFNSLLHAADDMQLY  SLLHAADDM        0.1374      11308.7                32.00     Sequence
IAs  327  KRLVPGYEAPINLVY  RLVPGYEAP        0.1361      11463.6                32.00     Sequence
IAs   89  NINFFVHDPFTLEPY  INFFVHDPF        0.1351      11587.7                32.00     Sequence
IAs  227  INYQFNSLLHAADDM  SLLHAADDM        0.1343      11693.5                32.00     Sequence
IAs  374  NPYLAFSAMLMAGLD  LAFSAMLMA        0.1342      11702.3                32.00     Sequence
IAs  428  RLEADHEYLTEGGVF  EYLTEGGVF        0.1333      11815.2                32.00     Sequence
IAs   67  DMLLLPDPETARIDP  DMLLLPDPE        0.1319      11993.5                32.00     Sequence
IAs  310  HHAPSLLAFTNPTVN  LAFTNPTVN        0.1315      12052.0                32.00     Sequence
IAs  228  NYQFNSLLHAADDMQ  SLLHAADDM        0.1303      12215.5                32.00     Sequence
IAs  322  TVNSYKRLVPGYEAP  RLVPGYEAP        0.1300      12253.1                32.00     Sequence
IAs  348  ACVRIPITGSNPKAK  ACVRIPITG        0.1299      12268.9                32.00     Sequence
IAs  323  VNSYKRLVPGYEAPI  RLVPGYEAP        0.1295      12320.6                32.00     Sequence
IAs   86  KTLNINFFVHDPFTL  FFVHDPFTL        0.1289      12393.9                32.00     Sequence
IAs  385  AGLDGIKNKIEPQAP  KNKIEPQAP        0.1254      12873.5                32.00     Sequence
IAs  229  YQFNSLLHAADDMQL  SLLHAADDM        0.1244      13008.7                32.00     Sequence
IAs   88  LNINFFVHDPFTLEP  INFFVHDPF        0.1241      13063.2                32.00     Sequence
IAs   87  TLNINFFVHDPFTLE  FFVHDPFTL        0.1226      13267.0                32.00     Sequence
IAs   52  FDGSSIRGFQSIHES  RGFQSIHES        0.1221      13335.8                32.00     Sequence
IAs  429  LEADHEYLTEGGVFT  EYLTEGGVF        0.1219      13368.6                32.00     Sequence
IAs   85  AKTLNINFFVHDPFT  INFFVHDPF        0.1213      13453.5                32.00     Sequence
IAs  392  NKIEPQAPVDKDLYE  NKIEPQAPV        0.1213      13455.8                32.00     Sequence
IAs  375  PYLAFSAMLMAGLDG  LAFSAMLMA        0.1209      13518.3                32.00     Sequence
IAs  362  KRLEFRSPDSSGNPY  KRLEFRSPD        0.1208      13527.3                32.00     Sequence
IAs   14  DEKVEYVDVRFCDLP  VDVRFCDLP        0.1199      13670.1                32.00     Sequence
IAs  376  YLAFSAMLMAGLDGI  LAFSAMLMA        0.1191      13785.5                32.00     Sequence
IAs  413  ASIPQTPTQLSDVID  ASIPQTPTQ        0.1189      13811.7                32.00     Sequence
IAs  377  LAFSAMLMAGLDGIK  FSAMLMAGL        0.1186      13855.3                32.00     Sequence
IAs   84  AAKTLNINFFVHDPF  INFFVHDPF        0.1182      13922.3                32.00     Sequence
IAs  311  HAPSLLAFTNPTVNS  LAFTNPTVN        0.1168      14131.3                32.00     Sequence
IAs   74  PETARIDPFRAAKTL  PETARIDPF        0.1156      14309.9                32.00     Sequence
IAs  273  GMHCHQSLWKDGAPL  SLWKDGAPL        0.1151      14394.9                32.00     Sequence
IAs  358  NPKAKRLEFRSPDSS  LEFRSPDSS        0.1148      14444.3                32.00     Sequence
IAs  275  HCHQSLWKDGAPLMY  SLWKDGAPL        0.1145      14480.6                32.00     Sequence
IAs   90  INFFVHDPFTLEPYS  INFFVHDPF        0.1130      14716.3                32.00     Sequence
IAs   15  EKVEYVDVRFCDLPG  VDVRFCDLP        0.1129      14734.5                32.00     Sequence
IAs  379  FSAMLMAGLDGIKNK  FSAMLMAGL        0.1125      14808.6                32.00     Sequence
IAs  430  EADHEYLTEGGVFTN  EYLTEGGVF        0.1124      14813.7                32.00     Sequence
IAs  183  GGYFPVAPNDQYVDL  FPVAPNDQY        0.1114      14981.4                32.00     Sequence
IAs  434  EYLTEGGVFTNDLIE  EYLTEGGVF        0.1104      15137.8                50.00     Sequence
IAs  274  MHCHQSLWKDGAPLM  SLWKDGAPL        0.1085      15457.2                50.00     Sequence
IAs  433  HEYLTEGGVFTNDLI  EYLTEGGVF        0.1078      15571.2                50.00     Sequence
IAs   31  MQHFTIPASAFDKSV  QHFTIPASA        0.1062      15841.7                50.00     Sequence
IAs   26  DLPGIMQHFTIPASA  QHFTIPASA        0.1062      15844.0                50.00     Sequence
IAs  359  PKAKRLEFRSPDSSG  LEFRSPDSS        0.1058      15914.4                50.00     Sequence
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IAs  431  ADHEYLTEGGVFTND  EYLTEGGVF        0.1052      16020.0               50.00     Sequence
IAs  351  RIPITGSNPKAKRLE  RIPITGSNP        0.1049      16067.0               50.00     Sequence
IAs   30  IMQHFTIPASAFDKS  QHFTIPASA        0.1040      16222.1               50.00     Sequence
IAs    9  FKLAKDEKVEYVDVR  AKDEKVEYV        0.1034      16329.9               50.00     Sequence
IAs    4  TPDDVFKLAKDEKVE  KLAKDEKVE        0.1034      16335.0               50.00     Sequence
IAs  363  RLEFRSPDSSGNPYL  LEFRSPDSS        0.1033      16358.6               50.00     Sequence
IAs  231  FNSLLHAADDMQLYK  SLLHAADDM        0.1027      16461.7               50.00     Sequence
IAs  329  LVPGYEAPINLVYSQ  VPGYEAPIN        0.1025      16494.7               50.00     Sequence
IAs  305  IGGLLHHAPSLLAFT  IGGLLHHAP        0.1025      16496.1               50.00     Sequence
IAs  302  RHYIGGLLHHAPSLL  LLHHAPSLL        0.1022      16544.9               50.00     Sequence
IAs  330  VPGYEAPINLVYSQR  VPGYEAPIN        0.1020      16580.0               50.00     Sequence
IAs  360  KAKRLEFRSPDSSGN  LEFRSPDSS        0.1019      16601.4               50.00     Sequence
IAs  378  AFSAMLMAGLDGIKN  FSAMLMAGL        0.1015      16665.7               50.00     Sequence
IAs   68  MLLLPDPETARIDPF  PETARIDPF        0.1015      16666.9               50.00     Sequence
IAs   27  LPGIMQHFTIPASAF  QHFTIPASA        0.1015      16677.4               50.00     Sequence
IAs  303  HYIGGLLHHAPSLLA  LLHHAPSLL        0.1010      16755.5               50.00     Sequence
IAs    6  DDVFKLAKDEKVEYV  KLAKDEKVE        0.1001      16925.2               50.00     Sequence
IAs  304  YIGGLLHHAPSLLAF  LLHHAPSLL        0.1001      16933.9               50.00     Sequence
IAs  239  DDMQLYKYIIKNTAW  KYIIKNTAW        0.0993      17078.2               50.00     Sequence
IAs  432  DHEYLTEGGVFTNDL  EYLTEGGVF        0.0987      17187.4               50.00     Sequence
IAs  232  NSLLHAADDMQLYKY  SLLHAADDM        0.0987      17188.5               50.00     Sequence
IAs   10  KLAKDEKVEYVDVRF  AKDEKVEYV        0.0986      17206.0               50.00     Sequence
IAs   69  LLLPDPETARIDPFR  PETARIDPF        0.0984      17240.3               50.00     Sequence
IAs  350  VRIPITGSNPKAKRL  IPITGSNPK        0.0982      17283.6               50.00     Sequence
IAs  279  SLWKDGAPLMYDETG  SLWKDGAPL        0.0980      17310.4               50.00     Sequence
IAs  277  HQSLWKDGAPLMYDE  SLWKDGAPL        0.0974      17434.4               50.00     Sequence
IAs  315  LLAFTNPTVNSYKRL  LAFTNPTVN        0.0971      17494.9               50.00     Sequence
IAs  240  DMQLYKYIIKNTAWQ  KYIIKNTAW        0.0968      17552.2               50.00     Sequence
IAs  103  YSRDPRNIARKAENY  RNIARKAEN        0.0966      17583.0               50.00     Sequence
IAs  356  GSNPKAKRLEFRSPD  KRLEFRSPD        0.0958      17740.4               50.00     Sequence
IAs  448  ETWISFKRENEIEPV  KRENEIEPV        0.0956      17774.2               50.00     Sequence
IAs  301  ARHYIGGLLHHAPSL  GLLHHAPSL        0.0954      17817.9               50.00     Sequence
IAs  276  CHQSLWKDGAPLMYD  SLWKDGAPL        0.0948      17929.5               50.00     Sequence
IAs   91  NFFVHDPFTLEPYSR  FFVHDPFTL        0.0945      17989.0               50.00     Sequence
IAs  364  LEFRSPDSSGNPYLA  RSPDSSGNP        0.0944      18013.7               50.00     Sequence
IAs  357  SNPKAKRLEFRSPDS  KRLEFRSPD        0.0938      18125.7               50.00     Sequence
IAs  245  KYIIKNTAWQNGKTV  KYIIKNTAW        0.0935      18183.1               50.00     Sequence
IAs   28  PGIMQHFTIPASAFD  QHFTIPASA        0.0932      18247.9               50.00     Sequence
IAs  244  YKYIIKNTAWQNGKT  KYIIKNTAW        0.0928      18321.1               50.00     Sequence
IAs  367  RSPDSSGNPYLAFSA  RSPDSSGNP        0.0928      18321.5               50.00     Sequence
IAs  349  CVRIPITGSNPKAKR  IPITGSNPK        0.0925      18387.9               50.00     Sequence
IAs   53  DGSSIRGFQSIHESD  RGFQSIHES        0.0923      18423.9               50.00     Sequence
IAs  278  QSLWKDGAPLMYDET  SLWKDGAPL        0.0923      18427.9               50.00     Sequence
IAs  175  RGYKVRHKGGYFPVA  RGYKVRHKG        0.0921      18450.1               50.00     Sequence
IAs  321  PTVNSYKRLVPGYEA  KRLVPGYEA        0.0920      18470.0               50.00     Sequence
IAs  119  ISTGIADTAYFGAEA  TGIADTAYF        0.0917      18546.3               50.00     Sequence
IAs  312  APSLLAFTNPTVNSY  LAFTNPTVN        0.0916      18566.6               50.00     Sequence
IAs  174  NRGYKVRHKGGYFPV  RGYKVRHKG        0.0913      18621.7               50.00     Sequence
IAs  241  MQLYKYIIKNTAWQN  KYIIKNTAW        0.0912      18647.7               50.00     Sequence
IAs  243  LYKYIIKNTAWQNGK  KYIIKNTAW        0.0908      18719.3               50.00     Sequence
IAs  104  SRDPRNIARKAENYL  RNIARKAEN        0.0907      18730.6               50.00     Sequence
IAs  461  PVNIRPHPYEFALYY  PVNIRPHPY        0.0904      18799.5               50.00     Sequence
IAs  173  PNRGYKVRHKGGYFP  RGYKVRHKG        0.0903      18822.1               50.00     Sequence
IAs  316  LAFTNPTVNSYKRLV  LAFTNPTVN        0.0900      18890.2               50.00     Sequence
IAs    7  DVFKLAKDEKVEYVD  KLAKDEKVE        0.0899      18894.7               50.00     Sequence
IAs   32  QHFTIPASAFDKSVF  QHFTIPASA        0.0899      18895.1               50.00     Sequence
IAs  371  SSGNPYLAFSAMLMA  LAFSAMLMA        0.0899      18895.5               50.00     Sequence
IAs    5  PDDVFKLAKDEKVEY  KLAKDEKVE        0.0895      18992.9               50.00     Sequence
IAs  313  PSLLAFTNPTVNSYK  LAFTNPTVN        0.0894      19003.2               50.00     Sequence
IAs  314  SLLAFTNPTVNSYKR  LAFTNPTVN        0.0893      19024.1               50.00     Sequence
IAs   92  FFVHDPFTLEPYSRD  FFVHDPFTL        0.0890      19080.8               50.00     Sequence
IAs  105  RDPRNIARKAENYLI  RNIARKAEN        0.0890      19082.9               50.00     Sequence
IAs  204  NLINSGFILEKGHHE  GFILEKGHH        0.0882      19255.0               50.00     Sequence
IAs   29  GIMQHFTIPASAFDK  QHFTIPASA        0.0882      19257.8               50.00     Sequence
IAs  172  SPNRGYKVRHKGGYF  NRGYKVRHK        0.0881      19272.5               50.00     Sequence
IAs  115  ENYLISTGIADTAYF  TGIADTAYF        0.0879      19313.2               50.00     Sequence
IAs  162  NTGAATEADGSPNRG  NTGAATEAD        0.0879      19315.1               50.00     Sequence
IAs  373  GNPYLAFSAMLMAGL  LAFSAMLMA        0.0879      19325.2               50.00     Sequence
IAs  259  VTFMPKPLFGDNGSG  VTFMPKPLF        0.0878      19331.4               50.00     Sequence
IAs  102  PYSRDPRNIARKAEN  RNIARKAEN        0.0876      19380.2               50.00     Sequence
IAs  384  MAGLDGIKNKIEPQA  GIKNKIEPQ        0.0876      19387.4               50.00     Sequence
IAs   54  GSSIRGFQSIHESDM  RGFQSIHES        0.0875      19401.6               50.00     Sequence
IAs  366  FRSPDSSGNPYLAFS  RSPDSSGNP        0.0875      19402.3               50.00     Sequence
IAs  116  NYLISTGIADTAYFG  TGIADTAYF        0.0874      19429.8               50.00     Sequence
IAs  352  IPITGSNPKAKRLEF  IPITGSNPK        0.0871      19478.0               50.00     Sequence
IAs  118  LISTGIADTAYFGAE  TGIADTAYF        0.0867      19570.5               50.00     Sequence
IAs   73  DPETARIDPFRAAKT  PETARIDPF        0.0862      19679.7               50.00     Sequence
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IAs  187  PVAPNDQYVDLRDKM  QYVDLRDKM         0.0861      19696.1            50.00     Sequence
IAs  449  TWISFKRENEIEPVN  KRENEIEPV         0.0861      19698.2            50.00     Sequence
IAs  117  YLISTGIADTAYFGA  TGIADTAYF         0.0860      19727.0            50.00     Sequence
IAs  372  SGNPYLAFSAMLMAG  LAFSAMLMA         0.0858      19771.0            50.00     Sequence
IAs  169  ADGSPNRGYKVRHKG  RGYKVRHKG         0.0857      19791.8            50.00     Sequence
IAs   94  VHDPFTLEPYSRDPR  DPFTLEPYS         0.0855      19817.7            50.00     Sequence
IAs  233  SLLHAADDMQLYKYI  SLLHAADDM         0.0854      19840.2            50.00     Sequence
IAs  242  QLYKYIIKNTAWQNG  KYIIKNTAW         0.0854      19840.9            50.00     Sequence
IAs  207  NSGFILEKGHHEVGS  GFILEKGHH         0.0854      19850.5            50.00     Sequence
IAs  451  ISFKRENEIEPVNIR  KRENEIEPV         0.0852      19897.0            50.00     Sequence
IAs   11  LAKDEKVEYVDVRFC  EKVEYVDVR         0.0851      19901.1            50.00     Sequence
IAs  453  FKRENEIEPVNIRPH  KRENEIEPV         0.0851      19916.4            50.00     Sequence
IAs  122  GIADTAYFGAEAEFY  YFGAEAEFY         0.0849      19955.6            50.00     Sequence
IAs  383  LMAGLDGIKNKIEPQ  GIKNKIEPQ         0.0848      19983.5            50.00     Sequence
IAs   70  LLPDPETARIDPFRA  PETARIDPF         0.0844      20062.8            50.00     Sequence
IAs  206  INSGFILEKGHHEVG  GFILEKGHH         0.0842      20103.4            50.00     Sequence
IAs  205  LINSGFILEKGHHEV  GFILEKGHH         0.0840      20142.4            50.00     Sequence
IAs   72  PDPETARIDPFRAAK  PETARIDPF         0.0836      20244.0            50.00     Sequence
IAs  395  EPQAPVDKDLYELPP  EPQAPVDKD         0.0835      20265.9            50.00     Sequence
IAs  365  EFRSPDSSGNPYLAF  SPDSSGNPY         0.0832      20333.5            50.00     Sequence
IAs  106  DPRNIARKAENYLIS  RNIARKAEN         0.0825      20485.2            50.00     Sequence
IAs   71  LPDPETARIDPFRAA  PETARIDPF         0.0821      20557.2            50.00     Sequence
IAs    8  VFKLAKDEKVEYVDV  KLAKDEKVE         0.0815      20699.4            50.00     Sequence
IAs  414  SIPQTPTQLSDVIDR  SIPQTPTQL         0.0810      20811.2            50.00     Sequence
IAs  188  VAPNDQYVDLRDKML  QYVDLRDKM         0.0808      20855.6            50.00     Sequence
IAs   12  AKDEKVEYVDVRFCD  EKVEYVDVR         0.0806      20901.0            50.00     Sequence
IAs  450  WISFKRENEIEPVNI  KRENEIEPV         0.0805      20935.4            50.00     Sequence
IAs  354  ITGSNPKAKRLEFRS  ITGSNPKAK         0.0805      20935.4            50.00     Sequence
IAs   13  KDEKVEYVDVRFCDL  EKVEYVDVR         0.0802      20990.3            50.00     Sequence
IAs  309  LHHAPSLLAFTNPTV  HAPSLLAFT         0.0799      21073.4            50.00     Sequence
IAs  320  NPTVNSYKRLVPGYE  NSYKRLVPG         0.0797      21118.3            50.00     Sequence
IAs  353  PITGSNPKAKRLEFR  ITGSNPKAK         0.0796      21122.7            50.00     Sequence
IAs  249  KNTAWQNGKTVTFMP  QNGKTVTFM         0.0794      21173.2            50.00     Sequence
IAs  161  WNTGAATEADGSPNR  ATEADGSPN         0.0792      21225.5            50.00     Sequence
IAs  171  GSPNRGYKVRHKGGY  RGYKVRHKG         0.0788      21324.3            50.00     Sequence
IAs  123  IADTAYFGAEAEFYI  YFGAEAEFY         0.0787      21333.8            50.00     Sequence
IAs   93  FVHDPFTLEPYSRDP  HDPFTLEPY         0.0784      21408.7            50.00     Sequence
IAs  380  SAMLMAGLDGIKNKI  SAMLMAGLD         0.0782      21444.1            50.00     Sequence
IAs  203  TNLINSGFILEKGHH  GFILEKGHH         0.0782      21446.7            50.00     Sequence
IAs  170  DGSPNRGYKVRHKGG  RGYKVRHKG         0.0782      21450.9            50.00     Sequence
IAs  452  SFKRENEIEPVNIRP  KRENEIEPV         0.0780      21499.9            50.00     Sequence
IAs  184  GYFPVAPNDQYVDLR  GYFPVAPND         0.0767      21805.4            50.00     Sequence
IAs  246  YIIKNTAWQNGKTVT  TAWQNGKTV         0.0765      21849.8            50.00     Sequence
IAs  266  LFGDNGSGMHCHQSL  SGMHCHQSL         0.0761      21949.3            50.00     Sequence
IAs  300  TARHYIGGLLHHAPS  RHYIGGLLH         0.0758      22014.0            50.00     Sequence
IAs  160  WWNTGAATEADGSPN  AATEADGSP         0.0757      22054.0            50.00     Sequence
IAs  404  LYELPPEEAASIPQT  EEAASIPQT         0.0750      22206.3            50.00     Sequence
IAs  318  FTNPTVNSYKRLVPG  PTVNSYKRL         0.0740      22457.1            50.00     Sequence
IAs  124  ADTAYFGAEAEFYIF  YFGAEAEFY         0.0736      22557.5            50.00     Sequence
IAs  267  FGDNGSGMHCHQSLW  SGMHCHQSL         0.0733      22620.8            50.00     Sequence
IAs  107  PRNIARKAENYLIST  RNIARKAEN         0.0731      22674.2            50.00     Sequence
IAs  189  APNDQYVDLRDKMLT  QYVDLRDKM         0.0730      22683.8            50.00     Sequence
IAs  248  IKNTAWQNGKTVTFM  QNGKTVTFM         0.0728      22754.6            50.00     Sequence
IAs  307  GLLHHAPSLLAFTNP  GLLHHAPSL         0.0727      22777.7            50.00     Sequence
IAs  306  GGLLHHAPSLLAFTN  LLHHAPSLL         0.0721      22919.9            50.00     Sequence
IAs  146  RANGSFYEVDAISGW  GSFYEVDAI         0.0720      22944.7            50.00     Sequence
IAs  147  ANGSFYEVDAISGWW  GSFYEVDAI         0.0715      23079.4            50.00     Sequence
IAs  308  LLHHAPSLLAFTNPT  SLLAFTNPT         0.0711      23162.7            50.00     Sequence
IAs  403  DLYELPPEEAASIPQ  PPEEAASIP         0.0709      23214.1            50.00     Sequence
IAs   76  TARIDPFRAAKTLNI  FRAAKTLNI         0.0698      23504.0            50.00     Sequence
IAs  260  TFMPKPLFGDNGSGM  TFMPKPLFG         0.0692      23649.6            50.00     Sequence
IAs  317  AFTNPTVNSYKRLVP  PTVNSYKRL         0.0686      23804.2            50.00     Sequence
IAs  159  GWWNTGAATEADGSP  NTGAATEAD         0.0685      23832.0            50.00     Sequence
IAs  127  AYFGAEAEFYIFDSV  YFGAEAEFY         0.0681      23936.2            50.00     Sequence
IAs  417  QTPTQLSDVIDRLEA  TPTQLSDVI         0.0676      24050.7            50.00     Sequence
IAs  415  IPQTPTQLSDVIDRL  TPTQLSDVI         0.0672      24177.5            50.00     Sequence
IAs  319  TNPTVNSYKRLVPGY  PTVNSYKRL         0.0666      24329.7            50.00     Sequence
IAs  126  TAYFGAEAEFYIFDS  TAYFGAEAE         0.0664      24363.4            50.00     Sequence
IAs  108  RNIARKAENYLISTG  RNIARKAEN         0.0658      24538.5            50.00     Sequence
IAs  416  PQTPTQLSDVIDRLE  TPTQLSDVI         0.0657      24549.1            50.00     Sequence
IAs  355  TGSNPKAKRLEFRSP  SNPKAKRLE         0.0656      24584.8            50.00     Sequence
IAs  281  WKDGAPLMYDETGYA  KDGAPLMYD         0.0655      24616.4            50.00     Sequence
IAs  368  SPDSSGNPYLAFSAM  NPYLAFSAM         0.0652      24684.4            50.00     Sequence
IAs  192  DQYVDLRDKMLTNLI  QYVDLRDKM         0.0651      24713.0            50.00     Sequence
IAs  128  YFGAEAEFYIFDSVS  YFGAEAEFY         0.0651      24715.2            50.00     Sequence
IAs  247  IIKNTAWQNGKTVTF  TAWQNGKTV         0.0646      24857.6            50.00     Sequence
IAs  393  KIEPQAPVDKDLYEL  APVDKDLYE         0.0642      24960.0            50.00     Sequence
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IAs  437  TEGGVFTNDLIETWI  GGVFTNDLI        0.0641      24993.2             50.00     Sequence
IAs  125  DTAYFGAEAEFYIFD  YFGAEAEFY        0.0638      25066.6             50.00     Sequence
IAs  272  SGMHCHQSLWKDGAP  QSLWKDGAP        0.0638      25071.2             50.00     Sequence
IAs  394  IEPQAPVDKDLYELP  QAPVDKDLY        0.0633      25216.2             50.00     Sequence
IAs  191  NDQYVDLRDKMLTNL  QYVDLRDKM        0.0625      25423.9             50.00     Sequence
IAs   51  AFDGSSIRGFQSIHE  SSIRGFQSI        0.0620      25574.8             50.00     Sequence
IAs  145  SRANGSFYEVDAISG  GSFYEVDAI        0.0619      25595.6             50.00     Sequence
IAs  280  LWKDGAPLMYDETGY  KDGAPLMYD        0.0619      25597.8             50.00     Sequence
IAs  370  DSSGNPYLAFSAMLM  PYLAFSAML        0.0618      25616.4             50.00     Sequence
IAs  144  DSRANGSFYEVDAIS  GSFYEVDAI        0.0612      25777.6             50.00     Sequence
IAs  369  PDSSGNPYLAFSAML  PYLAFSAML        0.0611      25825.1             50.00     Sequence
IAs  190  PNDQYVDLRDKMLTN  QYVDLRDKM        0.0607      25937.4             50.00     Sequence
IAs   95  HDPFTLEPYSRDPRN  DPFTLEPYS        0.0602      26073.0             50.00     Sequence
IAs  436  LTEGGVFTNDLIETW  GGVFTNDLI        0.0598      26175.6             50.00     Sequence
IAs  185  YFPVAPNDQYVDLRD  FPVAPNDQY        0.0598      26184.7             50.00     Sequence
IAs  193  QYVDLRDKMLTNLIN  QYVDLRDKM        0.0593      26331.8             50.00     Sequence
IAs   75  ETARIDPFRAAKTLN  DPFRAAKTL        0.0591      26379.7             50.00     Sequence
IAs  282  KDGAPLMYDETGYAG  KDGAPLMYD        0.0591      26391.7             50.00     Sequence
IAs  435  YLTEGGVFTNDLIET  GGVFTNDLI        0.0590      26396.3             50.00     Sequence
IAs   25  CDLPGIMQHFTIPAS  PGIMQHFTI        0.0590      26416.6             50.00     Sequence
IAs  418  TPTQLSDVIDRLEAD  TPTQLSDVI        0.0588      26452.6             50.00     Sequence
IAs   36  IPASAFDKSVFDDGL  IPASAFDKS        0.0588      26466.6             50.00     Sequence
IAs  114  AENYLISTGIADTAY  ISTGIADTA        0.0581      26660.3             50.00     Sequence
IAs  268  GDNGSGMHCHQSLWK  SGMHCHQSL        0.0579      26731.4             50.00     Sequence
IAs  445  DLIETWISFKRENEI  ISFKRENEI        0.0578      26746.5             50.00     Sequence
IAs   49  GLAFDGSSIRGFQSI  SSIRGFQSI        0.0574      26878.4             50.00     Sequence
IAs  158  SGWWNTGAATEADGS  NTGAATEAD        0.0571      26963.2             50.00     Sequence
IAs  186  FPVAPNDQYVDLRDK  FPVAPNDQY        0.0570      26972.3             50.00     Sequence
IAs  121  TGIADTAYFGAEAEF  TGIADTAYF        0.0568      27033.0             50.00     Sequence
IAs   96  DPFTLEPYSRDPRNI  DPFTLEPYS        0.0567      27083.7             50.00     Sequence
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IAs  202  LTNLINSGFILEKGH  TNLINSGFI        0.0563      27188.5             50.00     Sequence
IAs  269  DNGSGMHCHQSLWKD  SGMHCHQSL        0.0559      27320.6             50.00     Sequence
IAs  143  FDSRANGSFYEVDAI  GSFYEVDAI        0.0557      27372.4             50.00     Sequence
IAs  446  LIETWISFKRENEIE  WISFKRENE        0.0555      27437.9             50.00     Sequence
IAs  226  EINYQFNSLLHAADD  NSLLHAADD        0.0550      27567.1             50.00     Sequence
IAs   33  HFTIPASAFDKSVFD  IPASAFDKS        0.0550      27570.9             50.00     Sequence
IAs   34  FTIPASAFDKSVFDD  IPASAFDKS        0.0549      27603.8             50.00     Sequence
IAs  168  EADGSPNRGYKVRHK  NRGYKVRHK        0.0547      27658.2             50.00     Sequence
IAs  444  NDLIETWISFKRENE  TWISFKREN        0.0547      27658.8             50.00     Sequence
IAs   37  PASAFDKSVFDDGLA  KSVFDDGLA        0.0546      27691.7             50.00     Sequence
IAs  271  GSGMHCHQSLWKDGA  SGMHCHQSL        0.0546      27704.6             50.00     Sequence
IAs  198  RDKMLTNLINSGFIL  NLINSGFIL        0.0535      28025.7             50.00     Sequence
IAs  120  STGIADTAYFGAEAE  TGIADTAYF        0.0518      28547.5             50.00     Sequence
IAs  447  IETWISFKRENEIEP  ETWISFKRE        0.0517      28591.4             50.00     Sequence
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IAs  270  NGSGMHCHQSLWKDG  SGMHCHQSL        0.0510      28795.4             50.00     Sequence
IAs   99  TLEPYSRDPRNIARK  RDPRNIARK        0.0509      28818.1             50.00     Sequence
IAs   24  FCDLPGIMQHFTIPA  LPGIMQHFT        0.0509      28839.0             50.00     Sequence
IAs  157  ISGWWNTGAATEADG  NTGAATEAD        0.0508      28842.4             50.00     Sequence
IAs   38  ASAFDKSVFDDGLAF  KSVFDDGLA        0.0508      28850.6             50.00     Sequence
IAs  292  TGYAGLSDTARHYIG  TGYAGLSDT        0.0505      28940.0             50.00     Sequence
IAs   50  LAFDGSSIRGFQSIH  SSIRGFQSI        0.0505      28945.9             50.00     Sequence
IAs  299  DTARHYIGGLLHHAP  IGGLLHHAP        0.0505      28955.3             50.00     Sequence
IAs  164  GAATEADGSPNRGYK  AATEADGSP        0.0504      28974.1             50.00     Sequence
IAs  234  LLHAADDMQLYKYII  HAADDMQLY        0.0504      28991.1             50.00     Sequence
IAs  289  YDETGYAGLSDTARH  AGLSDTARH        0.0503      29004.2             50.00     Sequence
IAs  163  TGAATEADGSPNRGY  AATEADGSP        0.0502      29053.9             50.00     Sequence
IAs  109  NIARKAENYLISTGI  NIARKAENY        0.0501      29078.7             50.00     Sequence
IAs  235  LHAADDMQLYKYIIK  HAADDMQLY        0.0497      29192.8             50.00     Sequence
IAs   97  PFTLEPYSRDPRNIA  PYSRDPRNI        0.0495      29276.7             50.00     Sequence
IAs  382  MLMAGLDGIKNKIEP  DGIKNKIEP        0.0495      29277.9             50.00     Sequence
IAs  101  EPYSRDPRNIARKAE  RDPRNIARK        0.0494      29288.7             50.00     Sequence
IAs  290  DETGYAGLSDTARHY  AGLSDTARH        0.0491      29389.3             50.00     Sequence
IAs  165  AATEADGSPNRGYKV  AATEADGSP        0.0488      29485.8             50.00     Sequence
IAs  201  MLTNLINSGFILEKG  TNLINSGFI        0.0487      29517.7             50.00     Sequence
IAs  236  HAADDMQLYKYIIKN  HAADDMQLY        0.0483      29638.4             50.00     Sequence
IAs  199  DKMLTNLINSGFILE  TNLINSGFI        0.0483      29642.9             50.00     Sequence
IAs  238  ADDMQLYKYIIKNTA  YKYIIKNTA        0.0476      29875.0             50.00     Sequence
IAs  381  AMLMAGLDGIKNKIE  AGLDGIKNK        0.0475      29915.8             50.00     Sequence
IAs  291  ETGYAGLSDTARHYI  AGLSDTARH        0.0475      29917.1             50.00     Sequence
IAs  217  HEVGSGGQAEINYQF  GSGGQAEIN        0.0474      29937.8             50.00     Sequence
IAs  216  HHEVGSGGQAEINYQ  GSGGQAEIN        0.0472      29993.9             50.00     Sequence
IAs  200  KMLTNLINSGFILEK  TNLINSGFI        0.0471      30045.5             50.00     Sequence
IAs  208  SGFILEKGHHEVGSG  GFILEKGHH        0.0471      30051.1             50.00     Sequence
IAs  331  PGYEAPINLVYSQRN  APINLVYSQ        0.0468      30125.3             50.00     Sequence
IAs  113  KAENYLISTGIADTA  ISTGIADTA        0.0467      30166.7             50.00     Sequence
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IAs  214  KGHHEVGSGGQAEIN  GSGGQAEIN         0.0467      30175.9             50.00     Sequence
IAs  215  GHHEVGSGGQAEINY  GSGGQAEIN         0.0466      30198.1             50.00     Sequence
IAs   46  FDDGLAFDGSSIRGF  GLAFDGSSI         0.0465      30231.8             50.00     Sequence
IAs  332  GYEAPINLVYSQRNR  NLVYSQRNR         0.0464      30274.9             50.00     Sequence
IAs  209  GFILEKGHHEVGSGG  GFILEKGHH         0.0462      30332.7             50.00     Sequence
IAs  156  AISGWWNTGAATEAD  NTGAATEAD         0.0461      30365.2             50.00     Sequence
IAs  443  TNDLIETWISFKREN  ETWISFKRE         0.0459      30416.8             50.00     Sequence
IAs   47  DDGLAFDGSSIRGFQ  GLAFDGSSI         0.0459      30417.5             50.00     Sequence
IAs   98  FTLEPYSRDPRNIAR  PYSRDPRNI         0.0454      30608.6             50.00     Sequence
IAs  442  FTNDLIETWISFKRE  ETWISFKRE         0.0452      30645.4             50.00     Sequence
IAs  149  GSFYEVDAISGWWNT  GSFYEVDAI         0.0443      30945.6             50.00     Sequence
IAs  333  YEAPINLVYSQRNRS  APINLVYSQ         0.0442      30977.4             50.00     Sequence
IAs  462  VNIRPHPYEFALYYD  VNIRPHPYE         0.0441      31027.1             50.00     Sequence
IAs  148  NGSFYEVDAISGWWN  GSFYEVDAI         0.0436      31185.6             50.00     Sequence
IAs  334  EAPINLVYSQRNRSA  APINLVYSQ         0.0436      31205.2             50.00     Sequence
IAs   48  DGLAFDGSSIRGFQS  FDGSSIRGF         0.0433      31281.9             50.00     Sequence
IAs  293  GYAGLSDTARHYIGG  GYAGLSDTA         0.0429      31423.0             50.00     Sequence
IAs   39  SAFDKSVFDDGLAFD  KSVFDDGLA         0.0429      31446.8             50.00     Sequence
IAs  218  EVGSGGQAEINYQFN  GSGGQAEIN         0.0425      31576.0             50.00     Sequence
IAs  296  GLSDTARHYIGGLLH  RHYIGGLLH         0.0424      31595.5             50.00     Sequence
IAs  112  RKAENYLISTGIADT  RKAENYLIS         0.0424      31610.9             50.00     Sequence
IAs   41  FDKSVFDDGLAFDGS  KSVFDDGLA         0.0422      31655.4             50.00     Sequence
IAs  265  PLFGDNGSGMHCHQS  GSGMHCHQS         0.0422      31683.9             50.00     Sequence
IAs  111  ARKAENYLISTGIAD  RKAENYLIS         0.0419      31766.6             50.00     Sequence
IAs   43  KSVFDDGLAFDGSSI  KSVFDDGLA         0.0419      31774.8             50.00     Sequence
IAs    1  TEKTPDDVFKLAKDE  DVFKLAKDE         0.0413      31969.0             50.00     Sequence
IAs  166  ATEADGSPNRGYKVR  SPNRGYKVR         0.0410      32088.9             50.00     Sequence
IAs  219  VGSGGQAEINYQFNS  GSGGQAEIN         0.0409      32118.4             50.00     Sequence
IAs  438  EGGVFTNDLIETWIS  GGVFTNDLI         0.0407      32206.4             50.00     Sequence
IAs  100  LEPYSRDPRNIARKA  RDPRNIARK         0.0402      32353.1             50.00     Sequence
IAs  220  GSGGQAEINYQFNSL  GSGGQAEIN         0.0402      32378.0             50.00     Sequence
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IAs  298  SDTARHYIGGLLHHA  RHYIGGLLH         0.0400      32445.7             50.00     Sequence
IAs  297  LSDTARHYIGGLLHH  RHYIGGLLH         0.0396      32590.3             50.00     Sequence
IAs  110  IARKAENYLISTGIA  RKAENYLIS         0.0395      32606.2             50.00     Sequence
IAs    2  EKTPDDVFKLAKDEK  DVFKLAKDE         0.0392      32714.3             50.00     Sequence
IAs  197  LRDKMLTNLINSGFI  TNLINSGFI         0.0390      32788.0             50.00     Sequence
IAs  283  DGAPLMYDETGYAGL  GAPLMYDET         0.0373      33389.8             50.00     Sequence
IAs  337  INLVYSQRNRSACVR  QRNRSACVR         0.0371      33461.8             50.00     Sequence
IAs  421  QLSDVIDRLEADHEY  QLSDVIDRL         0.0369      33542.2             50.00     Sequence
IAs  335  APINLVYSQRNRSAC  APINLVYSQ         0.0369      33555.3             50.00     Sequence
IAs  221  SGGQAEINYQFNSLL  GGQAEINYQ         0.0368      33583.3             50.00     Sequence
IAs  338  NLVYSQRNRSACVRI  NLVYSQRNR         0.0366      33654.9             50.00     Sequence
IAs   44  SVFDDGLAFDGSSIR  LAFDGSSIR         0.0365      33687.0             50.00     Sequence
IAs  222  GGQAEINYQFNSLLH  GGQAEINYQ         0.0363      33773.5             50.00     Sequence
IAs  427  DRLEADHEYLTEGGV  RLEADHEYL         0.0362      33783.7             50.00     Sequence
IAs  288  MYDETGYAGLSDTAR  GYAGLSDTA         0.0356      34025.1             50.00     Sequence
IAs  194  YVDLRDKMLTNLINS  KMLTNLINS         0.0349      34269.7             50.00     Sequence
IAs    0  VTEKTPDDVFKLAKD  VTEKTPDDV         0.0347      34352.8             50.00     Sequence
IAs  439  GGVFTNDLIETWISF  GGVFTNDLI         0.0346      34400.8             50.00     Sequence
IAs  261  FMPKPLFGDNGSGMH  MPKPLFGDN         0.0345      34407.9             50.00     Sequence
IAs  237  AADDMQLYKYIIKNT  MQLYKYIIK         0.0345      34420.6             50.00     Sequence
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IAs  422  LSDVIDRLEADHEYL  RLEADHEYL         0.0343      34498.1             50.00     Sequence
IAs  294  YAGLSDTARHYIGGL  AGLSDTARH         0.0342      34529.9             50.00     Sequence
IAs  264  KPLFGDNGSGMHCHQ  NGSGMHCHQ         0.0339      34664.6             50.00     Sequence
IAs  155  DAISGWWNTGAATEA  GWWNTGAAT         0.0336      34754.4             50.00     Sequence
IAs  154  VDAISGWWNTGAATE  GWWNTGAAT         0.0335      34815.0             50.00     Sequence
IAs   45  VFDDGLAFDGSSIRG  LAFDGSSIR         0.0330      34969.8             50.00     Sequence
IAs  213  EKGHHEVGSGGQAEI  HEVGSGGQA         0.0330      35003.4             50.00     Sequence
IAs   42  DKSVFDDGLAFDGSS  KSVFDDGLA         0.0329      35026.6             50.00     Sequence
IAs  153  EVDAISGWWNTGAAT  SGWWNTGAA         0.0327      35100.9             50.00     Sequence
IAs  287  LMYDETGYAGLSDTA  TGYAGLSDT         0.0322      35285.6             50.00     Sequence
IAs  423  SDVIDRLEADHEYLT  RLEADHEYL         0.0319      35393.8             50.00     Sequence
IAs  152  YEVDAISGWWNTGAA  SGWWNTGAA         0.0318      35446.7             50.00     Sequence
IAs  195  VDLRDKMLTNLINSG  KMLTNLINS         0.0310      35752.9             50.00     Sequence
IAs  224  QAEINYQFNSLLHAA  QAEINYQFN         0.0310      35765.3             50.00     Sequence
IAs  420  TQLSDVIDRLEADHE  QLSDVIDRL         0.0306      35896.3             50.00     Sequence
IAs  210  FILEKGHHEVGSGGQ  FILEKGHHE         0.0306      35923.9             50.00     Sequence
IAs  295  AGLSDTARHYIGGLL  AGLSDTARH         0.0303      36023.2             50.00     Sequence
IAs  142  SFDSRANGSFYEVDA  ANGSFYEVD         0.0302      36060.2             50.00     Sequence
IAs  263  PKPLFGDNGSGMHCH  KPLFGDNGS         0.0301      36093.0             50.00     Sequence
IAs  419  PTQLSDVIDRLEADH  QLSDVIDRL         0.0298      36218.6             50.00     Sequence
IAs  141  VSFDSRANGSFYEVD  ANGSFYEVD         0.0292      36439.5             50.00     Sequence
IAs  150  SFYEVDAISGWWNTG  SFYEVDAIS         0.0290      36544.9             50.00     Sequence
IAs  225  AEINYQFNSLLHAAD  QFNSLLHAA         0.0289      36578.9             50.00     Sequence
IAs  426  IDRLEADHEYLTEGG  RLEADHEYL         0.0288      36601.9             50.00     Sequence
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         IAs  336  PINLVYSQRNRSACV  NLVYSQRNR        0.0286      36676.0               50.00     Sequence
         IAs  212  LEKGHHEVGSGGQAE  HEVGSGGQA        0.0283      36808.0               50.00     Sequence
         IAs  211  ILEKGHHEVGSGGQA  HEVGSGGQA        0.0281      36904.5               50.00     Sequence
         IAs  196  DLRDKMLTNLINSGF  KMLTNLINS        0.0278      37023.7               50.00     Sequence
         IAs  286  PLMYDETGYAGLSDT  TGYAGLSDT        0.0276      37098.3               50.00     Sequence
         IAs  284  GAPLMYDETGYAGLS  GAPLMYDET        0.0275      37127.6               50.00     Sequence
         IAs  424  DVIDRLEADHEYLTE  RLEADHEYL        0.0270      37332.6               50.00     Sequence
         IAs  425  VIDRLEADHEYLTEG  RLEADHEYL        0.0268      37402.1               50.00     Sequence
         IAs  167  TEADGSPNRGYKVRH  SPNRGYKVR        0.0267      37464.9               50.00     Sequence
         IAs  285  APLMYDETGYAGLSD  APLMYDETG        0.0265      37544.1               50.00     Sequence
         IAs  151  FYEVDAISGWWNTGA  YEVDAISGW        0.0251      38089.5               50.00     Sequence
         IAs  130  GAEAEFYIFDSVSFD  AEFYIFDSV        0.0245      38365.8               50.00     Sequence
         IAs  223  GQAEINYQFNSLLHA  QAEINYQFN        0.0243      38451.4               50.00     Sequence
         IAs  440  GVFTNDLIETWISFK  DLIETWISF        0.0239      38606.0               50.00     Sequence
         IAs  441  VFTNDLIETWISFKR  DLIETWISF        0.0234      38813.4               50.00     Sequence
         IAs  136  YIFDSVSFDSRANGS  YIFDSVSFD        0.0231      38958.9               50.00     Sequence
         IAs  132  EAEFYIFDSVSFDSR  AEFYIFDSV        0.0229      39023.5               50.00     Sequence
         IAs  131  AEAEFYIFDSVSFDS  AEFYIFDSV        0.0229      39044.2               50.00     Sequence
         IAs  133  AEFYIFDSVSFDSRA  AEFYIFDSV        0.0226      39163.1               50.00     Sequence
         IAs  129  FGAEAEFYIFDSVSF  AEFYIFDSV        0.0223      39272.6               50.00     Sequence
         IAs  135  FYIFDSVSFDSRANG  YIFDSVSFD        0.0223      39282.7               50.00     Sequence
         IAs  463  NIRPHPYEFALYYDV  HPYEFALYY        0.0223      39299.3               50.00     Sequence
         IAs  138  FDSVSFDSRANGSFY  FDSVSFDSR        0.0204      40075.2               50.00     Sequence
         IAs  137  IFDSVSFDSRANGSF  VSFDSRANG        0.0199      40318.8               50.00     Sequence
         IAs  134  EFYIFDSVSFDSRAN  YIFDSVSFD        0.0198      40355.0               50.00     Sequence
         IAs  140  SVSFDSRANGSFYEV  RANGSFYEV        0.0184      40989.1               50.00     Sequence
         IAs  139  DSVSFDSRANGSFYE  SRANGSFYE        0.0178      41259.2               50.00     Sequence
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Allele: IAs. Number of high binders 0. Number of weak binders 4. Number of peptides 464

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Explain the output. Go **back**.