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   19  EEGVTPLRARIAERL  VTPLRARIA        0.8435          5.4         SB     4.00   Rv2711, TB
   DRB1_0101   20  EGVTPLRARIAERLD  VTPLRARIA        0.8292          6.3         SB     4.00   Rv2711, TB
   DRB1_0101   21  GVTPLRARIAERLDQ  VTPLRARIA        0.8182          7.2         SB     8.00   Rv2711, TB
   DRB1_0101   18  EEEGVTPLRARIAER  VTPLRARIA        0.8066          8.1         SB     8.00   Rv2711, TB
   DRB1_0101   22  VTPLRARIAERLDQS  VTPLRARIA        0.8051          8.2         SB     8.00   Rv2711, TB
   DRB1_0101  112  ERRLVKVLNNPTTSP  LVKVLNNPT        0.7781         11.0         SB    16.00   Rv2711, TB
   DRB1_0101  111  VERRLVKVLNNPTTS  LVKVLNNPT        0.7741         11.5         SB    16.00   Rv2711, TB
   DRB1_0101  113  RRLVKVLNNPTTSPF  LVKVLNNPT        0.7728         11.7         SB    16.00   Rv2711, TB
   DRB1_0101   69  ALAIAVMRKHRLAER  IAVMRKHRL        0.7626         13.0         SB    16.00   Rv2711, TB
   DRB1_0101   17  LEEEGVTPLRARIAE  VTPLRARIA        0.7564         14.0         SB    16.00   Rv2711, TB
   DRB1_0101   61  LELTEKGRALAIAVM  TEKGRALAI        0.7494         15.1         SB    16.00   Rv2711, TB
   DRB1_0101   16  DLEEEGVTPLRARIA  VTPLRARIA        0.7291         18.7         SB    16.00   Rv2711, TB
   DRB1_0101   70  LAIAVMRKHRLAERL  IAVMRKHRL        0.7199         20.7         SB    16.00   Rv2711, TB
   DRB1_0101   68  RALAIAVMRKHRLAE  IAVMRKHRL        0.7184         21.1         SB    16.00   Rv2711, TB
   DRB1_0101   74  VMRKHRLAERLLVDV  KHRLAERLL        0.7181         21.1         SB    16.00   Rv2711, TB
   DRB1_0101  110  DVERRLVKVLNNPTT  LVKVLNNPT        0.7138         22.1         SB    16.00   Rv2711, TB
   DRB1_0101   60  HLELTEKGRALAIAV  TEKGRALAI        0.7124         22.5         SB    16.00   Rv2711, TB
   DRB1_0101   59  RHLELTEKGRALAIA  ELTEKGRAL        0.7110         22.8         SB    16.00   Rv2711, TB
   DRB1_0101   62  ELTEKGRALAIAVMR  TEKGRALAI        0.7100         23.0         SB    16.00   Rv2711, TB
   DRB1_0101   67  GRALAIAVMRKHRLA  IAVMRKHRL        0.7039         24.6         SB    32.00   Rv2711, TB
   DRB1_0101  153  LTELPAGSPVAVVVR  LPAGSPVAV        0.7015         25.3         SB    32.00   Rv2711, TB
   DRB1_0101  147  DANLVRLTELPAGSP  LVRLTELPA        0.7014         25.3         SB    32.00   Rv2711, TB
   DRB1_0101  152  RLTELPAGSPVAVVV  LPAGSPVAV        0.7007         25.5         SB    32.00   Rv2711, TB
   DRB1_0101  146  DDANLVRLTELPAGS  LVRLTELPA        0.6973         26.4         SB    32.00   Rv2711, TB
   DRB1_0101   63  LTEKGRALAIAVMRK  TEKGRALAI        0.6952         27.1         SB    32.00   Rv2711, TB
   DRB1_0101  114  RLVKVLNNPTTSPFG  LVKVLNNPT        0.6931         27.7         SB    32.00   Rv2711, TB
   DRB1_0101   72  IAVMRKHRLAERLLV  KHRLAERLL        0.6916         28.1         SB    32.00   Rv2711, TB
   DRB1_0101  151  VRLTELPAGSPVAVV  TELPAGSPV        0.6915         28.2         SB    32.00   Rv2711, TB
   DRB1_0101   23  TPLRARIAERLDQSG  LRARIAERL        0.6849         30.2         SB    32.00   Rv2711, TB
   DRB1_0101   75  MRKHRLAERLLVDVI  KHRLAERLL        0.6822         31.1         SB    32.00   Rv2711, TB
   DRB1_0101  150  LVRLTELPAGSPVAV  LTELPAGSP        0.6800         31.9         SB    32.00   Rv2711, TB
   DRB1_0101   71  AIAVMRKHRLAERLL  IAVMRKHRL        0.6756         33.4         SB    32.00   Rv2711, TB
   DRB1_0101  148  ANLVRLTELPAGSPV  LVRLTELPA        0.6741         34.0         SB    32.00   Rv2711, TB
   DRB1_0101   73  AVMRKHRLAERLLVD  KHRLAERLL        0.6699         35.6         SB    32.00   Rv2711, TB
   DRB1_0101  215  TLPHEMAHAVKVEKV  HEMAHAVKV        0.6692         35.9         SB    32.00   Rv2711, TB
   DRB1_0101   66  KGRALAIAVMRKHRL  IAVMRKHRL        0.6667         36.8         SB    32.00   Rv2711, TB
   DRB1_0101  100  ACRWEHVMSEDVERR  WEHVMSEDV        0.6635         38.1         SB    32.00   Rv2711, TB
   DRB1_0101   58  DRHLELTEKGRALAI  ELTEKGRAL        0.6556         41.5         SB    32.00   Rv2711, TB
   DRB1_0101   64  TEKGRALAIAVMRKH  KGRALAIAV        0.6494         44.4         SB    32.00   Rv2711, TB
   DRB1_0101  213  NVTLPHEMAHAVKVE  LPHEMAHAV        0.6401         49.1         SB    32.00   Rv2711, TB
   DRB1_0101  154  TELPAGSPVAVVVRQ  LPAGSPVAV        0.6371         50.7         WB    32.00   Rv2711, TB
   DRB1_0101  214  VTLPHEMAHAVKVEK  HEMAHAVKV        0.6328         53.1         WB    32.00   Rv2711, TB
   DRB1_0101   76  RKHRLAERLLVDVIG  KHRLAERLL        0.6302         54.7         WB    32.00   Rv2711, TB
   DRB1_0101  212  ENVTLPHEMAHAVKV  LPHEMAHAV        0.6286         55.6         WB    32.00   Rv2711, TB
   DRB1_0101  210  GHENVTLPHEMAHAV  NVTLPHEMA        0.6271         56.5         WB    32.00   Rv2711, TB
   DRB1_0101  161  PVAVVVRQLTEHVQG  VVRQLTEHV        0.6244         58.2         WB    32.00   Rv2711, TB
   DRB1_0101  109  EDVERRLVKVLNNPT  LVKVLNNPT        0.6242         58.4         WB    32.00   Rv2711, TB
   DRB1_0101  149  NLVRLTELPAGSPVA  LVRLTELPA        0.6235         58.8         WB    32.00   Rv2711, TB
   DRB1_0101  145  ADDANLVRLTELPAG  LVRLTELPA        0.6211         60.3         WB    32.00   Rv2711, TB
   DRB1_0101  162  VAVVVRQLTEHVQGD  VVRQLTEHV        0.6190         61.7         WB    32.00   Rv2711, TB
   DRB1_0101   24  PLRARIAERLDQSGP  LRARIAERL        0.6114         67.0         WB    32.00   Rv2711, TB
   DRB1_0101  101  CRWEHVMSEDVERRL  WEHVMSEDV        0.6081         69.4         WB    32.00   Rv2711, TB
   DRB1_0101  193  RVTVETTPGGGVTIV  VETTPGGGV        0.6080         69.5         WB    32.00   Rv2711, TB
   DRB1_0101   65  EKGRALAIAVMRKHR  GRALAIAVM        0.6078         69.7         WB    32.00   Rv2711, TB
   DRB1_0101  177  IDLITRLKDAGVVPN  ITRLKDAGV        0.6060         71.0         WB    32.00   Rv2711, TB
   DRB1_0101   50  DGLLRVAGDRHLELT  LRVAGDRHL        0.6058         71.2         WB    32.00   Rv2711, TB
   DRB1_0101  211  HENVTLPHEMAHAVK  NVTLPHEMA        0.6022         74.0         WB    32.00   Rv2711, TB
   DRB1_0101  202  GGVTIVIPGHENVTL  TIVIPGHEN        0.6014         74.6         WB    32.00   Rv2711, TB
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DRB1_0101  155  ELPAGSPVAVVVRQL  LPAGSPVAV         0.5950          80.0          WB    50.00   Rv2711, TB
DRB1_0101   51  GLLRVAGDRHLELTE  LRVAGDRHL         0.5905          84.0          WB    50.00   Rv2711, TB
DRB1_0101   42  QTVSRMERDGLLRVA  SRMERDGLL         0.5880          86.3          WB    50.00   Rv2711, TB
DRB1_0101  124  TSPFGNPIPGLVELG  FGNPIPGLV         0.5813          92.8          WB    50.00   Rv2711, TB
DRB1_0101  115  LVKVLNNPTTSPFGN  LVKVLNNPT         0.5802          93.9          WB    50.00   Rv2711, TB
DRB1_0101  160  SPVAVVVRQLTEHVQ  VVRQLTEHV         0.5777          96.5          WB    50.00   Rv2711, TB
DRB1_0101   99  EACRWEHVMSEDVER  WEHVMSEDV         0.5770          97.2          WB    50.00   Rv2711, TB
DRB1_0101   57  GDRHLELTEKGRALA  ELTEKGRAL         0.5759          98.4          WB    50.00   Rv2711, TB
DRB1_0101  156  LPAGSPVAVVVRQLT  LPAGSPVAV         0.5748          99.6          WB    50.00   Rv2711, TB
DRB1_0101   77  KHRLAERLLVDVIGL  KHRLAERLL         0.5673         108.0          WB    50.00   Rv2711, TB
DRB1_0101  102  RWEHVMSEDVERRLV  WEHVMSEDV         0.5587         118.5          WB    50.00   Rv2711, TB
DRB1_0101  144  GADDANLVRLTELPA  LVRLTELPA         0.5583         118.9          WB    50.00   Rv2711, TB
DRB1_0101  123  TTSPFGNPIPGLVEL  FGNPIPGLV         0.5579         119.6          WB    50.00   Rv2711, TB
DRB1_0101   49  RDGLLRVAGDRHLEL  LRVAGDRHL         0.5574         120.2          WB    50.00   Rv2711, TB
DRB1_0101   25  LRARIAERLDQSGPT  LRARIAERL         0.5560         122.0          WB    50.00   Rv2711, TB
DRB1_0101  159  GSPVAVVVRQLTEHV  PVAVVVRQL         0.5557         122.4          WB    50.00   Rv2711, TB
DRB1_0101  178  DLITRLKDAGVVPNA  ITRLKDAGV         0.5536         125.2          WB    50.00   Rv2711, TB
DRB1_0101  203  GVTIVIPGHENVTLP  TIVIPGHEN         0.5518         127.7          WB    50.00   Rv2711, TB
DRB1_0101  158  AGSPVAVVVRQLTEH  PVAVVVRQL         0.5502         129.8          WB    50.00   Rv2711, TB
DRB1_0101  175  GDIDLITRLKDAGVV  ITRLKDAGV         0.5488         131.9          WB    50.00   Rv2711, TB
DRB1_0101  176  DIDLITRLKDAGVVP  ITRLKDAGV         0.5472         134.2          WB    50.00   Rv2711, TB
DRB1_0101  179  LITRLKDAGVVPNAR  ITRLKDAGV         0.5467         134.9          WB    50.00   Rv2711, TB
DRB1_0101  209  PGHENVTLPHEMAHA  NVTLPHEMA         0.5418         142.2          WB    50.00   Rv2711, TB
DRB1_0101  163  AVVVRQLTEHVQGDI  VVRQLTEHV         0.5412         143.2          WB    50.00   Rv2711, TB
DRB1_0101  125  SPFGNPIPGLVELGV  FGNPIPGLV         0.5408         143.9          WB    50.00   Rv2711, TB
DRB1_0101  194  VTVETTPGGGVTIVI  VETTPGGGV         0.5350         153.2          WB    50.00   Rv2711, TB
DRB1_0101  183  LKDAGVVPNARVTVE  AGVVPNARV         0.5319         158.3          WB    50.00   Rv2711, TB
DRB1_0101   43  TVSRMERDGLLRVAG  SRMERDGLL         0.5312         159.6          WB    50.00   Rv2711, TB
DRB1_0101  182  RLKDAGVVPNARVTV  AGVVPNARV         0.5308         160.3          WB    50.00   Rv2711, TB
DRB1_0101   52  LLRVAGDRHLELTEK  LRVAGDRHL         0.5304         160.9          WB    50.00   Rv2711, TB
DRB1_0101  157  PAGSPVAVVVRQLTE  PVAVVVRQL         0.5262         168.3          WB    50.00   Rv2711, TB
DRB1_0101   35  QSGPTVSQTVSRMER  TVSQTVSRM         0.5196         180.9          WB    50.00   Rv2711, TB
DRB1_0101   41  SQTVSRMERDGLLRV  SRMERDGLL         0.5192         181.7          WB    50.00   Rv2711, TB
DRB1_0101   78  HRLAERLLVDVIGLP  AERLLVDVI         0.5167         186.7          WB    50.00   Rv2711, TB
DRB1_0101   79  RLAERLLVDVIGLPW  RLLVDVIGL         0.5167         186.7          WB    50.00   Rv2711, TB
DRB1_0101   36  SGPTVSQTVSRMERD  TVSQTVSRM         0.5139         192.3          WB    50.00   Rv2711, TB
DRB1_0101   30  AERLDQSGPTVSQTV  LDQSGPTVS         0.5080         205.1          WB    50.00   Rv2711, TB
DRB1_0101  180  ITRLKDAGVVPNARV  ITRLKDAGV         0.5043         213.4          WB    50.00   Rv2711, TB
DRB1_0101  126  PFGNPIPGLVELGVG  FGNPIPGLV         0.5021         218.5          WB    50.00   Rv2711, TB
DRB1_0101   56  AGDRHLELTEKGRAL  ELTEKGRAL         0.4975         229.8          WB    50.00   Rv2711, TB
DRB1_0101    6  TTEMYLRTIYDLEEE  MYLRTIYDL         0.4968         231.4          WB    50.00   Rv2711, TB
DRB1_0101    3  LVDTTEMYLRTIYDL  TTEMYLRTI         0.4957         234.2          WB    50.00   Rv2711, TB
DRB1_0101   82  ERLLVDVIGLPWEEV  RLLVDVIGL         0.4935         240.0          WB    50.00   Rv2711, TB
DRB1_0101   80  LAERLLVDVIGLPWE  RLLVDVIGL         0.4930         241.2          WB    50.00   Rv2711, TB
DRB1_0101   83  RLLVDVIGLPWEEVH  RLLVDVIGL         0.4927         242.0          WB    50.00   Rv2711, TB
DRB1_0101  174  QGDIDLITRLKDAGV  ITRLKDAGV         0.4920         243.9          WB    50.00   Rv2711, TB
DRB1_0101   98  AEACRWEHVMSEDVE  WEHVMSEDV         0.4915         245.2          WB    50.00   Rv2711, TB
DRB1_0101  192  ARVTVETTPGGGVTI  VETTPGGGV         0.4833         267.8          WB    50.00   Rv2711, TB
DRB1_0101  127  FGNPIPGLVELGVGP  FGNPIPGLV         0.4832         268.3          WB    50.00   Rv2711, TB
DRB1_0101  204  VTIVIPGHENVTLPH  TIVIPGHEN         0.4825         270.3          WB    50.00   Rv2711, TB
DRB1_0101    5  DTTEMYLRTIYDLEE  MYLRTIYDL         0.4820         271.5          WB    50.00   Rv2711, TB
DRB1_0101  122  PTTSPFGNPIPGLVE  FGNPIPGLV         0.4805         276.0          WB    50.00   Rv2711, TB
DRB1_0101  201  GGGVTIVIPGHENVT  TIVIPGHEN         0.4801         277.3          WB    50.00   Rv2711, TB
DRB1_0101  195  TVETTPGGGVTIVIP  TTPGGGVTI         0.4784         282.5          WB    50.00   Rv2711, TB
DRB1_0101  103  WEHVMSEDVERRLVK  WEHVMSEDV         0.4777         284.7          WB    50.00   Rv2711, TB
DRB1_0101   11  LRTIYDLEEEGVTPL  IYDLEEEGV         0.4776         284.8          WB    50.00   Rv2711, TB
DRB1_0101    0  MNELVDTTEMYLRTI  LVDTTEMYL         0.4776         285.0          WB    50.00   Rv2711, TB
DRB1_0101   44  VSRMERDGLLRVAGD  SRMERDGLL         0.4766         287.9          WB    50.00   Rv2711, TB
DRB1_0101   81  AERLLVDVIGLPWEE  RLLVDVIGL         0.4766         288.0          WB    50.00   Rv2711, TB
DRB1_0101    4  VDTTEMYLRTIYDLE  MYLRTIYDL         0.4755         291.5          WB    50.00   Rv2711, TB
DRB1_0101   84  LLVDVIGLPWEEVHA  VIGLPWEEV         0.4749         293.5          WB    50.00   Rv2711, TB
DRB1_0101    1  NELVDTTEMYLRTIY  DTTEMYLRT         0.4745         294.6          WB    50.00   Rv2711, TB
DRB1_0101    7  TEMYLRTIYDLEEEG  MYLRTIYDL         0.4738         296.7          WB    50.00   Rv2711, TB
DRB1_0101  181  TRLKDAGVVPNARVT  KDAGVVPNA         0.4709         306.4          WB    50.00   Rv2711, TB
DRB1_0101  208  IPGHENVTLPHEMAH  NVTLPHEMA         0.4668         320.2          WB    50.00   Rv2711, TB
DRB1_0101    2  ELVDTTEMYLRTIYD  DTTEMYLRT         0.4633         332.7          WB    50.00   Rv2711, TB
DRB1_0101   85  LVDVIGLPWEEVHAE  VIGLPWEEV         0.4614         339.5          WB    50.00   Rv2711, TB
DRB1_0101   97  HAEACRWEHVMSEDV  WEHVMSEDV         0.4611         340.8          WB    50.00   Rv2711, TB
DRB1_0101  169  LTEHVQGDIDLITRL  HVQGDIDLI         0.4597         345.6          WB    50.00   Rv2711, TB
DRB1_0101  121  NPTTSPFGNPIPGLV  FGNPIPGLV         0.4579         352.7          WB    50.00   Rv2711, TB
DRB1_0101  184  KDAGVVPNARVTVET  AGVVPNARV         0.4558         360.5          WB    50.00   Rv2711, TB
DRB1_0101  164  VVVRQLTEHVQGDID  VRQLTEHVQ         0.4534         370.1          WB    50.00   Rv2711, TB
DRB1_0101   47  MERDGLLRVAGDRHL  RDGLLRVAG         0.4532         371.2          WB    50.00   Rv2711, TB
DRB1_0101   37  GPTVSQTVSRMERDG  TVSQTVSRM         0.4483         391.1          WB    50.00   Rv2711, TB
DRB1_0101   48  ERDGLLRVAGDRHLE  LRVAGDRHL         0.4471         396.2          WB    50.00   Rv2711, TB
DRB1_0101   15  YDLEEEGVTPLRARI  EEGVTPLRA         0.4465         399.0          WB    50.00   Rv2711, TB
DRB1_0101   29  IAERLDQSGPTVSQT  RLDQSGPTV         0.4426         416.3          WB    50.00   Rv2711, TB
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   DRB1_0101    8  EMYLRTIYDLEEEGV  YLRTIYDLE          0.4418          419.8           WB    50.00   Rv2711, TB
   DRB1_0101   34  DQSGPTVSQTVSRME  TVSQTVSRM          0.4372          441.0           WB    50.00   Rv2711, TB
   DRB1_0101    9  MYLRTIYDLEEEGVT  YLRTIYDLE          0.4364          445.0           WB    50.00   Rv2711, TB
   DRB1_0101   45  SRMERDGLLRVAGDR  RDGLLRVAG          0.4357          448.2           WB    50.00   Rv2711, TB
   DRB1_0101   33  LDQSGPTVSQTVSRM  TVSQTVSRM          0.4341          456.4           WB    50.00   Rv2711, TB
   DRB1_0101   31  ERLDQSGPTVSQTVS  LDQSGPTVS          0.4319          467.4           WB    50.00   Rv2711, TB
   DRB1_0101   53  LRVAGDRHLELTEKG  LRVAGDRHL          0.4284          485.0           WB    50.00   Rv2711, TB
   DRB1_0101  196  VETTPGGGVTIVIPG  TTPGGGVTI          0.4260          498.0           WB    50.00   Rv2711, TB
   DRB1_0101   14  IYDLEEEGVTPLRAR  LEEEGVTPL          0.4188          538.3                 50.00   Rv2711, TB
   DRB1_0101   46  RMERDGLLRVAGDRH  RDGLLRVAG          0.4188          538.5                 50.00   Rv2711, TB
   DRB1_0101  170  TEHVQGDIDLITRLK  HVQGDIDLI          0.4174          546.3                 50.00   Rv2711, TB
   DRB1_0101  116  VKVLNNPTTSPFGNP  VKVLNNPTT          0.4155          557.8                 50.00   Rv2711, TB
   DRB1_0101  200  PGGGVTIVIPGHENV  TIVIPGHEN          0.4085          601.8                 50.00   Rv2711, TB
   DRB1_0101  172  HVQGDIDLITRLKDA  HVQGDIDLI          0.4052          623.5                 50.00   Rv2711, TB
   DRB1_0101  173  VQGDIDLITRLKDAG  DIDLITRLK          0.3998          661.0                 50.00   Rv2711, TB
   DRB1_0101   40  VSQTVSRMERDGLLR  SRMERDGLL          0.3989          667.6                 50.00   Rv2711, TB
   DRB1_0101  197  ETTPGGGVTIVIPGH  PGGGVTIVI          0.3989          667.8                 50.00   Rv2711, TB
   DRB1_0101   32  RLDQSGPTVSQTVSR  LDQSGPTVS          0.3987          668.8                 50.00   Rv2711, TB
   DRB1_0101  205  TIVIPGHENVTLPHE  TIVIPGHEN          0.3975          677.6                 50.00   Rv2711, TB
   DRB1_0101  168  QLTEHVQGDIDLITR  HVQGDIDLI          0.3967          683.5                 50.00   Rv2711, TB
   DRB1_0101  128  GNPIPGLVELGVGPE  IPGLVELGV          0.3948          698.3                 50.00   Rv2711, TB
   DRB1_0101  185  DAGVVPNARVTVETT  AGVVPNARV          0.3888          745.0                 50.00   Rv2711, TB
   DRB1_0101  171  EHVQGDIDLITRLKD  HVQGDIDLI          0.3887          745.4                 50.00   Rv2711, TB
   DRB1_0101  207  VIPGHENVTLPHEMA  NVTLPHEMA          0.3875          755.7                 50.00   Rv2711, TB
   DRB1_0101  143  PGADDANLVRLTELP  DDANLVRLT          0.3873          756.8                 50.00   Rv2711, TB
   DRB1_0101  107  MSEDVERRLVKVLNN  RRLVKVLNN          0.3867          762.3                 50.00   Rv2711, TB
   DRB1_0101  142  EPGADDANLVRLTEL  DDANLVRLT          0.3858          769.3                 50.00   Rv2711, TB
   DRB1_0101   38  PTVSQTVSRMERDGL  TVSQTVSRM          0.3855          771.6                 50.00   Rv2711, TB
   DRB1_0101  191  NARVTVETTPGGGVT  VETTPGGGV          0.3843          782.0                 50.00   Rv2711, TB
   DRB1_0101  198  TTPGGGVTIVIPGHE  PGGGVTIVI          0.3841          783.3                 50.00   Rv2711, TB
   DRB1_0101   86  VDVIGLPWEEVHAEA  VIGLPWEEV          0.3826          796.8                 50.00   Rv2711, TB
   DRB1_0101   10  YLRTIYDLEEEGVTP  IYDLEEEGV          0.3821          800.4                 50.00   Rv2711, TB
   DRB1_0101   12  RTIYDLEEEGVTPLR  IYDLEEEGV          0.3792          825.9                 50.00   Rv2711, TB
   DRB1_0101  108  SEDVERRLVKVLNNP  VERRLVKVL          0.3747          867.3                 50.00   Rv2711, TB
   DRB1_0101  186  AGVVPNARVTVETTP  AGVVPNARV          0.3713          899.9                 50.00   Rv2711, TB
   DRB1_0101  129  NPIPGLVELGVGPEP  PIPGLVELG          0.3679          933.3                 50.00   Rv2711, TB
   DRB1_0101  105  HVMSEDVERRLVKVL  SEDVERRLV          0.3677          936.1                 50.00   Rv2711, TB
   DRB1_0101   28  RIAERLDQSGPTVSQ  LDQSGPTVS          0.3651          962.6                 50.00   Rv2711, TB
   DRB1_0101  165  VVRQLTEHVQGDIDL  VRQLTEHVQ          0.3634          980.0                 50.00   Rv2711, TB
   DRB1_0101  199  TPGGGVTIVIPGHEN  TIVIPGHEN          0.3634          980.8                 50.00   Rv2711, TB
   DRB1_0101   39  TVSQTVSRMERDGLL  TVSQTVSRM          0.3633          981.7                 50.00   Rv2711, TB
   DRB1_0101   88  VIGLPWEEVHAEACR  VIGLPWEEV          0.3605         1011.3                 50.00   Rv2711, TB
   DRB1_0101  130  PIPGLVELGVGPEPG  PIPGLVELG          0.3518         1111.8                 50.00   Rv2711, TB
   DRB1_0101   90  GLPWEEVHAEACRWE  WEEVHAEAC          0.3504         1128.4                 50.00   Rv2711, TB
   DRB1_0101   87  DVIGLPWEEVHAEAC  VIGLPWEEV          0.3463         1179.0                 50.00   Rv2711, TB
   DRB1_0101  106  VMSEDVERRLVKVLN  SEDVERRLV          0.3428         1225.4                 50.00   Rv2711, TB
   DRB1_0101  167  RQLTEHVQGDIDLIT  HVQGDIDLI          0.3421         1234.4                 50.00   Rv2711, TB
   DRB1_0101   13  TIYDLEEEGVTPLRA  LEEEGVTPL          0.3397         1266.4                 50.00   Rv2711, TB
   DRB1_0101   89  IGLPWEEVHAEACRW  WEEVHAEAC          0.3366         1310.4                 50.00   Rv2711, TB
   DRB1_0101  104  EHVMSEDVERRLVKV  VMSEDVERR          0.3362         1315.6                 50.00   Rv2711, TB
   DRB1_0101  190  PNARVTVETTPGGGV  VETTPGGGV          0.3193         1579.6                 50.00   Rv2711, TB
   DRB1_0101   27  ARIAERLDQSGPTVS  LDQSGPTVS          0.3187         1590.1                 50.00   Rv2711, TB
   DRB1_0101  131  IPGLVELGVGPEPGA  IPGLVELGV          0.3141         1670.3                 50.00   Rv2711, TB
   DRB1_0101  166  VRQLTEHVQGDIDLI  HVQGDIDLI          0.3126         1698.2                 50.00   Rv2711, TB
   DRB1_0101  140  GPEPGADDANLVRLT  PGADDANLV          0.3069         1806.7                 50.00   Rv2711, TB
   DRB1_0101  141  PEPGADDANLVRLTE  DDANLVRLT          0.3016         1912.8                 50.00   Rv2711, TB
   DRB1_0101  187  GVVPNARVTVETTPG  VVPNARVTV          0.2944         2067.7                 50.00   Rv2711, TB
   DRB1_0101   91  LPWEEVHAEACRWEH  WEEVHAEAC          0.2920         2122.8                 50.00   Rv2711, TB
   DRB1_0101  120  NNPTTSPFGNPIPGL  TTSPFGNPI          0.2830         2340.8                 50.00   Rv2711, TB
   DRB1_0101   92  PWEEVHAEACRWEHV  EVHAEACRW          0.2798         2420.9                 50.00   Rv2711, TB
   DRB1_0101   93  WEEVHAEACRWEHVM  EVHAEACRW          0.2751         2549.3                 50.00   Rv2711, TB
   DRB1_0101  117  KVLNNPTTSPFGNPI  VLNNPTTSP          0.2718         2640.5                 50.00   Rv2711, TB
   DRB1_0101   26  RARIAERLDQSGPTV  IAERLDQSG          0.2686         2733.3                 50.00   Rv2711, TB
   DRB1_0101   54  RVAGDRHLELTEKGR  VAGDRHLEL          0.2652         2836.4                 50.00   Rv2711, TB
   DRB1_0101  132  PGLVELGVGPEPGAD  VELGVGPEP          0.2542         3196.3                 50.00   Rv2711, TB
   DRB1_0101   55  VAGDRHLELTEKGRA  RHLELTEKG          0.2517         3284.2                 50.00   Rv2711, TB
   DRB1_0101   95  EVHAEACRWEHVMSE  AEACRWEHV          0.2490         3378.6                 50.00   Rv2711, TB
   DRB1_0101   94  EEVHAEACRWEHVMS  AEACRWEHV          0.2401         3720.1                 50.00   Rv2711, TB
   DRB1_0101  133  GLVELGVGPEPGADD  LGVGPEPGA          0.2386         3781.2                 50.00   Rv2711, TB
   DRB1_0101  188  VVPNARVTVETTPGG  VTVETTPGG          0.2346         3948.7                 50.00   Rv2711, TB
   DRB1_0101  134  LVELGVGPEPGADDA  LGVGPEPGA          0.2333         4007.6                 50.00   Rv2711, TB
   DRB1_0101  206  IVIPGHENVTLPHEM  IVIPGHENV          0.2297         4165.2                 50.00   Rv2711, TB
   DRB1_0101  118  VLNNPTTSPFGNPIP  TTSPFGNPI          0.2291         4191.8                 50.00   Rv2711, TB
   DRB1_0101   96  VHAEACRWEHVMSED  AEACRWEHV          0.2271         4284.4                 50.00   Rv2711, TB
   DRB1_0101  189  VPNARVTVETTPGGG  VTVETTPGG          0.2269         4293.8                 50.00   Rv2711, TB
   DRB1_0101  139  VGPEPGADDANLVRL  PGADDANLV          0.2267         4303.5                 50.00   Rv2711, TB
   DRB1_0101  119  LNNPTTSPFGNPIPG  TTSPFGNPI          0.2164         4808.1                 50.00   Rv2711, TB
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   DRB1_0101  135  VELGVGPEPGADDAN  LGVGPEPGA         0.2078       5277.9                50.00   Rv2711, TB
   DRB1_0101  136  ELGVGPEPGADDANL  VGPEPGADD         0.2032       5547.0                50.00   Rv2711, TB
   DRB1_0101  137  LGVGPEPGADDANLV  VGPEPGADD         0.1956       6026.4                50.00   Rv2711, TB
   DRB1_0101  138  GVGPEPGADDANLVR  PGADDANLV         0.1859       6687.7                50.00   Rv2711, TB
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Allele: DRB1_0101. Number of high binders 40. Number of weak binders 103. Number of peptides 216

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0301  103  WEHVMSEDVERRLVK  VMSEDVERR         0.6357         51.5          WB     2.00   Rv2711, TB
   DRB1_0301  104  EHVMSEDVERRLVKV  VMSEDVERR         0.6175         62.7          WB     2.00   Rv2711, TB
   DRB1_0301  105  HVMSEDVERRLVKVL  VMSEDVERR         0.6046         72.1          WB     4.00   Rv2711, TB
   DRB1_0301  102  RWEHVMSEDVERRLV  HVMSEDVER         0.5850         89.1          WB     4.00   Rv2711, TB
   DRB1_0301   72  IAVMRKHRLAERLLV  IAVMRKHRL         0.5570        120.7          WB     4.00   Rv2711, TB
   DRB1_0301   71  AIAVMRKHRLAERLL  IAVMRKHRL         0.5419        142.1          WB     8.00   Rv2711, TB
   DRB1_0301   52  LLRVAGDRHLELTEK  LLRVAGDRH         0.5389        146.8          WB     8.00   Rv2711, TB
   DRB1_0301  101  CRWEHVMSEDVERRL  HVMSEDVER         0.5308        160.3          WB     8.00   Rv2711, TB
   DRB1_0301  106  VMSEDVERRLVKVLN  VMSEDVERR         0.5274        166.3          WB     8.00   Rv2711, TB
   DRB1_0301   51  GLLRVAGDRHLELTE  LLRVAGDRH         0.5230        174.4          WB     8.00   Rv2711, TB
   DRB1_0301    0  MNELVDTTEMYLRTI  ELVDTTEMY         0.5226        175.1          WB     8.00   Rv2711, TB
   DRB1_0301   50  DGLLRVAGDRHLELT  LLRVAGDRH         0.5223        175.7          WB     8.00   Rv2711, TB
   DRB1_0301   70  LAIAVMRKHRLAERL  IAVMRKHRL         0.5053        211.1          WB     8.00   Rv2711, TB
   DRB1_0301  172  HVQGDIDLITRLKDA  QGDIDLITR         0.5049        212.1          WB     8.00   Rv2711, TB
   DRB1_0301   68  RALAIAVMRKHRLAE  IAVMRKHRL         0.5044        213.2          WB     8.00   Rv2711, TB
   DRB1_0301  175  GDIDLITRLKDAGVV  IDLITRLKD         0.5027        217.2          WB     8.00   Rv2711, TB
   DRB1_0301  176  DIDLITRLKDAGVVP  IDLITRLKD         0.4968        231.4          WB     8.00   Rv2711, TB
   DRB1_0301  173  VQGDIDLITRLKDAG  VQGDIDLIT         0.4897        249.9          WB     8.00   Rv2711, TB
   DRB1_0301   49  RDGLLRVAGDRHLEL  LLRVAGDRH         0.4867        258.2          WB     8.00   Rv2711, TB
   DRB1_0301  174  QGDIDLITRLKDAGV  GDIDLITRL         0.4863        259.3          WB     8.00   Rv2711, TB
   DRB1_0301  170  TEHVQGDIDLITRLK  VQGDIDLIT         0.4803        276.8          WB     8.00   Rv2711, TB
   DRB1_0301  171  EHVQGDIDLITRLKD  VQGDIDLIT         0.4787        281.6          WB    16.00   Rv2711, TB
   DRB1_0301    1  NELVDTTEMYLRTIY  ELVDTTEMY         0.4770        286.9          WB    16.00   Rv2711, TB
   DRB1_0301   69  ALAIAVMRKHRLAER  IAVMRKHRL         0.4744        294.8          WB    16.00   Rv2711, TB
   DRB1_0301   44  VSRMERDGLLRVAGD  VSRMERDGL         0.4593        347.4          WB    16.00   Rv2711, TB
   DRB1_0301  100  ACRWEHVMSEDVERR  HVMSEDVER         0.4564        358.2          WB    16.00   Rv2711, TB
   DRB1_0301   10  YLRTIYDLEEEGVTP  YLRTIYDLE         0.4457        402.3          WB    16.00   Rv2711, TB
   DRB1_0301   43  TVSRMERDGLLRVAG  VSRMERDGL         0.4456        402.6          WB    16.00   Rv2711, TB
   DRB1_0301   67  GRALAIAVMRKHRLA  RALAIAVMR         0.4442        409.0          WB    16.00   Rv2711, TB
   DRB1_0301  177  IDLITRLKDAGVVPN  IDLITRLKD         0.4416        420.7          WB    16.00   Rv2711, TB
   DRB1_0301   42  QTVSRMERDGLLRVA  VSRMERDGL         0.4263        496.6          WB    16.00   Rv2711, TB
   DRB1_0301  169  LTEHVQGDIDLITRL  VQGDIDLIT         0.4248        504.5                16.00   Rv2711, TB
   DRB1_0301   41  SQTVSRMERDGLLRV  SQTVSRMER         0.4231        513.7                16.00   Rv2711, TB
   DRB1_0301    9  MYLRTIYDLEEEGVT  YLRTIYDLE         0.4207        527.5                16.00   Rv2711, TB
   DRB1_0301   75  MRKHRLAERLLVDVI  RKHRLAERL         0.4189        537.8                16.00   Rv2711, TB
   DRB1_0301    8  EMYLRTIYDLEEEGV  YLRTIYDLE         0.4182        541.6                16.00   Rv2711, TB
   DRB1_0301   66  KGRALAIAVMRKHRL  RALAIAVMR         0.4155        558.2                16.00   Rv2711, TB
   DRB1_0301   74  VMRKHRLAERLLVDV  RKHRLAERL         0.4105        589.2                16.00   Rv2711, TB
   DRB1_0301   76  RKHRLAERLLVDVIG  RKHRLAERL         0.4087        600.5                16.00   Rv2711, TB
   DRB1_0301    7  TEMYLRTIYDLEEEG  YLRTIYDLE         0.3973        679.6                16.00   Rv2711, TB
   DRB1_0301    2  ELVDTTEMYLRTIYD  ELVDTTEMY         0.3904        731.9                32.00   Rv2711, TB
   DRB1_0301   48  ERDGLLRVAGDRHLE  LLRVAGDRH         0.3866        762.9                32.00   Rv2711, TB
   DRB1_0301   73  AVMRKHRLAERLLVD  RKHRLAERL         0.3734        879.7                32.00   Rv2711, TB
   DRB1_0301   81  AERLLVDVIGLPWEE  RLLVDVIGL         0.3711        901.6                32.00   Rv2711, TB
   DRB1_0301   40  VSQTVSRMERDGLLR  SQTVSRMER         0.3687        926.2                32.00   Rv2711, TB
   DRB1_0301   38  PTVSQTVSRMERDGL  SQTVSRMER         0.3634        979.8                32.00   Rv2711, TB
   DRB1_0301  185  DAGVVPNARVTVETT  VVPNARVTV         0.3631        983.8                32.00   Rv2711, TB
   DRB1_0301   78  HRLAERLLVDVIGLP  HRLAERLLV         0.3608       1008.0                32.00   Rv2711, TB
   DRB1_0301   80  LAERLLVDVIGLPWE  RLLVDVIGL         0.3569       1052.0                32.00   Rv2711, TB
   DRB1_0301   46  RMERDGLLRVAGDRH  RMERDGLLR         0.3527       1100.1                32.00   Rv2711, TB
   DRB1_0301   47  MERDGLLRVAGDRHL  LLRVAGDRH         0.3515       1115.2                32.00   Rv2711, TB
   DRB1_0301   45  SRMERDGLLRVAGDR  RMERDGLLR         0.3499       1134.0                32.00   Rv2711, TB
   DRB1_0301  178  DLITRLKDAGVVPNA  LITRLKDAG         0.3493       1142.0                32.00   Rv2711, TB
   DRB1_0301   11  LRTIYDLEEEGVTPL  IYDLEEEGV         0.3487       1149.4                32.00   Rv2711, TB
   DRB1_0301    6  TTEMYLRTIYDLEEE  YLRTIYDLE         0.3473       1166.9                32.00   Rv2711, TB
   DRB1_0301   79  RLAERLLVDVIGLPW  AERLLVDVI         0.3400       1262.3                32.00   Rv2711, TB
   DRB1_0301  115  LVKVLNNPTTSPFGN  LVKVLNNPT         0.3381       1288.8                32.00   Rv2711, TB
   DRB1_0301   77  KHRLAERLLVDVIGL  HRLAERLLV         0.3369       1306.2                32.00   Rv2711, TB
   DRB1_0301   37  GPTVSQTVSRMERDG  PTVSQTVSR         0.3329       1363.4                32.00   Rv2711, TB
   DRB1_0301  211  HENVTLPHEMAHAVK  VTLPHEMAH         0.3278       1441.2                32.00   Rv2711, TB
   DRB1_0301   99  EACRWEHVMSEDVER  HVMSEDVER         0.3268       1456.0                32.00   Rv2711, TB
   DRB1_0301   65  EKGRALAIAVMRKHR  RALAIAVMR         0.3266       1460.0                32.00   Rv2711, TB
   DRB1_0301   59  RHLELTEKGRALAIA  HLELTEKGR         0.3265       1461.6                32.00   Rv2711, TB
   DRB1_0301   60  HLELTEKGRALAIAV  HLELTEKGR         0.3255       1476.6                32.00   Rv2711, TB
   DRB1_0301  114  RLVKVLNNPTTSPFG  LVKVLNNPT         0.3246       1491.1                32.00   Rv2711, TB
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DRB1_0301   53  LRVAGDRHLELTEKG  LRVAGDRHL         0.3239        1503.1              32.00   Rv2711, TB
DRB1_0301  212  ENVTLPHEMAHAVKV  VTLPHEMAH         0.3227        1523.0              32.00   Rv2711, TB
DRB1_0301   36  SGPTVSQTVSRMERD  PTVSQTVSR         0.3215        1542.6              32.00   Rv2711, TB
DRB1_0301  168  QLTEHVQGDIDLITR  VQGDIDLIT         0.3212        1547.0              32.00   Rv2711, TB
DRB1_0301  184  KDAGVVPNARVTVET  DAGVVPNAR         0.3204        1561.5              32.00   Rv2711, TB
DRB1_0301  204  VTIVIPGHENVTLPH  VTIVIPGHE         0.3201        1566.5              32.00   Rv2711, TB
DRB1_0301   58  DRHLELTEKGRALAI  HLELTEKGR         0.3196        1574.3              32.00   Rv2711, TB
DRB1_0301  113  RRLVKVLNNPTTSPF  LVKVLNNPT         0.3175        1610.0              32.00   Rv2711, TB
DRB1_0301  186  AGVVPNARVTVETTP  VVPNARVTV         0.3172        1616.5              32.00   Rv2711, TB
DRB1_0301   82  ERLLVDVIGLPWEEV  LLVDVIGLP         0.3084        1778.2              32.00   Rv2711, TB
DRB1_0301   39  TVSQTVSRMERDGLL  TVSQTVSRM         0.3065        1813.7              32.00   Rv2711, TB
DRB1_0301  187  GVVPNARVTVETTPG  VVPNARVTV         0.3060        1824.7              32.00   Rv2711, TB
DRB1_0301   35  QSGPTVSQTVSRMER  PTVSQTVSR         0.3042        1861.0              32.00   Rv2711, TB
DRB1_0301   12  RTIYDLEEEGVTPLR  IYDLEEEGV         0.3032        1880.6              32.00   Rv2711, TB
DRB1_0301  188  VVPNARVTVETTPGG  VVPNARVTV         0.2994        1960.2              50.00   Rv2711, TB
DRB1_0301    5  DTTEMYLRTIYDLEE  YLRTIYDLE         0.2991        1966.1              50.00   Rv2711, TB
DRB1_0301  210  GHENVTLPHEMAHAV  ENVTLPHEM         0.2979        1991.5              50.00   Rv2711, TB
DRB1_0301   83  RLLVDVIGLPWEEVH  RLLVDVIGL         0.2917        2130.4              50.00   Rv2711, TB
DRB1_0301   28  RIAERLDQSGPTVSQ  RIAERLDQS         0.2904        2160.8              50.00   Rv2711, TB
DRB1_0301   98  AEACRWEHVMSEDVE  CRWEHVMSE         0.2894        2183.3              50.00   Rv2711, TB
DRB1_0301  179  LITRLKDAGVVPNAR  LITRLKDAG         0.2884        2208.0              50.00   Rv2711, TB
DRB1_0301  183  LKDAGVVPNARVTVE  DAGVVPNAR         0.2870        2239.5              50.00   Rv2711, TB
DRB1_0301  203  GVTIVIPGHENVTLP  VTIVIPGHE         0.2866        2251.3              50.00   Rv2711, TB
DRB1_0301   25  LRARIAERLDQSGPT  LRARIAERL         0.2824        2353.7              50.00   Rv2711, TB
DRB1_0301   57  GDRHLELTEKGRALA  HLELTEKGR         0.2823        2358.0              50.00   Rv2711, TB
DRB1_0301   13  TIYDLEEEGVTPLRA  IYDLEEEGV         0.2799        2418.5              50.00   Rv2711, TB
DRB1_0301   27  ARIAERLDQSGPTVS  RIAERLDQS         0.2773        2488.5              50.00   Rv2711, TB
DRB1_0301  112  ERRLVKVLNNPTTSP  LVKVLNNPT         0.2731        2603.4              50.00   Rv2711, TB
DRB1_0301  182  RLKDAGVVPNARVTV  DAGVVPNAR         0.2726        2618.0              50.00   Rv2711, TB
DRB1_0301   24  PLRARIAERLDQSGP  PLRARIAER         0.2703        2684.1              50.00   Rv2711, TB
DRB1_0301   54  RVAGDRHLELTEKGR  VAGDRHLEL         0.2692        2717.6              50.00   Rv2711, TB
DRB1_0301  213  NVTLPHEMAHAVKVE  VTLPHEMAH         0.2687        2732.4              50.00   Rv2711, TB
DRB1_0301  160  SPVAVVVRQLTEHVQ  VAVVVRQLT         0.2686        2732.8              50.00   Rv2711, TB
DRB1_0301  162  VAVVVRQLTEHVQGD  VAVVVRQLT         0.2675        2766.4              50.00   Rv2711, TB
DRB1_0301    3  LVDTTEMYLRTIYDL  LVDTTEMYL         0.2674        2770.6              50.00   Rv2711, TB
DRB1_0301  161  PVAVVVRQLTEHVQG  VAVVVRQLT         0.2641        2870.8              50.00   Rv2711, TB
DRB1_0301   26  RARIAERLDQSGPTV  RIAERLDQS         0.2605        2984.2              50.00   Rv2711, TB
DRB1_0301   55  VAGDRHLELTEKGRA  VAGDRHLEL         0.2603        2989.6              50.00   Rv2711, TB
DRB1_0301  167  RQLTEHVQGDIDLIT  VQGDIDLIT         0.2602        2994.0              50.00   Rv2711, TB
DRB1_0301  209  PGHENVTLPHEMAHA  ENVTLPHEM         0.2597        3011.7              50.00   Rv2711, TB
DRB1_0301   97  HAEACRWEHVMSEDV  CRWEHVMSE         0.2558        3141.2              50.00   Rv2711, TB
DRB1_0301  143  PGADDANLVRLTELP  ADDANLVRL         0.2511        3305.2              50.00   Rv2711, TB
DRB1_0301  159  GSPVAVVVRQLTEHV  VAVVVRQLT         0.2488        3389.2              50.00   Rv2711, TB
DRB1_0301    4  VDTTEMYLRTIYDLE  VDTTEMYLR         0.2485        3397.0              50.00   Rv2711, TB
DRB1_0301  202  GGVTIVIPGHENVTL  VTIVIPGHE         0.2483        3407.6              50.00   Rv2711, TB
DRB1_0301  144  GADDANLVRLTELPA  ADDANLVRL         0.2470        3455.7              50.00   Rv2711, TB
DRB1_0301   14  IYDLEEEGVTPLRAR  IYDLEEEGV         0.2462        3483.7              50.00   Rv2711, TB
DRB1_0301  142  EPGADDANLVRLTEL  GADDANLVR         0.2416        3660.9              50.00   Rv2711, TB
DRB1_0301   21  GVTPLRARIAERLDQ  GVTPLRARI         0.2407        3697.8              50.00   Rv2711, TB
DRB1_0301  164  VVVRQLTEHVQGDID  VRQLTEHVQ         0.2379        3810.2              50.00   Rv2711, TB
DRB1_0301   34  DQSGPTVSQTVSRME  PTVSQTVSR         0.2373        3837.0              50.00   Rv2711, TB
DRB1_0301  116  VKVLNNPTTSPFGNP  VKVLNNPTT         0.2371        3845.2              50.00   Rv2711, TB
DRB1_0301  111  VERRLVKVLNNPTTS  LVKVLNNPT         0.2360        3891.3              50.00   Rv2711, TB
DRB1_0301   23  TPLRARIAERLDQSG  LRARIAERL         0.2346        3948.5              50.00   Rv2711, TB
DRB1_0301  214  VTLPHEMAHAVKVEK  LPHEMAHAV         0.2342        3965.8              50.00   Rv2711, TB
DRB1_0301  107  MSEDVERRLVKVLNN  MSEDVERRL         0.2336        3992.2              50.00   Rv2711, TB
DRB1_0301  166  VRQLTEHVQGDIDLI  VRQLTEHVQ         0.2315        4083.2              50.00   Rv2711, TB
DRB1_0301  215  TLPHEMAHAVKVEKV  LPHEMAHAV         0.2290        4197.2              50.00   Rv2711, TB
DRB1_0301  163  AVVVRQLTEHVQGDI  VRQLTEHVQ         0.2276        4260.6              50.00   Rv2711, TB
DRB1_0301  110  DVERRLVKVLNNPTT  DVERRLVKV         0.2268        4295.6              50.00   Rv2711, TB
DRB1_0301  145  ADDANLVRLTELPAG  ADDANLVRL         0.2262        4325.4              50.00   Rv2711, TB
DRB1_0301   22  VTPLRARIAERLDQS  PLRARIAER         0.2242        4419.3              50.00   Rv2711, TB
DRB1_0301   96  VHAEACRWEHVMSED  CRWEHVMSE         0.2241        4424.6              50.00   Rv2711, TB
DRB1_0301   19  EEGVTPLRARIAERL  GVTPLRARI         0.2228        4486.9              50.00   Rv2711, TB
DRB1_0301  165  VVRQLTEHVQGDIDL  VRQLTEHVQ         0.2223        4511.8              50.00   Rv2711, TB
DRB1_0301   33  LDQSGPTVSQTVSRM  PTVSQTVSR         0.2217        4539.5              50.00   Rv2711, TB
DRB1_0301   56  AGDRHLELTEKGRAL  HLELTEKGR         0.2212        4565.4              50.00   Rv2711, TB
DRB1_0301   64  TEKGRALAIAVMRKH  RALAIAVMR         0.2193        4661.3              50.00   Rv2711, TB
DRB1_0301  140  GPEPGADDANLVRLT  GPEPGADDA         0.2158        4838.8              50.00   Rv2711, TB
DRB1_0301   20  EGVTPLRARIAERLD  GVTPLRARI         0.2157        4846.2              50.00   Rv2711, TB
DRB1_0301  180  ITRLKDAGVVPNARV  ITRLKDAGV         0.2150        4881.1              50.00   Rv2711, TB
DRB1_0301  109  EDVERRLVKVLNNPT  DVERRLVKV         0.2132        4981.3              50.00   Rv2711, TB
DRB1_0301  205  TIVIPGHENVTLPHE  IVIPGHENV         0.2119        5047.2              50.00   Rv2711, TB
DRB1_0301   29  IAERLDQSGPTVSQT  ERLDQSGPT         0.2109        5106.2              50.00   Rv2711, TB
DRB1_0301  208  IPGHENVTLPHEMAH  ENVTLPHEM         0.2106        5120.8              50.00   Rv2711, TB
DRB1_0301  189  VPNARVTVETTPGGG  VPNARVTVE         0.2106        5122.0              50.00   Rv2711, TB
DRB1_0301  148  ANLVRLTELPAGSPV  LVRLTELPA         0.2050        5441.1              50.00   Rv2711, TB
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   DRB1_0301  149  NLVRLTELPAGSPVA  NLVRLTELP        0.2042       5486.6                 50.00   Rv2711, TB
   DRB1_0301   84  LLVDVIGLPWEEVHA  LLVDVIGLP        0.2031       5553.6                 50.00   Rv2711, TB
   DRB1_0301   95  EVHAEACRWEHVMSE  AEACRWEHV        0.2006       5704.0                 50.00   Rv2711, TB
   DRB1_0301   30  AERLDQSGPTVSQTV  AERLDQSGP        0.2006       5706.3                 50.00   Rv2711, TB
   DRB1_0301  141  PEPGADDANLVRLTE  GADDANLVR        0.1994       5782.6                 50.00   Rv2711, TB
   DRB1_0301   61  LELTEKGRALAIAVM  LELTEKGRA        0.1987       5825.9                 50.00   Rv2711, TB
   DRB1_0301  108  SEDVERRLVKVLNNP  DVERRLVKV        0.1982       5854.8                 50.00   Rv2711, TB
   DRB1_0301  158  AGSPVAVVVRQLTEH  PVAVVVRQL        0.1973       5914.8                 50.00   Rv2711, TB
   DRB1_0301   32  RLDQSGPTVSQTVSR  LDQSGPTVS        0.1960       5998.0                 50.00   Rv2711, TB
   DRB1_0301   18  EEEGVTPLRARIAER  GVTPLRARI        0.1956       6022.8                 50.00   Rv2711, TB
   DRB1_0301  201  GGGVTIVIPGHENVT  VTIVIPGHE        0.1940       6126.7                 50.00   Rv2711, TB
   DRB1_0301  206  IVIPGHENVTLPHEM  IVIPGHENV        0.1912       6315.9                 50.00   Rv2711, TB
   DRB1_0301  150  LVRLTELPAGSPVAV  LVRLTELPA        0.1902       6384.8                 50.00   Rv2711, TB
   DRB1_0301  147  DANLVRLTELPAGSP  LVRLTELPA        0.1828       6915.0                 50.00   Rv2711, TB
   DRB1_0301   31  ERLDQSGPTVSQTVS  LDQSGPTVS        0.1768       7380.0                 50.00   Rv2711, TB
   DRB1_0301  139  VGPEPGADDANLVRL  GPEPGADDA        0.1752       7508.2                 50.00   Rv2711, TB
   DRB1_0301  146  DDANLVRLTELPAGS  ANLVRLTEL        0.1744       7575.4                 50.00   Rv2711, TB
   DRB1_0301   62  ELTEKGRALAIAVMR  ELTEKGRAL        0.1737       7634.5                 50.00   Rv2711, TB
   DRB1_0301  181  TRLKDAGVVPNARVT  RLKDAGVVP        0.1737       7636.5                 50.00   Rv2711, TB
   DRB1_0301   17  LEEEGVTPLRARIAE  EEGVTPLRA        0.1727       7713.8                 50.00   Rv2711, TB
   DRB1_0301   63  LTEKGRALAIAVMRK  RALAIAVMR        0.1710       7858.2                 50.00   Rv2711, TB
   DRB1_0301  156  LPAGSPVAVVVRQLT  LPAGSPVAV        0.1662       8280.1                 50.00   Rv2711, TB
   DRB1_0301  191  NARVTVETTPGGGVT  NARVTVETT        0.1643       8449.6                 50.00   Rv2711, TB
   DRB1_0301  157  PAGSPVAVVVRQLTE  SPVAVVVRQ        0.1631       8561.5                 50.00   Rv2711, TB
   DRB1_0301  190  PNARVTVETTPGGGV  NARVTVETT        0.1602       8832.7                 50.00   Rv2711, TB
   DRB1_0301  207  VIPGHENVTLPHEMA  ENVTLPHEM        0.1537       9476.6                 50.00   Rv2711, TB
   DRB1_0301  151  VRLTELPAGSPVAVV  RLTELPAGS        0.1532       9532.3                 50.00   Rv2711, TB
   DRB1_0301   16  DLEEEGVTPLRARIA  EEGVTPLRA        0.1472      10170.3                 50.00   Rv2711, TB
   DRB1_0301  138  GVGPEPGADDANLVR  GPEPGADDA        0.1405      10933.3                 50.00   Rv2711, TB
   DRB1_0301  117  KVLNNPTTSPFGNPI  KVLNNPTTS        0.1405      10933.5                 50.00   Rv2711, TB
   DRB1_0301   94  EEVHAEACRWEHVMS  EEVHAEACR        0.1387      11143.8                 50.00   Rv2711, TB
   DRB1_0301  134  LVELGVGPEPGADDA  LVELGVGPE        0.1380      11232.3                 50.00   Rv2711, TB
   DRB1_0301  155  ELPAGSPVAVVVRQL  LPAGSPVAV        0.1355      11540.1                 50.00   Rv2711, TB
   DRB1_0301  200  PGGGVTIVIPGHENV  VTIVIPGHE        0.1257      12832.4                 50.00   Rv2711, TB
   DRB1_0301   15  YDLEEEGVTPLRARI  EEGVTPLRA        0.1254      12876.4                 50.00   Rv2711, TB
   DRB1_0301  133  GLVELGVGPEPGADD  LVELGVGPE        0.1212      13472.7                 50.00   Rv2711, TB
   DRB1_0301  152  RLTELPAGSPVAVVV  RLTELPAGS        0.1163      14206.9                 50.00   Rv2711, TB
   DRB1_0301   93  WEEVHAEACRWEHVM  EEVHAEACR        0.1160      14250.7                 50.00   Rv2711, TB
   DRB1_0301  137  LGVGPEPGADDANLV  GPEPGADDA        0.1122      14857.9                 50.00   Rv2711, TB
   DRB1_0301  154  TELPAGSPVAVVVRQ  LPAGSPVAV        0.1111      15033.5                 50.00   Rv2711, TB
   DRB1_0301  132  PGLVELGVGPEPGAD  LVELGVGPE        0.1103      15163.7                 50.00   Rv2711, TB
   DRB1_0301  131  IPGLVELGVGPEPGA  LVELGVGPE        0.1091      15351.7                 50.00   Rv2711, TB
   DRB1_0301   88  VIGLPWEEVHAEACR  LPWEEVHAE        0.1010      16756.4                 50.00   Rv2711, TB
   DRB1_0301  153  LTELPAGSPVAVVVR  LPAGSPVAV        0.1005      16846.6                 50.00   Rv2711, TB
   DRB1_0301   85  LVDVIGLPWEEVHAE  LVDVIGLPW        0.0996      17028.2                 50.00   Rv2711, TB
   DRB1_0301  125  SPFGNPIPGLVELGV  FGNPIPGLV        0.0976      17389.6                 50.00   Rv2711, TB
   DRB1_0301  135  VELGVGPEPGADDAN  LGVGPEPGA        0.0927      18330.7                 50.00   Rv2711, TB
   DRB1_0301   91  LPWEEVHAEACRWEH  LPWEEVHAE        0.0924      18393.4                 50.00   Rv2711, TB
   DRB1_0301  124  TSPFGNPIPGLVELG  FGNPIPGLV        0.0920      18475.8                 50.00   Rv2711, TB
   DRB1_0301   92  PWEEVHAEACRWEHV  EEVHAEACR        0.0911      18661.2                 50.00   Rv2711, TB
   DRB1_0301   89  IGLPWEEVHAEACRW  LPWEEVHAE        0.0911      18669.1                 50.00   Rv2711, TB
   DRB1_0301   86  VDVIGLPWEEVHAEA  VIGLPWEEV        0.0900      18890.0                 50.00   Rv2711, TB
   DRB1_0301  136  ELGVGPEPGADDANL  LGVGPEPGA        0.0898      18927.8                 50.00   Rv2711, TB
   DRB1_0301  126  PFGNPIPGLVELGVG  FGNPIPGLV        0.0866      19591.9                 50.00   Rv2711, TB
   DRB1_0301  127  FGNPIPGLVELGVGP  FGNPIPGLV        0.0863      19647.3                 50.00   Rv2711, TB
   DRB1_0301  123  TTSPFGNPIPGLVEL  FGNPIPGLV        0.0847      19998.8                 50.00   Rv2711, TB
   DRB1_0301   87  DVIGLPWEEVHAEAC  VIGLPWEEV        0.0840      20157.4                 50.00   Rv2711, TB
   DRB1_0301   90  GLPWEEVHAEACRWE  LPWEEVHAE        0.0820      20586.6                 50.00   Rv2711, TB
   DRB1_0301  199  TPGGGVTIVIPGHEN  VTIVIPGHE        0.0787      21343.4                 50.00   Rv2711, TB
   DRB1_0301  118  VLNNPTTSPFGNPIP  LNNPTTSPF        0.0782      21460.4                 50.00   Rv2711, TB
   DRB1_0301  192  ARVTVETTPGGGVTI  ARVTVETTP        0.0763      21905.6                 50.00   Rv2711, TB
   DRB1_0301  130  PIPGLVELGVGPEPG  IPGLVELGV        0.0758      22015.9                 50.00   Rv2711, TB
   DRB1_0301  122  PTTSPFGNPIPGLVE  FGNPIPGLV        0.0670      24224.9                 50.00   Rv2711, TB
   DRB1_0301  129  NPIPGLVELGVGPEP  IPGLVELGV        0.0669      24252.1                 50.00   Rv2711, TB
   DRB1_0301  193  RVTVETTPGGGVTIV  RVTVETTPG        0.0656      24588.2                 50.00   Rv2711, TB
   DRB1_0301  121  NPTTSPFGNPIPGLV  NPTTSPFGN        0.0636      25128.5                 50.00   Rv2711, TB
   DRB1_0301  195  TVETTPGGGVTIVIP  TVETTPGGG        0.0612      25799.9                 50.00   Rv2711, TB
   DRB1_0301  194  VTVETTPGGGVTIVI  TVETTPGGG        0.0595      26263.5                 50.00   Rv2711, TB
   DRB1_0301  198  TTPGGGVTIVIPGHE  VTIVIPGHE        0.0590      26417.1                 50.00   Rv2711, TB
   DRB1_0301  119  LNNPTTSPFGNPIPG  LNNPTTSPF        0.0584      26589.8                 50.00   Rv2711, TB
   DRB1_0301  120  NNPTTSPFGNPIPGL  NPTTSPFGN        0.0564      27167.6                 50.00   Rv2711, TB
   DRB1_0301  128  GNPIPGLVELGVGPE  IPGLVELGV        0.0556      27387.2                 50.00   Rv2711, TB
   DRB1_0301  196  VETTPGGGVTIVIPG  VETTPGGGV        0.0447      30816.6                 50.00   Rv2711, TB
   DRB1_0301  197  ETTPGGGVTIVIPGH  ETTPGGGVT        0.0432      31319.8                 50.00   Rv2711, TB
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Allele: DRB1_0301. Number of high binders 0. Number of weak binders 31. Number of peptides 216
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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0401  113  RRLVKVLNNPTTSPF  VKVLNNPTT         0.8348          6.0         SB     0.10    Rv2711, TB
   DRB1_0401  112  ERRLVKVLNNPTTSP  RRLVKVLNN         0.8224          6.8         SB     0.10    Rv2711, TB
   DRB1_0401  111  VERRLVKVLNNPTTS  RRLVKVLNN         0.7984          8.9         SB     0.20    Rv2711, TB
   DRB1_0401  114  RLVKVLNNPTTSPFG  VKVLNNPTT         0.7813         10.7         SB     0.30    Rv2711, TB
   DRB1_0401  110  DVERRLVKVLNNPTT  RRLVKVLNN         0.7688         12.2         SB     0.40    Rv2711, TB
   DRB1_0401  115  LVKVLNNPTTSPFGN  VKVLNNPTT         0.7273         19.1         SB     1.00    Rv2711, TB
   DRB1_0401  109  EDVERRLVKVLNNPT  RRLVKVLNN         0.6913         28.2         SB     2.00    Rv2711, TB
   DRB1_0401  116  VKVLNNPTTSPFGNP  VKVLNNPTT         0.6011         74.9         WB     8.00    Rv2711, TB
   DRB1_0401  108  SEDVERRLVKVLNNP  RRLVKVLNN         0.5902         84.2         WB     8.00    Rv2711, TB
   DRB1_0401   66  KGRALAIAVMRKHRL  RALAIAVMR         0.5481        132.9         WB    16.00    Rv2711, TB
   DRB1_0401   65  EKGRALAIAVMRKHR  RALAIAVMR         0.5457        136.4         WB    16.00    Rv2711, TB
   DRB1_0401  149  NLVRLTELPAGSPVA  LVRLTELPA         0.5375        149.1         WB    16.00    Rv2711, TB
   DRB1_0401   67  GRALAIAVMRKHRLA  RALAIAVMR         0.5315        159.0         WB    16.00    Rv2711, TB
   DRB1_0401  150  LVRLTELPAGSPVAV  LVRLTELPA         0.5151        189.9         WB    16.00    Rv2711, TB
   DRB1_0401  148  ANLVRLTELPAGSPV  LVRLTELPA         0.5094        202.0         WB    16.00    Rv2711, TB
   DRB1_0401   68  RALAIAVMRKHRLAE  RALAIAVMR         0.4911        246.2         WB    16.00    Rv2711, TB
   DRB1_0401   64  TEKGRALAIAVMRKH  RALAIAVMR         0.4786        281.8         WB    32.00    Rv2711, TB
   DRB1_0401   81  AERLLVDVIGLPWEE  RLLVDVIGL         0.4764        288.7         WB    32.00    Rv2711, TB
   DRB1_0401  147  DANLVRLTELPAGSP  LVRLTELPA         0.4721        302.4         WB    32.00    Rv2711, TB
   DRB1_0401   82  ERLLVDVIGLPWEEV  RLLVDVIGL         0.4697        310.4         WB    32.00    Rv2711, TB
   DRB1_0401   80  LAERLLVDVIGLPWE  RLLVDVIGL         0.4636        331.6         WB    32.00    Rv2711, TB
   DRB1_0401   79  RLAERLLVDVIGLPW  RLLVDVIGL         0.4523        374.6         WB    32.00    Rv2711, TB
   DRB1_0401   83  RLLVDVIGLPWEEVH  RLLVDVIGL         0.4503        382.7         WB    32.00    Rv2711, TB
   DRB1_0401  179  LITRLKDAGVVPNAR  RLKDAGVVP         0.4428        415.1         WB    32.00    Rv2711, TB
   DRB1_0401   78  HRLAERLLVDVIGLP  RLLVDVIGL         0.4384        435.6         WB    32.00    Rv2711, TB
   DRB1_0401  178  DLITRLKDAGVVPNA  RLKDAGVVP         0.4316        468.5         WB    32.00    Rv2711, TB
   DRB1_0401  107  MSEDVERRLVKVLNN  RRLVKVLNN         0.4289        482.8         WB    32.00    Rv2711, TB
   DRB1_0401  151  VRLTELPAGSPVAVV  RLTELPAGS         0.4193        535.5                32.00    Rv2711, TB
   DRB1_0401    8  EMYLRTIYDLEEEGV  EMYLRTIYD         0.4118        580.6                32.00    Rv2711, TB
   DRB1_0401   77  KHRLAERLLVDVIGL  RLLVDVIGL         0.4114        583.0                32.00    Rv2711, TB
   DRB1_0401    7  TEMYLRTIYDLEEEG  EMYLRTIYD         0.4032        637.5                32.00    Rv2711, TB
   DRB1_0401  177  IDLITRLKDAGVVPN  LITRLKDAG         0.4029        639.0                32.00    Rv2711, TB
   DRB1_0401   63  LTEKGRALAIAVMRK  RALAIAVMR         0.4021        645.0                32.00    Rv2711, TB
   DRB1_0401  180  ITRLKDAGVVPNARV  RLKDAGVVP         0.4018        647.2                32.00    Rv2711, TB
   DRB1_0401  181  TRLKDAGVVPNARVT  RLKDAGVVP         0.4012        651.1                32.00    Rv2711, TB
   DRB1_0401  146  DDANLVRLTELPAGS  LVRLTELPA         0.3987        669.1                32.00    Rv2711, TB
   DRB1_0401  210  GHENVTLPHEMAHAV  GHENVTLPH         0.3982        672.9                32.00    Rv2711, TB
   DRB1_0401  182  RLKDAGVVPNARVTV  RLKDAGVVP         0.3847        778.8                50.00    Rv2711, TB
   DRB1_0401  117  KVLNNPTTSPFGNPI  KVLNNPTTS         0.3800        819.0                50.00    Rv2711, TB
   DRB1_0401  209  PGHENVTLPHEMAHA  GHENVTLPH         0.3761        854.5                50.00    Rv2711, TB
   DRB1_0401    6  TTEMYLRTIYDLEEE  EMYLRTIYD         0.3756        859.4                50.00    Rv2711, TB
   DRB1_0401   49  RDGLLRVAGDRHLEL  LLRVAGDRH         0.3620        995.6                50.00    Rv2711, TB
   DRB1_0401    5  DTTEMYLRTIYDLEE  EMYLRTIYD         0.3612       1004.1                50.00    Rv2711, TB
   DRB1_0401   46  RMERDGLLRVAGDRH  RMERDGLLR         0.3607       1009.6                50.00    Rv2711, TB
   DRB1_0401  208  IPGHENVTLPHEMAH  GHENVTLPH         0.3605       1012.0                50.00    Rv2711, TB
   DRB1_0401  176  DIDLITRLKDAGVVP  LITRLKDAG         0.3561       1060.7                50.00    Rv2711, TB
   DRB1_0401   50  DGLLRVAGDRHLELT  LLRVAGDRH         0.3546       1078.4                50.00    Rv2711, TB
   DRB1_0401   45  SRMERDGLLRVAGDR  RMERDGLLR         0.3544       1080.8                50.00    Rv2711, TB
   DRB1_0401   51  GLLRVAGDRHLELTE  LLRVAGDRH         0.3473       1166.3                50.00    Rv2711, TB
   DRB1_0401   76  RKHRLAERLLVDVIG  RLAERLLVD         0.3470       1170.2                50.00    Rv2711, TB
   DRB1_0401   10  YLRTIYDLEEEGVTP  LRTIYDLEE         0.3464       1178.7                50.00    Rv2711, TB
   DRB1_0401   44  VSRMERDGLLRVAGD  RMERDGLLR         0.3444       1204.5                50.00    Rv2711, TB
   DRB1_0401  162  VAVVVRQLTEHVQGD  VVVRQLTEH         0.3431       1221.7                50.00    Rv2711, TB
   DRB1_0401  173  VQGDIDLITRLKDAG  VQGDIDLIT         0.3428       1224.5                50.00    Rv2711, TB
   DRB1_0401  100  ACRWEHVMSEDVERR  WEHVMSEDV         0.3428       1224.5                50.00    Rv2711, TB
   DRB1_0401    9  MYLRTIYDLEEEGVT  LRTIYDLEE         0.3428       1224.7                50.00    Rv2711, TB
   DRB1_0401   75  MRKHRLAERLLVDVI  RLAERLLVD         0.3418       1238.5                50.00    Rv2711, TB
   DRB1_0401   62  ELTEKGRALAIAVMR  RALAIAVMR         0.3382       1287.0                50.00    Rv2711, TB
   DRB1_0401  190  PNARVTVETTPGGGV  RVTVETTPG         0.3356       1323.8                50.00    Rv2711, TB
   DRB1_0401  103  WEHVMSEDVERRLVK  WEHVMSEDV         0.3333       1357.5                50.00    Rv2711, TB
   DRB1_0401  191  NARVTVETTPGGGVT  RVTVETTPG         0.3329       1363.3                50.00    Rv2711, TB
   DRB1_0401  161  PVAVVVRQLTEHVQG  VVVRQLTEH         0.3327       1366.3                50.00    Rv2711, TB
   DRB1_0401  163  AVVVRQLTEHVQGDI  VVVRQLTEH         0.3317       1382.0                50.00    Rv2711, TB
   DRB1_0401  207  VIPGHENVTLPHEMA  GHENVTLPH         0.3306       1398.4                50.00    Rv2711, TB
   DRB1_0401   52  LLRVAGDRHLELTEK  LLRVAGDRH         0.3296       1412.6                50.00    Rv2711, TB
   DRB1_0401   48  ERDGLLRVAGDRHLE  LLRVAGDRH         0.3249       1487.1                50.00    Rv2711, TB
   DRB1_0401   43  TVSRMERDGLLRVAG  RMERDGLLR         0.3171       1618.0                50.00    Rv2711, TB
   DRB1_0401  102  RWEHVMSEDVERRLV  WEHVMSEDV         0.3158       1641.0                50.00    Rv2711, TB
   DRB1_0401   74  VMRKHRLAERLLVDV  HRLAERLLV         0.3137       1679.2                50.00    Rv2711, TB
   DRB1_0401  152  RLTELPAGSPVAVVV  RLTELPAGS         0.3102       1744.1                50.00    Rv2711, TB
   DRB1_0401   57  GDRHLELTEKGRALA  RHLELTEKG         0.3098       1751.3                50.00    Rv2711, TB
   DRB1_0401  101  CRWEHVMSEDVERRL  WEHVMSEDV         0.3090       1766.8                50.00    Rv2711, TB
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DRB1_0401   58  DRHLELTEKGRALAI  RHLELTEKG         0.3083        1778.8                 50.00   Rv2711, TB
DRB1_0401    4  VDTTEMYLRTIYDLE  EMYLRTIYD         0.3076        1792.6                 50.00   Rv2711, TB
DRB1_0401   59  RHLELTEKGRALAIA  RHLELTEKG         0.3068        1809.3                 50.00   Rv2711, TB
DRB1_0401  192  ARVTVETTPGGGVTI  RVTVETTPG         0.3060        1824.1                 50.00   Rv2711, TB
DRB1_0401  145  ADDANLVRLTELPAG  LVRLTELPA         0.3060        1825.0                 50.00   Rv2711, TB
DRB1_0401  164  VVVRQLTEHVQGDID  VVVRQLTEH         0.3059        1827.0                 50.00   Rv2711, TB
DRB1_0401  172  HVQGDIDLITRLKDA  VQGDIDLIT         0.3052        1840.0                 50.00   Rv2711, TB
DRB1_0401   56  AGDRHLELTEKGRAL  RHLELTEKG         0.3037        1871.0                 50.00   Rv2711, TB
DRB1_0401   53  LRVAGDRHLELTEKG  RHLELTEKG         0.3029        1886.3                 50.00   Rv2711, TB
DRB1_0401  215  TLPHEMAHAVKVEKV  HEMAHAVKV         0.3019        1906.7                 50.00   Rv2711, TB
DRB1_0401   69  ALAIAVMRKHRLAER  LAIAVMRKH         0.3004        1938.9                 50.00   Rv2711, TB
DRB1_0401  104  EHVMSEDVERRLVKV  EHVMSEDVE         0.3002        1941.7                 50.00   Rv2711, TB
DRB1_0401  171  EHVQGDIDLITRLKD  VQGDIDLIT         0.2999        1949.1                 50.00   Rv2711, TB
DRB1_0401  189  VPNARVTVETTPGGG  RVTVETTPG         0.2989        1968.9                 50.00   Rv2711, TB
DRB1_0401   99  EACRWEHVMSEDVER  WEHVMSEDV         0.2981        1987.8                 50.00   Rv2711, TB
DRB1_0401  214  VTLPHEMAHAVKVEK  HEMAHAVKV         0.2930        2099.7                 50.00   Rv2711, TB
DRB1_0401  160  SPVAVVVRQLTEHVQ  VVVRQLTEH         0.2929        2102.5                 50.00   Rv2711, TB
DRB1_0401  175  GDIDLITRLKDAGVV  LITRLKDAG         0.2926        2109.8                 50.00   Rv2711, TB
DRB1_0401   28  RIAERLDQSGPTVSQ  RIAERLDQS         0.2902        2164.5                 50.00   Rv2711, TB
DRB1_0401   11  LRTIYDLEEEGVTPL  LRTIYDLEE         0.2901        2167.7                 50.00   Rv2711, TB
DRB1_0401   47  MERDGLLRVAGDRHL  LLRVAGDRH         0.2886        2201.0                 50.00   Rv2711, TB
DRB1_0401  170  TEHVQGDIDLITRLK  VQGDIDLIT         0.2867        2248.2                 50.00   Rv2711, TB
DRB1_0401  211  HENVTLPHEMAHAVK  NVTLPHEMA         0.2863        2258.4                 50.00   Rv2711, TB
DRB1_0401   55  VAGDRHLELTEKGRA  RHLELTEKG         0.2863        2258.8                 50.00   Rv2711, TB
DRB1_0401    2  ELVDTTEMYLRTIYD  ELVDTTEMY         0.2858        2270.7                 50.00   Rv2711, TB
DRB1_0401  213  NVTLPHEMAHAVKVE  NVTLPHEMA         0.2822        2361.2                 50.00   Rv2711, TB
DRB1_0401   70  LAIAVMRKHRLAERL  LAIAVMRKH         0.2795        2429.5                 50.00   Rv2711, TB
DRB1_0401  193  RVTVETTPGGGVTIV  RVTVETTPG         0.2795        2431.2                 50.00   Rv2711, TB
DRB1_0401  206  IVIPGHENVTLPHEM  GHENVTLPH         0.2793        2435.0                 50.00   Rv2711, TB
DRB1_0401   73  AVMRKHRLAERLLVD  MRKHRLAER         0.2773        2488.5                 50.00   Rv2711, TB
DRB1_0401   27  ARIAERLDQSGPTVS  RIAERLDQS         0.2730        2606.5                 50.00   Rv2711, TB
DRB1_0401   42  QTVSRMERDGLLRVA  RMERDGLLR         0.2728        2612.9                 50.00   Rv2711, TB
DRB1_0401  144  GADDANLVRLTELPA  LVRLTELPA         0.2689        2726.7                 50.00   Rv2711, TB
DRB1_0401  212  ENVTLPHEMAHAVKV  NVTLPHEMA         0.2686        2732.7                 50.00   Rv2711, TB
DRB1_0401  188  VVPNARVTVETTPGG  RVTVETTPG         0.2683        2743.2                 50.00   Rv2711, TB
DRB1_0401   26  RARIAERLDQSGPTV  RIAERLDQS         0.2677        2761.2                 50.00   Rv2711, TB
DRB1_0401   37  GPTVSQTVSRMERDG  PTVSQTVSR         0.2656        2823.7                 50.00   Rv2711, TB
DRB1_0401   98  AEACRWEHVMSEDVE  ACRWEHVMS         0.2651        2840.7                 50.00   Rv2711, TB
DRB1_0401   38  PTVSQTVSRMERDGL  PTVSQTVSR         0.2637        2882.3                 50.00   Rv2711, TB
DRB1_0401   36  SGPTVSQTVSRMERD  PTVSQTVSR         0.2602        2993.5                 50.00   Rv2711, TB
DRB1_0401   25  LRARIAERLDQSGPT  RIAERLDQS         0.2595        3016.0                 50.00   Rv2711, TB
DRB1_0401   12  RTIYDLEEEGVTPLR  RTIYDLEEE         0.2588        3039.0                 50.00   Rv2711, TB
DRB1_0401   72  IAVMRKHRLAERLLV  MRKHRLAER         0.2588        3040.5                 50.00   Rv2711, TB
DRB1_0401  174  QGDIDLITRLKDAGV  LITRLKDAG         0.2570        3098.5                 50.00   Rv2711, TB
DRB1_0401   54  RVAGDRHLELTEKGR  RHLELTEKG         0.2567        3108.8                 50.00   Rv2711, TB
DRB1_0401    0  MNELVDTTEMYLRTI  ELVDTTEMY         0.2564        3121.0                 50.00   Rv2711, TB
DRB1_0401  205  TIVIPGHENVTLPHE  GHENVTLPH         0.2559        3136.6                 50.00   Rv2711, TB
DRB1_0401    1  NELVDTTEMYLRTIY  ELVDTTEMY         0.2526        3251.9                 50.00   Rv2711, TB
DRB1_0401    3  LVDTTEMYLRTIYDL  EMYLRTIYD         0.2484        3401.1                 50.00   Rv2711, TB
DRB1_0401   84  LLVDVIGLPWEEVHA  LLVDVIGLP         0.2449        3534.4                 50.00   Rv2711, TB
DRB1_0401   19  EEGVTPLRARIAERL  EEGVTPLRA         0.2415        3667.5                 50.00   Rv2711, TB
DRB1_0401   71  AIAVMRKHRLAERLL  IAVMRKHRL         0.2409        3690.8                 50.00   Rv2711, TB
DRB1_0401   35  QSGPTVSQTVSRMER  PTVSQTVSR         0.2406        3700.5                 50.00   Rv2711, TB
DRB1_0401  165  VVRQLTEHVQGDIDL  VVRQLTEHV         0.2398        3732.9                 50.00   Rv2711, TB
DRB1_0401  131  IPGLVELGVGPEPGA  GLVELGVGP         0.2393        3752.4                 50.00   Rv2711, TB
DRB1_0401  159  GSPVAVVVRQLTEHV  VVVRQLTEH         0.2385        3785.6                 50.00   Rv2711, TB
DRB1_0401   97  HAEACRWEHVMSEDV  ACRWEHVMS         0.2373        3837.0                 50.00   Rv2711, TB
DRB1_0401  169  LTEHVQGDIDLITRL  EHVQGDIDL         0.2355        3913.2                 50.00   Rv2711, TB
DRB1_0401  183  LKDAGVVPNARVTVE  LKDAGVVPN         0.2341        3970.1                 50.00   Rv2711, TB
DRB1_0401   41  SQTVSRMERDGLLRV  RMERDGLLR         0.2336        3993.9                 50.00   Rv2711, TB
DRB1_0401  132  PGLVELGVGPEPGAD  GLVELGVGP         0.2322        4052.8                 50.00   Rv2711, TB
DRB1_0401   29  IAERLDQSGPTVSQT  ERLDQSGPT         0.2316        4081.9                 50.00   Rv2711, TB
DRB1_0401  105  HVMSEDVERRLVKVL  HVMSEDVER         0.2298        4159.6                 50.00   Rv2711, TB
DRB1_0401   31  ERLDQSGPTVSQTVS  ERLDQSGPT         0.2295        4173.8                 50.00   Rv2711, TB
DRB1_0401   24  PLRARIAERLDQSGP  RIAERLDQS         0.2292        4188.1                 50.00   Rv2711, TB
DRB1_0401  130  PIPGLVELGVGPEPG  GLVELGVGP         0.2266        4308.6                 50.00   Rv2711, TB
DRB1_0401  187  GVVPNARVTVETTPG  NARVTVETT         0.2254        4365.2                 50.00   Rv2711, TB
DRB1_0401   22  VTPLRARIAERLDQS  RIAERLDQS         0.2230        4476.1                 50.00   Rv2711, TB
DRB1_0401   18  EEEGVTPLRARIAER  VTPLRARIA         0.2218        4534.9                 50.00   Rv2711, TB
DRB1_0401   16  DLEEEGVTPLRARIA  DLEEEGVTP         0.2217        4541.7                 50.00   Rv2711, TB
DRB1_0401   30  AERLDQSGPTVSQTV  ERLDQSGPT         0.2207        4591.1                 50.00   Rv2711, TB
DRB1_0401   90  GLPWEEVHAEACRWE  GLPWEEVHA         0.2171        4771.0                 50.00   Rv2711, TB
DRB1_0401   61  LELTEKGRALAIAVM  KGRALAIAV         0.2161        4825.5                 50.00   Rv2711, TB
DRB1_0401   87  DVIGLPWEEVHAEAC  GLPWEEVHA         0.2156        4849.6                 50.00   Rv2711, TB
DRB1_0401   88  VIGLPWEEVHAEACR  GLPWEEVHA         0.2153        4864.9                 50.00   Rv2711, TB
DRB1_0401  200  PGGGVTIVIPGHENV  GGGVTIVIP         0.2139        4940.8                 50.00   Rv2711, TB
DRB1_0401   23  TPLRARIAERLDQSG  LRARIAERL         0.2139        4943.2                 50.00   Rv2711, TB
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   DRB1_0401  168  QLTEHVQGDIDLITR  EHVQGDIDL        0.2119       5047.8               50.00   Rv2711, TB
   DRB1_0401  204  VTIVIPGHENVTLPH  TIVIPGHEN        0.2116       5068.2               50.00   Rv2711, TB
   DRB1_0401  201  GGGVTIVIPGHENVT  GGGVTIVIP        0.2113       5081.5               50.00   Rv2711, TB
   DRB1_0401   85  LVDVIGLPWEEVHAE  GLPWEEVHA        0.2101       5148.0               50.00   Rv2711, TB
   DRB1_0401   13  TIYDLEEEGVTPLRA  DLEEEGVTP        0.2099       5157.6               50.00   Rv2711, TB
   DRB1_0401   15  YDLEEEGVTPLRARI  YDLEEEGVT        0.2073       5309.1               50.00   Rv2711, TB
   DRB1_0401   14  IYDLEEEGVTPLRAR  DLEEEGVTP        0.2061       5374.9               50.00   Rv2711, TB
   DRB1_0401   89  IGLPWEEVHAEACRW  GLPWEEVHA        0.2053       5422.4               50.00   Rv2711, TB
   DRB1_0401   96  VHAEACRWEHVMSED  ACRWEHVMS        0.2039       5508.1               50.00   Rv2711, TB
   DRB1_0401   32  RLDQSGPTVSQTVSR  RLDQSGPTV        0.1991       5797.6               50.00   Rv2711, TB
   DRB1_0401   86  VDVIGLPWEEVHAEA  GLPWEEVHA        0.1983       5849.7               50.00   Rv2711, TB
   DRB1_0401   17  LEEEGVTPLRARIAE  EEGVTPLRA        0.1969       5939.8               50.00   Rv2711, TB
   DRB1_0401   21  GVTPLRARIAERLDQ  VTPLRARIA        0.1967       5953.3               50.00   Rv2711, TB
   DRB1_0401  133  GLVELGVGPEPGADD  GLVELGVGP        0.1954       6034.6               50.00   Rv2711, TB
   DRB1_0401  202  GGVTIVIPGHENVTL  TIVIPGHEN        0.1944       6104.8               50.00   Rv2711, TB
   DRB1_0401   20  EGVTPLRARIAERLD  VTPLRARIA        0.1941       6120.6               50.00   Rv2711, TB
   DRB1_0401   34  DQSGPTVSQTVSRME  PTVSQTVSR        0.1907       6354.0               50.00   Rv2711, TB
   DRB1_0401  199  TPGGGVTIVIPGHEN  GGGVTIVIP        0.1889       6478.0               50.00   Rv2711, TB
   DRB1_0401   95  EVHAEACRWEHVMSE  ACRWEHVMS        0.1872       6599.1               50.00   Rv2711, TB
   DRB1_0401   40  VSQTVSRMERDGLLR  RMERDGLLR        0.1842       6814.7               50.00   Rv2711, TB
   DRB1_0401  118  VLNNPTTSPFGNPIP  VLNNPTTSP        0.1833       6878.3               50.00   Rv2711, TB
   DRB1_0401  129  NPIPGLVELGVGPEP  GLVELGVGP        0.1830       6903.4               50.00   Rv2711, TB
   DRB1_0401  153  LTELPAGSPVAVVVR  LTELPAGSP        0.1814       7025.9               50.00   Rv2711, TB
   DRB1_0401  167  RQLTEHVQGDIDLIT  EHVQGDIDL        0.1809       7058.5               50.00   Rv2711, TB
   DRB1_0401   33  LDQSGPTVSQTVSRM  PTVSQTVSR        0.1781       7277.7               50.00   Rv2711, TB
   DRB1_0401  186  AGVVPNARVTVETTP  VVPNARVTV        0.1781       7282.1               50.00   Rv2711, TB
   DRB1_0401  143  PGADDANLVRLTELP  GADDANLVR        0.1778       7301.5               50.00   Rv2711, TB
   DRB1_0401  203  GVTIVIPGHENVTLP  TIVIPGHEN        0.1769       7376.6               50.00   Rv2711, TB
   DRB1_0401  185  DAGVVPNARVTVETT  DAGVVPNAR        0.1763       7418.7               50.00   Rv2711, TB
   DRB1_0401  184  KDAGVVPNARVTVET  DAGVVPNAR        0.1741       7602.5               50.00   Rv2711, TB
   DRB1_0401   94  EEVHAEACRWEHVMS  ACRWEHVMS        0.1734       7662.3               50.00   Rv2711, TB
   DRB1_0401  158  AGSPVAVVVRQLTEH  VVVRQLTEH        0.1725       7731.0               50.00   Rv2711, TB
   DRB1_0401  106  VMSEDVERRLVKVLN  VMSEDVERR        0.1721       7763.5               50.00   Rv2711, TB
   DRB1_0401  141  PEPGADDANLVRLTE  GADDANLVR        0.1709       7868.7               50.00   Rv2711, TB
   DRB1_0401  166  VRQLTEHVQGDIDLI  RQLTEHVQG        0.1699       7953.5               50.00   Rv2711, TB
   DRB1_0401   60  HLELTEKGRALAIAV  KGRALAIAV        0.1682       8100.5               50.00   Rv2711, TB
   DRB1_0401  142  EPGADDANLVRLTEL  GADDANLVR        0.1675       8163.3               50.00   Rv2711, TB
   DRB1_0401  198  TTPGGGVTIVIPGHE  GGGVTIVIP        0.1656       8336.7               50.00   Rv2711, TB
   DRB1_0401  124  TSPFGNPIPGLVELG  PFGNPIPGL        0.1483      10048.9               50.00   Rv2711, TB
   DRB1_0401  128  GNPIPGLVELGVGPE  GLVELGVGP        0.1454      10370.3               50.00   Rv2711, TB
   DRB1_0401  140  GPEPGADDANLVRLT  GADDANLVR        0.1445      10468.3               50.00   Rv2711, TB
   DRB1_0401  123  TTSPFGNPIPGLVEL  SPFGNPIPG        0.1440      10525.7               50.00   Rv2711, TB
   DRB1_0401   39  TVSQTVSRMERDGLL  TVSQTVSRM        0.1434      10595.0               50.00   Rv2711, TB
   DRB1_0401  122  PTTSPFGNPIPGLVE  SPFGNPIPG        0.1375      11289.6               50.00   Rv2711, TB
   DRB1_0401  197  ETTPGGGVTIVIPGH  PGGGVTIVI        0.1335      11792.5               50.00   Rv2711, TB
   DRB1_0401  121  NPTTSPFGNPIPGLV  TSPFGNPIP        0.1333      11823.9               50.00   Rv2711, TB
   DRB1_0401  194  VTVETTPGGGVTIVI  VTVETTPGG        0.1332      11829.6               50.00   Rv2711, TB
   DRB1_0401  125  SPFGNPIPGLVELGV  PFGNPIPGL        0.1324      11940.1               50.00   Rv2711, TB
   DRB1_0401   91  LPWEEVHAEACRWEH  EEVHAEACR        0.1263      12750.4               50.00   Rv2711, TB
   DRB1_0401   93  WEEVHAEACRWEHVM  EEVHAEACR        0.1241      13062.6               50.00   Rv2711, TB
   DRB1_0401  126  PFGNPIPGLVELGVG  PFGNPIPGL        0.1221      13339.1               50.00   Rv2711, TB
   DRB1_0401  154  TELPAGSPVAVVVRQ  LPAGSPVAV        0.1219      13374.7               50.00   Rv2711, TB
   DRB1_0401  127  FGNPIPGLVELGVGP  GLVELGVGP        0.1190      13789.9               50.00   Rv2711, TB
   DRB1_0401  139  VGPEPGADDANLVRL  GADDANLVR        0.1168      14124.3               50.00   Rv2711, TB
   DRB1_0401  155  ELPAGSPVAVVVRQL  LPAGSPVAV        0.1150      14407.5               50.00   Rv2711, TB
   DRB1_0401  120  NNPTTSPFGNPIPGL  TSPFGNPIP        0.1113      14996.5               50.00   Rv2711, TB
   DRB1_0401  156  LPAGSPVAVVVRQLT  LPAGSPVAV        0.1110      15049.6               50.00   Rv2711, TB
   DRB1_0401   92  PWEEVHAEACRWEHV  EEVHAEACR        0.1087      15427.8               50.00   Rv2711, TB
   DRB1_0401  196  VETTPGGGVTIVIPG  PGGGVTIVI        0.1054      15977.2               50.00   Rv2711, TB
   DRB1_0401  135  VELGVGPEPGADDAN  LGVGPEPGA        0.1052      16017.0               50.00   Rv2711, TB
   DRB1_0401  134  LVELGVGPEPGADDA  LGVGPEPGA        0.1020      16580.8               50.00   Rv2711, TB
   DRB1_0401  136  ELGVGPEPGADDANL  LGVGPEPGA        0.0983      17254.3               50.00   Rv2711, TB
   DRB1_0401  119  LNNPTTSPFGNPIPG  TSPFGNPIP        0.0952      17840.9               50.00   Rv2711, TB
   DRB1_0401  137  LGVGPEPGADDANLV  LGVGPEPGA        0.0950      17896.4               50.00   Rv2711, TB
   DRB1_0401  138  GVGPEPGADDANLVR  GADDANLVR        0.0928      18311.8               50.00   Rv2711, TB
   DRB1_0401  157  PAGSPVAVVVRQLTE  PAGSPVAVV        0.0920      18480.6               50.00   Rv2711, TB
   DRB1_0401  195  TVETTPGGGVTIVIP  GGGVTIVIP        0.0815      20701.4               50.00   Rv2711, TB
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Allele: DRB1_0401. Number of high binders 7. Number of weak binders 20. Number of peptides 216

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0404  113  RRLVKVLNNPTTSPF  RLVKVLNNP        0.8714          4.0         SB    0.05   Rv2711, TB
   DRB1_0404  112  ERRLVKVLNNPTTSP  RLVKVLNNP        0.8674          4.2         SB    0.05   Rv2711, TB
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DRB1_0404  111  VERRLVKVLNNPTTS  RLVKVLNNP         0.8600          4.6          SB     0.05   Rv2711, TB
DRB1_0404  114  RLVKVLNNPTTSPFG  RLVKVLNNP         0.8595          4.6          SB     0.05   Rv2711, TB
DRB1_0404  110  DVERRLVKVLNNPTT  RLVKVLNNP         0.8287          6.4          SB     0.15   Rv2711, TB
DRB1_0404  115  LVKVLNNPTTSPFGN  LVKVLNNPT         0.7882          9.9          SB     0.40   Rv2711, TB
DRB1_0404  109  EDVERRLVKVLNNPT  RLVKVLNNP         0.7471         15.4          SB     2.00   Rv2711, TB
DRB1_0404    7  TEMYLRTIYDLEEEG  YLRTIYDLE         0.6603         39.5          SB     8.00   Rv2711, TB
DRB1_0404    6  TTEMYLRTIYDLEEE  YLRTIYDLE         0.6534         42.5          SB     8.00   Rv2711, TB
DRB1_0404    8  EMYLRTIYDLEEEGV  YLRTIYDLE         0.6513         43.5          SB     8.00   Rv2711, TB
DRB1_0404    5  DTTEMYLRTIYDLEE  YLRTIYDLE         0.6205         60.7          WB     8.00   Rv2711, TB
DRB1_0404  148  ANLVRLTELPAGSPV  LVRLTELPA         0.6041         72.5          WB    16.00   Rv2711, TB
DRB1_0404  147  DANLVRLTELPAGSP  NLVRLTELP         0.6022         74.0          WB    16.00   Rv2711, TB
DRB1_0404  108  SEDVERRLVKVLNNP  RLVKVLNNP         0.5996         76.1          WB    16.00   Rv2711, TB
DRB1_0404  149  NLVRLTELPAGSPVA  LVRLTELPA         0.5815         92.6          WB    16.00   Rv2711, TB
DRB1_0404  146  DDANLVRLTELPAGS  NLVRLTELP         0.5777         96.4          WB    16.00   Rv2711, TB
DRB1_0404    4  VDTTEMYLRTIYDLE  EMYLRTIYD         0.5624        113.8          WB    16.00   Rv2711, TB
DRB1_0404  116  VKVLNNPTTSPFGNP  KVLNNPTTS         0.5482        132.8          WB    16.00   Rv2711, TB
DRB1_0404    9  MYLRTIYDLEEEGVT  YLRTIYDLE         0.5420        141.9          WB    16.00   Rv2711, TB
DRB1_0404  145  ADDANLVRLTELPAG  NLVRLTELP         0.5264        168.1          WB    16.00   Rv2711, TB
DRB1_0404   81  AERLLVDVIGLPWEE  RLLVDVIGL         0.5241        172.3          WB    32.00   Rv2711, TB
DRB1_0404   80  LAERLLVDVIGLPWE  RLLVDVIGL         0.5151        190.0          WB    32.00   Rv2711, TB
DRB1_0404   82  ERLLVDVIGLPWEEV  RLLVDVIGL         0.5144        191.4          WB    32.00   Rv2711, TB
DRB1_0404   83  RLLVDVIGLPWEEVH  RLLVDVIGL         0.5059        209.8          WB    32.00   Rv2711, TB
DRB1_0404  150  LVRLTELPAGSPVAV  LVRLTELPA         0.4963        232.8          WB    32.00   Rv2711, TB
DRB1_0404   66  KGRALAIAVMRKHRL  RALAIAVMR         0.4870        257.3          WB    32.00   Rv2711, TB
DRB1_0404   67  GRALAIAVMRKHRLA  RALAIAVMR         0.4846        264.2          WB    32.00   Rv2711, TB
DRB1_0404   79  RLAERLLVDVIGLPW  RLLVDVIGL         0.4782        283.1          WB    32.00   Rv2711, TB
DRB1_0404   78  HRLAERLLVDVIGLP  RLLVDVIGL         0.4737        297.3          WB    32.00   Rv2711, TB
DRB1_0404   68  RALAIAVMRKHRLAE  RALAIAVMR         0.4711        305.7          WB    32.00   Rv2711, TB
DRB1_0404   65  EKGRALAIAVMRKHR  RALAIAVMR         0.4559        360.3          WB    32.00   Rv2711, TB
DRB1_0404  144  GADDANLVRLTELPA  NLVRLTELP         0.4483        391.3          WB    32.00   Rv2711, TB
DRB1_0404  178  DLITRLKDAGVVPNA  LITRLKDAG         0.4464        399.4          WB    32.00   Rv2711, TB
DRB1_0404  177  IDLITRLKDAGVVPN  LITRLKDAG         0.4376        439.2          WB    32.00   Rv2711, TB
DRB1_0404   77  KHRLAERLLVDVIGL  RLLVDVIGL         0.4305        474.3          WB    32.00   Rv2711, TB
DRB1_0404    3  LVDTTEMYLRTIYDL  EMYLRTIYD         0.4283        485.9          WB    32.00   Rv2711, TB
DRB1_0404  176  DIDLITRLKDAGVVP  LITRLKDAG         0.4238        510.2                32.00   Rv2711, TB
DRB1_0404  161  PVAVVVRQLTEHVQG  VVVRQLTEH         0.4234        512.0                32.00   Rv2711, TB
DRB1_0404   64  TEKGRALAIAVMRKH  RALAIAVMR         0.4207        527.6                32.00   Rv2711, TB
DRB1_0404   10  YLRTIYDLEEEGVTP  YLRTIYDLE         0.4203        529.7                32.00   Rv2711, TB
DRB1_0404  162  VAVVVRQLTEHVQGD  VVVRQLTEH         0.4193        535.3                32.00   Rv2711, TB
DRB1_0404  179  LITRLKDAGVVPNAR  LITRLKDAG         0.4020        646.0                50.00   Rv2711, TB
DRB1_0404  163  AVVVRQLTEHVQGDI  VVVRQLTEH         0.3982        672.7                50.00   Rv2711, TB
DRB1_0404  190  PNARVTVETTPGGGV  RVTVETTPG         0.3970        681.8                50.00   Rv2711, TB
DRB1_0404  191  NARVTVETTPGGGVT  RVTVETTPG         0.3944        700.7                50.00   Rv2711, TB
DRB1_0404    2  ELVDTTEMYLRTIYD  TTEMYLRTI         0.3924        716.5                50.00   Rv2711, TB
DRB1_0404  160  SPVAVVVRQLTEHVQ  VAVVVRQLT         0.3877        753.9                50.00   Rv2711, TB
DRB1_0404  164  VVVRQLTEHVQGDID  VVVRQLTEH         0.3862        766.3                50.00   Rv2711, TB
DRB1_0404  203  GVTIVIPGHENVTLP  IVIPGHENV         0.3805        815.1                50.00   Rv2711, TB
DRB1_0404   84  LLVDVIGLPWEEVHA  LLVDVIGLP         0.3764        852.1                50.00   Rv2711, TB
DRB1_0404  175  GDIDLITRLKDAGVV  LITRLKDAG         0.3747        867.6                50.00   Rv2711, TB
DRB1_0404  117  KVLNNPTTSPFGNPI  KVLNNPTTS         0.3717        895.7                50.00   Rv2711, TB
DRB1_0404  189  VPNARVTVETTPGGG  RVTVETTPG         0.3712        901.1                50.00   Rv2711, TB
DRB1_0404    0  MNELVDTTEMYLRTI  ELVDTTEMY         0.3689        923.5                50.00   Rv2711, TB
DRB1_0404   69  ALAIAVMRKHRLAER  LAIAVMRKH         0.3673        939.8                50.00   Rv2711, TB
DRB1_0404   70  LAIAVMRKHRLAERL  LAIAVMRKH         0.3666        946.8                50.00   Rv2711, TB
DRB1_0404  202  GGVTIVIPGHENVTL  GVTIVIPGH         0.3664        948.6                50.00   Rv2711, TB
DRB1_0404  151  VRLTELPAGSPVAVV  VRLTELPAG         0.3643        971.3                50.00   Rv2711, TB
DRB1_0404  204  VTIVIPGHENVTLPH  IVIPGHENV         0.3637        977.3                50.00   Rv2711, TB
DRB1_0404  188  VVPNARVTVETTPGG  RVTVETTPG         0.3635        979.5                50.00   Rv2711, TB
DRB1_0404   50  DGLLRVAGDRHLELT  LLRVAGDRH         0.3629        985.9                50.00   Rv2711, TB
DRB1_0404   63  LTEKGRALAIAVMRK  RALAIAVMR         0.3618        997.4                50.00   Rv2711, TB
DRB1_0404  205  TIVIPGHENVTLPHE  IVIPGHENV         0.3554       1068.5                50.00   Rv2711, TB
DRB1_0404  159  GSPVAVVVRQLTEHV  VAVVVRQLT         0.3537       1088.2                50.00   Rv2711, TB
DRB1_0404    1  NELVDTTEMYLRTIY  ELVDTTEMY         0.3499       1134.8                50.00   Rv2711, TB
DRB1_0404   49  RDGLLRVAGDRHLEL  LLRVAGDRH         0.3490       1145.9                50.00   Rv2711, TB
DRB1_0404  107  MSEDVERRLVKVLNN  RRLVKVLNN         0.3479       1159.6                50.00   Rv2711, TB
DRB1_0404  126  PFGNPIPGLVELGVG  PIPGLVELG         0.3472       1167.9                50.00   Rv2711, TB
DRB1_0404   51  GLLRVAGDRHLELTE  LRVAGDRHL         0.3393       1272.5                50.00   Rv2711, TB
DRB1_0404  171  EHVQGDIDLITRLKD  HVQGDIDLI         0.3392       1274.1                50.00   Rv2711, TB
DRB1_0404  170  TEHVQGDIDLITRLK  HVQGDIDLI         0.3382       1288.2                50.00   Rv2711, TB
DRB1_0404  192  ARVTVETTPGGGVTI  RVTVETTPG         0.3371       1303.4                50.00   Rv2711, TB
DRB1_0404  201  GGGVTIVIPGHENVT  GVTIVIPGH         0.3357       1323.2                50.00   Rv2711, TB
DRB1_0404  128  GNPIPGLVELGVGPE  PIPGLVELG         0.3344       1341.6                50.00   Rv2711, TB
DRB1_0404  187  GVVPNARVTVETTPG  VVPNARVTV         0.3341       1346.0                50.00   Rv2711, TB
DRB1_0404  127  FGNPIPGLVELGVGP  PIPGLVELG         0.3316       1383.2                50.00   Rv2711, TB
DRB1_0404   76  RKHRLAERLLVDVIG  HRLAERLLV         0.3308       1394.5                50.00   Rv2711, TB
DRB1_0404  169  LTEHVQGDIDLITRL  EHVQGDIDL         0.3294       1416.2                50.00   Rv2711, TB
DRB1_0404  129  NPIPGLVELGVGPEP  PIPGLVELG         0.3275       1445.3                50.00   Rv2711, TB
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DRB1_0404  206  IVIPGHENVTLPHEM  IVIPGHENV        0.3217       1539.8              50.00   Rv2711, TB
DRB1_0404   85  LVDVIGLPWEEVHAE  LVDVIGLPW        0.3198       1570.7              50.00   Rv2711, TB
DRB1_0404  174  QGDIDLITRLKDAGV  LITRLKDAG        0.3171       1618.1              50.00   Rv2711, TB
DRB1_0404   48  ERDGLLRVAGDRHLE  GLLRVAGDR        0.3170       1619.0              50.00   Rv2711, TB
DRB1_0404  165  VVRQLTEHVQGDIDL  VVRQLTEHV        0.3164       1629.5              50.00   Rv2711, TB
DRB1_0404  125  SPFGNPIPGLVELGV  PIPGLVELG        0.3099       1749.0              50.00   Rv2711, TB
DRB1_0404   62  ELTEKGRALAIAVMR  RALAIAVMR        0.3057       1830.7              50.00   Rv2711, TB
DRB1_0404   52  LLRVAGDRHLELTEK  LRVAGDRHL        0.3053       1838.3              50.00   Rv2711, TB
DRB1_0404  130  PIPGLVELGVGPEPG  PIPGLVELG        0.3053       1838.9              50.00   Rv2711, TB
DRB1_0404  193  RVTVETTPGGGVTIV  RVTVETTPG        0.3043       1858.0              50.00   Rv2711, TB
DRB1_0404  172  HVQGDIDLITRLKDA  HVQGDIDLI        0.2976       1997.0              50.00   Rv2711, TB
DRB1_0404  168  QLTEHVQGDIDLITR  EHVQGDIDL        0.2957       2039.2              50.00   Rv2711, TB
DRB1_0404  186  AGVVPNARVTVETTP  VVPNARVTV        0.2942       2071.8              50.00   Rv2711, TB
DRB1_0404  152  RLTELPAGSPVAVVV  RLTELPAGS        0.2942       2072.5              50.00   Rv2711, TB
DRB1_0404  200  PGGGVTIVIPGHENV  GVTIVIPGH        0.2889       2194.8              50.00   Rv2711, TB
DRB1_0404  158  AGSPVAVVVRQLTEH  VAVVVRQLT        0.2882       2212.0              50.00   Rv2711, TB
DRB1_0404  180  ITRLKDAGVVPNARV  TRLKDAGVV        0.2858       2268.7              50.00   Rv2711, TB
DRB1_0404   47  MERDGLLRVAGDRHL  GLLRVAGDR        0.2858       2268.8              50.00   Rv2711, TB
DRB1_0404  185  DAGVVPNARVTVETT  VVPNARVTV        0.2794       2431.3              50.00   Rv2711, TB
DRB1_0404  143  PGADDANLVRLTELP  NLVRLTELP        0.2790       2444.1              50.00   Rv2711, TB
DRB1_0404   75  MRKHRLAERLLVDVI  HRLAERLLV        0.2764       2512.4              50.00   Rv2711, TB
DRB1_0404   87  DVIGLPWEEVHAEAC  VIGLPWEEV        0.2746       2561.4              50.00   Rv2711, TB
DRB1_0404  124  TSPFGNPIPGLVELG  PFGNPIPGL        0.2745       2563.8              50.00   Rv2711, TB
DRB1_0404   86  VDVIGLPWEEVHAEA  VIGLPWEEV        0.2718       2641.2              50.00   Rv2711, TB
DRB1_0404   99  EACRWEHVMSEDVER  EACRWEHVM        0.2715       2650.9              50.00   Rv2711, TB
DRB1_0404  181  TRLKDAGVVPNARVT  TRLKDAGVV        0.2710       2664.0              50.00   Rv2711, TB
DRB1_0404  173  VQGDIDLITRLKDAG  LITRLKDAG        0.2647       2853.4              50.00   Rv2711, TB
DRB1_0404   97  HAEACRWEHVMSEDV  EACRWEHVM        0.2627       2914.9              50.00   Rv2711, TB
DRB1_0404   53  LRVAGDRHLELTEKG  LRVAGDRHL        0.2602       2993.9              50.00   Rv2711, TB
DRB1_0404  167  RQLTEHVQGDIDLIT  HVQGDIDLI        0.2573       3088.2              50.00   Rv2711, TB
DRB1_0404   98  AEACRWEHVMSEDVE  EACRWEHVM        0.2566       3112.0              50.00   Rv2711, TB
DRB1_0404   74  VMRKHRLAERLLVDV  HRLAERLLV        0.2521       3267.7              50.00   Rv2711, TB
DRB1_0404   28  RIAERLDQSGPTVSQ  RIAERLDQS        0.2504       3328.8              50.00   Rv2711, TB
DRB1_0404   88  VIGLPWEEVHAEACR  VIGLPWEEV        0.2490       3379.3              50.00   Rv2711, TB
DRB1_0404  131  IPGLVELGVGPEPGA  GLVELGVGP        0.2480       3418.5              50.00   Rv2711, TB
DRB1_0404   27  ARIAERLDQSGPTVS  RIAERLDQS        0.2449       3533.3              50.00   Rv2711, TB
DRB1_0404  123  TTSPFGNPIPGLVEL  TTSPFGNPI        0.2447       3540.2              50.00   Rv2711, TB
DRB1_0404  153  LTELPAGSPVAVVVR  ELPAGSPVA        0.2440       3567.0              50.00   Rv2711, TB
DRB1_0404  122  PTTSPFGNPIPGLVE  TTSPFGNPI        0.2435       3587.4              50.00   Rv2711, TB
DRB1_0404  118  VLNNPTTSPFGNPIP  VLNNPTTSP        0.2433       3593.5              50.00   Rv2711, TB
DRB1_0404   96  VHAEACRWEHVMSED  EACRWEHVM        0.2408       3693.9              50.00   Rv2711, TB
DRB1_0404   46  RMERDGLLRVAGDRH  GLLRVAGDR        0.2396       3741.9              50.00   Rv2711, TB
DRB1_0404  199  TPGGGVTIVIPGHEN  GVTIVIPGH        0.2378       3814.7              50.00   Rv2711, TB
DRB1_0404   20  EGVTPLRARIAERLD  VTPLRARIA        0.2370       3848.2              50.00   Rv2711, TB
DRB1_0404  182  RLKDAGVVPNARVTV  LKDAGVVPN        0.2360       3891.7              50.00   Rv2711, TB
DRB1_0404  121  NPTTSPFGNPIPGLV  TTSPFGNPI        0.2335       3997.9              50.00   Rv2711, TB
DRB1_0404  184  KDAGVVPNARVTVET  VVPNARVTV        0.2322       4055.6              50.00   Rv2711, TB
DRB1_0404   19  EEGVTPLRARIAERL  VTPLRARIA        0.2302       4144.4              50.00   Rv2711, TB
DRB1_0404   30  AERLDQSGPTVSQTV  RLDQSGPTV        0.2273       4272.6              50.00   Rv2711, TB
DRB1_0404  132  PGLVELGVGPEPGAD  GLVELGVGP        0.2267       4300.2              50.00   Rv2711, TB
DRB1_0404   26  RARIAERLDQSGPTV  RIAERLDQS        0.2263       4321.5              50.00   Rv2711, TB
DRB1_0404   32  RLDQSGPTVSQTVSR  RLDQSGPTV        0.2253       4369.7              50.00   Rv2711, TB
DRB1_0404   29  IAERLDQSGPTVSQT  RLDQSGPTV        0.2247       4398.2              50.00   Rv2711, TB
DRB1_0404  154  TELPAGSPVAVVVRQ  ELPAGSPVA        0.2243       4413.4              50.00   Rv2711, TB
DRB1_0404   71  AIAVMRKHRLAERLL  IAVMRKHRL        0.2240       4429.3              50.00   Rv2711, TB
DRB1_0404   21  GVTPLRARIAERLDQ  VTPLRARIA        0.2229       4483.4              50.00   Rv2711, TB
DRB1_0404  157  PAGSPVAVVVRQLTE  VAVVVRQLT        0.2204       4608.0              50.00   Rv2711, TB
DRB1_0404  183  LKDAGVVPNARVTVE  VVPNARVTV        0.2202       4616.3              50.00   Rv2711, TB
DRB1_0404  155  ELPAGSPVAVVVRQL  ELPAGSPVA        0.2197       4642.4              50.00   Rv2711, TB
DRB1_0404   36  SGPTVSQTVSRMERD  PTVSQTVSR        0.2195       4653.1              50.00   Rv2711, TB
DRB1_0404  120  NNPTTSPFGNPIPGL  TTSPFGNPI        0.2193       4660.7              50.00   Rv2711, TB
DRB1_0404   31  ERLDQSGPTVSQTVS  RLDQSGPTV        0.2186       4697.0              50.00   Rv2711, TB
DRB1_0404   61  LELTEKGRALAIAVM  KGRALAIAV        0.2172       4766.2              50.00   Rv2711, TB
DRB1_0404  207  VIPGHENVTLPHEMA  VIPGHENVT        0.2161       4823.5              50.00   Rv2711, TB
DRB1_0404  133  GLVELGVGPEPGADD  GLVELGVGP        0.2159       4835.4              50.00   Rv2711, TB
DRB1_0404   73  AVMRKHRLAERLLVD  HRLAERLLV        0.2149       4890.2              50.00   Rv2711, TB
DRB1_0404   38  PTVSQTVSRMERDGL  PTVSQTVSR        0.2139       4942.5              50.00   Rv2711, TB
DRB1_0404   18  EEEGVTPLRARIAER  VTPLRARIA        0.2129       4996.1              50.00   Rv2711, TB
DRB1_0404   37  GPTVSQTVSRMERDG  PTVSQTVSR        0.2111       5093.5              50.00   Rv2711, TB
DRB1_0404  100  ACRWEHVMSEDVERR  HVMSEDVER        0.2106       5118.4              50.00   Rv2711, TB
DRB1_0404   22  VTPLRARIAERLDQS  VTPLRARIA        0.2102       5141.4              50.00   Rv2711, TB
DRB1_0404   72  IAVMRKHRLAERLLV  IAVMRKHRL        0.2097       5168.6              50.00   Rv2711, TB
DRB1_0404   45  SRMERDGLLRVAGDR  DGLLRVAGD        0.2082       5258.2              50.00   Rv2711, TB
DRB1_0404  166  VRQLTEHVQGDIDLI  HVQGDIDLI        0.2066       5348.6              50.00   Rv2711, TB
DRB1_0404   95  EVHAEACRWEHVMSE  EACRWEHVM        0.2065       5351.6              50.00   Rv2711, TB
DRB1_0404  215  TLPHEMAHAVKVEKV  HEMAHAVKV        0.2055       5412.7              50.00   Rv2711, TB
DRB1_0404  119  LNNPTTSPFGNPIPG  PTTSPFGNP        0.2054       5419.3              50.00   Rv2711, TB
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   DRB1_0404   35  QSGPTVSQTVSRMER  PTVSQTVSR        0.2034       5536.8               50.00   Rv2711, TB
   DRB1_0404  198  TTPGGGVTIVIPGHE  GVTIVIPGH        0.2010       5680.6               50.00   Rv2711, TB
   DRB1_0404  102  RWEHVMSEDVERRLV  HVMSEDVER        0.2000       5741.9               50.00   Rv2711, TB
   DRB1_0404   17  LEEEGVTPLRARIAE  VTPLRARIA        0.1982       5857.3               50.00   Rv2711, TB
   DRB1_0404  213  NVTLPHEMAHAVKVE  NVTLPHEMA        0.1960       5996.3               50.00   Rv2711, TB
   DRB1_0404  101  CRWEHVMSEDVERRL  HVMSEDVER        0.1879       6546.7               50.00   Rv2711, TB
   DRB1_0404   44  VSRMERDGLLRVAGD  RMERDGLLR        0.1867       6632.2               50.00   Rv2711, TB
   DRB1_0404  103  WEHVMSEDVERRLVK  HVMSEDVER        0.1859       6688.1               50.00   Rv2711, TB
   DRB1_0404  212  ENVTLPHEMAHAVKV  NVTLPHEMA        0.1859       6690.7               50.00   Rv2711, TB
   DRB1_0404  214  VTLPHEMAHAVKVEK  HEMAHAVKV        0.1845       6790.8               50.00   Rv2711, TB
   DRB1_0404  105  HVMSEDVERRLVKVL  HVMSEDVER        0.1820       6977.5               50.00   Rv2711, TB
   DRB1_0404   94  EEVHAEACRWEHVMS  EACRWEHVM        0.1794       7174.9               50.00   Rv2711, TB
   DRB1_0404   25  LRARIAERLDQSGPT  RIAERLDQS        0.1784       7257.6               50.00   Rv2711, TB
   DRB1_0404   34  DQSGPTVSQTVSRME  PTVSQTVSR        0.1776       7315.6               50.00   Rv2711, TB
   DRB1_0404  134  LVELGVGPEPGADDA  LVELGVGPE        0.1769       7373.4               50.00   Rv2711, TB
   DRB1_0404  104  EHVMSEDVERRLVKV  HVMSEDVER        0.1758       7461.8               50.00   Rv2711, TB
   DRB1_0404   33  LDQSGPTVSQTVSRM  PTVSQTVSR        0.1743       7587.7               50.00   Rv2711, TB
   DRB1_0404   23  TPLRARIAERLDQSG  RIAERLDQS        0.1740       7608.6               50.00   Rv2711, TB
   DRB1_0404  156  LPAGSPVAVVVRQLT  VAVVVRQLT        0.1723       7749.7               50.00   Rv2711, TB
   DRB1_0404  106  VMSEDVERRLVKVLN  VERRLVKVL        0.1722       7760.6               50.00   Rv2711, TB
   DRB1_0404   16  DLEEEGVTPLRARIA  LEEEGVTPL        0.1698       7960.7               50.00   Rv2711, TB
   DRB1_0404   24  PLRARIAERLDQSGP  RIAERLDQS        0.1690       8035.1               50.00   Rv2711, TB
   DRB1_0404   43  TVSRMERDGLLRVAG  RMERDGLLR        0.1670       8212.0               50.00   Rv2711, TB
   DRB1_0404  211  HENVTLPHEMAHAVK  NVTLPHEMA        0.1621       8657.0               50.00   Rv2711, TB
   DRB1_0404   60  HLELTEKGRALAIAV  KGRALAIAV        0.1610       8759.9               50.00   Rv2711, TB
   DRB1_0404  197  ETTPGGGVTIVIPGH  GVTIVIPGH        0.1609       8764.2               50.00   Rv2711, TB
   DRB1_0404   39  TVSQTVSRMERDGLL  TVSQTVSRM        0.1590       8946.5               50.00   Rv2711, TB
   DRB1_0404   89  IGLPWEEVHAEACRW  IGLPWEEVH        0.1558       9265.6               50.00   Rv2711, TB
   DRB1_0404  210  GHENVTLPHEMAHAV  NVTLPHEMA        0.1554       9309.3               50.00   Rv2711, TB
   DRB1_0404   42  QTVSRMERDGLLRVA  VSRMERDGL        0.1507       9792.2               50.00   Rv2711, TB
   DRB1_0404   11  LRTIYDLEEEGVTPL  LRTIYDLEE        0.1470      10191.2               50.00   Rv2711, TB
   DRB1_0404   41  SQTVSRMERDGLLRV  VSRMERDGL        0.1417      10793.8               50.00   Rv2711, TB
   DRB1_0404  142  EPGADDANLVRLTEL  EPGADDANL        0.1380      11230.1               50.00   Rv2711, TB
   DRB1_0404   57  GDRHLELTEKGRALA  RHLELTEKG        0.1375      11294.8               50.00   Rv2711, TB
   DRB1_0404   58  DRHLELTEKGRALAI  RHLELTEKG        0.1332      11826.9               50.00   Rv2711, TB
   DRB1_0404   56  AGDRHLELTEKGRAL  RHLELTEKG        0.1325      11924.4               50.00   Rv2711, TB
   DRB1_0404  208  IPGHENVTLPHEMAH  IPGHENVTL        0.1309      12128.2               50.00   Rv2711, TB
   DRB1_0404  194  VTVETTPGGGVTIVI  VTVETTPGG        0.1243      13026.3               50.00   Rv2711, TB
   DRB1_0404  209  PGHENVTLPHEMAHA  NVTLPHEMA        0.1237      13110.2               50.00   Rv2711, TB
   DRB1_0404   15  YDLEEEGVTPLRARI  LEEEGVTPL        0.1232      13178.4               50.00   Rv2711, TB
   DRB1_0404   40  VSQTVSRMERDGLLR  VSRMERDGL        0.1222      13323.4               50.00   Rv2711, TB
   DRB1_0404   93  WEEVHAEACRWEHVM  EACRWEHVM        0.1211      13482.8               50.00   Rv2711, TB
   DRB1_0404  135  VELGVGPEPGADDAN  ELGVGPEPG        0.1208      13531.6               50.00   Rv2711, TB
   DRB1_0404   55  VAGDRHLELTEKGRA  RHLELTEKG        0.1201      13638.0               50.00   Rv2711, TB
   DRB1_0404   59  RHLELTEKGRALAIA  RHLELTEKG        0.1200      13644.5               50.00   Rv2711, TB
   DRB1_0404   54  RVAGDRHLELTEKGR  RHLELTEKG        0.1167      14138.5               50.00   Rv2711, TB
   DRB1_0404   14  IYDLEEEGVTPLRAR  LEEEGVTPL        0.1110      15044.7               50.00   Rv2711, TB
   DRB1_0404  136  ELGVGPEPGADDANL  ELGVGPEPG        0.1108      15073.4               50.00   Rv2711, TB
   DRB1_0404   12  RTIYDLEEEGVTPLR  TIYDLEEEG        0.1045      16147.2               50.00   Rv2711, TB
   DRB1_0404   13  TIYDLEEEGVTPLRA  TIYDLEEEG        0.1028      16434.5               50.00   Rv2711, TB
   DRB1_0404  196  VETTPGGGVTIVIPG  GGVTIVIPG        0.0991      17106.7               50.00   Rv2711, TB
   DRB1_0404  137  LGVGPEPGADDANLV  LGVGPEPGA        0.0974      17434.6               50.00   Rv2711, TB
   DRB1_0404   90  GLPWEEVHAEACRWE  GLPWEEVHA        0.0910      18688.7               50.00   Rv2711, TB
   DRB1_0404  141  PEPGADDANLVRLTE  EPGADDANL        0.0906      18750.7               50.00   Rv2711, TB
   DRB1_0404  140  GPEPGADDANLVRLT  EPGADDANL        0.0894      19000.9               50.00   Rv2711, TB
   DRB1_0404  139  VGPEPGADDANLVRL  EPGADDANL        0.0871      19476.1               50.00   Rv2711, TB
   DRB1_0404  195  TVETTPGGGVTIVIP  TTPGGGVTI        0.0868      19549.8               50.00   Rv2711, TB
   DRB1_0404   92  PWEEVHAEACRWEHV  EVHAEACRW        0.0823      20518.1               50.00   Rv2711, TB
   DRB1_0404  138  GVGPEPGADDANLVR  EPGADDANL        0.0760      21979.2               50.00   Rv2711, TB
   DRB1_0404   91  LPWEEVHAEACRWEH  EVHAEACRW        0.0726      22794.5               50.00   Rv2711, TB
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Allele: DRB1_0404. Number of high binders 10. Number of weak binders 26. Number of peptides 216

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      Allele  pos         peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0405  111  VERRLVKVLNNPTTS  LVKVLNNPT        0.7370         17.2         SB     2.00   Rv2711, TB
   DRB1_0405  112  ERRLVKVLNNPTTSP  LVKVLNNPT        0.7345         17.7         SB     2.00   Rv2711, TB
   DRB1_0405  110  DVERRLVKVLNNPTT  LVKVLNNPT        0.7336         17.9         SB     2.00   Rv2711, TB
   DRB1_0405  113  RRLVKVLNNPTTSPF  LVKVLNNPT        0.7236         19.9         SB     2.00   Rv2711, TB
   DRB1_0405    6  TTEMYLRTIYDLEEE  EMYLRTIYD        0.7219         20.3         SB     2.00   Rv2711, TB
   DRB1_0405    5  DTTEMYLRTIYDLEE  EMYLRTIYD        0.7131         22.3         SB     2.00   Rv2711, TB
   DRB1_0405  109  EDVERRLVKVLNNPT  LVKVLNNPT        0.7075         23.7         SB     4.00   Rv2711, TB
   DRB1_0405    7  TEMYLRTIYDLEEEG  EMYLRTIYD        0.6963         26.7         SB     4.00   Rv2711, TB
   DRB1_0405   99  EACRWEHVMSEDVER  CRWEHVMSE        0.6940         27.4         SB     4.00   Rv2711, TB
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DRB1_0405  100  ACRWEHVMSEDVERR  CRWEHVMSE        0.6881        29.2         SB     4.00   Rv2711, TB
DRB1_0405   98  AEACRWEHVMSEDVE  CRWEHVMSE        0.6819        31.2         SB     4.00   Rv2711, TB
DRB1_0405    8  EMYLRTIYDLEEEGV  EMYLRTIYD        0.6775        32.8         SB     4.00   Rv2711, TB
DRB1_0405    4  VDTTEMYLRTIYDLE  EMYLRTIYD        0.6651        37.5         SB     8.00   Rv2711, TB
DRB1_0405  114  RLVKVLNNPTTSPFG  LVKVLNNPT        0.6640        37.9         SB     8.00   Rv2711, TB
DRB1_0405   97  HAEACRWEHVMSEDV  CRWEHVMSE        0.6505        43.9         SB     8.00   Rv2711, TB
DRB1_0405  147  DANLVRLTELPAGSP  LVRLTELPA        0.6488        44.7         SB     8.00   Rv2711, TB
DRB1_0405  101  CRWEHVMSEDVERRL  CRWEHVMSE        0.6464        45.9         SB     8.00   Rv2711, TB
DRB1_0405  148  ANLVRLTELPAGSPV  LVRLTELPA        0.6450        46.6         SB     8.00   Rv2711, TB
DRB1_0405  149  NLVRLTELPAGSPVA  LVRLTELPA        0.6277        56.2         WB     8.00   Rv2711, TB
DRB1_0405    3  LVDTTEMYLRTIYDL  EMYLRTIYD        0.6255        57.5         WB    16.00   Rv2711, TB
DRB1_0405  146  DDANLVRLTELPAGS  LVRLTELPA        0.6203        60.9         WB    16.00   Rv2711, TB
DRB1_0405    2  ELVDTTEMYLRTIYD  EMYLRTIYD        0.6183        62.2         WB    16.00   Rv2711, TB
DRB1_0405  115  LVKVLNNPTTSPFGN  VKVLNNPTT        0.6141        65.0         WB    16.00   Rv2711, TB
DRB1_0405  108  SEDVERRLVKVLNNP  RRLVKVLNN        0.5933        81.5         WB    16.00   Rv2711, TB
DRB1_0405  150  LVRLTELPAGSPVAV  LVRLTELPA        0.5881        86.2         WB    16.00   Rv2711, TB
DRB1_0405  145  ADDANLVRLTELPAG  LVRLTELPA        0.5782        96.0         WB    16.00   Rv2711, TB
DRB1_0405    9  MYLRTIYDLEEEGVT  YLRTIYDLE        0.5669       108.4         WB    16.00   Rv2711, TB
DRB1_0405   96  VHAEACRWEHVMSED  CRWEHVMSE        0.5391       146.5         WB    32.00   Rv2711, TB
DRB1_0405  107  MSEDVERRLVKVLNN  RRLVKVLNN        0.5247       171.2         WB    32.00   Rv2711, TB
DRB1_0405  102  RWEHVMSEDVERRLV  WEHVMSEDV        0.5151       189.8         WB    32.00   Rv2711, TB
DRB1_0405  177  IDLITRLKDAGVVPN  TRLKDAGVV        0.5141       192.0         WB    32.00   Rv2711, TB
DRB1_0405   82  ERLLVDVIGLPWEEV  LLVDVIGLP        0.5117       197.0         WB    32.00   Rv2711, TB
DRB1_0405  178  DLITRLKDAGVVPNA  TRLKDAGVV        0.5106       199.4         WB    32.00   Rv2711, TB
DRB1_0405   83  RLLVDVIGLPWEEVH  LLVDVIGLP        0.5096       201.6         WB    32.00   Rv2711, TB
DRB1_0405  176  DIDLITRLKDAGVVP  ITRLKDAGV        0.5068       207.8         WB    32.00   Rv2711, TB
DRB1_0405   10  YLRTIYDLEEEGVTP  YLRTIYDLE        0.5058       210.0         WB    32.00   Rv2711, TB
DRB1_0405   81  AERLLVDVIGLPWEE  RLLVDVIGL        0.4986       226.9         WB    32.00   Rv2711, TB
DRB1_0405  179  LITRLKDAGVVPNAR  TRLKDAGVV        0.4882       254.0         WB    32.00   Rv2711, TB
DRB1_0405    0  MNELVDTTEMYLRTI  LVDTTEMYL        0.4855       261.7         WB    32.00   Rv2711, TB
DRB1_0405    1  NELVDTTEMYLRTIY  LVDTTEMYL        0.4842       265.4         WB    32.00   Rv2711, TB
DRB1_0405   84  LLVDVIGLPWEEVHA  LLVDVIGLP        0.4805       276.0         WB    32.00   Rv2711, TB
DRB1_0405  175  GDIDLITRLKDAGVV  ITRLKDAGV        0.4802       277.2         WB    32.00   Rv2711, TB
DRB1_0405  116  VKVLNNPTTSPFGNP  VKVLNNPTT        0.4724       301.4         WB    50.00   Rv2711, TB
DRB1_0405  180  ITRLKDAGVVPNARV  RLKDAGVVP        0.4722       302.2         WB    50.00   Rv2711, TB
DRB1_0405   80  LAERLLVDVIGLPWE  RLLVDVIGL        0.4710       305.9         WB    50.00   Rv2711, TB
DRB1_0405  144  GADDANLVRLTELPA  LVRLTELPA        0.4612       340.3         WB    50.00   Rv2711, TB
DRB1_0405   79  RLAERLLVDVIGLPW  RLLVDVIGL        0.4537       368.9         WB    50.00   Rv2711, TB
DRB1_0405  162  VAVVVRQLTEHVQGD  VVRQLTEHV        0.4499       384.4         WB    50.00   Rv2711, TB
DRB1_0405  163  AVVVRQLTEHVQGDI  VVRQLTEHV        0.4497       385.4         WB    50.00   Rv2711, TB
DRB1_0405  181  TRLKDAGVVPNARVT  RLKDAGVVP        0.4427       415.9         WB    50.00   Rv2711, TB
DRB1_0405  171  EHVQGDIDLITRLKD  EHVQGDIDL        0.4365       444.7         WB    50.00   Rv2711, TB
DRB1_0405   95  EVHAEACRWEHVMSE  CRWEHVMSE        0.4353       450.4         WB    50.00   Rv2711, TB
DRB1_0405  161  PVAVVVRQLTEHVQG  VVRQLTEHV        0.4301       476.2         WB    50.00   Rv2711, TB
DRB1_0405  164  VVVRQLTEHVQGDID  VVRQLTEHV        0.4266       494.7         WB    50.00   Rv2711, TB
DRB1_0405  174  QGDIDLITRLKDAGV  DIDLITRLK        0.4264       495.7         WB    50.00   Rv2711, TB
DRB1_0405   78  HRLAERLLVDVIGLP  RLLVDVIGL        0.4264       495.8         WB    50.00   Rv2711, TB
DRB1_0405   77  KHRLAERLLVDVIGL  LAERLLVDV        0.4185       540.3               50.00   Rv2711, TB
DRB1_0405  169  LTEHVQGDIDLITRL  HVQGDIDLI        0.4179       543.3               50.00   Rv2711, TB
DRB1_0405  170  TEHVQGDIDLITRLK  HVQGDIDLI        0.4172       547.5               50.00   Rv2711, TB
DRB1_0405   45  SRMERDGLLRVAGDR  RMERDGLLR        0.4155       558.1               50.00   Rv2711, TB
DRB1_0405   44  VSRMERDGLLRVAGD  RMERDGLLR        0.4149       561.4               50.00   Rv2711, TB
DRB1_0405   85  LVDVIGLPWEEVHAE  VDVIGLPWE        0.4108       586.8               50.00   Rv2711, TB
DRB1_0405  168  QLTEHVQGDIDLITR  HVQGDIDLI        0.4094       596.0               50.00   Rv2711, TB
DRB1_0405  172  HVQGDIDLITRLKDA  IDLITRLKD        0.4065       615.3               50.00   Rv2711, TB
DRB1_0405  160  SPVAVVVRQLTEHVQ  VVVRQLTEH        0.4058       619.5               50.00   Rv2711, TB
DRB1_0405   88  VIGLPWEEVHAEACR  GLPWEEVHA        0.4009       653.4               50.00   Rv2711, TB
DRB1_0405   50  DGLLRVAGDRHLELT  LLRVAGDRH        0.3992       665.5               50.00   Rv2711, TB
DRB1_0405   46  RMERDGLLRVAGDRH  RMERDGLLR        0.3985       670.6               50.00   Rv2711, TB
DRB1_0405  173  VQGDIDLITRLKDAG  DIDLITRLK        0.3962       687.4               50.00   Rv2711, TB
DRB1_0405  126  PFGNPIPGLVELGVG  FGNPIPGLV        0.3948       697.7               50.00   Rv2711, TB
DRB1_0405   86  VDVIGLPWEEVHAEA  VDVIGLPWE        0.3941       703.1               50.00   Rv2711, TB
DRB1_0405  125  SPFGNPIPGLVELGV  FGNPIPGLV        0.3925       715.2               50.00   Rv2711, TB
DRB1_0405   49  RDGLLRVAGDRHLEL  LLRVAGDRH        0.3905       730.8               50.00   Rv2711, TB
DRB1_0405  127  FGNPIPGLVELGVGP  FGNPIPGLV        0.3900       735.2               50.00   Rv2711, TB
DRB1_0405   89  IGLPWEEVHAEACRW  LPWEEVHAE        0.3892       741.5               50.00   Rv2711, TB
DRB1_0405  167  RQLTEHVQGDIDLIT  HVQGDIDLI        0.3880       751.3               50.00   Rv2711, TB
DRB1_0405   87  DVIGLPWEEVHAEAC  LPWEEVHAE        0.3874       756.0               50.00   Rv2711, TB
DRB1_0405   48  ERDGLLRVAGDRHLE  LLRVAGDRH        0.3856       770.8               50.00   Rv2711, TB
DRB1_0405  207  VIPGHENVTLPHEMA  HENVTLPHE        0.3830       793.3               50.00   Rv2711, TB
DRB1_0405   47  MERDGLLRVAGDRHL  DGLLRVAGD        0.3828       795.1               50.00   Rv2711, TB
DRB1_0405   76  RKHRLAERLLVDVIG  RLAERLLVD        0.3800       819.4               50.00   Rv2711, TB
DRB1_0405   64  TEKGRALAIAVMRKH  GRALAIAVM        0.3782       835.0               50.00   Rv2711, TB
DRB1_0405  208  IPGHENVTLPHEMAH  GHENVTLPH        0.3782       835.1               50.00   Rv2711, TB
DRB1_0405   51  GLLRVAGDRHLELTE  LLRVAGDRH        0.3775       841.3               50.00   Rv2711, TB
DRB1_0405   63  LTEKGRALAIAVMRK  KGRALAIAV        0.3718       894.9               50.00   Rv2711, TB
DRB1_0405   65  EKGRALAIAVMRKHR  GRALAIAVM        0.3680       932.3               50.00   Rv2711, TB
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DRB1_0405  159  GSPVAVVVRQLTEHV  VVVRQLTEH         0.3669         944.4                 50.00   Rv2711, TB
DRB1_0405   52  LLRVAGDRHLELTEK  LRVAGDRHL         0.3661         952.5                 50.00   Rv2711, TB
DRB1_0405  124  TSPFGNPIPGLVELG  FGNPIPGLV         0.3655         958.2                 50.00   Rv2711, TB
DRB1_0405  206  IVIPGHENVTLPHEM  GHENVTLPH         0.3650         963.7                 50.00   Rv2711, TB
DRB1_0405  209  PGHENVTLPHEMAHA  HENVTLPHE         0.3646         967.9                 50.00   Rv2711, TB
DRB1_0405  205  TIVIPGHENVTLPHE  TIVIPGHEN         0.3633         981.8                 50.00   Rv2711, TB
DRB1_0405   11  LRTIYDLEEEGVTPL  LRTIYDLEE         0.3612        1004.0                 50.00   Rv2711, TB
DRB1_0405  165  VVRQLTEHVQGDIDL  VVRQLTEHV         0.3604        1013.0                 50.00   Rv2711, TB
DRB1_0405   20  EGVTPLRARIAERLD  GVTPLRARI         0.3602        1015.0                 50.00   Rv2711, TB
DRB1_0405  199  TPGGGVTIVIPGHEN  GGVTIVIPG         0.3587        1030.9                 50.00   Rv2711, TB
DRB1_0405  200  PGGGVTIVIPGHENV  GGVTIVIPG         0.3581        1038.6                 50.00   Rv2711, TB
DRB1_0405  201  GGGVTIVIPGHENVT  GGVTIVIPG         0.3578        1042.0                 50.00   Rv2711, TB
DRB1_0405  151  VRLTELPAGSPVAVV  VRLTELPAG         0.3576        1044.2                 50.00   Rv2711, TB
DRB1_0405  103  WEHVMSEDVERRLVK  WEHVMSEDV         0.3559        1063.6                 50.00   Rv2711, TB
DRB1_0405   66  KGRALAIAVMRKHRL  KGRALAIAV         0.3552        1070.8                 50.00   Rv2711, TB
DRB1_0405   90  GLPWEEVHAEACRWE  LPWEEVHAE         0.3545        1079.8                 50.00   Rv2711, TB
DRB1_0405  182  RLKDAGVVPNARVTV  RLKDAGVVP         0.3530        1097.6                 50.00   Rv2711, TB
DRB1_0405  128  GNPIPGLVELGVGPE  NPIPGLVEL         0.3514        1115.8                 50.00   Rv2711, TB
DRB1_0405  210  GHENVTLPHEMAHAV  GHENVTLPH         0.3503        1129.9                 50.00   Rv2711, TB
DRB1_0405  166  VRQLTEHVQGDIDLI  VRQLTEHVQ         0.3490        1145.1                 50.00   Rv2711, TB
DRB1_0405  202  GGVTIVIPGHENVTL  GVTIVIPGH         0.3489        1146.7                 50.00   Rv2711, TB
DRB1_0405   43  TVSRMERDGLLRVAG  MERDGLLRV         0.3471        1169.5                 50.00   Rv2711, TB
DRB1_0405   18  EEEGVTPLRARIAER  GVTPLRARI         0.3471        1170.0                 50.00   Rv2711, TB
DRB1_0405   19  EEGVTPLRARIAERL  GVTPLRARI         0.3468        1173.2                 50.00   Rv2711, TB
DRB1_0405   37  GPTVSQTVSRMERDG  VSQTVSRME         0.3448        1199.4                 50.00   Rv2711, TB
DRB1_0405   36  SGPTVSQTVSRMERD  VSQTVSRME         0.3437        1213.7                 50.00   Rv2711, TB
DRB1_0405  123  TTSPFGNPIPGLVEL  FGNPIPGLV         0.3434        1216.7                 50.00   Rv2711, TB
DRB1_0405   75  MRKHRLAERLLVDVI  RLAERLLVD         0.3432        1219.2                 50.00   Rv2711, TB
DRB1_0405   17  LEEEGVTPLRARIAE  GVTPLRARI         0.3424        1230.7                 50.00   Rv2711, TB
DRB1_0405  129  NPIPGLVELGVGPEP  GLVELGVGP         0.3395        1269.5                 50.00   Rv2711, TB
DRB1_0405  106  VMSEDVERRLVKVLN  VERRLVKVL         0.3375        1297.5                 50.00   Rv2711, TB
DRB1_0405  158  AGSPVAVVVRQLTEH  PVAVVVRQL         0.3350        1333.0                 50.00   Rv2711, TB
DRB1_0405   35  QSGPTVSQTVSRMER  PTVSQTVSR         0.3341        1345.4                 50.00   Rv2711, TB
DRB1_0405   62  ELTEKGRALAIAVMR  GRALAIAVM         0.3294        1416.3                 50.00   Rv2711, TB
DRB1_0405   21  GVTPLRARIAERLDQ  TPLRARIAE         0.3225        1526.5                 50.00   Rv2711, TB
DRB1_0405  117  KVLNNPTTSPFGNPI  KVLNNPTTS         0.3217        1539.0                 50.00   Rv2711, TB
DRB1_0405   67  GRALAIAVMRKHRLA  GRALAIAVM         0.3215        1541.9                 50.00   Rv2711, TB
DRB1_0405   42  QTVSRMERDGLLRVA  SRMERDGLL         0.3213        1545.6                 50.00   Rv2711, TB
DRB1_0405   38  PTVSQTVSRMERDGL  VSQTVSRME         0.3182        1598.6                 50.00   Rv2711, TB
DRB1_0405   34  DQSGPTVSQTVSRME  PTVSQTVSR         0.3131        1689.3                 50.00   Rv2711, TB
DRB1_0405  130  PIPGLVELGVGPEPG  LVELGVGPE         0.3123        1703.8                 50.00   Rv2711, TB
DRB1_0405   16  DLEEEGVTPLRARIA  LEEEGVTPL         0.3111        1726.0                 50.00   Rv2711, TB
DRB1_0405  190  PNARVTVETTPGGGV  NARVTVETT         0.3102        1742.8                 50.00   Rv2711, TB
DRB1_0405   23  TPLRARIAERLDQSG  TPLRARIAE         0.3096        1754.8                 50.00   Rv2711, TB
DRB1_0405   74  VMRKHRLAERLLVDV  RLAERLLVD         0.3088        1769.0                 50.00   Rv2711, TB
DRB1_0405   15  YDLEEEGVTPLRARI  YDLEEEGVT         0.3087        1772.1                 50.00   Rv2711, TB
DRB1_0405  198  TTPGGGVTIVIPGHE  GGVTIVIPG         0.3081        1783.8                 50.00   Rv2711, TB
DRB1_0405  211  HENVTLPHEMAHAVK  HENVTLPHE         0.3072        1801.6                 50.00   Rv2711, TB
DRB1_0405   53  LRVAGDRHLELTEKG  LRVAGDRHL         0.3048        1848.6                 50.00   Rv2711, TB
DRB1_0405  131  IPGLVELGVGPEPGA  LVELGVGPE         0.3044        1855.8                 50.00   Rv2711, TB
DRB1_0405   22  VTPLRARIAERLDQS  TPLRARIAE         0.3035        1874.1                 50.00   Rv2711, TB
DRB1_0405  215  TLPHEMAHAVKVEKV  HEMAHAVKV         0.3031        1881.6                 50.00   Rv2711, TB
DRB1_0405  122  PTTSPFGNPIPGLVE  FGNPIPGLV         0.3007        1931.4                 50.00   Rv2711, TB
DRB1_0405  188  VVPNARVTVETTPGG  NARVTVETT         0.2997        1952.8                 50.00   Rv2711, TB
DRB1_0405  204  VTIVIPGHENVTLPH  IVIPGHENV         0.2994        1959.4                 50.00   Rv2711, TB
DRB1_0405  189  VPNARVTVETTPGGG  NARVTVETT         0.2986        1975.8                 50.00   Rv2711, TB
DRB1_0405  132  PGLVELGVGPEPGAD  LVELGVGPE         0.2972        2007.4                 50.00   Rv2711, TB
DRB1_0405   12  RTIYDLEEEGVTPLR  YDLEEEGVT         0.2965        2022.5                 50.00   Rv2711, TB
DRB1_0405  191  NARVTVETTPGGGVT  RVTVETTPG         0.2964        2023.3                 50.00   Rv2711, TB
DRB1_0405  203  GVTIVIPGHENVTLP  GVTIVIPGH         0.2938        2081.4                 50.00   Rv2711, TB
DRB1_0405   73  AVMRKHRLAERLLVD  RLAERLLVD         0.2909        2148.4                 50.00   Rv2711, TB
DRB1_0405   61  LELTEKGRALAIAVM  KGRALAIAV         0.2899        2170.5                 50.00   Rv2711, TB
DRB1_0405   13  TIYDLEEEGVTPLRA  YDLEEEGVT         0.2896        2177.9                 50.00   Rv2711, TB
DRB1_0405   91  LPWEEVHAEACRWEH  LPWEEVHAE         0.2884        2206.2                 50.00   Rv2711, TB
DRB1_0405   41  SQTVSRMERDGLLRV  SRMERDGLL         0.2852        2285.9                 50.00   Rv2711, TB
DRB1_0405  214  VTLPHEMAHAVKVEK  MAHAVKVEK         0.2818        2371.1                 50.00   Rv2711, TB
DRB1_0405  105  HVMSEDVERRLVKVL  VERRLVKVL         0.2815        2378.3                 50.00   Rv2711, TB
DRB1_0405   14  IYDLEEEGVTPLRAR  YDLEEEGVT         0.2771        2494.5                 50.00   Rv2711, TB
DRB1_0405   68  RALAIAVMRKHRLAE  RALAIAVMR         0.2751        2548.8                 50.00   Rv2711, TB
DRB1_0405  187  GVVPNARVTVETTPG  NARVTVETT         0.2741        2575.8                 50.00   Rv2711, TB
DRB1_0405  197  ETTPGGGVTIVIPGH  GGVTIVIPG         0.2730        2605.9                 50.00   Rv2711, TB
DRB1_0405   40  VSQTVSRMERDGLLR  VSQTVSRME         0.2730        2607.9                 50.00   Rv2711, TB
DRB1_0405   31  ERLDQSGPTVSQTVS  RLDQSGPTV         0.2686        2732.8                 50.00   Rv2711, TB
DRB1_0405   39  TVSQTVSRMERDGLL  VSQTVSRME         0.2681        2750.4                 50.00   Rv2711, TB
DRB1_0405  133  GLVELGVGPEPGADD  LVELGVGPE         0.2661        2809.0                 50.00   Rv2711, TB
DRB1_0405   32  RLDQSGPTVSQTVSR  RLDQSGPTV         0.2656        2822.9                 50.00   Rv2711, TB
DRB1_0405  157  PAGSPVAVVVRQLTE  PVAVVVRQL         0.2615        2952.4                 50.00   Rv2711, TB
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   DRB1_0405   30  AERLDQSGPTVSQTV  RLDQSGPTV        0.2581       3061.8               50.00   Rv2711, TB
   DRB1_0405   94  EEVHAEACRWEHVMS  ACRWEHVMS        0.2559       3135.9               50.00   Rv2711, TB
   DRB1_0405   26  RARIAERLDQSGPTV  RARIAERLD        0.2545       3183.6               50.00   Rv2711, TB
   DRB1_0405   25  LRARIAERLDQSGPT  RARIAERLD        0.2542       3195.7               50.00   Rv2711, TB
   DRB1_0405  183  LKDAGVVPNARVTVE  AGVVPNARV        0.2535       3219.1               50.00   Rv2711, TB
   DRB1_0405  192  ARVTVETTPGGGVTI  RVTVETTPG        0.2528       3245.2               50.00   Rv2711, TB
   DRB1_0405  118  VLNNPTTSPFGNPIP  VLNNPTTSP        0.2526       3252.5               50.00   Rv2711, TB
   DRB1_0405  186  AGVVPNARVTVETTP  NARVTVETT        0.2512       3300.0               50.00   Rv2711, TB
   DRB1_0405   29  IAERLDQSGPTVSQT  RLDQSGPTV        0.2509       3311.4               50.00   Rv2711, TB
   DRB1_0405  213  NVTLPHEMAHAVKVE  LPHEMAHAV        0.2498       3352.4               50.00   Rv2711, TB
   DRB1_0405   33  LDQSGPTVSQTVSRM  PTVSQTVSR        0.2486       3393.3               50.00   Rv2711, TB
   DRB1_0405  212  ENVTLPHEMAHAVKV  VTLPHEMAH        0.2477       3428.3               50.00   Rv2711, TB
   DRB1_0405   72  IAVMRKHRLAERLLV  VMRKHRLAE        0.2456       3507.8               50.00   Rv2711, TB
   DRB1_0405  104  EHVMSEDVERRLVKV  HVMSEDVER        0.2441       3563.0               50.00   Rv2711, TB
   DRB1_0405   24  PLRARIAERLDQSGP  RARIAERLD        0.2438       3577.5               50.00   Rv2711, TB
   DRB1_0405  121  NPTTSPFGNPIPGLV  FGNPIPGLV        0.2432       3597.6               50.00   Rv2711, TB
   DRB1_0405  156  LPAGSPVAVVVRQLT  PVAVVVRQL        0.2381       3805.0               50.00   Rv2711, TB
   DRB1_0405   69  ALAIAVMRKHRLAER  LAIAVMRKH        0.2367       3862.1               50.00   Rv2711, TB
   DRB1_0405  143  PGADDANLVRLTELP  ANLVRLTEL        0.2354       3918.0               50.00   Rv2711, TB
   DRB1_0405  185  DAGVVPNARVTVETT  AGVVPNARV        0.2344       3960.0               50.00   Rv2711, TB
   DRB1_0405   28  RIAERLDQSGPTVSQ  ERLDQSGPT        0.2343       3962.8               50.00   Rv2711, TB
   DRB1_0405   70  LAIAVMRKHRLAERL  IAVMRKHRL        0.2310       4107.4               50.00   Rv2711, TB
   DRB1_0405  142  EPGADDANLVRLTEL  ANLVRLTEL        0.2301       4147.0               50.00   Rv2711, TB
   DRB1_0405  134  LVELGVGPEPGADDA  LVELGVGPE        0.2288       4203.6               50.00   Rv2711, TB
   DRB1_0405  155  ELPAGSPVAVVVRQL  PVAVVVRQL        0.2260       4336.5               50.00   Rv2711, TB
   DRB1_0405   71  AIAVMRKHRLAERLL  VMRKHRLAE        0.2256       4354.1               50.00   Rv2711, TB
   DRB1_0405   27  ARIAERLDQSGPTVS  ERLDQSGPT        0.2222       4516.8               50.00   Rv2711, TB
   DRB1_0405  152  RLTELPAGSPVAVVV  LPAGSPVAV        0.2221       4522.5               50.00   Rv2711, TB
   DRB1_0405  193  RVTVETTPGGGVTIV  RVTVETTPG        0.2211       4572.6               50.00   Rv2711, TB
   DRB1_0405  153  LTELPAGSPVAVVVR  LPAGSPVAV        0.2205       4602.1               50.00   Rv2711, TB
   DRB1_0405  196  VETTPGGGVTIVIPG  GGVTIVIPG        0.2167       4796.0               50.00   Rv2711, TB
   DRB1_0405   60  HLELTEKGRALAIAV  KGRALAIAV        0.2097       5173.3               50.00   Rv2711, TB
   DRB1_0405  141  PEPGADDANLVRLTE  EPGADDANL        0.2082       5256.2               50.00   Rv2711, TB
   DRB1_0405  184  KDAGVVPNARVTVET  AGVVPNARV        0.2074       5302.7               50.00   Rv2711, TB
   DRB1_0405  154  TELPAGSPVAVVVRQ  PAGSPVAVV        0.1983       5848.0               50.00   Rv2711, TB
   DRB1_0405  140  GPEPGADDANLVRLT  EPGADDANL        0.1950       6065.3               50.00   Rv2711, TB
   DRB1_0405  120  NNPTTSPFGNPIPGL  TTSPFGNPI        0.1942       6117.5               50.00   Rv2711, TB
   DRB1_0405   92  PWEEVHAEACRWEHV  PWEEVHAEA        0.1938       6144.0               50.00   Rv2711, TB
   DRB1_0405   55  VAGDRHLELTEKGRA  DRHLELTEK        0.1903       6381.2               50.00   Rv2711, TB
   DRB1_0405  119  LNNPTTSPFGNPIPG  PTTSPFGNP        0.1887       6491.8               50.00   Rv2711, TB
   DRB1_0405   54  RVAGDRHLELTEKGR  DRHLELTEK        0.1876       6569.1               50.00   Rv2711, TB
   DRB1_0405  195  TVETTPGGGVTIVIP  GGGVTIVIP        0.1865       6643.8               50.00   Rv2711, TB
   DRB1_0405   57  GDRHLELTEKGRALA  DRHLELTEK        0.1860       6680.2               50.00   Rv2711, TB
   DRB1_0405   56  AGDRHLELTEKGRAL  GDRHLELTE        0.1841       6822.2               50.00   Rv2711, TB
   DRB1_0405  194  VTVETTPGGGVTIVI  VTVETTPGG        0.1782       7269.5               50.00   Rv2711, TB
   DRB1_0405   59  RHLELTEKGRALAIA  LELTEKGRA        0.1693       8002.6               50.00   Rv2711, TB
   DRB1_0405  139  VGPEPGADDANLVRL  EPGADDANL        0.1676       8158.5               50.00   Rv2711, TB
   DRB1_0405   58  DRHLELTEKGRALAI  LELTEKGRA        0.1562       9224.3               50.00   Rv2711, TB
   DRB1_0405  137  LGVGPEPGADDANLV  PGADDANLV        0.1480      10085.0               50.00   Rv2711, TB
   DRB1_0405   93  WEEVHAEACRWEHVM  WEEVHAEAC        0.1467      10221.5               50.00   Rv2711, TB
   DRB1_0405  135  VELGVGPEPGADDAN  VELGVGPEP        0.1466      10235.0               50.00   Rv2711, TB
   DRB1_0405  138  GVGPEPGADDANLVR  EPGADDANL        0.1448      10440.1               50.00   Rv2711, TB
   DRB1_0405  136  ELGVGPEPGADDANL  ELGVGPEPG        0.1401      10981.5               50.00   Rv2711, TB
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Allele: DRB1_0405. Number of high binders 18. Number of weak binders 38. Number of peptides 216

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0701   47  MERDGLLRVAGDRHL  LRVAGDRHL        0.8705          4.1         SB     1.00   Rv2711, TB
   DRB1_0701   48  ERDGLLRVAGDRHLE  LRVAGDRHL        0.8545          4.8         SB     2.00   Rv2711, TB
   DRB1_0701   49  RDGLLRVAGDRHLEL  LRVAGDRHL        0.8504          5.0         SB     2.00   Rv2711, TB
   DRB1_0701   50  DGLLRVAGDRHLELT  LRVAGDRHL        0.8262          6.6         SB     4.00   Rv2711, TB
   DRB1_0701   51  GLLRVAGDRHLELTE  LRVAGDRHL        0.8090          7.9         SB     4.00   Rv2711, TB
   DRB1_0701   52  LLRVAGDRHLELTEK  LRVAGDRHL        0.7892          9.8         SB     4.00   Rv2711, TB
   DRB1_0701   53  LRVAGDRHLELTEKG  LRVAGDRHL        0.7637         12.9         SB     8.00   Rv2711, TB
   DRB1_0701    0  MNELVDTTEMYLRTI  LVDTTEMYL        0.7233         20.0         SB     8.00   Rv2711, TB
   DRB1_0701    1  NELVDTTEMYLRTIY  LVDTTEMYL        0.7040         24.6         SB    16.00   Rv2711, TB
   DRB1_0701    3  LVDTTEMYLRTIYDL  LVDTTEMYL        0.6915         28.2         SB    16.00   Rv2711, TB
   DRB1_0701    2  ELVDTTEMYLRTIYD  LVDTTEMYL        0.6777         32.7         SB    16.00   Rv2711, TB
   DRB1_0701   19  EEGVTPLRARIAERL  LRARIAERL        0.6401         49.1         SB    16.00   Rv2711, TB
   DRB1_0701   67  GRALAIAVMRKHRLA  IAVMRKHRL        0.6296         55.0         WB    16.00   Rv2711, TB
   DRB1_0701   71  AIAVMRKHRLAERLL  RKHRLAERL        0.6081         69.4         WB    16.00   Rv2711, TB
   DRB1_0701   72  IAVMRKHRLAERLLV  HRLAERLLV        0.6073         70.0         WB    16.00   Rv2711, TB
   DRB1_0701   20  EGVTPLRARIAERLD  LRARIAERL        0.6047         72.0         WB    16.00   Rv2711, TB
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DRB1_0701  159  GSPVAVVVRQLTEHV  VVRQLTEHV        0.5987       76.9        WB    32.00   Rv2711, TB
DRB1_0701  109  EDVERRLVKVLNNPT  LVKVLNNPT        0.5943       80.6        WB    32.00   Rv2711, TB
DRB1_0701   70  LAIAVMRKHRLAERL  RKHRLAERL        0.5873       86.9        WB    32.00   Rv2711, TB
DRB1_0701   66  KGRALAIAVMRKHRL  IAVMRKHRL        0.5869       87.3        WB    32.00   Rv2711, TB
DRB1_0701   68  RALAIAVMRKHRLAE  IAVMRKHRL        0.5820       92.1        WB    32.00   Rv2711, TB
DRB1_0701  110  DVERRLVKVLNNPTT  LVKVLNNPT        0.5753       99.0        WB    32.00   Rv2711, TB
DRB1_0701  175  GDIDLITRLKDAGVV  ITRLKDAGV        0.5706      104.2        WB    32.00   Rv2711, TB
DRB1_0701   21  GVTPLRARIAERLDQ  LRARIAERL        0.5599      117.0        WB    32.00   Rv2711, TB
DRB1_0701   97  HAEACRWEHVMSEDV  WEHVMSEDV        0.5509      128.9        WB    32.00   Rv2711, TB
DRB1_0701  212  ENVTLPHEMAHAVKV  HEMAHAVKV        0.5482      132.7        WB    32.00   Rv2711, TB
DRB1_0701  160  SPVAVVVRQLTEHVQ  VVRQLTEHV        0.5443      138.5        WB    32.00   Rv2711, TB
DRB1_0701  182  RLKDAGVVPNARVTV  VVPNARVTV        0.5283      164.6        WB    32.00   Rv2711, TB
DRB1_0701  155  ELPAGSPVAVVVRQL  PVAVVVRQL        0.5263      168.2        WB    32.00   Rv2711, TB
DRB1_0701  156  LPAGSPVAVVVRQLT  PVAVVVRQL        0.5218      176.7        WB    32.00   Rv2711, TB
DRB1_0701  111  VERRLVKVLNNPTTS  LVKVLNNPT        0.5213      177.6        WB    32.00   Rv2711, TB
DRB1_0701  113  RRLVKVLNNPTTSPF  LNNPTTSPF        0.5206      178.9        WB    32.00   Rv2711, TB
DRB1_0701   73  AVMRKHRLAERLLVD  HRLAERLLV        0.5175      185.0        WB    32.00   Rv2711, TB
DRB1_0701  174  QGDIDLITRLKDAGV  ITRLKDAGV        0.5134      193.4        WB    32.00   Rv2711, TB
DRB1_0701   69  ALAIAVMRKHRLAER  IAVMRKHRL        0.5129      194.5        WB    32.00   Rv2711, TB
DRB1_0701   22  VTPLRARIAERLDQS  LRARIAERL        0.5101      200.4        WB    32.00   Rv2711, TB
DRB1_0701   98  AEACRWEHVMSEDVE  WEHVMSEDV        0.5095      201.7        WB    32.00   Rv2711, TB
DRB1_0701  176  DIDLITRLKDAGVVP  ITRLKDAGV        0.5039      214.3        WB    32.00   Rv2711, TB
DRB1_0701  213  NVTLPHEMAHAVKVE  HEMAHAVKV        0.5035      215.4        WB    32.00   Rv2711, TB
DRB1_0701  200  PGGGVTIVIPGHENV  IVIPGHENV        0.4971      230.7        WB    32.00   Rv2711, TB
DRB1_0701  157  PAGSPVAVVVRQLTE  PVAVVVRQL        0.4929      241.4        WB    32.00   Rv2711, TB
DRB1_0701   99  EACRWEHVMSEDVER  WEHVMSEDV        0.4922      243.3        WB    32.00   Rv2711, TB
DRB1_0701  215  TLPHEMAHAVKVEKV  HEMAHAVKV        0.4917      244.7        WB    32.00   Rv2711, TB
DRB1_0701  181  TRLKDAGVVPNARVT  GVVPNARVT        0.4907      247.3        WB    32.00   Rv2711, TB
DRB1_0701  180  ITRLKDAGVVPNARV  AGVVPNARV        0.4838      266.5        WB    32.00   Rv2711, TB
DRB1_0701  142  EPGADDANLVRLTEL  ANLVRLTEL        0.4826      269.9        WB    32.00   Rv2711, TB
DRB1_0701  183  LKDAGVVPNARVTVE  VVPNARVTV        0.4763      289.1        WB    32.00   Rv2711, TB
DRB1_0701  161  PVAVVVRQLTEHVQG  VVRQLTEHV        0.4723      301.9        WB    32.00   Rv2711, TB
DRB1_0701  114  RLVKVLNNPTTSPFG  LVKVLNNPT        0.4715      304.3        WB    32.00   Rv2711, TB
DRB1_0701  177  IDLITRLKDAGVVPN  ITRLKDAGV        0.4638      330.7        WB    32.00   Rv2711, TB
DRB1_0701   23  TPLRARIAERLDQSG  LRARIAERL        0.4629      334.0        WB    32.00   Rv2711, TB
DRB1_0701  201  GGGVTIVIPGHENVT  IVIPGHENV        0.4611      340.4        WB    32.00   Rv2711, TB
DRB1_0701   74  VMRKHRLAERLLVDV  HRLAERLLV        0.4609      341.4        WB    32.00   Rv2711, TB
DRB1_0701  190  PNARVTVETTPGGGV  VETTPGGGV        0.4609      341.5        WB    32.00   Rv2711, TB
DRB1_0701  101  CRWEHVMSEDVERRL  WEHVMSEDV        0.4553      362.7        WB    32.00   Rv2711, TB
DRB1_0701   16  DLEEEGVTPLRARIA  VTPLRARIA        0.4538      368.4        WB    50.00   Rv2711, TB
DRB1_0701  214  VTLPHEMAHAVKVEK  HEMAHAVKV        0.4480      392.7        WB    50.00   Rv2711, TB
DRB1_0701  100  ACRWEHVMSEDVERR  WEHVMSEDV        0.4473      395.4        WB    50.00   Rv2711, TB
DRB1_0701  112  ERRLVKVLNNPTTSP  LVKVLNNPT        0.4465      399.0        WB    50.00   Rv2711, TB
DRB1_0701  144  GADDANLVRLTELPA  ANLVRLTEL        0.4438      410.7        WB    50.00   Rv2711, TB
DRB1_0701   24  PLRARIAERLDQSGP  LRARIAERL        0.4380      437.1        WB    50.00   Rv2711, TB
DRB1_0701  105  HVMSEDVERRLVKVL  VERRLVKVL        0.4353      450.4        WB    50.00   Rv2711, TB
DRB1_0701  191  NARVTVETTPGGGVT  VETTPGGGV        0.4347      453.5        WB    50.00   Rv2711, TB
DRB1_0701   89  IGLPWEEVHAEACRW  EVHAEACRW        0.4320      466.6        WB    50.00   Rv2711, TB
DRB1_0701  202  GGVTIVIPGHENVTL  IVIPGHENV        0.4320      466.8        WB    50.00   Rv2711, TB
DRB1_0701  184  KDAGVVPNARVTVET  VVPNARVTV        0.4304      474.9        WB    50.00   Rv2711, TB
DRB1_0701  158  AGSPVAVVVRQLTEH  PVAVVVRQL        0.4297      478.7        WB    50.00   Rv2711, TB
DRB1_0701  192  ARVTVETTPGGGVTI  VETTPGGGV        0.4294      479.9        WB    50.00   Rv2711, TB
DRB1_0701   90  GLPWEEVHAEACRWE  EVHAEACRW        0.4255      500.8              50.00   Rv2711, TB
DRB1_0701  178  DLITRLKDAGVVPNA  ITRLKDAGV        0.4254      501.4              50.00   Rv2711, TB
DRB1_0701   25  LRARIAERLDQSGPT  LRARIAERL        0.4249      504.0              50.00   Rv2711, TB
DRB1_0701  102  RWEHVMSEDVERRLV  WEHVMSEDV        0.4221      519.2              50.00   Rv2711, TB
DRB1_0701   75  MRKHRLAERLLVDVI  HRLAERLLV        0.4169      549.7              50.00   Rv2711, TB
DRB1_0701  115  LVKVLNNPTTSPFGN  LVKVLNNPT        0.4151      560.2              50.00   Rv2711, TB
DRB1_0701  143  PGADDANLVRLTELP  ANLVRLTEL        0.4149      561.6              50.00   Rv2711, TB
DRB1_0701  106  VMSEDVERRLVKVLN  VERRLVKVL        0.4062      617.1              50.00   Rv2711, TB
DRB1_0701   17  LEEEGVTPLRARIAE  VTPLRARIA        0.4054      622.0              50.00   Rv2711, TB
DRB1_0701  193  RVTVETTPGGGVTIV  VETTPGGGV        0.4020      645.5              50.00   Rv2711, TB
DRB1_0701   34  DQSGPTVSQTVSRME  TVSQTVSRM        0.3993      664.7              50.00   Rv2711, TB
DRB1_0701  121  NPTTSPFGNPIPGLV  FGNPIPGLV        0.3976      677.0              50.00   Rv2711, TB
DRB1_0701  107  MSEDVERRLVKVLNN  VERRLVKVL        0.3927      714.0              50.00   Rv2711, TB
DRB1_0701  179  LITRLKDAGVVPNAR  ITRLKDAGV        0.3890      743.2              50.00   Rv2711, TB
DRB1_0701  122  PTTSPFGNPIPGLVE  FGNPIPGLV        0.3878      753.1              50.00   Rv2711, TB
DRB1_0701  203  GVTIVIPGHENVTLP  IVIPGHENV        0.3849      777.0              50.00   Rv2711, TB
DRB1_0701  185  DAGVVPNARVTVETT  VVPNARVTV        0.3840      784.0              50.00   Rv2711, TB
DRB1_0701   91  LPWEEVHAEACRWEH  EVHAEACRW        0.3833      790.6              50.00   Rv2711, TB
DRB1_0701  117  KVLNNPTTSPFGNPI  TTSPFGNPI        0.3831      792.3              50.00   Rv2711, TB
DRB1_0701    5  DTTEMYLRTIYDLEE  MYLRTIYDL        0.3824      797.8              50.00   Rv2711, TB
DRB1_0701  194  VTVETTPGGGVTIVI  VETTPGGGV        0.3815      805.6              50.00   Rv2711, TB
DRB1_0701    4  VDTTEMYLRTIYDLE  MYLRTIYDL        0.3789      828.8              50.00   Rv2711, TB
DRB1_0701  103  WEHVMSEDVERRLVK  WEHVMSEDV        0.3769      847.3              50.00   Rv2711, TB
DRB1_0701   79  RLAERLLVDVIGLPW  LVDVIGLPW        0.3743      870.8              50.00   Rv2711, TB
DRB1_0701  162  VAVVVRQLTEHVQGD  VVRQLTEHV        0.3741      873.5              50.00   Rv2711, TB
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DRB1_0701   76  RKHRLAERLLVDVIG  HRLAERLLV        0.3722        891.2              50.00   Rv2711, TB
DRB1_0701  123  TTSPFGNPIPGLVEL  FGNPIPGLV        0.3684        928.5              50.00   Rv2711, TB
DRB1_0701   18  EEEGVTPLRARIAER  VTPLRARIA        0.3671        942.1              50.00   Rv2711, TB
DRB1_0701   33  LDQSGPTVSQTVSRM  TVSQTVSRM        0.3636        977.7              50.00   Rv2711, TB
DRB1_0701  204  VTIVIPGHENVTLPH  IVIPGHENV        0.3634        979.9              50.00   Rv2711, TB
DRB1_0701  195  TVETTPGGGVTIVIP  VETTPGGGV        0.3612       1004.3              50.00   Rv2711, TB
DRB1_0701  186  AGVVPNARVTVETTP  VVPNARVTV        0.3599       1018.2              50.00   Rv2711, TB
DRB1_0701   35  QSGPTVSQTVSRMER  TVSQTVSRM        0.3581       1037.7              50.00   Rv2711, TB
DRB1_0701  145  ADDANLVRLTELPAG  ANLVRLTEL        0.3575       1044.4              50.00   Rv2711, TB
DRB1_0701   58  DRHLELTEKGRALAI  ELTEKGRAL        0.3516       1113.2              50.00   Rv2711, TB
DRB1_0701   92  PWEEVHAEACRWEHV  EVHAEACRW        0.3502       1130.4              50.00   Rv2711, TB
DRB1_0701  163  AVVVRQLTEHVQGDI  VVRQLTEHV        0.3497       1136.8              50.00   Rv2711, TB
DRB1_0701  187  GVVPNARVTVETTPG  VVPNARVTV        0.3423       1231.3              50.00   Rv2711, TB
DRB1_0701  118  VLNNPTTSPFGNPIP  TTSPFGNPI        0.3385       1283.9              50.00   Rv2711, TB
DRB1_0701   80  LAERLLVDVIGLPWE  LVDVIGLPW        0.3379       1292.1              50.00   Rv2711, TB
DRB1_0701  196  VETTPGGGVTIVIPG  VETTPGGGV        0.3362       1315.8              50.00   Rv2711, TB
DRB1_0701   39  TVSQTVSRMERDGLL  SRMERDGLL        0.3359       1320.6              50.00   Rv2711, TB
DRB1_0701  205  TIVIPGHENVTLPHE  IVIPGHENV        0.3334       1356.7              50.00   Rv2711, TB
DRB1_0701  108  SEDVERRLVKVLNNP  VERRLVKVL        0.3287       1427.1              50.00   Rv2711, TB
DRB1_0701  206  IVIPGHENVTLPHEM  IVIPGHENV        0.3274       1446.9              50.00   Rv2711, TB
DRB1_0701   93  WEEVHAEACRWEHVM  EVHAEACRW        0.3262       1465.5              50.00   Rv2711, TB
DRB1_0701    6  TTEMYLRTIYDLEEE  MYLRTIYDL        0.3250       1484.9              50.00   Rv2711, TB
DRB1_0701   46  RMERDGLLRVAGDRH  LLRVAGDRH        0.3234       1510.5              50.00   Rv2711, TB
DRB1_0701   41  SQTVSRMERDGLLRV  MERDGLLRV        0.3227       1523.0              50.00   Rv2711, TB
DRB1_0701  152  RLTELPAGSPVAVVV  AGSPVAVVV        0.3177       1606.7              50.00   Rv2711, TB
DRB1_0701   62  ELTEKGRALAIAVMR  RALAIAVMR        0.3140       1672.7              50.00   Rv2711, TB
DRB1_0701  146  DDANLVRLTELPAGS  ANLVRLTEL        0.3124       1702.7              50.00   Rv2711, TB
DRB1_0701   61  LELTEKGRALAIAVM  GRALAIAVM        0.3118       1714.0              50.00   Rv2711, TB
DRB1_0701   40  VSQTVSRMERDGLLR  SRMERDGLL        0.3104       1739.0              50.00   Rv2711, TB
DRB1_0701   36  SGPTVSQTVSRMERD  VSQTVSRME        0.3078       1789.1              50.00   Rv2711, TB
DRB1_0701   56  AGDRHLELTEKGRAL  ELTEKGRAL        0.3077       1791.3              50.00   Rv2711, TB
DRB1_0701  164  VVVRQLTEHVQGDID  VVRQLTEHV        0.3068       1807.8              50.00   Rv2711, TB
DRB1_0701   82  ERLLVDVIGLPWEEV  LVDVIGLPW        0.3047       1850.4              50.00   Rv2711, TB
DRB1_0701  153  LTELPAGSPVAVVVR  AGSPVAVVV        0.3047       1850.9              50.00   Rv2711, TB
DRB1_0701   59  RHLELTEKGRALAIA  ELTEKGRAL        0.3037       1870.6              50.00   Rv2711, TB
DRB1_0701   57  GDRHLELTEKGRALA  ELTEKGRAL        0.3018       1909.9              50.00   Rv2711, TB
DRB1_0701  148  ANLVRLTELPAGSPV  ANLVRLTEL        0.2988       1972.7              50.00   Rv2711, TB
DRB1_0701   81  AERLLVDVIGLPWEE  LVDVIGLPW        0.2984       1979.9              50.00   Rv2711, TB
DRB1_0701   60  HLELTEKGRALAIAV  ELTEKGRAL        0.2953       2048.4              50.00   Rv2711, TB
DRB1_0701   77  KHRLAERLLVDVIGL  HRLAERLLV        0.2944       2068.0              50.00   Rv2711, TB
DRB1_0701  147  DANLVRLTELPAGSP  ANLVRLTEL        0.2939       2079.5              50.00   Rv2711, TB
DRB1_0701   94  EEVHAEACRWEHVMS  EVHAEACRW        0.2917       2128.8              50.00   Rv2711, TB
DRB1_0701   63  LTEKGRALAIAVMRK  ALAIAVMRK        0.2901       2166.3              50.00   Rv2711, TB
DRB1_0701  124  TSPFGNPIPGLVELG  FGNPIPGLV        0.2893       2186.4              50.00   Rv2711, TB
DRB1_0701  188  VVPNARVTVETTPGG  VVPNARVTV        0.2875       2229.1              50.00   Rv2711, TB
DRB1_0701   11  LRTIYDLEEEGVTPL  LEEEGVTPL        0.2871       2237.5              50.00   Rv2711, TB
DRB1_0701  119  LNNPTTSPFGNPIPG  TTSPFGNPI        0.2825       2352.8              50.00   Rv2711, TB
DRB1_0701   83  RLLVDVIGLPWEEVH  LVDVIGLPW        0.2821       2361.5              50.00   Rv2711, TB
DRB1_0701   95  EVHAEACRWEHVMSE  EVHAEACRW        0.2815       2377.5              50.00   Rv2711, TB
DRB1_0701  116  VKVLNNPTTSPFGNP  LNNPTTSPF        0.2790       2442.4              50.00   Rv2711, TB
DRB1_0701    7  TEMYLRTIYDLEEEG  MYLRTIYDL        0.2788       2449.3              50.00   Rv2711, TB
DRB1_0701  125  SPFGNPIPGLVELGV  FGNPIPGLV        0.2771       2495.0              50.00   Rv2711, TB
DRB1_0701   38  PTVSQTVSRMERDGL  VSQTVSRME        0.2763       2516.2              50.00   Rv2711, TB
DRB1_0701   15  YDLEEEGVTPLRARI  GVTPLRARI        0.2748       2557.3              50.00   Rv2711, TB
DRB1_0701  165  VVRQLTEHVQGDIDL  VVRQLTEHV        0.2736       2590.2              50.00   Rv2711, TB
DRB1_0701   37  GPTVSQTVSRMERDG  VSQTVSRME        0.2681       2748.6              50.00   Rv2711, TB
DRB1_0701  154  TELPAGSPVAVVVRQ  AGSPVAVVV        0.2650       2842.2              50.00   Rv2711, TB
DRB1_0701   64  TEKGRALAIAVMRKH  ALAIAVMRK        0.2642       2867.1              50.00   Rv2711, TB
DRB1_0701   42  QTVSRMERDGLLRVA  MERDGLLRV        0.2639       2878.1              50.00   Rv2711, TB
DRB1_0701  149  NLVRLTELPAGSPVA  ELPAGSPVA        0.2598       3007.4              50.00   Rv2711, TB
DRB1_0701   65  EKGRALAIAVMRKHR  AIAVMRKHR        0.2584       3052.7              50.00   Rv2711, TB
DRB1_0701  126  PFGNPIPGLVELGVG  FGNPIPGLV        0.2573       3089.1              50.00   Rv2711, TB
DRB1_0701  150  LVRLTELPAGSPVAV  ELPAGSPVA        0.2511       3305.6              50.00   Rv2711, TB
DRB1_0701  151  VRLTELPAGSPVAVV  ELPAGSPVA        0.2505       3324.1              50.00   Rv2711, TB
DRB1_0701   84  LLVDVIGLPWEEVHA  LVDVIGLPW        0.2505       3327.4              50.00   Rv2711, TB
DRB1_0701  127  FGNPIPGLVELGVGP  FGNPIPGLV        0.2458       3500.2              50.00   Rv2711, TB
DRB1_0701    8  EMYLRTIYDLEEEGV  MYLRTIYDL        0.2456       3508.3              50.00   Rv2711, TB
DRB1_0701   54  RVAGDRHLELTEKGR  VAGDRHLEL        0.2361       3888.2              50.00   Rv2711, TB
DRB1_0701   12  RTIYDLEEEGVTPLR  LEEEGVTPL        0.2360       3892.3              50.00   Rv2711, TB
DRB1_0701   78  HRLAERLLVDVIGLP  HRLAERLLV        0.2344       3959.5              50.00   Rv2711, TB
DRB1_0701  120  NNPTTSPFGNPIPGL  TTSPFGNPI        0.2264       4318.1              50.00   Rv2711, TB
DRB1_0701  198  TTPGGGVTIVIPGHE  VTIVIPGHE        0.2257       4351.1              50.00   Rv2711, TB
DRB1_0701    9  MYLRTIYDLEEEGVT  MYLRTIYDL        0.2235       4453.2              50.00   Rv2711, TB
DRB1_0701   55  VAGDRHLELTEKGRA  VAGDRHLEL        0.2210       4578.3              50.00   Rv2711, TB
DRB1_0701  199  TPGGGVTIVIPGHEN  VTIVIPGHE        0.2208       4584.7              50.00   Rv2711, TB
DRB1_0701   27  ARIAERLDQSGPTVS  LDQSGPTVS        0.2167       4791.5              50.00   Rv2711, TB
DRB1_0701   13  TIYDLEEEGVTPLRA  LEEEGVTPL        0.2153       4868.9              50.00   Rv2711, TB
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   DRB1_0701   85  LVDVIGLPWEEVHAE  LVDVIGLPW        0.2124       5023.2                50.00   Rv2711, TB
   DRB1_0701   30  AERLDQSGPTVSQTV  SGPTVSQTV        0.2119       5048.2                50.00   Rv2711, TB
   DRB1_0701   43  TVSRMERDGLLRVAG  MERDGLLRV        0.2090       5212.7                50.00   Rv2711, TB
   DRB1_0701  208  IPGHENVTLPHEMAH  ENVTLPHEM        0.1942       6118.6                50.00   Rv2711, TB
   DRB1_0701   31  ERLDQSGPTVSQTVS  SGPTVSQTV        0.1925       6226.2                50.00   Rv2711, TB
   DRB1_0701   28  RIAERLDQSGPTVSQ  LDQSGPTVS        0.1901       6392.9                50.00   Rv2711, TB
   DRB1_0701  210  GHENVTLPHEMAHAV  LPHEMAHAV        0.1889       6473.8                50.00   Rv2711, TB
   DRB1_0701  207  VIPGHENVTLPHEMA  ENVTLPHEM        0.1883       6519.2                50.00   Rv2711, TB
   DRB1_0701   87  DVIGLPWEEVHAEAC  WEEVHAEAC        0.1880       6536.6                50.00   Rv2711, TB
   DRB1_0701  167  RQLTEHVQGDIDLIT  LTEHVQGDI        0.1846       6785.7                50.00   Rv2711, TB
   DRB1_0701   32  RLDQSGPTVSQTVSR  SGPTVSQTV        0.1841       6819.4                50.00   Rv2711, TB
   DRB1_0701  166  VRQLTEHVQGDIDLI  LTEHVQGDI        0.1773       7341.8                50.00   Rv2711, TB
   DRB1_0701   14  IYDLEEEGVTPLRAR  LEEEGVTPL        0.1745       7569.7                50.00   Rv2711, TB
   DRB1_0701   44  VSRMERDGLLRVAGD  MERDGLLRV        0.1728       7707.1                50.00   Rv2711, TB
   DRB1_0701   29  IAERLDQSGPTVSQT  LDQSGPTVS        0.1692       8015.0                50.00   Rv2711, TB
   DRB1_0701   45  SRMERDGLLRVAGDR  MERDGLLRV        0.1615       8711.9                50.00   Rv2711, TB
   DRB1_0701   88  VIGLPWEEVHAEACR  WEEVHAEAC        0.1613       8727.9                50.00   Rv2711, TB
   DRB1_0701  211  HENVTLPHEMAHAVK  LPHEMAHAV        0.1585       8998.7                50.00   Rv2711, TB
   DRB1_0701  168  QLTEHVQGDIDLITR  LTEHVQGDI        0.1522       9629.6                50.00   Rv2711, TB
   DRB1_0701  209  PGHENVTLPHEMAHA  ENVTLPHEM        0.1515       9706.5                50.00   Rv2711, TB
   DRB1_0701  104  EHVMSEDVERRLVKV  MSEDVERRL        0.1380      11234.9                50.00   Rv2711, TB
   DRB1_0701   26  RARIAERLDQSGPTV  RLDQSGPTV        0.1367      11387.5                50.00   Rv2711, TB
   DRB1_0701  169  LTEHVQGDIDLITRL  LTEHVQGDI        0.1348      11630.3                50.00   Rv2711, TB
   DRB1_0701  189  VPNARVTVETTPGGG  TVETTPGGG        0.1096      15273.0                50.00   Rv2711, TB
   DRB1_0701   10  YLRTIYDLEEEGVTP  LRTIYDLEE        0.1078      15574.2                50.00   Rv2711, TB
   DRB1_0701  171  EHVQGDIDLITRLKD  VQGDIDLIT        0.1024      16504.2                50.00   Rv2711, TB
   DRB1_0701  170  TEHVQGDIDLITRLK  VQGDIDLIT        0.1010      16764.0                50.00   Rv2711, TB
   DRB1_0701   96  VHAEACRWEHVMSED  CRWEHVMSE        0.0982      17277.6                50.00   Rv2711, TB
   DRB1_0701  172  HVQGDIDLITRLKDA  VQGDIDLIT        0.0968      17552.2                50.00   Rv2711, TB
   DRB1_0701  139  VGPEPGADDANLVRL  ADDANLVRL        0.0907      18734.7                50.00   Rv2711, TB
   DRB1_0701  173  VQGDIDLITRLKDAG  VQGDIDLIT        0.0815      20698.5                50.00   Rv2711, TB
   DRB1_0701  128  GNPIPGLVELGVGPE  LVELGVGPE        0.0797      21103.5                50.00   Rv2711, TB
   DRB1_0701  140  GPEPGADDANLVRLT  ADDANLVRL        0.0797      21117.6                50.00   Rv2711, TB
   DRB1_0701   86  VDVIGLPWEEVHAEA  VIGLPWEEV        0.0771      21720.8                50.00   Rv2711, TB
   DRB1_0701  197  ETTPGGGVTIVIPGH  TTPGGGVTI        0.0743      22378.8                50.00   Rv2711, TB
   DRB1_0701  141  PEPGADDANLVRLTE  ADDANLVRL        0.0678      24008.0                50.00   Rv2711, TB
   DRB1_0701  138  GVGPEPGADDANLVR  GADDANLVR        0.0589      26431.7                50.00   Rv2711, TB
   DRB1_0701  134  LVELGVGPEPGADDA  GPEPGADDA        0.0570      26995.6                50.00   Rv2711, TB
   DRB1_0701  137  LGVGPEPGADDANLV  PGADDANLV        0.0568      27043.8                50.00   Rv2711, TB
   DRB1_0701  136  ELGVGPEPGADDANL  GPEPGADDA        0.0520      28474.7                50.00   Rv2711, TB
   DRB1_0701  132  PGLVELGVGPEPGAD  GVGPEPGAD        0.0514      28685.0                50.00   Rv2711, TB
   DRB1_0701  135  VELGVGPEPGADDAN  GPEPGADDA        0.0508      28860.9                50.00   Rv2711, TB
   DRB1_0701  130  PIPGLVELGVGPEPG  LVELGVGPE        0.0492      29357.9                50.00   Rv2711, TB
   DRB1_0701  133  GLVELGVGPEPGADD  GVGPEPGAD        0.0489      29470.5                50.00   Rv2711, TB
   DRB1_0701  131  IPGLVELGVGPEPGA  ELGVGPEPG        0.0483      29638.1                50.00   Rv2711, TB
   DRB1_0701  129  NPIPGLVELGVGPEP  LVELGVGPE        0.0470      30052.7                50.00   Rv2711, TB
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Allele: DRB1_0701. Number of high binders 12. Number of weak binders 56. Number of peptides 216

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0802   71  AIAVMRKHRLAERLL  AVMRKHRLA        0.6780         32.6          SB     0.80   Rv2711, TB
   DRB1_0802   70  LAIAVMRKHRLAERL  AVMRKHRLA        0.6655         37.3          SB     0.80   Rv2711, TB
   DRB1_0802   72  IAVMRKHRLAERLLV  AVMRKHRLA        0.6531         42.7          SB     1.00   Rv2711, TB
   DRB1_0802   69  ALAIAVMRKHRLAER  AVMRKHRLA        0.6149         64.5          WB     2.00   Rv2711, TB
   DRB1_0802   73  AVMRKHRLAERLLVD  AVMRKHRLA        0.5993         76.3          WB     4.00   Rv2711, TB
   DRB1_0802   68  RALAIAVMRKHRLAE  AVMRKHRLA        0.5970         78.3          WB     4.00   Rv2711, TB
   DRB1_0802   67  GRALAIAVMRKHRLA  AVMRKHRLA        0.5695        105.4          WB     4.00   Rv2711, TB
   DRB1_0802  159  GSPVAVVVRQLTEHV  VAVVVRQLT        0.5335        155.6          WB     8.00   Rv2711, TB
   DRB1_0802  161  PVAVVVRQLTEHVQG  VAVVVRQLT        0.5134        193.4          WB     8.00   Rv2711, TB
   DRB1_0802   21  GVTPLRARIAERLDQ  GVTPLRARI        0.5109        198.7          WB     8.00   Rv2711, TB
   DRB1_0802  160  SPVAVVVRQLTEHVQ  VAVVVRQLT        0.5050        211.8          WB     8.00   Rv2711, TB
   DRB1_0802   20  EGVTPLRARIAERLD  GVTPLRARI        0.5025        217.7          WB     8.00   Rv2711, TB
   DRB1_0802  158  AGSPVAVVVRQLTEH  VAVVVRQLT        0.4897        249.9          WB     8.00   Rv2711, TB
   DRB1_0802  178  DLITRLKDAGVVPNA  LITRLKDAG        0.4750        293.2          WB    16.00   Rv2711, TB
   DRB1_0802  177  IDLITRLKDAGVVPN  LITRLKDAG        0.4740        296.3          WB    16.00   Rv2711, TB
   DRB1_0802   66  KGRALAIAVMRKHRL  AIAVMRKHR        0.4646        328.1          WB    16.00   Rv2711, TB
   DRB1_0802  157  PAGSPVAVVVRQLTE  VAVVVRQLT        0.4628        334.5          WB    16.00   Rv2711, TB
   DRB1_0802  176  DIDLITRLKDAGVVP  LITRLKDAG        0.4617        338.4          WB    16.00   Rv2711, TB
   DRB1_0802  111  VERRLVKVLNNPTTS  LVKVLNNPT        0.4568        357.0          WB    16.00   Rv2711, TB
   DRB1_0802  110  DVERRLVKVLNNPTT  LVKVLNNPT        0.4500        384.3          WB    16.00   Rv2711, TB
   DRB1_0802  179  LITRLKDAGVVPNAR  LITRLKDAG        0.4483        391.2          WB    16.00   Rv2711, TB
   DRB1_0802   19  EEGVTPLRARIAERL  GVTPLRARI        0.4481        391.9          WB    16.00   Rv2711, TB
   DRB1_0802  156  LPAGSPVAVVVRQLT  PVAVVVRQL        0.4444        408.0          WB    16.00   Rv2711, TB
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DRB1_0802  175  GDIDLITRLKDAGVV  LITRLKDAG         0.4389        432.9          WB    16.00   Rv2711, TB
DRB1_0802  112  ERRLVKVLNNPTTSP  RLVKVLNNP         0.4365        444.6          WB    16.00   Rv2711, TB
DRB1_0802   22  VTPLRARIAERLDQS  VTPLRARIA         0.4305        474.5          WB    16.00   Rv2711, TB
DRB1_0802  174  QGDIDLITRLKDAGV  LITRLKDAG         0.4166        551.0                16.00   Rv2711, TB
DRB1_0802  113  RRLVKVLNNPTTSPF  LVKVLNNPT         0.4058        619.8                32.00   Rv2711, TB
DRB1_0802   37  GPTVSQTVSRMERDG  GPTVSQTVS         0.4055        621.4                32.00   Rv2711, TB
DRB1_0802   18  EEEGVTPLRARIAER  GVTPLRARI         0.4028        639.8                32.00   Rv2711, TB
DRB1_0802  109  EDVERRLVKVLNNPT  LVKVLNNPT         0.3999        660.1                32.00   Rv2711, TB
DRB1_0802  114  RLVKVLNNPTTSPFG  LVKVLNNPT         0.3958        690.6                32.00   Rv2711, TB
DRB1_0802   76  RKHRLAERLLVDVIG  RKHRLAERL         0.3902        733.5                32.00   Rv2711, TB
DRB1_0802  149  NLVRLTELPAGSPVA  NLVRLTELP         0.3833        790.2                32.00   Rv2711, TB
DRB1_0802  162  VAVVVRQLTEHVQGD  VAVVVRQLT         0.3814        806.7                32.00   Rv2711, TB
DRB1_0802  148  ANLVRLTELPAGSPV  NLVRLTELP         0.3788        830.0                32.00   Rv2711, TB
DRB1_0802   74  VMRKHRLAERLLVDV  RKHRLAERL         0.3786        831.5                32.00   Rv2711, TB
DRB1_0802   36  SGPTVSQTVSRMERD  GPTVSQTVS         0.3756        859.3                32.00   Rv2711, TB
DRB1_0802   17  LEEEGVTPLRARIAE  GVTPLRARI         0.3751        864.0                32.00   Rv2711, TB
DRB1_0802   75  MRKHRLAERLLVDVI  RKHRLAERL         0.3746        868.4                32.00   Rv2711, TB
DRB1_0802   40  VSQTVSRMERDGLLR  VSQTVSRME         0.3743        871.0                32.00   Rv2711, TB
DRB1_0802  173  VQGDIDLITRLKDAG  LITRLKDAG         0.3689        924.2                32.00   Rv2711, TB
DRB1_0802   16  DLEEEGVTPLRARIA  GVTPLRARI         0.3620        995.6                32.00   Rv2711, TB
DRB1_0802   35  QSGPTVSQTVSRMER  GPTVSQTVS         0.3598       1019.7                32.00   Rv2711, TB
DRB1_0802   38  PTVSQTVSRMERDGL  TVSQTVSRM         0.3593       1025.2                32.00   Rv2711, TB
DRB1_0802   39  TVSQTVSRMERDGLL  VSQTVSRME         0.3591       1027.1                32.00   Rv2711, TB
DRB1_0802   62  ELTEKGRALAIAVMR  LTEKGRALA         0.3581       1037.7                32.00   Rv2711, TB
DRB1_0802  147  DANLVRLTELPAGSP  NLVRLTELP         0.3578       1041.4                32.00   Rv2711, TB
DRB1_0802   65  EKGRALAIAVMRKHR  AIAVMRKHR         0.3530       1096.6                32.00   Rv2711, TB
DRB1_0802    4  VDTTEMYLRTIYDLE  YLRTIYDLE         0.3494       1140.9                32.00   Rv2711, TB
DRB1_0802   61  LELTEKGRALAIAVM  LTEKGRALA         0.3479       1158.7                32.00   Rv2711, TB
DRB1_0802   43  TVSRMERDGLLRVAG  TVSRMERDG         0.3474       1165.7                32.00   Rv2711, TB
DRB1_0802    6  TTEMYLRTIYDLEEE  YLRTIYDLE         0.3416       1241.1                32.00   Rv2711, TB
DRB1_0802  182  RLKDAGVVPNARVTV  RLKDAGVVP         0.3405       1255.4                32.00   Rv2711, TB
DRB1_0802   24  PLRARIAERLDQSGP  LRARIAERL         0.3403       1258.9                32.00   Rv2711, TB
DRB1_0802    5  DTTEMYLRTIYDLEE  YLRTIYDLE         0.3378       1293.3                32.00   Rv2711, TB
DRB1_0802   63  LTEKGRALAIAVMRK  LTEKGRALA         0.3351       1330.8                32.00   Rv2711, TB
DRB1_0802  146  DDANLVRLTELPAGS  NLVRLTELP         0.3351       1331.4                32.00   Rv2711, TB
DRB1_0802   41  SQTVSRMERDGLLRV  SQTVSRMER         0.3294       1416.8                32.00   Rv2711, TB
DRB1_0802   49  RDGLLRVAGDRHLEL  RDGLLRVAG         0.3283       1433.7                32.00   Rv2711, TB
DRB1_0802   23  TPLRARIAERLDQSG  LRARIAERL         0.3272       1450.6                32.00   Rv2711, TB
DRB1_0802   46  RMERDGLLRVAGDRH  RMERDGLLR         0.3270       1454.1                32.00   Rv2711, TB
DRB1_0802   60  HLELTEKGRALAIAV  LTEKGRALA         0.3267       1457.9                32.00   Rv2711, TB
DRB1_0802  108  SEDVERRLVKVLNNP  VERRLVKVL         0.3260       1470.0                32.00   Rv2711, TB
DRB1_0802   25  LRARIAERLDQSGPT  LRARIAERL         0.3256       1476.2                32.00   Rv2711, TB
DRB1_0802  126  PFGNPIPGLVELGVG  FGNPIPGLV         0.3247       1489.7                32.00   Rv2711, TB
DRB1_0802  124  TSPFGNPIPGLVELG  FGNPIPGLV         0.3232       1514.1                32.00   Rv2711, TB
DRB1_0802  155  ELPAGSPVAVVVRQL  PVAVVVRQL         0.3220       1534.4                32.00   Rv2711, TB
DRB1_0802  187  GVVPNARVTVETTPG  GVVPNARVT         0.3185       1593.5                50.00   Rv2711, TB
DRB1_0802  181  TRLKDAGVVPNARVT  RLKDAGVVP         0.3184       1595.4                50.00   Rv2711, TB
DRB1_0802  123  TTSPFGNPIPGLVEL  FGNPIPGLV         0.3184       1595.5                50.00   Rv2711, TB
DRB1_0802   48  ERDGLLRVAGDRHLE  RDGLLRVAG         0.3146       1661.5                50.00   Rv2711, TB
DRB1_0802   34  DQSGPTVSQTVSRME  GPTVSQTVS         0.3125       1699.8                50.00   Rv2711, TB
DRB1_0802  115  LVKVLNNPTTSPFGN  LVKVLNNPT         0.3118       1712.8                50.00   Rv2711, TB
DRB1_0802  127  FGNPIPGLVELGVGP  FGNPIPGLV         0.3101       1744.8                50.00   Rv2711, TB
DRB1_0802  125  SPFGNPIPGLVELGV  FGNPIPGLV         0.3082       1780.5                50.00   Rv2711, TB
DRB1_0802   45  SRMERDGLLRVAGDR  RMERDGLLR         0.3059       1826.5                50.00   Rv2711, TB
DRB1_0802  145  ADDANLVRLTELPAG  NLVRLTELP         0.3056       1832.2                50.00   Rv2711, TB
DRB1_0802  122  PTTSPFGNPIPGLVE  FGNPIPGLV         0.3027       1890.4                50.00   Rv2711, TB
DRB1_0802    7  TEMYLRTIYDLEEEG  YLRTIYDLE         0.3020       1904.5                50.00   Rv2711, TB
DRB1_0802  201  GGGVTIVIPGHENVT  GGVTIVIPG         0.3009       1927.9                50.00   Rv2711, TB
DRB1_0802   59  RHLELTEKGRALAIA  LTEKGRALA         0.2998       1950.8                50.00   Rv2711, TB
DRB1_0802  186  AGVVPNARVTVETTP  GVVPNARVT         0.2956       2042.1                50.00   Rv2711, TB
DRB1_0802   77  KHRLAERLLVDVIGL  KHRLAERLL         0.2940       2076.8                50.00   Rv2711, TB
DRB1_0802   33  LDQSGPTVSQTVSRM  GPTVSQTVS         0.2929       2103.1                50.00   Rv2711, TB
DRB1_0802   47  MERDGLLRVAGDRHL  RDGLLRVAG         0.2908       2149.6                50.00   Rv2711, TB
DRB1_0802   42  QTVSRMERDGLLRVA  TVSRMERDG         0.2903       2161.8                50.00   Rv2711, TB
DRB1_0802   44  VSRMERDGLLRVAGD  RMERDGLLR         0.2900       2169.7                50.00   Rv2711, TB
DRB1_0802  106  VMSEDVERRLVKVLN  VERRLVKVL         0.2857       2273.0                50.00   Rv2711, TB
DRB1_0802  213  NVTLPHEMAHAVKVE  NVTLPHEMA         0.2844       2303.3                50.00   Rv2711, TB
DRB1_0802  107  MSEDVERRLVKVLNN  VERRLVKVL         0.2841       2311.1                50.00   Rv2711, TB
DRB1_0802  185  DAGVVPNARVTVETT  GVVPNARVT         0.2834       2330.5                50.00   Rv2711, TB
DRB1_0802  144  GADDANLVRLTELPA  NLVRLTELP         0.2809       2392.5                50.00   Rv2711, TB
DRB1_0802   58  DRHLELTEKGRALAI  LTEKGRALA         0.2809       2393.6                50.00   Rv2711, TB
DRB1_0802  200  PGGGVTIVIPGHENV  GVTIVIPGH         0.2797       2424.4                50.00   Rv2711, TB
DRB1_0802  121  NPTTSPFGNPIPGLV  FGNPIPGLV         0.2779       2472.8                50.00   Rv2711, TB
DRB1_0802   32  RLDQSGPTVSQTVSR  RLDQSGPTV         0.2777       2476.9                50.00   Rv2711, TB
DRB1_0802   15  YDLEEEGVTPLRARI  GVTPLRARI         0.2775       2483.8                50.00   Rv2711, TB
DRB1_0802  202  GGVTIVIPGHENVTL  GGVTIVIPG         0.2769       2498.8                50.00   Rv2711, TB
DRB1_0802   64  TEKGRALAIAVMRKH  KGRALAIAV         0.2765       2510.6                50.00   Rv2711, TB
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DRB1_0802   51  GLLRVAGDRHLELTE  LLRVAGDRH        0.2763        2516.1               50.00   Rv2711, TB
DRB1_0802  180  ITRLKDAGVVPNARV  RLKDAGVVP        0.2755        2536.7               50.00   Rv2711, TB
DRB1_0802  215  TLPHEMAHAVKVEKV  HEMAHAVKV        0.2742        2572.2               50.00   Rv2711, TB
DRB1_0802  212  ENVTLPHEMAHAVKV  NVTLPHEMA        0.2730        2607.9               50.00   Rv2711, TB
DRB1_0802   52  LLRVAGDRHLELTEK  LLRVAGDRH        0.2716        2645.7               50.00   Rv2711, TB
DRB1_0802   57  GDRHLELTEKGRALA  LTEKGRALA        0.2715        2648.9               50.00   Rv2711, TB
DRB1_0802    8  EMYLRTIYDLEEEGV  YLRTIYDLE        0.2709        2666.1               50.00   Rv2711, TB
DRB1_0802    9  MYLRTIYDLEEEGVT  YLRTIYDLE        0.2700        2691.7               50.00   Rv2711, TB
DRB1_0802  150  LVRLTELPAGSPVAV  LVRLTELPA        0.2664        2801.0               50.00   Rv2711, TB
DRB1_0802    3  LVDTTEMYLRTIYDL  TTEMYLRTI        0.2654        2829.0               50.00   Rv2711, TB
DRB1_0802  214  VTLPHEMAHAVKVEK  HEMAHAVKV        0.2645        2857.5               50.00   Rv2711, TB
DRB1_0802   10  YLRTIYDLEEEGVTP  YLRTIYDLE        0.2630        2903.8               50.00   Rv2711, TB
DRB1_0802  183  LKDAGVVPNARVTVE  GVVPNARVT        0.2611        2965.1               50.00   Rv2711, TB
DRB1_0802  184  KDAGVVPNARVTVET  GVVPNARVT        0.2557        3145.0               50.00   Rv2711, TB
DRB1_0802   50  DGLLRVAGDRHLELT  LLRVAGDRH        0.2527        3248.0               50.00   Rv2711, TB
DRB1_0802  199  TPGGGVTIVIPGHEN  GGVTIVIPG        0.2494        3365.5               50.00   Rv2711, TB
DRB1_0802   26  RARIAERLDQSGPTV  RARIAERLD        0.2489        3382.6               50.00   Rv2711, TB
DRB1_0802  188  VVPNARVTVETTPGG  VVPNARVTV        0.2482        3407.8               50.00   Rv2711, TB
DRB1_0802  172  HVQGDIDLITRLKDA  DIDLITRLK        0.2471        3451.1               50.00   Rv2711, TB
DRB1_0802  164  VVVRQLTEHVQGDID  VVRQLTEHV        0.2460        3490.5               50.00   Rv2711, TB
DRB1_0802    2  ELVDTTEMYLRTIYD  TTEMYLRTI        0.2426        3622.8               50.00   Rv2711, TB
DRB1_0802  163  AVVVRQLTEHVQGDI  VVRQLTEHV        0.2417        3658.2               50.00   Rv2711, TB
DRB1_0802  105  HVMSEDVERRLVKVL  VERRLVKVL        0.2410        3686.5               50.00   Rv2711, TB
DRB1_0802   84  LLVDVIGLPWEEVHA  LVDVIGLPW        0.2404        3710.4               50.00   Rv2711, TB
DRB1_0802   53  LRVAGDRHLELTEKG  RVAGDRHLE        0.2378        3815.1               50.00   Rv2711, TB
DRB1_0802  198  TTPGGGVTIVIPGHE  GGVTIVIPG        0.2373        3837.2               50.00   Rv2711, TB
DRB1_0802   85  LVDVIGLPWEEVHAE  LVDVIGLPW        0.2367        3863.1               50.00   Rv2711, TB
DRB1_0802   31  ERLDQSGPTVSQTVS  RLDQSGPTV        0.2360        3892.0               50.00   Rv2711, TB
DRB1_0802  128  GNPIPGLVELGVGPE  PIPGLVELG        0.2335        3999.0               50.00   Rv2711, TB
DRB1_0802  189  VPNARVTVETTPGGG  RVTVETTPG        0.2298        4158.9               50.00   Rv2711, TB
DRB1_0802  165  VVRQLTEHVQGDIDL  VVRQLTEHV        0.2270        4288.3               50.00   Rv2711, TB
DRB1_0802  197  ETTPGGGVTIVIPGH  GVTIVIPGH        0.2242        4420.2               50.00   Rv2711, TB
DRB1_0802  210  GHENVTLPHEMAHAV  NVTLPHEMA        0.2212        4564.9               50.00   Rv2711, TB
DRB1_0802  190  PNARVTVETTPGGGV  PNARVTVET        0.2186        4695.0               50.00   Rv2711, TB
DRB1_0802  116  VKVLNNPTTSPFGNP  VKVLNNPTT        0.2182        4715.2               50.00   Rv2711, TB
DRB1_0802  211  HENVTLPHEMAHAVK  NVTLPHEMA        0.2173        4762.5               50.00   Rv2711, TB
DRB1_0802   56  AGDRHLELTEKGRAL  ELTEKGRAL        0.2070        5327.0               50.00   Rv2711, TB
DRB1_0802  209  PGHENVTLPHEMAHA  NVTLPHEMA        0.2068        5333.8               50.00   Rv2711, TB
DRB1_0802    1  NELVDTTEMYLRTIY  VDTTEMYLR        0.2058        5392.7               50.00   Rv2711, TB
DRB1_0802  129  NPIPGLVELGVGPEP  PIPGLVELG        0.2046        5461.7               50.00   Rv2711, TB
DRB1_0802   88  VIGLPWEEVHAEACR  VIGLPWEEV        0.2033        5544.0               50.00   Rv2711, TB
DRB1_0802  171  EHVQGDIDLITRLKD  DIDLITRLK        0.2027        5580.3               50.00   Rv2711, TB
DRB1_0802  130  PIPGLVELGVGPEPG  PIPGLVELG        0.1975        5901.7               50.00   Rv2711, TB
DRB1_0802  191  NARVTVETTPGGGVT  RVTVETTPG        0.1959        6003.4               50.00   Rv2711, TB
DRB1_0802  143  PGADDANLVRLTELP  NLVRLTELP        0.1956        6024.6               50.00   Rv2711, TB
DRB1_0802   83  RLLVDVIGLPWEEVH  LVDVIGLPW        0.1955        6032.5               50.00   Rv2711, TB
DRB1_0802  154  TELPAGSPVAVVVRQ  ELPAGSPVA        0.1942        6117.5               50.00   Rv2711, TB
DRB1_0802  192  ARVTVETTPGGGVTI  RVTVETTPG        0.1933        6172.6               50.00   Rv2711, TB
DRB1_0802  193  RVTVETTPGGGVTIV  RVTVETTPG        0.1908        6343.5               50.00   Rv2711, TB
DRB1_0802   78  HRLAERLLVDVIGLP  HRLAERLLV        0.1902        6383.5               50.00   Rv2711, TB
DRB1_0802   87  DVIGLPWEEVHAEAC  VIGLPWEEV        0.1888        6484.5               50.00   Rv2711, TB
DRB1_0802  120  NNPTTSPFGNPIPGL  TSPFGNPIP        0.1879        6546.4               50.00   Rv2711, TB
DRB1_0802  208  IPGHENVTLPHEMAH  NVTLPHEMA        0.1870        6613.8               50.00   Rv2711, TB
DRB1_0802   86  VDVIGLPWEEVHAEA  GLPWEEVHA        0.1836        6856.7               50.00   Rv2711, TB
DRB1_0802   89  IGLPWEEVHAEACRW  GLPWEEVHA        0.1836        6859.5               50.00   Rv2711, TB
DRB1_0802  203  GVTIVIPGHENVTLP  GVTIVIPGH        0.1806        7081.3               50.00   Rv2711, TB
DRB1_0802   54  RVAGDRHLELTEKGR  RVAGDRHLE        0.1747        7550.8               50.00   Rv2711, TB
DRB1_0802   28  RIAERLDQSGPTVSQ  RIAERLDQS        0.1738        7628.4               50.00   Rv2711, TB
DRB1_0802  153  LTELPAGSPVAVVVR  ELPAGSPVA        0.1727        7716.9               50.00   Rv2711, TB
DRB1_0802   82  ERLLVDVIGLPWEEV  LVDVIGLPW        0.1723        7751.3               50.00   Rv2711, TB
DRB1_0802  207  VIPGHENVTLPHEMA  NVTLPHEMA        0.1718        7795.8               50.00   Rv2711, TB
DRB1_0802  196  VETTPGGGVTIVIPG  GGVTIVIPG        0.1689        8041.6               50.00   Rv2711, TB
DRB1_0802  104  EHVMSEDVERRLVKV  DVERRLVKV        0.1678        8135.0               50.00   Rv2711, TB
DRB1_0802   27  ARIAERLDQSGPTVS  RIAERLDQS        0.1671        8197.1               50.00   Rv2711, TB
DRB1_0802  118  VLNNPTTSPFGNPIP  TSPFGNPIP        0.1664        8265.0               50.00   Rv2711, TB
DRB1_0802   95  EVHAEACRWEHVMSE  VHAEACRWE        0.1649        8392.3               50.00   Rv2711, TB
DRB1_0802  151  VRLTELPAGSPVAVV  VRLTELPAG        0.1620        8665.4               50.00   Rv2711, TB
DRB1_0802   96  VHAEACRWEHVMSED  VHAEACRWE        0.1616        8705.1               50.00   Rv2711, TB
DRB1_0802   90  GLPWEEVHAEACRWE  GLPWEEVHA        0.1606        8793.7               50.00   Rv2711, TB
DRB1_0802  103  WEHVMSEDVERRLVK  WEHVMSEDV        0.1592        8932.2               50.00   Rv2711, TB
DRB1_0802   55  VAGDRHLELTEKGRA  RHLELTEKG        0.1584        9005.3               50.00   Rv2711, TB
DRB1_0802   94  EEVHAEACRWEHVMS  VHAEACRWE        0.1577        9081.0               50.00   Rv2711, TB
DRB1_0802    0  MNELVDTTEMYLRTI  VDTTEMYLR        0.1572        9124.3               50.00   Rv2711, TB
DRB1_0802   97  HAEACRWEHVMSEDV  EACRWEHVM        0.1572        9131.1               50.00   Rv2711, TB
DRB1_0802   79  RLAERLLVDVIGLPW  LVDVIGLPW        0.1543        9418.0               50.00   Rv2711, TB
DRB1_0802   30  AERLDQSGPTVSQTV  RLDQSGPTV        0.1539        9463.1               50.00   Rv2711, TB
DRB1_0802  133  GLVELGVGPEPGADD  GLVELGVGP        0.1538        9464.9               50.00   Rv2711, TB
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   DRB1_0802   98  AEACRWEHVMSEDVE  EACRWEHVM        0.1536       9488.7                50.00   Rv2711, TB
   DRB1_0802   99  EACRWEHVMSEDVER  WEHVMSEDV        0.1530       9550.5                50.00   Rv2711, TB
   DRB1_0802   81  AERLLVDVIGLPWEE  LVDVIGLPW        0.1527       9581.5                50.00   Rv2711, TB
   DRB1_0802   29  IAERLDQSGPTVSQT  RLDQSGPTV        0.1488       9989.9                50.00   Rv2711, TB
   DRB1_0802   80  LAERLLVDVIGLPWE  LVDVIGLPW        0.1481      10072.4                50.00   Rv2711, TB
   DRB1_0802  119  LNNPTTSPFGNPIPG  TSPFGNPIP        0.1442      10500.0                50.00   Rv2711, TB
   DRB1_0802  100  ACRWEHVMSEDVERR  WEHVMSEDV        0.1441      10513.6                50.00   Rv2711, TB
   DRB1_0802  132  PGLVELGVGPEPGAD  GLVELGVGP        0.1409      10888.0                50.00   Rv2711, TB
   DRB1_0802  102  RWEHVMSEDVERRLV  WEHVMSEDV        0.1371      11340.8                50.00   Rv2711, TB
   DRB1_0802  170  TEHVQGDIDLITRLK  DIDLITRLK        0.1368      11376.0                50.00   Rv2711, TB
   DRB1_0802  152  RLTELPAGSPVAVVV  ELPAGSPVA        0.1352      11575.1                50.00   Rv2711, TB
   DRB1_0802  101  CRWEHVMSEDVERRL  WEHVMSEDV        0.1325      11921.9                50.00   Rv2711, TB
   DRB1_0802  166  VRQLTEHVQGDIDLI  VRQLTEHVQ        0.1317      12027.0                50.00   Rv2711, TB
   DRB1_0802  117  KVLNNPTTSPFGNPI  VLNNPTTSP        0.1294      12324.1                50.00   Rv2711, TB
   DRB1_0802   12  RTIYDLEEEGVTPLR  TIYDLEEEG        0.1281      12507.7                50.00   Rv2711, TB
   DRB1_0802   11  LRTIYDLEEEGVTPL  TIYDLEEEG        0.1277      12552.6                50.00   Rv2711, TB
   DRB1_0802  131  IPGLVELGVGPEPGA  GLVELGVGP        0.1271      12640.1                50.00   Rv2711, TB
   DRB1_0802   14  IYDLEEEGVTPLRAR  YDLEEEGVT        0.1239      13082.1                50.00   Rv2711, TB
   DRB1_0802  195  TVETTPGGGVTIVIP  GGGVTIVIP        0.1197      13689.9                50.00   Rv2711, TB
   DRB1_0802  206  IVIPGHENVTLPHEM  IVIPGHENV        0.1179      13965.8                50.00   Rv2711, TB
   DRB1_0802  194  VTVETTPGGGVTIVI  VTVETTPGG        0.1178      13978.8                50.00   Rv2711, TB
   DRB1_0802   93  WEEVHAEACRWEHVM  VHAEACRWE        0.1162      14216.4                50.00   Rv2711, TB
   DRB1_0802  204  VTIVIPGHENVTLPH  IVIPGHENV        0.1122      14851.9                50.00   Rv2711, TB
   DRB1_0802   13  TIYDLEEEGVTPLRA  TIYDLEEEG        0.1115      14966.8                50.00   Rv2711, TB
   DRB1_0802  205  TIVIPGHENVTLPHE  TIVIPGHEN        0.1089      15382.2                50.00   Rv2711, TB
   DRB1_0802   92  PWEEVHAEACRWEHV  PWEEVHAEA        0.1074      15649.6                50.00   Rv2711, TB
   DRB1_0802   91  LPWEEVHAEACRWEH  VHAEACRWE        0.1037      16275.6                50.00   Rv2711, TB
   DRB1_0802  167  RQLTEHVQGDIDLIT  RQLTEHVQG        0.0993      17071.7                50.00   Rv2711, TB
   DRB1_0802  134  LVELGVGPEPGADDA  LVELGVGPE        0.0957      17757.9                50.00   Rv2711, TB
   DRB1_0802  135  VELGVGPEPGADDAN  VELGVGPEP        0.0940      18083.2                50.00   Rv2711, TB
   DRB1_0802  142  EPGADDANLVRLTEL  GADDANLVR        0.0848      19978.7                50.00   Rv2711, TB
   DRB1_0802  169  LTEHVQGDIDLITRL  HVQGDIDLI        0.0704      23336.0                50.00   Rv2711, TB
   DRB1_0802  141  PEPGADDANLVRLTE  GADDANLVR        0.0670      24213.1                50.00   Rv2711, TB
   DRB1_0802  136  ELGVGPEPGADDANL  ELGVGPEPG        0.0667      24301.5                50.00   Rv2711, TB
   DRB1_0802  168  QLTEHVQGDIDLITR  HVQGDIDLI        0.0603      26033.0                50.00   Rv2711, TB
   DRB1_0802  140  GPEPGADDANLVRLT  DDANLVRLT        0.0592      26362.0                50.00   Rv2711, TB
   DRB1_0802  137  LGVGPEPGADDANLV  LGVGPEPGA        0.0479      29778.2                50.00   Rv2711, TB
   DRB1_0802  138  GVGPEPGADDANLVR  GADDANLVR        0.0455      30568.9                50.00   Rv2711, TB
   DRB1_0802  139  VGPEPGADDANLVRL  GADDANLVR        0.0437      31153.2                50.00   Rv2711, TB
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Allele: DRB1_0802. Number of high binders 3. Number of weak binders 23. Number of peptides 216

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_0901   75  MRKHRLAERLLVDVI  KHRLAERLL        0.6550         41.8         SB     2.00   Rv2711, TB
   DRB1_0901   74  VMRKHRLAERLLVDV  KHRLAERLL        0.6499         44.2         SB     2.00   Rv2711, TB
   DRB1_0901   73  AVMRKHRLAERLLVD  KHRLAERLL        0.6451         46.5         SB     2.00   Rv2711, TB
   DRB1_0901   72  IAVMRKHRLAERLLV  KHRLAERLL        0.6250         57.8         WB     4.00   Rv2711, TB
   DRB1_0901   76  RKHRLAERLLVDVIG  KHRLAERLL        0.6216         60.0         WB     4.00   Rv2711, TB
   DRB1_0901  215  TLPHEMAHAVKVEKV  HEMAHAVKV        0.6079         69.6         WB     4.00   Rv2711, TB
   DRB1_0901  101  CRWEHVMSEDVERRL  WEHVMSEDV        0.5818         92.3         WB     8.00   Rv2711, TB
   DRB1_0901  100  ACRWEHVMSEDVERR  WEHVMSEDV        0.5777         96.5         WB     8.00   Rv2711, TB
   DRB1_0901  213  NVTLPHEMAHAVKVE  HEMAHAVKV        0.5772         97.0         WB     8.00   Rv2711, TB
   DRB1_0901  214  VTLPHEMAHAVKVEK  HEMAHAVKV        0.5712        103.5         WB     8.00   Rv2711, TB
   DRB1_0901   21  GVTPLRARIAERLDQ  LRARIAERL        0.5688        106.2         WB     8.00   Rv2711, TB
   DRB1_0901   20  EGVTPLRARIAERLD  LRARIAERL        0.5686        106.4         WB     8.00   Rv2711, TB
   DRB1_0901   99  EACRWEHVMSEDVER  WEHVMSEDV        0.5637        112.2         WB     8.00   Rv2711, TB
   DRB1_0901  102  RWEHVMSEDVERRLV  WEHVMSEDV        0.5611        115.5         WB     8.00   Rv2711, TB
   DRB1_0901   71  AIAVMRKHRLAERLL  KHRLAERLL        0.5578        119.6         WB     8.00   Rv2711, TB
   DRB1_0901   22  VTPLRARIAERLDQS  LRARIAERL        0.5554        122.8         WB     8.00   Rv2711, TB
   DRB1_0901   77  KHRLAERLLVDVIGL  KHRLAERLL        0.5519        127.5         WB     8.00   Rv2711, TB
   DRB1_0901   98  AEACRWEHVMSEDVE  WEHVMSEDV        0.5473        134.1         WB    16.00   Rv2711, TB
   DRB1_0901   23  TPLRARIAERLDQSG  LRARIAERL        0.5370        149.8         WB    16.00   Rv2711, TB
   DRB1_0901   19  EEGVTPLRARIAERL  TPLRARIAE        0.5265        167.9         WB    16.00   Rv2711, TB
   DRB1_0901    8  EMYLRTIYDLEEEGV  YLRTIYDLE        0.5192        181.6         WB    16.00   Rv2711, TB
   DRB1_0901  103  WEHVMSEDVERRLVK  WEHVMSEDV        0.5180        184.1         WB    16.00   Rv2711, TB
   DRB1_0901  212  ENVTLPHEMAHAVKV  HEMAHAVKV        0.5156        188.8         WB    16.00   Rv2711, TB
   DRB1_0901   65  EKGRALAIAVMRKHR  KGRALAIAV        0.5104        199.7         WB    16.00   Rv2711, TB
   DRB1_0901   64  TEKGRALAIAVMRKH  EKGRALAIA        0.5009        221.4         WB    16.00   Rv2711, TB
   DRB1_0901   66  KGRALAIAVMRKHRL  KGRALAIAV        0.4986        227.0         WB    16.00   Rv2711, TB
   DRB1_0901  127  FGNPIPGLVELGVGP  FGNPIPGLV        0.4985        227.4         WB    16.00   Rv2711, TB
   DRB1_0901  126  PFGNPIPGLVELGVG  FGNPIPGLV        0.4919        244.1         WB    32.00   Rv2711, TB
   DRB1_0901   63  LTEKGRALAIAVMRK  KGRALAIAV        0.4862        259.7         WB    32.00   Rv2711, TB
   DRB1_0901    9  MYLRTIYDLEEEGVT  YLRTIYDLE        0.4793        279.8         WB    32.00   Rv2711, TB
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DRB1_0901  155  ELPAGSPVAVVVRQL  ELPAGSPVA         0.4769         287.1          WB    32.00   Rv2711, TB
DRB1_0901  125  SPFGNPIPGLVELGV  FGNPIPGLV         0.4679         316.6          WB    32.00   Rv2711, TB
DRB1_0901  153  LTELPAGSPVAVVVR  ELPAGSPVA         0.4679         316.6          WB    32.00   Rv2711, TB
DRB1_0901   62  ELTEKGRALAIAVMR  EKGRALAIA         0.4676         317.6          WB    32.00   Rv2711, TB
DRB1_0901    6  TTEMYLRTIYDLEEE  YLRTIYDLE         0.4656         324.3          WB    32.00   Rv2711, TB
DRB1_0901  180  ITRLKDAGVVPNARV  ITRLKDAGV         0.4651         326.1          WB    32.00   Rv2711, TB
DRB1_0901  186  AGVVPNARVTVETTP  AGVVPNARV         0.4632         332.9          WB    32.00   Rv2711, TB
DRB1_0901  111  VERRLVKVLNNPTTS  RRLVKVLNN         0.4627         334.8          WB    32.00   Rv2711, TB
DRB1_0901    7  TEMYLRTIYDLEEEG  YLRTIYDLE         0.4627         334.8          WB    32.00   Rv2711, TB
DRB1_0901  154  TELPAGSPVAVVVRQ  ELPAGSPVA         0.4612         340.1          WB    32.00   Rv2711, TB
DRB1_0901  169  LTEHVQGDIDLITRL  EHVQGDIDL         0.4573         355.1          WB    32.00   Rv2711, TB
DRB1_0901   67  GRALAIAVMRKHRLA  RALAIAVMR         0.4552         363.1          WB    32.00   Rv2711, TB
DRB1_0901  178  DLITRLKDAGVVPNA  ITRLKDAGV         0.4538         368.7          WB    32.00   Rv2711, TB
DRB1_0901   10  YLRTIYDLEEEGVTP  YLRTIYDLE         0.4537         369.1          WB    32.00   Rv2711, TB
DRB1_0901  168  QLTEHVQGDIDLITR  LTEHVQGDI         0.4518         376.5          WB    32.00   Rv2711, TB
DRB1_0901  177  IDLITRLKDAGVVPN  ITRLKDAGV         0.4505         382.1          WB    32.00   Rv2711, TB
DRB1_0901  179  LITRLKDAGVVPNAR  ITRLKDAGV         0.4501         383.5          WB    32.00   Rv2711, TB
DRB1_0901  167  RQLTEHVQGDIDLIT  LTEHVQGDI         0.4493         387.1          WB    32.00   Rv2711, TB
DRB1_0901  110  DVERRLVKVLNNPTT  VERRLVKVL         0.4481         392.2          WB    32.00   Rv2711, TB
DRB1_0901    5  DTTEMYLRTIYDLEE  YLRTIYDLE         0.4455         403.1          WB    32.00   Rv2711, TB
DRB1_0901  176  DIDLITRLKDAGVVP  ITRLKDAGV         0.4448         406.2          WB    32.00   Rv2711, TB
DRB1_0901  185  DAGVVPNARVTVETT  AGVVPNARV         0.4440         410.0          WB    32.00   Rv2711, TB
DRB1_0901  165  VVRQLTEHVQGDIDL  LTEHVQGDI         0.4402         426.8          WB    32.00   Rv2711, TB
DRB1_0901   18  EEEGVTPLRARIAER  EGVTPLRAR         0.4396         430.0          WB    32.00   Rv2711, TB
DRB1_0901  152  RLTELPAGSPVAVVV  ELPAGSPVA         0.4392         431.6          WB    32.00   Rv2711, TB
DRB1_0901   97  HAEACRWEHVMSEDV  WEHVMSEDV         0.4391         432.3          WB    32.00   Rv2711, TB
DRB1_0901  104  EHVMSEDVERRLVKV  EHVMSEDVE         0.4386         434.5          WB    32.00   Rv2711, TB
DRB1_0901  151  VRLTELPAGSPVAVV  ELPAGSPVA         0.4378         438.5          WB    32.00   Rv2711, TB
DRB1_0901  166  VRQLTEHVQGDIDLI  LTEHVQGDI         0.4367         443.4          WB    32.00   Rv2711, TB
DRB1_0901  124  TSPFGNPIPGLVELG  FGNPIPGLV         0.4360         447.0          WB    32.00   Rv2711, TB
DRB1_0901   39  TVSQTVSRMERDGLL  VSQTVSRME         0.4341         456.0          WB    32.00   Rv2711, TB
DRB1_0901  150  LVRLTELPAGSPVAV  ELPAGSPVA         0.4334         459.6          WB    32.00   Rv2711, TB
DRB1_0901  112  ERRLVKVLNNPTTSP  VKVLNNPTT         0.4327         463.4          WB    32.00   Rv2711, TB
DRB1_0901   24  PLRARIAERLDQSGP  LRARIAERL         0.4323         465.0          WB    32.00   Rv2711, TB
DRB1_0901  128  GNPIPGLVELGVGPE  NPIPGLVEL         0.4323         465.0          WB    32.00   Rv2711, TB
DRB1_0901   50  DGLLRVAGDRHLELT  LRVAGDRHL         0.4317         468.2          WB    32.00   Rv2711, TB
DRB1_0901   36  SGPTVSQTVSRMERD  VSQTVSRME         0.4309         472.0          WB    32.00   Rv2711, TB
DRB1_0901  113  RRLVKVLNNPTTSPF  VKVLNNPTT         0.4306         474.0          WB    32.00   Rv2711, TB
DRB1_0901   17  LEEEGVTPLRARIAE  EGVTPLRAR         0.4272         491.7          WB    32.00   Rv2711, TB
DRB1_0901   38  PTVSQTVSRMERDGL  VSQTVSRME         0.4252         502.3                50.00   Rv2711, TB
DRB1_0901   40  VSQTVSRMERDGLLR  VSQTVSRME         0.4245         506.3                50.00   Rv2711, TB
DRB1_0901  149  NLVRLTELPAGSPVA  NLVRLTELP         0.4242         507.9                50.00   Rv2711, TB
DRB1_0901  156  LPAGSPVAVVVRQLT  LPAGSPVAV         0.4224         517.9                50.00   Rv2711, TB
DRB1_0901  164  VVVRQLTEHVQGDID  LTEHVQGDI         0.4211         524.9                50.00   Rv2711, TB
DRB1_0901   34  DQSGPTVSQTVSRME  GPTVSQTVS         0.4180         543.3                50.00   Rv2711, TB
DRB1_0901   35  QSGPTVSQTVSRMER  VSQTVSRME         0.4170         549.2                50.00   Rv2711, TB
DRB1_0901  184  KDAGVVPNARVTVET  AGVVPNARV         0.4161         554.5                50.00   Rv2711, TB
DRB1_0901  211  HENVTLPHEMAHAVK  NVTLPHEMA         0.4147         562.7                50.00   Rv2711, TB
DRB1_0901   49  RDGLLRVAGDRHLEL  LRVAGDRHL         0.4145         564.0                50.00   Rv2711, TB
DRB1_0901   61  LELTEKGRALAIAVM  EKGRALAIA         0.4131         572.4                50.00   Rv2711, TB
DRB1_0901   78  HRLAERLLVDVIGLP  HRLAERLLV         0.4122         578.0                50.00   Rv2711, TB
DRB1_0901  175  GDIDLITRLKDAGVV  ITRLKDAGV         0.4111         585.3                50.00   Rv2711, TB
DRB1_0901  129  NPIPGLVELGVGPEP  NPIPGLVEL         0.4109         586.1                50.00   Rv2711, TB
DRB1_0901  181  TRLKDAGVVPNARVT  AGVVPNARV         0.4103         590.4                50.00   Rv2711, TB
DRB1_0901  148  ANLVRLTELPAGSPV  LVRLTELPA         0.4101         591.2                50.00   Rv2711, TB
DRB1_0901   37  GPTVSQTVSRMERDG  VSQTVSRME         0.4076         607.5                50.00   Rv2711, TB
DRB1_0901   88  VIGLPWEEVHAEACR  VIGLPWEEV         0.4061         617.7                50.00   Rv2711, TB
DRB1_0901   91  LPWEEVHAEACRWEH  EEVHAEACR         0.4060         618.3                50.00   Rv2711, TB
DRB1_0901  183  LKDAGVVPNARVTVE  AGVVPNARV         0.4056         620.9                50.00   Rv2711, TB
DRB1_0901   90  GLPWEEVHAEACRWE  EEVHAEACR         0.4048         626.3                50.00   Rv2711, TB
DRB1_0901   51  GLLRVAGDRHLELTE  LRVAGDRHL         0.4028         640.2                50.00   Rv2711, TB
DRB1_0901   68  RALAIAVMRKHRLAE  RALAIAVMR         0.4025         642.0                50.00   Rv2711, TB
DRB1_0901  182  RLKDAGVVPNARVTV  AGVVPNARV         0.4021         644.8                50.00   Rv2711, TB
DRB1_0901   48  ERDGLLRVAGDRHLE  LRVAGDRHL         0.4014         649.8                50.00   Rv2711, TB
DRB1_0901  163  AVVVRQLTEHVQGDI  VVRQLTEHV         0.4008         653.9                50.00   Rv2711, TB
DRB1_0901  123  TTSPFGNPIPGLVEL  FGNPIPGLV         0.3995         663.1                50.00   Rv2711, TB
DRB1_0901    4  VDTTEMYLRTIYDLE  YLRTIYDLE         0.3958         690.4                50.00   Rv2711, TB
DRB1_0901  107  MSEDVERRLVKVLNN  MSEDVERRL         0.3949         697.4                50.00   Rv2711, TB
DRB1_0901  210  GHENVTLPHEMAHAV  NVTLPHEMA         0.3937         705.9                50.00   Rv2711, TB
DRB1_0901  109  EDVERRLVKVLNNPT  VERRLVKVL         0.3927         713.9                50.00   Rv2711, TB
DRB1_0901  147  DANLVRLTELPAGSP  NLVRLTELP         0.3907         729.4                50.00   Rv2711, TB
DRB1_0901  106  VMSEDVERRLVKVLN  MSEDVERRL         0.3887         745.6                50.00   Rv2711, TB
DRB1_0901   92  PWEEVHAEACRWEHV  WEEVHAEAC         0.3877         753.9                50.00   Rv2711, TB
DRB1_0901   16  DLEEEGVTPLRARIA  EGVTPLRAR         0.3838         786.2                50.00   Rv2711, TB
DRB1_0901  207  VIPGHENVTLPHEMA  IPGHENVTL         0.3837         787.1                50.00   Rv2711, TB
DRB1_0901  122  PTTSPFGNPIPGLVE  FGNPIPGLV         0.3804         816.0                50.00   Rv2711, TB
DRB1_0901   31  ERLDQSGPTVSQTVS  LDQSGPTVS         0.3793         825.6                50.00   Rv2711, TB
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DRB1_0901   47  MERDGLLRVAGDRHL  LRVAGDRHL         0.3788        829.7                 50.00   Rv2711, TB
DRB1_0901   32  RLDQSGPTVSQTVSR  LDQSGPTVS         0.3762        853.4                 50.00   Rv2711, TB
DRB1_0901  108  SEDVERRLVKVLNNP  VERRLVKVL         0.3758        857.3                 50.00   Rv2711, TB
DRB1_0901  209  PGHENVTLPHEMAHA  NVTLPHEMA         0.3750        864.8                 50.00   Rv2711, TB
DRB1_0901   33  LDQSGPTVSQTVSRM  LDQSGPTVS         0.3749        865.2                 50.00   Rv2711, TB
DRB1_0901   25  LRARIAERLDQSGPT  LRARIAERL         0.3746        868.2                 50.00   Rv2711, TB
DRB1_0901  161  PVAVVVRQLTEHVQG  VAVVVRQLT         0.3738        875.8                 50.00   Rv2711, TB
DRB1_0901  146  DDANLVRLTELPAGS  NLVRLTELP         0.3735        878.5                 50.00   Rv2711, TB
DRB1_0901   70  LAIAVMRKHRLAERL  RKHRLAERL         0.3710        902.8                 50.00   Rv2711, TB
DRB1_0901  114  RLVKVLNNPTTSPFG  VKVLNNPTT         0.3705        907.4                 50.00   Rv2711, TB
DRB1_0901   41  SQTVSRMERDGLLRV  QTVSRMERD         0.3701        912.0                 50.00   Rv2711, TB
DRB1_0901    0  MNELVDTTEMYLRTI  LVDTTEMYL         0.3688        924.3                 50.00   Rv2711, TB
DRB1_0901   93  WEEVHAEACRWEHVM  WEEVHAEAC         0.3659        954.1                 50.00   Rv2711, TB
DRB1_0901  105  HVMSEDVERRLVKVL  HVMSEDVER         0.3650        964.0                 50.00   Rv2711, TB
DRB1_0901    1  NELVDTTEMYLRTIY  LVDTTEMYL         0.3645        968.8                 50.00   Rv2711, TB
DRB1_0901  121  NPTTSPFGNPIPGLV  FGNPIPGLV         0.3626        988.5                 50.00   Rv2711, TB
DRB1_0901  160  SPVAVVVRQLTEHVQ  SPVAVVVRQ         0.3570       1050.0                 50.00   Rv2711, TB
DRB1_0901  170  TEHVQGDIDLITRLK  EHVQGDIDL         0.3567       1053.6                 50.00   Rv2711, TB
DRB1_0901   89  IGLPWEEVHAEACRW  WEEVHAEAC         0.3567       1054.0                 50.00   Rv2711, TB
DRB1_0901  145  ADDANLVRLTELPAG  NLVRLTELP         0.3554       1069.5                 50.00   Rv2711, TB
DRB1_0901  137  LGVGPEPGADDANLV  LGVGPEPGA         0.3543       1081.8                 50.00   Rv2711, TB
DRB1_0901  208  IPGHENVTLPHEMAH  IPGHENVTL         0.3538       1087.6                 50.00   Rv2711, TB
DRB1_0901  115  LVKVLNNPTTSPFGN  VKVLNNPTT         0.3526       1102.2                 50.00   Rv2711, TB
DRB1_0901   30  AERLDQSGPTVSQTV  LDQSGPTVS         0.3489       1146.9                 50.00   Rv2711, TB
DRB1_0901  158  AGSPVAVVVRQLTEH  AGSPVAVVV         0.3471       1169.5                 50.00   Rv2711, TB
DRB1_0901  134  LVELGVGPEPGADDA  LGVGPEPGA         0.3459       1185.3                 50.00   Rv2711, TB
DRB1_0901   42  QTVSRMERDGLLRVA  QTVSRMERD         0.3450       1195.9                 50.00   Rv2711, TB
DRB1_0901  162  VAVVVRQLTEHVQGD  VVRQLTEHV         0.3428       1225.0                 50.00   Rv2711, TB
DRB1_0901    2  ELVDTTEMYLRTIYD  ELVDTTEMY         0.3419       1236.8                 50.00   Rv2711, TB
DRB1_0901  159  GSPVAVVVRQLTEHV  VAVVVRQLT         0.3404       1257.0                 50.00   Rv2711, TB
DRB1_0901  116  VKVLNNPTTSPFGNP  VKVLNNPTT         0.3393       1272.3                 50.00   Rv2711, TB
DRB1_0901  133  GLVELGVGPEPGADD  LGVGPEPGA         0.3392       1273.1                 50.00   Rv2711, TB
DRB1_0901   60  HLELTEKGRALAIAV  EKGRALAIA         0.3391       1274.7                 50.00   Rv2711, TB
DRB1_0901  157  PAGSPVAVVVRQLTE  PAGSPVAVV         0.3375       1297.5                 50.00   Rv2711, TB
DRB1_0901   44  VSRMERDGLLRVAGD  ERDGLLRVA         0.3374       1298.8                 50.00   Rv2711, TB
DRB1_0901   87  DVIGLPWEEVHAEAC  VIGLPWEEV         0.3351       1332.1                 50.00   Rv2711, TB
DRB1_0901   52  LLRVAGDRHLELTEK  LRVAGDRHL         0.3348       1335.2                 50.00   Rv2711, TB
DRB1_0901  135  VELGVGPEPGADDAN  LGVGPEPGA         0.3348       1336.5                 50.00   Rv2711, TB
DRB1_0901  136  ELGVGPEPGADDANL  LGVGPEPGA         0.3343       1343.4                 50.00   Rv2711, TB
DRB1_0901  131  IPGLVELGVGPEPGA  LGVGPEPGA         0.3333       1357.8                 50.00   Rv2711, TB
DRB1_0901   94  EEVHAEACRWEHVMS  EVHAEACRW         0.3318       1380.5                 50.00   Rv2711, TB
DRB1_0901  130  PIPGLVELGVGPEPG  IPGLVELGV         0.3315       1383.9                 50.00   Rv2711, TB
DRB1_0901  171  EHVQGDIDLITRLKD  EHVQGDIDL         0.3292       1419.9                 50.00   Rv2711, TB
DRB1_0901  132  PGLVELGVGPEPGAD  LGVGPEPGA         0.3249       1486.3                 50.00   Rv2711, TB
DRB1_0901   15  YDLEEEGVTPLRARI  YDLEEEGVT         0.3246       1492.2                 50.00   Rv2711, TB
DRB1_0901  118  VLNNPTTSPFGNPIP  LNNPTTSPF         0.3236       1508.7                 50.00   Rv2711, TB
DRB1_0901   83  RLLVDVIGLPWEEVH  VIGLPWEEV         0.3187       1589.3                 50.00   Rv2711, TB
DRB1_0901   14  IYDLEEEGVTPLRAR  IYDLEEEGV         0.3184       1595.0                 50.00   Rv2711, TB
DRB1_0901  205  TIVIPGHENVTLPHE  TIVIPGHEN         0.3182       1599.4                 50.00   Rv2711, TB
DRB1_0901   82  ERLLVDVIGLPWEEV  LLVDVIGLP         0.3152       1651.2                 50.00   Rv2711, TB
DRB1_0901  204  VTIVIPGHENVTLPH  TIVIPGHEN         0.3147       1661.2                 50.00   Rv2711, TB
DRB1_0901   95  EVHAEACRWEHVMSE  EVHAEACRW         0.3136       1680.9                 50.00   Rv2711, TB
DRB1_0901  144  GADDANLVRLTELPA  NLVRLTELP         0.3130       1691.4                 50.00   Rv2711, TB
DRB1_0901  187  GVVPNARVTVETTPG  VVPNARVTV         0.3127       1696.2                 50.00   Rv2711, TB
DRB1_0901   96  VHAEACRWEHVMSED  RWEHVMSED         0.3125       1699.9                 50.00   Rv2711, TB
DRB1_0901  117  KVLNNPTTSPFGNPI  LNNPTTSPF         0.3123       1704.2                 50.00   Rv2711, TB
DRB1_0901   53  LRVAGDRHLELTEKG  LRVAGDRHL         0.3119       1710.7                 50.00   Rv2711, TB
DRB1_0901   69  ALAIAVMRKHRLAER  MRKHRLAER         0.3104       1739.1                 50.00   Rv2711, TB
DRB1_0901   43  TVSRMERDGLLRVAG  SRMERDGLL         0.3094       1757.8                 50.00   Rv2711, TB
DRB1_0901   45  SRMERDGLLRVAGDR  ERDGLLRVA         0.3086       1772.8                 50.00   Rv2711, TB
DRB1_0901   79  RLAERLLVDVIGLPW  RLAERLLVD         0.3083       1779.8                 50.00   Rv2711, TB
DRB1_0901  206  IVIPGHENVTLPHEM  IVIPGHENV         0.3047       1849.1                 50.00   Rv2711, TB
DRB1_0901  174  QGDIDLITRLKDAGV  ITRLKDAGV         0.2997       1951.9                 50.00   Rv2711, TB
DRB1_0901  196  VETTPGGGVTIVIPG  VETTPGGGV         0.2996       1955.2                 50.00   Rv2711, TB
DRB1_0901   59  RHLELTEKGRALAIA  EKGRALAIA         0.2989       1970.5                 50.00   Rv2711, TB
DRB1_0901   86  VDVIGLPWEEVHAEA  VIGLPWEEV         0.2967       2016.7                 50.00   Rv2711, TB
DRB1_0901   46  RMERDGLLRVAGDRH  ERDGLLRVA         0.2941       2075.5                 50.00   Rv2711, TB
DRB1_0901  203  GVTIVIPGHENVTLP  VIPGHENVT         0.2939       2079.3                 50.00   Rv2711, TB
DRB1_0901  119  LNNPTTSPFGNPIPG  LNNPTTSPF         0.2923       2114.6                 50.00   Rv2711, TB
DRB1_0901   11  LRTIYDLEEEGVTPL  IYDLEEEGV         0.2911       2144.0                 50.00   Rv2711, TB
DRB1_0901   84  LLVDVIGLPWEEVHA  VIGLPWEEV         0.2910       2145.7                 50.00   Rv2711, TB
DRB1_0901    3  LVDTTEMYLRTIYDL  LVDTTEMYL         0.2869       2243.8                 50.00   Rv2711, TB
DRB1_0901   29  IAERLDQSGPTVSQT  LDQSGPTVS         0.2865       2251.8                 50.00   Rv2711, TB
DRB1_0901   26  RARIAERLDQSGPTV  RARIAERLD         0.2822       2359.8                 50.00   Rv2711, TB
DRB1_0901  202  GGVTIVIPGHENVTL  IVIPGHENV         0.2812       2384.6                 50.00   Rv2711, TB
DRB1_0901  195  TVETTPGGGVTIVIP  VETTPGGGV         0.2806       2401.3                 50.00   Rv2711, TB
DRB1_0901   80  LAERLLVDVIGLPWE  ERLLVDVIG         0.2775       2483.6                 50.00   Rv2711, TB
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   DRB1_0901   12  RTIYDLEEEGVTPLR  IYDLEEEGV        0.2768       2502.3              50.00  Rv2711, TB
   DRB1_0901  201  GGGVTIVIPGHENVT  VIPGHENVT        0.2752       2545.2              50.00  Rv2711, TB
   DRB1_0901   85  LVDVIGLPWEEVHAE  VIGLPWEEV        0.2733       2599.0              50.00  Rv2711, TB
   DRB1_0901  120  NNPTTSPFGNPIPGL  TTSPFGNPI        0.2722       2630.4              50.00  Rv2711, TB
   DRB1_0901  188  VVPNARVTVETTPGG  VVPNARVTV        0.2611       2966.7              50.00  Rv2711, TB
   DRB1_0901   13  TIYDLEEEGVTPLRA  YDLEEEGVT        0.2598       3006.6              50.00  Rv2711, TB
   DRB1_0901  194  VTVETTPGGGVTIVI  ETTPGGGVT        0.2586       3046.5              50.00  Rv2711, TB
   DRB1_0901  200  PGGGVTIVIPGHENV  IVIPGHENV        0.2483       3404.4              50.00  Rv2711, TB
   DRB1_0901   58  DRHLELTEKGRALAI  LTEKGRALA        0.2482       3410.8              50.00  Rv2711, TB
   DRB1_0901   81  AERLLVDVIGLPWEE  ERLLVDVIG        0.2465       3474.0              50.00  Rv2711, TB
   DRB1_0901  197  ETTPGGGVTIVIPGH  ETTPGGGVT        0.2431       3601.4              50.00  Rv2711, TB
   DRB1_0901  192  ARVTVETTPGGGVTI  VETTPGGGV        0.2392       3758.5              50.00  Rv2711, TB
   DRB1_0901  193  RVTVETTPGGGVTIV  VETTPGGGV        0.2391       3761.5              50.00  Rv2711, TB
   DRB1_0901   28  RIAERLDQSGPTVSQ  RLDQSGPTV        0.2351       3930.4              50.00  Rv2711, TB
   DRB1_0901   55  VAGDRHLELTEKGRA  AGDRHLELT        0.2325       4040.6              50.00  Rv2711, TB
   DRB1_0901  191  NARVTVETTPGGGVT  VETTPGGGV        0.2293       4184.6              50.00  Rv2711, TB
   DRB1_0901  199  TPGGGVTIVIPGHEN  PGGGVTIVI        0.2276       4262.2              50.00  Rv2711, TB
   DRB1_0901  172  HVQGDIDLITRLKDA  HVQGDIDLI        0.2257       4348.9              50.00  Rv2711, TB
   DRB1_0901   57  GDRHLELTEKGRALA  LTEKGRALA        0.2248       4390.0              50.00  Rv2711, TB
   DRB1_0901   56  AGDRHLELTEKGRAL  LELTEKGRA        0.2247       4395.5              50.00  Rv2711, TB
   DRB1_0901  189  VPNARVTVETTPGGG  VPNARVTVE        0.2238       4440.5              50.00  Rv2711, TB
   DRB1_0901   54  RVAGDRHLELTEKGR  AGDRHLELT        0.2195       4648.9              50.00  Rv2711, TB
   DRB1_0901   27  ARIAERLDQSGPTVS  RLDQSGPTV        0.2156       4851.2              50.00  Rv2711, TB
   DRB1_0901  198  TTPGGGVTIVIPGHE  PGGGVTIVI        0.2075       5296.6              50.00  Rv2711, TB
   DRB1_0901  138  GVGPEPGADDANLVR  VGPEPGADD        0.2069       5332.7              50.00  Rv2711, TB
   DRB1_0901  139  VGPEPGADDANLVRL  VGPEPGADD        0.1981       5863.4              50.00  Rv2711, TB
   DRB1_0901  143  PGADDANLVRLTELP  NLVRLTELP        0.1935       6160.4              50.00  Rv2711, TB
   DRB1_0901  190  PNARVTVETTPGGGV  VETTPGGGV        0.1930       6197.3              50.00  Rv2711, TB
   DRB1_0901  173  VQGDIDLITRLKDAG  DIDLITRLK        0.1500       9865.2              50.00  Rv2711, TB
   DRB1_0901  142  EPGADDANLVRLTEL  ANLVRLTEL        0.1313      12082.8              50.00  Rv2711, TB
   DRB1_0901  140  GPEPGADDANLVRLT  EPGADDANL        0.1101      15189.5              50.00  Rv2711, TB
   DRB1_0901  141  PEPGADDANLVRLTE  EPGADDANL        0.0910      18677.4              50.00  Rv2711, TB
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Allele: DRB1_0901. Number of high binders 3. Number of weak binders 66. Number of peptides 216

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1101  112  ERRLVKVLNNPTTSP  LVKVLNNPT        0.8493          5.1          SB     0.10  Rv2711, TB
   DRB1_1101  113  RRLVKVLNNPTTSPF  VKVLNNPTT        0.8435          5.4          SB     0.15  Rv2711, TB
   DRB1_1101  111  VERRLVKVLNNPTTS  LVKVLNNPT        0.8379          5.8          SB     0.15  Rv2711, TB
   DRB1_1101  110  DVERRLVKVLNNPTT  LVKVLNNPT        0.8037          8.4          SB     0.40  Rv2711, TB
   DRB1_1101  114  RLVKVLNNPTTSPFG  VKVLNNPTT        0.7985          8.8          SB     0.40  Rv2711, TB
   DRB1_1101   69  ALAIAVMRKHRLAER  IAVMRKHRL        0.7703         12.0          SB     0.80  Rv2711, TB
   DRB1_1101   70  LAIAVMRKHRLAERL  LAIAVMRKH        0.7693         12.1          SB     0.80  Rv2711, TB
   DRB1_1101  109  EDVERRLVKVLNNPT  RRLVKVLNN        0.7525         14.6          SB     1.00  Rv2711, TB
   DRB1_1101   68  RALAIAVMRKHRLAE  LAIAVMRKH        0.7392         16.8          SB     2.00  Rv2711, TB
   DRB1_1101  115  LVKVLNNPTTSPFGN  VKVLNNPTT        0.7075         23.7          SB     2.00  Rv2711, TB
   DRB1_1101   71  AIAVMRKHRLAERLL  IAVMRKHRL        0.6975         26.4          SB     4.00  Rv2711, TB
   DRB1_1101   67  GRALAIAVMRKHRLA  LAIAVMRKH        0.6891         28.9          SB     4.00  Rv2711, TB
   DRB1_1101   72  IAVMRKHRLAERLLV  IAVMRKHRL        0.6669         36.7          SB     4.00  Rv2711, TB
   DRB1_1101  108  SEDVERRLVKVLNNP  RRLVKVLNN        0.6555         41.6          SB     4.00  Rv2711, TB
   DRB1_1101   66  KGRALAIAVMRKHRL  LAIAVMRKH        0.5978         77.6          WB     8.00  Rv2711, TB
   DRB1_1101  160  SPVAVVVRQLTEHVQ  VAVVVRQLT        0.5851         89.0          WB     8.00  Rv2711, TB
   DRB1_1101  107  MSEDVERRLVKVLNN  RRLVKVLNN        0.5822         91.9          WB     8.00  Rv2711, TB
   DRB1_1101   73  AVMRKHRLAERLLVD  AVMRKHRLA        0.5813         92.8          WB     8.00  Rv2711, TB
   DRB1_1101  159  GSPVAVVVRQLTEHV  VAVVVRQLT        0.5789         95.2          WB     8.00  Rv2711, TB
   DRB1_1101  147  DANLVRLTELPAGSP  LVRLTELPA        0.5729        101.7          WB     8.00  Rv2711, TB
   DRB1_1101  161  PVAVVVRQLTEHVQG  VAVVVRQLT        0.5728        101.7          WB     8.00  Rv2711, TB
   DRB1_1101  148  ANLVRLTELPAGSPV  LVRLTELPA        0.5628        113.4          WB    16.00  Rv2711, TB
   DRB1_1101  162  VAVVVRQLTEHVQGD  VAVVVRQLT        0.5553        123.0          WB    16.00  Rv2711, TB
   DRB1_1101   74  VMRKHRLAERLLVDV  KHRLAERLL        0.5484        132.4          WB    16.00  Rv2711, TB
   DRB1_1101   19  EEGVTPLRARIAERL  VTPLRARIA        0.5453        136.9          WB    16.00  Rv2711, TB
   DRB1_1101  149  NLVRLTELPAGSPVA  LVRLTELPA        0.5393        146.2          WB    16.00  Rv2711, TB
   DRB1_1101   75  MRKHRLAERLLVDVI  HRLAERLLV        0.5251        170.5          WB    16.00  Rv2711, TB
   DRB1_1101  146  DDANLVRLTELPAGS  LVRLTELPA        0.5250        170.6          WB    16.00  Rv2711, TB
   DRB1_1101   20  EGVTPLRARIAERLD  VTPLRARIA        0.5203        179.5          WB    16.00  Rv2711, TB
   DRB1_1101   18  EEEGVTPLRARIAER  VTPLRARIA        0.5094        202.0          WB    16.00  Rv2711, TB
   DRB1_1101  158  AGSPVAVVVRQLTEH  VAVVVRQLT        0.5088        203.3          WB    16.00  Rv2711, TB
   DRB1_1101   76  RKHRLAERLLVDVIG  HRLAERLLV        0.4875        255.9          WB    16.00  Rv2711, TB
   DRB1_1101   21  GVTPLRARIAERLDQ  VTPLRARIA        0.4693        311.8          WB    32.00  Rv2711, TB
   DRB1_1101   65  EKGRALAIAVMRKHR  LAIAVMRKH        0.4668        320.2          WB    32.00  Rv2711, TB
   DRB1_1101  116  VKVLNNPTTSPFGNP  VKVLNNPTT        0.4640        330.2          WB    32.00  Rv2711, TB
   DRB1_1101  150  LVRLTELPAGSPVAV  LVRLTELPA        0.4632        333.0          WB    32.00  Rv2711, TB
   DRB1_1101  145  ADDANLVRLTELPAG  LVRLTELPA        0.4619        337.5          WB    32.00  Rv2711, TB
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DRB1_1101   77  KHRLAERLLVDVIGL  HRLAERLLV         0.4528        372.6          WB    32.00   Rv2711, TB
DRB1_1101    6  TTEMYLRTIYDLEEE  EMYLRTIYD         0.4444        408.2          WB    32.00   Rv2711, TB
DRB1_1101   17  LEEEGVTPLRARIAE  VTPLRARIA         0.4431        413.9          WB    32.00   Rv2711, TB
DRB1_1101    5  DTTEMYLRTIYDLEE  EMYLRTIYD         0.4394        430.6          WB    32.00   Rv2711, TB
DRB1_1101   60  HLELTEKGRALAIAV  LTEKGRALA         0.4296        478.9          WB    32.00   Rv2711, TB
DRB1_1101    7  TEMYLRTIYDLEEEG  EMYLRTIYD         0.4227        516.2                32.00   Rv2711, TB
DRB1_1101  174  QGDIDLITRLKDAGV  IDLITRLKD         0.4155        557.8                32.00   Rv2711, TB
DRB1_1101    4  VDTTEMYLRTIYDLE  EMYLRTIYD         0.4147        562.8                32.00   Rv2711, TB
DRB1_1101  175  GDIDLITRLKDAGVV  IDLITRLKD         0.4123        577.6                32.00   Rv2711, TB
DRB1_1101  157  PAGSPVAVVVRQLTE  VAVVVRQLT         0.4122        578.4                32.00   Rv2711, TB
DRB1_1101  144  GADDANLVRLTELPA  LVRLTELPA         0.4067        613.5                32.00   Rv2711, TB
DRB1_1101   61  LELTEKGRALAIAVM  LTEKGRALA         0.4063        616.1                32.00   Rv2711, TB
DRB1_1101   59  RHLELTEKGRALAIA  LTEKGRALA         0.3923        716.8                32.00   Rv2711, TB
DRB1_1101  106  VMSEDVERRLVKVLN  ERRLVKVLN         0.3922        717.5                32.00   Rv2711, TB
DRB1_1101   62  ELTEKGRALAIAVMR  LTEKGRALA         0.3840        784.9                32.00   Rv2711, TB
DRB1_1101   49  RDGLLRVAGDRHLEL  LLRVAGDRH         0.3837        786.7                32.00   Rv2711, TB
DRB1_1101    8  EMYLRTIYDLEEEGV  EMYLRTIYD         0.3803        816.6                32.00   Rv2711, TB
DRB1_1101   16  DLEEEGVTPLRARIA  VTPLRARIA         0.3789        828.7                32.00   Rv2711, TB
DRB1_1101  176  DIDLITRLKDAGVVP  IDLITRLKD         0.3788        829.6                32.00   Rv2711, TB
DRB1_1101   63  LTEKGRALAIAVMRK  LTEKGRALA         0.3728        885.9                32.00   Rv2711, TB
DRB1_1101   51  GLLRVAGDRHLELTE  LLRVAGDRH         0.3644        969.6                32.00   Rv2711, TB
DRB1_1101   46  RMERDGLLRVAGDRH  RDGLLRVAG         0.3627        987.6                32.00   Rv2711, TB
DRB1_1101  173  VQGDIDLITRLKDAG  IDLITRLKD         0.3590       1027.9                32.00   Rv2711, TB
DRB1_1101   52  LLRVAGDRHLELTEK  LLRVAGDRH         0.3576       1043.3                32.00   Rv2711, TB
DRB1_1101   48  ERDGLLRVAGDRHLE  RDGLLRVAG         0.3563       1058.0                32.00   Rv2711, TB
DRB1_1101   47  MERDGLLRVAGDRHL  RDGLLRVAG         0.3553       1069.5                32.00   Rv2711, TB
DRB1_1101  212  ENVTLPHEMAHAVKV  NVTLPHEMA         0.3544       1081.0                32.00   Rv2711, TB
DRB1_1101   38  PTVSQTVSRMERDGL  SQTVSRMER         0.3536       1090.4                50.00   Rv2711, TB
DRB1_1101   50  DGLLRVAGDRHLELT  LLRVAGDRH         0.3531       1095.3                50.00   Rv2711, TB
DRB1_1101   64  TEKGRALAIAVMRKH  LAIAVMRKH         0.3530       1096.8                50.00   Rv2711, TB
DRB1_1101   78  HRLAERLLVDVIGLP  HRLAERLLV         0.3495       1140.0                50.00   Rv2711, TB
DRB1_1101  177  IDLITRLKDAGVVPN  IDLITRLKD         0.3491       1143.9                50.00   Rv2711, TB
DRB1_1101   58  DRHLELTEKGRALAI  LTEKGRALA         0.3459       1184.5                50.00   Rv2711, TB
DRB1_1101  213  NVTLPHEMAHAVKVE  VTLPHEMAH         0.3391       1275.2                50.00   Rv2711, TB
DRB1_1101  211  HENVTLPHEMAHAVK  NVTLPHEMA         0.3360       1319.1                50.00   Rv2711, TB
DRB1_1101    3  LVDTTEMYLRTIYDL  TEMYLRTIY         0.3352       1329.6                50.00   Rv2711, TB
DRB1_1101   39  TVSQTVSRMERDGLL  SQTVSRMER         0.3320       1377.5                50.00   Rv2711, TB
DRB1_1101  163  AVVVRQLTEHVQGDI  AVVVRQLTE         0.3275       1445.1                50.00   Rv2711, TB
DRB1_1101  210  GHENVTLPHEMAHAV  NVTLPHEMA         0.3209       1552.3                50.00   Rv2711, TB
DRB1_1101   40  VSQTVSRMERDGLLR  SQTVSRMER         0.3199       1569.7                50.00   Rv2711, TB
DRB1_1101   22  VTPLRARIAERLDQS  VTPLRARIA         0.3195       1576.2                50.00   Rv2711, TB
DRB1_1101  156  LPAGSPVAVVVRQLT  VAVVVRQLT         0.3182       1599.4                50.00   Rv2711, TB
DRB1_1101   37  GPTVSQTVSRMERDG  SQTVSRMER         0.3099       1748.8                50.00   Rv2711, TB
DRB1_1101   45  SRMERDGLLRVAGDR  RDGLLRVAG         0.3029       1886.8                50.00   Rv2711, TB
DRB1_1101  172  HVQGDIDLITRLKDA  IDLITRLKD         0.2958       2037.1                50.00   Rv2711, TB
DRB1_1101  100  ACRWEHVMSEDVERR  WEHVMSEDV         0.2927       2105.8                50.00   Rv2711, TB
DRB1_1101  185  DAGVVPNARVTVETT  VVPNARVTV         0.2926       2109.3                50.00   Rv2711, TB
DRB1_1101   57  GDRHLELTEKGRALA  LTEKGRALA         0.2892       2187.7                50.00   Rv2711, TB
DRB1_1101   99  EACRWEHVMSEDVER  WEHVMSEDV         0.2806       2400.1                50.00   Rv2711, TB
DRB1_1101  186  AGVVPNARVTVETTP  VVPNARVTV         0.2793       2435.0                50.00   Rv2711, TB
DRB1_1101    2  ELVDTTEMYLRTIYD  TEMYLRTIY         0.2704       2681.7                50.00   Rv2711, TB
DRB1_1101  184  KDAGVVPNARVTVET  VVPNARVTV         0.2686       2733.9                50.00   Rv2711, TB
DRB1_1101   41  SQTVSRMERDGLLRV  SQTVSRMER         0.2650       2843.1                50.00   Rv2711, TB
DRB1_1101   36  SGPTVSQTVSRMERD  SQTVSRMER         0.2627       2913.4                50.00   Rv2711, TB
DRB1_1101  209  PGHENVTLPHEMAHA  NVTLPHEMA         0.2626       2918.1                50.00   Rv2711, TB
DRB1_1101  214  VTLPHEMAHAVKVEK  VTLPHEMAH         0.2589       3037.1                50.00   Rv2711, TB
DRB1_1101   44  VSRMERDGLLRVAGD  RDGLLRVAG         0.2496       3356.5                50.00   Rv2711, TB
DRB1_1101  164  VVVRQLTEHVQGDID  VVRQLTEHV         0.2494       3365.0                50.00   Rv2711, TB
DRB1_1101   43  TVSRMERDGLLRVAG  RMERDGLLR         0.2489       3382.7                50.00   Rv2711, TB
DRB1_1101   98  AEACRWEHVMSEDVE  ACRWEHVMS         0.2483       3404.2                50.00   Rv2711, TB
DRB1_1101  183  LKDAGVVPNARVTVE  AGVVPNARV         0.2404       3708.2                50.00   Rv2711, TB
DRB1_1101  151  VRLTELPAGSPVAVV  LTELPAGSP         0.2401       3721.1                50.00   Rv2711, TB
DRB1_1101  101  CRWEHVMSEDVERRL  WEHVMSEDV         0.2388       3775.2                50.00   Rv2711, TB
DRB1_1101   83  RLLVDVIGLPWEEVH  LVDVIGLPW         0.2377       3820.4                50.00   Rv2711, TB
DRB1_1101   82  ERLLVDVIGLPWEEV  LVDVIGLPW         0.2341       3973.1                50.00   Rv2711, TB
DRB1_1101   80  LAERLLVDVIGLPWE  ERLLVDVIG         0.2329       4025.5                50.00   Rv2711, TB
DRB1_1101  105  HVMSEDVERRLVKVL  EDVERRLVK         0.2328       4026.7                50.00   Rv2711, TB
DRB1_1101   84  LLVDVIGLPWEEVHA  LVDVIGLPW         0.2288       4204.4                50.00   Rv2711, TB
DRB1_1101   97  HAEACRWEHVMSEDV  ACRWEHVMS         0.2275       4265.0                50.00   Rv2711, TB
DRB1_1101   79  RLAERLLVDVIGLPW  ERLLVDVIG         0.2254       4361.3                50.00   Rv2711, TB
DRB1_1101  171  EHVQGDIDLITRLKD  IDLITRLKD         0.2253       4365.8                50.00   Rv2711, TB
DRB1_1101  215  TLPHEMAHAVKVEKV  HEMAHAVKV         0.2251       4378.5                50.00   Rv2711, TB
DRB1_1101    9  MYLRTIYDLEEEGVT  YLRTIYDLE         0.2251       4378.9                50.00   Rv2711, TB
DRB1_1101   35  QSGPTVSQTVSRMER  SQTVSRMER         0.2238       4441.8                50.00   Rv2711, TB
DRB1_1101  143  PGADDANLVRLTELP  DANLVRLTE         0.2199       4632.1                50.00   Rv2711, TB
DRB1_1101  187  GVVPNARVTVETTPG  VVPNARVTV         0.2184       4705.8                50.00   Rv2711, TB
DRB1_1101   81  AERLLVDVIGLPWEE  LVDVIGLPW         0.2163       4814.9                50.00   Rv2711, TB
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DRB1_1101   53  LRVAGDRHLELTEKG  VAGDRHLEL       0.2135      4961.1             50.00  Rv2711, TB
DRB1_1101  178  DLITRLKDAGVVPNA  LITRLKDAG       0.2132      4979.8             50.00  Rv2711, TB
DRB1_1101  182  RLKDAGVVPNARVTV  AGVVPNARV       0.2132      4981.2             50.00  Rv2711, TB
DRB1_1101   85  LVDVIGLPWEEVHAE  LVDVIGLPW       0.2121      5041.3             50.00  Rv2711, TB
DRB1_1101  165  VVRQLTEHVQGDIDL  VVRQLTEHV       0.2091      5202.2             50.00  Rv2711, TB
DRB1_1101  208  IPGHENVTLPHEMAH  NVTLPHEMA       0.2048      5453.8             50.00  Rv2711, TB
DRB1_1101   15  YDLEEEGVTPLRARI  GVTPLRARI       0.2034      5534.8             50.00  Rv2711, TB
DRB1_1101  102  RWEHVMSEDVERRLV  WEHVMSEDV       0.2031      5557.0             50.00  Rv2711, TB
DRB1_1101  179  LITRLKDAGVVPNAR  LITRLKDAG       0.1954      6037.4             50.00  Rv2711, TB
DRB1_1101   42  QTVSRMERDGLLRVA  RMERDGLLR       0.1944      6100.9             50.00  Rv2711, TB
DRB1_1101  103  WEHVMSEDVERRLVK  WEHVMSEDV       0.1931      6187.8             50.00  Rv2711, TB
DRB1_1101  202  GGVTIVIPGHENVTL  VTIVIPGHE       0.1909      6339.1             50.00  Rv2711, TB
DRB1_1101  180  ITRLKDAGVVPNARV  ITRLKDAGV       0.1868      6624.0             50.00  Rv2711, TB
DRB1_1101   10  YLRTIYDLEEEGVTP  YLRTIYDLE       0.1854      6729.9             50.00  Rv2711, TB
DRB1_1101  152  RLTELPAGSPVAVVV  LTELPAGSP       0.1848      6773.7             50.00  Rv2711, TB
DRB1_1101  203  GVTIVIPGHENVTLP  VTIVIPGHE       0.1847      6779.1             50.00  Rv2711, TB
DRB1_1101   95  EVHAEACRWEHVMSE  EVHAEACRW       0.1840      6828.4             50.00  Rv2711, TB
DRB1_1101  188  VVPNARVTVETTPGG  VVPNARVTV       0.1818      6994.1             50.00  Rv2711, TB
DRB1_1101  201  GGGVTIVIPGHENVT  VTIVIPGHE       0.1799      7136.6             50.00  Rv2711, TB
DRB1_1101  129  NPIPGLVELGVGPEP  IPGLVELGV       0.1741      7598.9             50.00  Rv2711, TB
DRB1_1101  181  TRLKDAGVVPNARVT  LKDAGVVPN       0.1727      7718.7             50.00  Rv2711, TB
DRB1_1101  128  GNPIPGLVELGVGPE  IPGLVELGV       0.1712      7843.8             50.00  Rv2711, TB
DRB1_1101   24  PLRARIAERLDQSGP  RARIAERLD       0.1690      8030.6             50.00  Rv2711, TB
DRB1_1101   56  AGDRHLELTEKGRAL  RHLELTEKG       0.1674      8168.6             50.00  Rv2711, TB
DRB1_1101  130  PIPGLVELGVGPEPG  IPGLVELGV       0.1671      8196.9             50.00  Rv2711, TB
DRB1_1101  142  EPGADDANLVRLTEL  DANLVRLTE       0.1651      8379.5             50.00  Rv2711, TB
DRB1_1101  127  FGNPIPGLVELGVGP  IPGLVELGV       0.1646      8427.1             50.00  Rv2711, TB
DRB1_1101   54  RVAGDRHLELTEKGR  VAGDRHLEL       0.1645      8431.2             50.00  Rv2711, TB
DRB1_1101   23  TPLRARIAERLDQSG  RARIAERLD       0.1633      8547.3             50.00  Rv2711, TB
DRB1_1101   96  VHAEACRWEHVMSED  ACRWEHVMS       0.1625      8616.3             50.00  Rv2711, TB
DRB1_1101   94  EEVHAEACRWEHVMS  EVHAEACRW       0.1624      8628.0             50.00  Rv2711, TB
DRB1_1101  204  VTIVIPGHENVTLPH  TIVIPGHEN       0.1596      8891.6             50.00  Rv2711, TB
DRB1_1101  104  EHVMSEDVERRLVKV  SEDVERRLV       0.1561      9231.3             50.00  Rv2711, TB
DRB1_1101    1  NELVDTTEMYLRTIY  TEMYLRTIY       0.1536      9487.3             50.00  Rv2711, TB
DRB1_1101   25  LRARIAERLDQSGPT  ARIAERLDQ       0.1523      9619.7             50.00  Rv2711, TB
DRB1_1101   55  VAGDRHLELTEKGRA  RHLELTEKG       0.1508      9776.7             50.00  Rv2711, TB
DRB1_1101  126  PFGNPIPGLVELGVG  IPGLVELGV       0.1503      9838.3             50.00  Rv2711, TB
DRB1_1101  200  PGGGVTIVIPGHENV  VTIVIPGHE       0.1481     10066.1             50.00  Rv2711, TB
DRB1_1101  131  IPGLVELGVGPEPGA  IPGLVELGV       0.1460     10298.5             50.00  Rv2711, TB
DRB1_1101  166  VRQLTEHVQGDIDLI  RQLTEHVQG       0.1450     10416.1             50.00  Rv2711, TB
DRB1_1101  207  VIPGHENVTLPHEMA  NVTLPHEMA       0.1425     10694.5             50.00  Rv2711, TB
DRB1_1101   86  VDVIGLPWEEVHAEA  VIGLPWEEV       0.1375     11299.5             50.00  Rv2711, TB
DRB1_1101  125  SPFGNPIPGLVELGV  IPGLVELGV       0.1361     11469.1             50.00  Rv2711, TB
DRB1_1101  124  TSPFGNPIPGLVELG  TSPFGNPIP       0.1360     11477.1             50.00  Rv2711, TB
DRB1_1101  190  PNARVTVETTPGGGV  RVTVETTPG       0.1360     11482.6             50.00  Rv2711, TB
DRB1_1101  191  NARVTVETTPGGGVT  RVTVETTPG       0.1346     11654.5             50.00  Rv2711, TB
DRB1_1101  205  TIVIPGHENVTLPHE  TIVIPGHEN       0.1333     11817.7             50.00  Rv2711, TB
DRB1_1101   34  DQSGPTVSQTVSRME  VSQTVSRME       0.1311     12101.7             50.00  Rv2711, TB
DRB1_1101  133  GLVELGVGPEPGADD  VELGVGPEP       0.1288     12413.1             50.00  Rv2711, TB
DRB1_1101  153  LTELPAGSPVAVVVR  LTELPAGSP       0.1287     12425.7             50.00  Rv2711, TB
DRB1_1101   26  RARIAERLDQSGPTV  ARIAERLDQ       0.1283     12477.3             50.00  Rv2711, TB
DRB1_1101  123  TTSPFGNPIPGLVEL  TSPFGNPIP       0.1241     13055.5             50.00  Rv2711, TB
DRB1_1101   93  WEEVHAEACRWEHVM  EVHAEACRW       0.1231     13200.7             50.00  Rv2711, TB
DRB1_1101  132  PGLVELGVGPEPGAD  VELGVGPEP       0.1221     13348.1             50.00  Rv2711, TB
DRB1_1101  189  VPNARVTVETTPGGG  NARVTVETT       0.1212     13475.3             50.00  Rv2711, TB
DRB1_1101    0  MNELVDTTEMYLRTI  LVDTTEMYL       0.1209     13510.8             50.00  Rv2711, TB
DRB1_1101  192  ARVTVETTPGGGVTI  RVTVETTPG       0.1201     13635.9             50.00  Rv2711, TB
DRB1_1101  199  TPGGGVTIVIPGHEN  VTIVIPGHE       0.1163     14202.9             50.00  Rv2711, TB
DRB1_1101  134  LVELGVGPEPGADDA  VELGVGPEP       0.1135     14641.6             50.00  Rv2711, TB
DRB1_1101   92  PWEEVHAEACRWEHV  EVHAEACRW       0.1122     14857.6             50.00  Rv2711, TB
DRB1_1101  122  PTTSPFGNPIPGLVE  TSPFGNPIP       0.1112     15019.4             50.00  Rv2711, TB
DRB1_1101  117  KVLNNPTTSPFGNPI  KVLNNPTTS       0.1060     15889.5             50.00  Rv2711, TB
DRB1_1101  141  PEPGADDANLVRLTE  DANLVRLTE       0.1045     16146.5             50.00  Rv2711, TB
DRB1_1101  167  RQLTEHVQGDIDLIT  RQLTEHVQG       0.1039     16238.6             50.00  Rv2711, TB
DRB1_1101  121  NPTTSPFGNPIPGLV  TSPFGNPIP       0.1027     16464.6             50.00  Rv2711, TB
DRB1_1101   87  DVIGLPWEEVHAEAC  VIGLPWEEV       0.1012     16735.6             50.00  Rv2711, TB
DRB1_1101   27  ARIAERLDQSGPTVS  ARIAERLDQ       0.0969     17515.2             50.00  Rv2711, TB
DRB1_1101   14  IYDLEEEGVTPLRAR  IYDLEEEGV       0.0965     17601.0             50.00  Rv2711, TB
DRB1_1101  135  VELGVGPEPGADDAN  VELGVGPEP       0.0942     18039.9             50.00  Rv2711, TB
DRB1_1101  170  TEHVQGDIDLITRLK  VQGDIDLIT       0.0926     18366.6             50.00  Rv2711, TB
DRB1_1101  193  RVTVETTPGGGVTIV  RVTVETTPG       0.0901     18863.6             50.00  Rv2711, TB
DRB1_1101   91  LPWEEVHAEACRWEH  EVHAEACRW       0.0882     19253.4             50.00  Rv2711, TB
DRB1_1101  155  ELPAGSPVAVVVRQL  LPAGSPVAV       0.0838     20189.5             50.00  Rv2711, TB
DRB1_1101  206  IVIPGHENVTLPHEM  GHENVTLPH       0.0834     20290.2             50.00  Rv2711, TB
DRB1_1101  169  LTEHVQGDIDLITRL  HVQGDIDLI       0.0772     21688.7             50.00  Rv2711, TB
DRB1_1101   88  VIGLPWEEVHAEACR  VIGLPWEEV       0.0755     22100.1             50.00  Rv2711, TB
DRB1_1101   11  LRTIYDLEEEGVTPL  TIYDLEEEG       0.0740     22459.3             50.00  Rv2711, TB
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   DRB1_1101   13  TIYDLEEEGVTPLRA  IYDLEEEGV          0.0727      22775.7                 50.00   Rv2711, TB
   DRB1_1101   33  LDQSGPTVSQTVSRM  PTVSQTVSR          0.0710      23182.5                 50.00   Rv2711, TB
   DRB1_1101   90  GLPWEEVHAEACRWE  EVHAEACRW          0.0695      23578.1                 50.00   Rv2711, TB
   DRB1_1101   28  RIAERLDQSGPTVSQ  IAERLDQSG          0.0680      23954.6                 50.00   Rv2711, TB
   DRB1_1101   12  RTIYDLEEEGVTPLR  YDLEEEGVT          0.0680      23955.9                 50.00   Rv2711, TB
   DRB1_1101   29  IAERLDQSGPTVSQT  RLDQSGPTV          0.0667      24303.6                 50.00   Rv2711, TB
   DRB1_1101  118  VLNNPTTSPFGNPIP  VLNNPTTSP          0.0663      24393.2                 50.00   Rv2711, TB
   DRB1_1101  168  QLTEHVQGDIDLITR  HVQGDIDLI          0.0662      24436.0                 50.00   Rv2711, TB
   DRB1_1101  120  NNPTTSPFGNPIPGL  TSPFGNPIP          0.0641      24976.7                 50.00   Rv2711, TB
   DRB1_1101  198  TTPGGGVTIVIPGHE  VTIVIPGHE          0.0628      25330.8                 50.00   Rv2711, TB
   DRB1_1101   32  RLDQSGPTVSQTVSR  RLDQSGPTV          0.0597      26206.2                 50.00   Rv2711, TB
   DRB1_1101   89  IGLPWEEVHAEACRW  EVHAEACRW          0.0596      26244.5                 50.00   Rv2711, TB
   DRB1_1101  136  ELGVGPEPGADDANL  LGVGPEPGA          0.0584      26593.2                 50.00   Rv2711, TB
   DRB1_1101   30  AERLDQSGPTVSQTV  RLDQSGPTV          0.0522      28436.2                 50.00   Rv2711, TB
   DRB1_1101  119  LNNPTTSPFGNPIPG  TSPFGNPIP          0.0496      29244.0                 50.00   Rv2711, TB
   DRB1_1101  154  TELPAGSPVAVVVRQ  LPAGSPVAV          0.0462      30332.7                 50.00   Rv2711, TB
   DRB1_1101  194  VTVETTPGGGVTIVI  VTVETTPGG          0.0448      30784.3                 50.00   Rv2711, TB
   DRB1_1101  137  LGVGPEPGADDANLV  LGVGPEPGA          0.0438      31139.1                 50.00   Rv2711, TB
   DRB1_1101   31  ERLDQSGPTVSQTVS  LDQSGPTVS          0.0397      32525.8                 50.00   Rv2711, TB
   DRB1_1101  140  GPEPGADDANLVRLT  DDANLVRLT          0.0370      33491.8                 50.00   Rv2711, TB
   DRB1_1101  197  ETTPGGGVTIVIPGH  GGVTIVIPG          0.0344      34469.0                 50.00   Rv2711, TB
   DRB1_1101  195  TVETTPGGGVTIVIP  TTPGGGVTI          0.0320      35352.1                 50.00   Rv2711, TB
   DRB1_1101  196  VETTPGGGVTIVIPG  GGVTIVIPG          0.0263      37601.8                 50.00   Rv2711, TB
   DRB1_1101  139  VGPEPGADDANLVRL  VGPEPGADD          0.0115      44133.9                 50.00   Rv2711, TB
   DRB1_1101  138  GVGPEPGADDANLVR  VGPEPGADD          0.0089      45404.3                 50.00   Rv2711, TB
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Allele: DRB1_1101. Number of high binders 14. Number of weak binders 28. Number of peptides 216

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random    Identity
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   DRB1_1302   66  KGRALAIAVMRKHRL  IAVMRKHRL          0.6850         30.2          SB      2.00   Rv2711, TB
   DRB1_1302   67  GRALAIAVMRKHRLA  IAVMRKHRL          0.6598         39.7          SB      4.00   Rv2711, TB
   DRB1_1302  182  RLKDAGVVPNARVTV  AGVVPNARV          0.6471         45.5          SB      4.00   Rv2711, TB
   DRB1_1302  183  LKDAGVVPNARVTVE  AGVVPNARV          0.6209         60.4          WB      4.00   Rv2711, TB
   DRB1_1302  110  DVERRLVKVLNNPTT  LVKVLNNPT          0.6135         65.5          WB      4.00   Rv2711, TB
   DRB1_1302  111  VERRLVKVLNNPTTS  LVKVLNNPT          0.6042         72.4          WB      8.00   Rv2711, TB
   DRB1_1302  113  RRLVKVLNNPTTSPF  LVKVLNNPT          0.6019         74.3          WB      8.00   Rv2711, TB
   DRB1_1302  184  KDAGVVPNARVTVET  AGVVPNARV          0.6008         75.2          WB      8.00   Rv2711, TB
   DRB1_1302   68  RALAIAVMRKHRLAE  IAVMRKHRL          0.6004         75.5          WB      8.00   Rv2711, TB
   DRB1_1302  112  ERRLVKVLNNPTTSP  LVKVLNNPT          0.5987         76.9          WB      8.00   Rv2711, TB
   DRB1_1302   69  ALAIAVMRKHRLAER  IAVMRKHRL          0.5883         86.0          WB      8.00   Rv2711, TB
   DRB1_1302  109  EDVERRLVKVLNNPT  LVKVLNNPT          0.5871         87.2          WB      8.00   Rv2711, TB
   DRB1_1302  185  DAGVVPNARVTVETT  AGVVPNARV          0.5845         89.6          WB      8.00   Rv2711, TB
   DRB1_1302   70  LAIAVMRKHRLAERL  IAVMRKHRL          0.5835         90.6          WB      8.00   Rv2711, TB
   DRB1_1302  186  AGVVPNARVTVETTP  AGVVPNARV          0.5725        102.1          WB      8.00   Rv2711, TB
   DRB1_1302   71  AIAVMRKHRLAERLL  IAVMRKHRL          0.5713        103.4          WB      8.00   Rv2711, TB
   DRB1_1302   72  IAVMRKHRLAERLLV  IAVMRKHRL          0.5592        117.9          WB      8.00   Rv2711, TB
   DRB1_1302   62  ELTEKGRALAIAVMR  KGRALAIAV          0.5566        121.2          WB      8.00   Rv2711, TB
   DRB1_1302  181  TRLKDAGVVPNARVT  AGVVPNARV          0.5510        128.7          WB      8.00   Rv2711, TB
   DRB1_1302   61  LELTEKGRALAIAVM  KGRALAIAV          0.5469        134.7          WB      8.00   Rv2711, TB
   DRB1_1302   64  TEKGRALAIAVMRKH  KGRALAIAV          0.5464        135.3          WB      8.00   Rv2711, TB
   DRB1_1302   63  LTEKGRALAIAVMRK  KGRALAIAV          0.5407        144.0          WB      8.00   Rv2711, TB
   DRB1_1302  180  ITRLKDAGVVPNARV  AGVVPNARV          0.5377        148.7          WB      8.00   Rv2711, TB
   DRB1_1302  114  RLVKVLNNPTTSPFG  LVKVLNNPT          0.5277        165.7          WB     16.00   Rv2711, TB
   DRB1_1302  160  SPVAVVVRQLTEHVQ  VVRQLTEHV          0.5244        171.7          WB     16.00   Rv2711, TB
   DRB1_1302  159  GSPVAVVVRQLTEHV  VVRQLTEHV          0.5231        174.2          WB     16.00   Rv2711, TB
   DRB1_1302  215  TLPHEMAHAVKVEKV  LPHEMAHAV          0.5166        186.8          WB     16.00   Rv2711, TB
   DRB1_1302   65  EKGRALAIAVMRKHR  KGRALAIAV          0.5110        198.4          WB     16.00   Rv2711, TB
   DRB1_1302  161  PVAVVVRQLTEHVQG  VVRQLTEHV          0.5034        215.6          WB     16.00   Rv2711, TB
   DRB1_1302  115  LVKVLNNPTTSPFGN  LVKVLNNPT          0.5001        223.3          WB     16.00   Rv2711, TB
   DRB1_1302  214  VTLPHEMAHAVKVEK  LPHEMAHAV          0.4926        242.2          WB     16.00   Rv2711, TB
   DRB1_1302   60  HLELTEKGRALAIAV  KGRALAIAV          0.4824        270.6          WB     16.00   Rv2711, TB
   DRB1_1302  162  VAVVVRQLTEHVQGD  VVRQLTEHV          0.4753        292.1          WB     16.00   Rv2711, TB
   DRB1_1302  213  NVTLPHEMAHAVKVE  LPHEMAHAV          0.4750        293.1          WB     16.00   Rv2711, TB
   DRB1_1302  212  ENVTLPHEMAHAVKV  LPHEMAHAV          0.4727        300.4          WB     16.00   Rv2711, TB
   DRB1_1302  210  GHENVTLPHEMAHAV  LPHEMAHAV          0.4527        372.9          WB     16.00   Rv2711, TB
   DRB1_1302  211  HENVTLPHEMAHAVK  LPHEMAHAV          0.4425        416.6          WB     32.00   Rv2711, TB
   DRB1_1302  163  AVVVRQLTEHVQGDI  VVRQLTEHV          0.4401        427.4          WB     32.00   Rv2711, TB
   DRB1_1302   79  RLAERLLVDVIGLPW  RLLVDVIGL          0.4208        526.9                 32.00   Rv2711, TB
   DRB1_1302   80  LAERLLVDVIGLPWE  RLLVDVIGL          0.4183        541.2                 32.00   Rv2711, TB
   DRB1_1302  150  LVRLTELPAGSPVAV  LPAGSPVAV          0.4166        551.3                 32.00   Rv2711, TB
   DRB1_1302  187  GVVPNARVTVETTPG  VVPNARVTV          0.4157        556.9                 32.00   Rv2711, TB
   DRB1_1302  152  RLTELPAGSPVAVVV  LPAGSPVAV          0.4111        584.8                 32.00   Rv2711, TB
   DRB1_1302  151  VRLTELPAGSPVAVV  LPAGSPVAV          0.4109        586.4                 32.00   Rv2711, TB
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DRB1_1302  153  LTELPAGSPVAVVVR  LPAGSPVAV       0.4001      659.2             32.00  Rv2711, TB
DRB1_1302   81  AERLLVDVIGLPWEE  RLLVDVIGL       0.3986      670.0             32.00  Rv2711, TB
DRB1_1302  155  ELPAGSPVAVVVRQL  LPAGSPVAV       0.3957      691.4             32.00  Rv2711, TB
DRB1_1302  156  LPAGSPVAVVVRQLT  LPAGSPVAV       0.3932      709.9             32.00  Rv2711, TB
DRB1_1302  165  VVRQLTEHVQGDIDL  VVRQLTEHV       0.3869      759.9             32.00  Rv2711, TB
DRB1_1302  164  VVVRQLTEHVQGDID  VVRQLTEHV       0.3839      785.6             32.00  Rv2711, TB
DRB1_1302  154  TELPAGSPVAVVVRQ  LPAGSPVAV       0.3837      786.6             32.00  Rv2711, TB
DRB1_1302  116  VKVLNNPTTSPFGNP  VKVLNNPTT       0.3830      792.6             32.00  Rv2711, TB
DRB1_1302   82  ERLLVDVIGLPWEEV  RLLVDVIGL       0.3752      862.9             32.00  Rv2711, TB
DRB1_1302   59  RHLELTEKGRALAIA  TEKGRALAI       0.3704      908.5             32.00  Rv2711, TB
DRB1_1302   58  DRHLELTEKGRALAI  TEKGRALAI       0.3688      924.4             32.00  Rv2711, TB
DRB1_1302   47  MERDGLLRVAGDRHL  LRVAGDRHL       0.3587     1031.2             32.00  Rv2711, TB
DRB1_1302   83  RLLVDVIGLPWEEVH  RLLVDVIGL       0.3515     1115.5             32.00  Rv2711, TB
DRB1_1302  177  IDLITRLKDAGVVPN  ITRLKDAGV       0.3449     1198.1             32.00  Rv2711, TB
DRB1_1302  175  GDIDLITRLKDAGVV  ITRLKDAGV       0.3407     1253.4             32.00  Rv2711, TB
DRB1_1302  178  DLITRLKDAGVVPNA  ITRLKDAGV       0.3392     1273.2             32.00  Rv2711, TB
DRB1_1302  179  LITRLKDAGVVPNAR  ITRLKDAGV       0.3338     1350.6             32.00  Rv2711, TB
DRB1_1302  188  VVPNARVTVETTPGG  VVPNARVTV       0.3324     1371.3             32.00  Rv2711, TB
DRB1_1302   78  HRLAERLLVDVIGLP  RLLVDVIGL       0.3273     1448.3             50.00  Rv2711, TB
DRB1_1302   34  DQSGPTVSQTVSRME  TVSQTVSRM       0.3266     1459.4             50.00  Rv2711, TB
DRB1_1302   33  LDQSGPTVSQTVSRM  TVSQTVSRM       0.3250     1484.7             50.00  Rv2711, TB
DRB1_1302   35  QSGPTVSQTVSRMER  TVSQTVSRM       0.3220     1533.6             50.00  Rv2711, TB
DRB1_1302  176  DIDLITRLKDAGVVP  ITRLKDAGV       0.3148     1659.4             50.00  Rv2711, TB
DRB1_1302   73  AVMRKHRLAERLLVD  RKHRLAERL       0.3133     1686.0             50.00  Rv2711, TB
DRB1_1302   77  KHRLAERLLVDVIGL  RLLVDVIGL       0.3114     1721.0             50.00  Rv2711, TB
DRB1_1302   48  ERDGLLRVAGDRHLE  LLRVAGDRH       0.3084     1777.5             50.00  Rv2711, TB
DRB1_1302  117  KVLNNPTTSPFGNPI  LNNPTTSPF       0.3051     1841.8             50.00  Rv2711, TB
DRB1_1302    1  NELVDTTEMYLRTIY  LVDTTEMYL       0.3032     1879.4             50.00  Rv2711, TB
DRB1_1302  174  QGDIDLITRLKDAGV  ITRLKDAGV       0.3019     1907.4             50.00  Rv2711, TB
DRB1_1302   36  SGPTVSQTVSRMERD  TVSQTVSRM       0.2981     1986.7             50.00  Rv2711, TB
DRB1_1302   74  VMRKHRLAERLLVDV  RKHRLAERL       0.2979     1991.7             50.00  Rv2711, TB
DRB1_1302   41  SQTVSRMERDGLLRV  MERDGLLRV       0.2951     2053.2             50.00  Rv2711, TB
DRB1_1302   49  RDGLLRVAGDRHLEL  LLRVAGDRH       0.2949     2056.4             50.00  Rv2711, TB
DRB1_1302  158  AGSPVAVVVRQLTEH  AVVVRQLTE       0.2911     2143.1             50.00  Rv2711, TB
DRB1_1302    0  MNELVDTTEMYLRTI  LVDTTEMYL       0.2868     2244.7             50.00  Rv2711, TB
DRB1_1302   75  MRKHRLAERLLVDVI  RKHRLAERL       0.2861     2263.5             50.00  Rv2711, TB
DRB1_1302   19  EEGVTPLRARIAERL  LRARIAERL       0.2834     2329.7             50.00  Rv2711, TB
DRB1_1302   42  QTVSRMERDGLLRVA  MERDGLLRV       0.2811     2388.7             50.00  Rv2711, TB
DRB1_1302   16  DLEEEGVTPLRARIA  GVTPLRARI       0.2810     2391.8             50.00  Rv2711, TB
DRB1_1302    2  ELVDTTEMYLRTIYD  LVDTTEMYL       0.2781     2466.0             50.00  Rv2711, TB
DRB1_1302   15  YDLEEEGVTPLRARI  GVTPLRARI       0.2775     2482.1             50.00  Rv2711, TB
DRB1_1302   37  GPTVSQTVSRMERDG  TVSQTVSRM       0.2753     2542.2             50.00  Rv2711, TB
DRB1_1302   46  RMERDGLLRVAGDRH  LLRVAGDRH       0.2749     2555.3             50.00  Rv2711, TB
DRB1_1302  193  RVTVETTPGGGVTIV  VETTPGGGV       0.2724     2622.9             50.00  Rv2711, TB
DRB1_1302  202  GGVTIVIPGHENVTL  VIPGHENVT       0.2708     2668.9             50.00  Rv2711, TB
DRB1_1302   50  DGLLRVAGDRHLELT  LLRVAGDRH       0.2705     2678.4             50.00  Rv2711, TB
DRB1_1302  194  VTVETTPGGGVTIVI  VETTPGGGV       0.2690     2723.2             50.00  Rv2711, TB
DRB1_1302   76  RKHRLAERLLVDVIG  RKHRLAERL       0.2650     2842.4             50.00  Rv2711, TB
DRB1_1302  192  ARVTVETTPGGGVTI  TTPGGGVTI       0.2643     2864.7             50.00  Rv2711, TB
DRB1_1302   39  TVSQTVSRMERDGLL  TVSQTVSRM       0.2622     2930.6             50.00  Rv2711, TB
DRB1_1302   43  TVSRMERDGLLRVAG  MERDGLLRV       0.2604     2987.3             50.00  Rv2711, TB
DRB1_1302   89  IGLPWEEVHAEACRW  EVHAEACRW       0.2586     3046.8             50.00  Rv2711, TB
DRB1_1302  157  PAGSPVAVVVRQLTE  VAVVVRQLT       0.2580     3067.0             50.00  Rv2711, TB
DRB1_1302  201  GGGVTIVIPGHENVT  VIPGHENVT       0.2573     3090.7             50.00  Rv2711, TB
DRB1_1302    3  LVDTTEMYLRTIYDL  LVDTTEMYL       0.2572     3094.6             50.00  Rv2711, TB
DRB1_1302   17  LEEEGVTPLRARIAE  GVTPLRARI       0.2570     3101.2             50.00  Rv2711, TB
DRB1_1302   97  HAEACRWEHVMSEDV  WEHVMSEDV       0.2569     3102.9             50.00  Rv2711, TB
DRB1_1302   98  AEACRWEHVMSEDVE  WEHVMSEDV       0.2561     3129.2             50.00  Rv2711, TB
DRB1_1302  195  TVETTPGGGVTIVIP  TTPGGGVTI       0.2560     3133.1             50.00  Rv2711, TB
DRB1_1302   51  GLLRVAGDRHLELTE  LLRVAGDRH       0.2560     3134.3             50.00  Rv2711, TB
DRB1_1302  108  SEDVERRLVKVLNNP  RRLVKVLNN       0.2545     3183.3             50.00  Rv2711, TB
DRB1_1302   90  GLPWEEVHAEACRWE  EVHAEACRW       0.2533     3227.4             50.00  Rv2711, TB
DRB1_1302   20  EGVTPLRARIAERLD  GVTPLRARI       0.2522     3264.5             50.00  Rv2711, TB
DRB1_1302  196  VETTPGGGVTIVIPG  VETTPGGGV       0.2518     3280.4             50.00  Rv2711, TB
DRB1_1302  204  VTIVIPGHENVTLPH  VIPGHENVT       0.2508     3314.1             50.00  Rv2711, TB
DRB1_1302  100  ACRWEHVMSEDVERR  WEHVMSEDV       0.2499     3347.4             50.00  Rv2711, TB
DRB1_1302  203  GVTIVIPGHENVTLP  VIPGHENVT       0.2494     3366.7             50.00  Rv2711, TB
DRB1_1302   99  EACRWEHVMSEDVER  WEHVMSEDV       0.2493     3369.8             50.00  Rv2711, TB
DRB1_1302  101  CRWEHVMSEDVERRL  WEHVMSEDV       0.2493     3370.7             50.00  Rv2711, TB
DRB1_1302   91  LPWEEVHAEACRWEH  EVHAEACRW       0.2462     3483.7             50.00  Rv2711, TB
DRB1_1302   38  PTVSQTVSRMERDGL  TVSQTVSRM       0.2455     3508.9             50.00  Rv2711, TB
DRB1_1302  102  RWEHVMSEDVERRLV  WEHVMSEDV       0.2411     3681.9             50.00  Rv2711, TB
DRB1_1302   92  PWEEVHAEACRWEHV  EVHAEACRW       0.2402     3718.5             50.00  Rv2711, TB
DRB1_1302   44  VSRMERDGLLRVAGD  MERDGLLRV       0.2401     3720.0             50.00  Rv2711, TB
DRB1_1302   18  EEEGVTPLRARIAER  GVTPLRARI       0.2391     3760.4             50.00  Rv2711, TB
DRB1_1302  118  VLNNPTTSPFGNPIP  LNNPTTSPF       0.2368     3855.5             50.00  Rv2711, TB
DRB1_1302   52  LLRVAGDRHLELTEK  LLRVAGDRH       0.2354     3916.6             50.00  Rv2711, TB
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DRB1_1302   93  WEEVHAEACRWEHVM  EVHAEACRW         0.2353       3921.4                 50.00   Rv2711, TB
DRB1_1302   84  LLVDVIGLPWEEVHA  LVDVIGLPW         0.2335       3997.8                 50.00   Rv2711, TB
DRB1_1302  107  MSEDVERRLVKVLNN  RRLVKVLNN         0.2321       4056.8                 50.00   Rv2711, TB
DRB1_1302   21  GVTPLRARIAERLDQ  GVTPLRARI         0.2266       4309.1                 50.00   Rv2711, TB
DRB1_1302  103  WEHVMSEDVERRLVK  WEHVMSEDV         0.2259       4340.8                 50.00   Rv2711, TB
DRB1_1302   57  GDRHLELTEKGRALA  ELTEKGRAL         0.2211       4569.6                 50.00   Rv2711, TB
DRB1_1302   45  SRMERDGLLRVAGDR  MERDGLLRV         0.2201       4623.2                 50.00   Rv2711, TB
DRB1_1302  205  TIVIPGHENVTLPHE  VIPGHENVT         0.2194       4657.3                 50.00   Rv2711, TB
DRB1_1302  169  LTEHVQGDIDLITRL  GDIDLITRL         0.2128       4999.9                 50.00   Rv2711, TB
DRB1_1302  145  ADDANLVRLTELPAG  ANLVRLTEL         0.2126       5013.1                 50.00   Rv2711, TB
DRB1_1302  200  PGGGVTIVIPGHENV  IVIPGHENV         0.2125       5018.8                 50.00   Rv2711, TB
DRB1_1302  198  TTPGGGVTIVIPGHE  TTPGGGVTI         0.2104       5135.0                 50.00   Rv2711, TB
DRB1_1302  206  IVIPGHENVTLPHEM  VIPGHENVT         0.2096       5179.4                 50.00   Rv2711, TB
DRB1_1302  170  TEHVQGDIDLITRLK  GDIDLITRL         0.2061       5374.4                 50.00   Rv2711, TB
DRB1_1302   31  ERLDQSGPTVSQTVS  RLDQSGPTV         0.2047       5460.3                 50.00   Rv2711, TB
DRB1_1302  144  GADDANLVRLTELPA  ANLVRLTEL         0.2011       5678.1                 50.00   Rv2711, TB
DRB1_1302   85  LVDVIGLPWEEVHAE  LVDVIGLPW         0.2008       5696.7                 50.00   Rv2711, TB
DRB1_1302   95  EVHAEACRWEHVMSE  EVHAEACRW         0.2004       5717.0                 50.00   Rv2711, TB
DRB1_1302   94  EEVHAEACRWEHVMS  EVHAEACRW         0.1994       5779.1                 50.00   Rv2711, TB
DRB1_1302   30  AERLDQSGPTVSQTV  RLDQSGPTV         0.1921       6258.7                 50.00   Rv2711, TB
DRB1_1302   32  RLDQSGPTVSQTVSR  RLDQSGPTV         0.1916       6288.0                 50.00   Rv2711, TB
DRB1_1302    5  DTTEMYLRTIYDLEE  LRTIYDLEE         0.1907       6354.9                 50.00   Rv2711, TB
DRB1_1302   27  ARIAERLDQSGPTVS  RLDQSGPTV         0.1904       6372.0                 50.00   Rv2711, TB
DRB1_1302    4  VDTTEMYLRTIYDLE  TTEMYLRTI         0.1899       6408.5                 50.00   Rv2711, TB
DRB1_1302  142  EPGADDANLVRLTEL  ANLVRLTEL         0.1891       6461.0                 50.00   Rv2711, TB
DRB1_1302   28  RIAERLDQSGPTVSQ  RLDQSGPTV         0.1867       6635.4                 50.00   Rv2711, TB
DRB1_1302  171  EHVQGDIDLITRLKD  GDIDLITRL         0.1853       6736.9                 50.00   Rv2711, TB
DRB1_1302  119  LNNPTTSPFGNPIPG  LNNPTTSPF         0.1849       6764.8                 50.00   Rv2711, TB
DRB1_1302  146  DDANLVRLTELPAGS  ANLVRLTEL         0.1840       6826.5                 50.00   Rv2711, TB
DRB1_1302   29  IAERLDQSGPTVSQT  RLDQSGPTV         0.1832       6891.5                 50.00   Rv2711, TB
DRB1_1302   56  AGDRHLELTEKGRAL  ELTEKGRAL         0.1830       6905.5                 50.00   Rv2711, TB
DRB1_1302  147  DANLVRLTELPAGSP  ANLVRLTEL         0.1821       6968.0                 50.00   Rv2711, TB
DRB1_1302  166  VRQLTEHVQGDIDLI  HVQGDIDLI         0.1819       6983.3                 50.00   Rv2711, TB
DRB1_1302  207  VIPGHENVTLPHEMA  VIPGHENVT         0.1818       6994.1                 50.00   Rv2711, TB
DRB1_1302  197  ETTPGGGVTIVIPGH  TTPGGGVTI         0.1809       7061.7                 50.00   Rv2711, TB
DRB1_1302  148  ANLVRLTELPAGSPV  ANLVRLTEL         0.1801       7123.5                 50.00   Rv2711, TB
DRB1_1302  190  PNARVTVETTPGGGV  VETTPGGGV         0.1794       7174.7                 50.00   Rv2711, TB
DRB1_1302  143  PGADDANLVRLTELP  ANLVRLTEL         0.1793       7187.6                 50.00   Rv2711, TB
DRB1_1302  149  NLVRLTELPAGSPVA  ELPAGSPVA         0.1768       7381.6                 50.00   Rv2711, TB
DRB1_1302  191  NARVTVETTPGGGVT  VETTPGGGV         0.1762       7433.2                 50.00   Rv2711, TB
DRB1_1302    6  TTEMYLRTIYDLEEE  LRTIYDLEE         0.1761       7440.4                 50.00   Rv2711, TB
DRB1_1302  199  TPGGGVTIVIPGHEN  VTIVIPGHE         0.1747       7552.9                 50.00   Rv2711, TB
DRB1_1302   22  VTPLRARIAERLDQS  LRARIAERL         0.1725       7736.2                 50.00   Rv2711, TB
DRB1_1302  121  NPTTSPFGNPIPGLV  FGNPIPGLV         0.1704       7911.0                 50.00   Rv2711, TB
DRB1_1302  123  TTSPFGNPIPGLVEL  FGNPIPGLV         0.1696       7979.2                 50.00   Rv2711, TB
DRB1_1302   40  VSQTVSRMERDGLLR  SRMERDGLL         0.1672       8190.3                 50.00   Rv2711, TB
DRB1_1302   26  RARIAERLDQSGPTV  RLDQSGPTV         0.1670       8212.1                 50.00   Rv2711, TB
DRB1_1302   53  LRVAGDRHLELTEKG  LRVAGDRHL         0.1656       8330.0                 50.00   Rv2711, TB
DRB1_1302  208  IPGHENVTLPHEMAH  IPGHENVTL         0.1621       8659.2                 50.00   Rv2711, TB
DRB1_1302  167  RQLTEHVQGDIDLIT  HVQGDIDLI         0.1603       8826.5                 50.00   Rv2711, TB
DRB1_1302  168  QLTEHVQGDIDLITR  HVQGDIDLI         0.1514       9714.7                 50.00   Rv2711, TB
DRB1_1302   23  TPLRARIAERLDQSG  LRARIAERL         0.1481      10070.2                 50.00   Rv2711, TB
DRB1_1302    7  TEMYLRTIYDLEEEG  LRTIYDLEE         0.1465      10248.8                 50.00   Rv2711, TB
DRB1_1302  209  PGHENVTLPHEMAHA  ENVTLPHEM         0.1464      10255.5                 50.00   Rv2711, TB
DRB1_1302  122  PTTSPFGNPIPGLVE  FGNPIPGLV         0.1455      10354.3                 50.00   Rv2711, TB
DRB1_1302   11  LRTIYDLEEEGVTPL  LEEEGVTPL         0.1449      10425.5                 50.00   Rv2711, TB
DRB1_1302  139  VGPEPGADDANLVRL  ADDANLVRL         0.1436      10571.5                 50.00   Rv2711, TB
DRB1_1302   25  LRARIAERLDQSGPT  LRARIAERL         0.1415      10812.7                 50.00   Rv2711, TB
DRB1_1302  140  GPEPGADDANLVRLT  ADDANLVRL         0.1414      10832.5                 50.00   Rv2711, TB
DRB1_1302  172  HVQGDIDLITRLKDA  GDIDLITRL         0.1406      10920.0                 50.00   Rv2711, TB
DRB1_1302  106  VMSEDVERRLVKVLN  VERRLVKVL         0.1402      10973.2                 50.00   Rv2711, TB
DRB1_1302   24  PLRARIAERLDQSGP  LRARIAERL         0.1385      11167.6                 50.00   Rv2711, TB
DRB1_1302  125  SPFGNPIPGLVELGV  FGNPIPGLV         0.1381      11226.7                 50.00   Rv2711, TB
DRB1_1302  105  HVMSEDVERRLVKVL  VERRLVKVL         0.1377      11268.1                 50.00   Rv2711, TB
DRB1_1302   14  IYDLEEEGVTPLRAR  LEEEGVTPL         0.1339      11741.9                 50.00   Rv2711, TB
DRB1_1302  124  TSPFGNPIPGLVELG  FGNPIPGLV         0.1318      12015.4                 50.00   Rv2711, TB
DRB1_1302  173  VQGDIDLITRLKDAG  GDIDLITRL         0.1284      12465.8                 50.00   Rv2711, TB
DRB1_1302  141  PEPGADDANLVRLTE  ADDANLVRL         0.1270      12654.3                 50.00   Rv2711, TB
DRB1_1302   13  TIYDLEEEGVTPLRA  LEEEGVTPL         0.1266      12708.8                 50.00   Rv2711, TB
DRB1_1302   12  RTIYDLEEEGVTPLR  LEEEGVTPL         0.1251      12919.1                 50.00   Rv2711, TB
DRB1_1302  126  PFGNPIPGLVELGVG  FGNPIPGLV         0.1237      13108.1                 50.00   Rv2711, TB
DRB1_1302  120  NNPTTSPFGNPIPGL  TTSPFGNPI         0.1163      14199.2                 50.00   Rv2711, TB
DRB1_1302  127  FGNPIPGLVELGVGP  FGNPIPGLV         0.1161      14244.4                 50.00   Rv2711, TB
DRB1_1302  104  EHVMSEDVERRLVKV  DVERRLVKV         0.1138      14595.9                 50.00   Rv2711, TB
DRB1_1302  189  VPNARVTVETTPGGG  RVTVETTPG         0.1099      15221.2                 50.00   Rv2711, TB
DRB1_1302    8  EMYLRTIYDLEEEGV  LRTIYDLEE         0.1086      15444.0                 50.00   Rv2711, TB
DRB1_1302  128  GNPIPGLVELGVGPE  LVELGVGPE         0.0992      17102.4                 50.00   Rv2711, TB
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   DRB1_1302    9  MYLRTIYDLEEEGVT  LRTIYDLEE         0.0945      17986.3                50.00   Rv2711, TB
   DRB1_1302   55  VAGDRHLELTEKGRA  LELTEKGRA         0.0875      19393.2                50.00   Rv2711, TB
   DRB1_1302  129  NPIPGLVELGVGPEP  LVELGVGPE         0.0852      19890.3                50.00   Rv2711, TB
   DRB1_1302  138  GVGPEPGADDANLVR  PGADDANLV         0.0812      20762.8                50.00   Rv2711, TB
   DRB1_1302   87  DVIGLPWEEVHAEAC  WEEVHAEAC         0.0811      20781.5                50.00   Rv2711, TB
   DRB1_1302   88  VIGLPWEEVHAEACR  WEEVHAEAC         0.0809      20832.1                50.00   Rv2711, TB
   DRB1_1302  137  LGVGPEPGADDANLV  PGADDANLV         0.0707      23255.1                50.00   Rv2711, TB
   DRB1_1302   54  RVAGDRHLELTEKGR  VAGDRHLEL         0.0684      23855.0                50.00   Rv2711, TB
   DRB1_1302  131  IPGLVELGVGPEPGA  LVELGVGPE         0.0649      24765.0                50.00   Rv2711, TB
   DRB1_1302  130  PIPGLVELGVGPEPG  LVELGVGPE         0.0617      25659.6                50.00   Rv2711, TB
   DRB1_1302   86  VDVIGLPWEEVHAEA  VIGLPWEEV         0.0539      27912.8                50.00   Rv2711, TB
   DRB1_1302  133  GLVELGVGPEPGADD  LVELGVGPE         0.0533      28073.0                50.00   Rv2711, TB
   DRB1_1302   10  YLRTIYDLEEEGVTP  LRTIYDLEE         0.0529      28211.9                50.00   Rv2711, TB
   DRB1_1302  132  PGLVELGVGPEPGAD  LVELGVGPE         0.0515      28632.6                50.00   Rv2711, TB
   DRB1_1302  134  LVELGVGPEPGADDA  LVELGVGPE         0.0488      29488.1                50.00   Rv2711, TB
   DRB1_1302   96  VHAEACRWEHVMSED  EACRWEHVM         0.0396      32583.6                50.00   Rv2711, TB
   DRB1_1302  136  ELGVGPEPGADDANL  LGVGPEPGA         0.0341      34578.5                50.00   Rv2711, TB
   DRB1_1302  135  VELGVGPEPGADDAN  LGVGPEPGA         0.0340      34624.9                50.00   Rv2711, TB
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Allele: DRB1_1302. Number of high binders 3. Number of weak binders 35. Number of peptides 216

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       Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB1_1501  113  RRLVKVLNNPTTSPF  LVKVLNNPT         0.7507         14.8         SB     0.80   Rv2711, TB
   DRB1_1501  112  ERRLVKVLNNPTTSP  LVKVLNNPT         0.7470         15.4         SB     0.80   Rv2711, TB
   DRB1_1501  111  VERRLVKVLNNPTTS  LVKVLNNPT         0.7279         19.0         SB     1.00   Rv2711, TB
   DRB1_1501  114  RLVKVLNNPTTSPFG  LVKVLNNPT         0.7248         19.6         SB     1.00   Rv2711, TB
   DRB1_1501   19  EEGVTPLRARIAERL  GVTPLRARI         0.6999         25.7         SB     2.00   Rv2711, TB
   DRB1_1501  110  DVERRLVKVLNNPTT  LVKVLNNPT         0.6986         26.1         SB     2.00   Rv2711, TB
   DRB1_1501   18  EEEGVTPLRARIAER  GVTPLRARI         0.6941         27.4         SB     2.00   Rv2711, TB
   DRB1_1501   20  EGVTPLRARIAERLD  GVTPLRARI         0.6883         29.2         SB     2.00   Rv2711, TB
   DRB1_1501   17  LEEEGVTPLRARIAE  GVTPLRARI         0.6713         35.0         SB     4.00   Rv2711, TB
   DRB1_1501   70  LAIAVMRKHRLAERL  IAVMRKHRL         0.6573         40.8         SB     4.00   Rv2711, TB
   DRB1_1501   16  DLEEEGVTPLRARIA  GVTPLRARI         0.6504         43.9         SB     4.00   Rv2711, TB
   DRB1_1501   69  ALAIAVMRKHRLAER  IAVMRKHRL         0.6395         49.4         SB     4.00   Rv2711, TB
   DRB1_1501   71  AIAVMRKHRLAERLL  IAVMRKHRL         0.6370         50.8         WB     4.00   Rv2711, TB
   DRB1_1501   68  RALAIAVMRKHRLAE  IAVMRKHRL         0.6304         54.6         WB     4.00   Rv2711, TB
   DRB1_1501   21  GVTPLRARIAERLDQ  GVTPLRARI         0.6224         59.4         WB     8.00   Rv2711, TB
   DRB1_1501  109  EDVERRLVKVLNNPT  LVKVLNNPT         0.6114         67.0         WB     8.00   Rv2711, TB
   DRB1_1501   72  IAVMRKHRLAERLLV  AVMRKHRLA         0.5807         93.4         WB     8.00   Rv2711, TB
   DRB1_1501  115  LVKVLNNPTTSPFGN  LVKVLNNPT         0.5795         94.6         WB     8.00   Rv2711, TB
   DRB1_1501   67  GRALAIAVMRKHRLA  IAVMRKHRL         0.5770         97.1         WB     8.00   Rv2711, TB
   DRB1_1501   66  KGRALAIAVMRKHRL  RALAIAVMR         0.5589        118.3         WB    16.00   Rv2711, TB
   DRB1_1501  161  PVAVVVRQLTEHVQG  VVVRQLTEH         0.5302        161.3         WB    16.00   Rv2711, TB
   DRB1_1501  162  VAVVVRQLTEHVQGD  VVVRQLTEH         0.5253        170.0         WB    16.00   Rv2711, TB
   DRB1_1501  160  SPVAVVVRQLTEHVQ  VVVRQLTEH         0.5145        191.2         WB    16.00   Rv2711, TB
   DRB1_1501  175  GDIDLITRLKDAGVV  LITRLKDAG         0.5052        211.4         WB    16.00   Rv2711, TB
   DRB1_1501   73  AVMRKHRLAERLLVD  AVMRKHRLA         0.5046        212.7         WB    16.00   Rv2711, TB
   DRB1_1501  163  AVVVRQLTEHVQGDI  VVVRQLTEH         0.5022        218.4         WB    16.00   Rv2711, TB
   DRB1_1501  159  GSPVAVVVRQLTEHV  VVVRQLTEH         0.4901        248.9         WB    16.00   Rv2711, TB
   DRB1_1501  176  DIDLITRLKDAGVVP  LITRLKDAG         0.4872        256.8         WB    32.00   Rv2711, TB
   DRB1_1501   15  YDLEEEGVTPLRARI  GVTPLRARI         0.4857        261.1         WB    32.00   Rv2711, TB
   DRB1_1501  177  IDLITRLKDAGVVPN  LITRLKDAG         0.4763        288.9         WB    32.00   Rv2711, TB
   DRB1_1501  174  QGDIDLITRLKDAGV  LITRLKDAG         0.4735        297.8         WB    32.00   Rv2711, TB
   DRB1_1501  164  VVVRQLTEHVQGDID  VVVRQLTEH         0.4705        307.6         WB    32.00   Rv2711, TB
   DRB1_1501   65  EKGRALAIAVMRKHR  RALAIAVMR         0.4693        311.7         WB    32.00   Rv2711, TB
   DRB1_1501    4  VDTTEMYLRTIYDLE  TEMYLRTIY         0.4614        339.6         WB    32.00   Rv2711, TB
   DRB1_1501   49  RDGLLRVAGDRHLEL  GLLRVAGDR         0.4535        369.9         WB    32.00   Rv2711, TB
   DRB1_1501   62  ELTEKGRALAIAVMR  LTEKGRALA         0.4502        383.4         WB    32.00   Rv2711, TB
   DRB1_1501   63  LTEKGRALAIAVMRK  LTEKGRALA         0.4476        394.4         WB    32.00   Rv2711, TB
   DRB1_1501  178  DLITRLKDAGVVPNA  LITRLKDAG         0.4471        396.3         WB    32.00   Rv2711, TB
   DRB1_1501   64  TEKGRALAIAVMRKH  RALAIAVMR         0.4452        404.5         WB    32.00   Rv2711, TB
   DRB1_1501    5  DTTEMYLRTIYDLEE  TEMYLRTIY         0.4414        421.4         WB    32.00   Rv2711, TB
   DRB1_1501   60  HLELTEKGRALAIAV  LTEKGRALA         0.4375        439.5         WB    32.00   Rv2711, TB
   DRB1_1501   50  DGLLRVAGDRHLELT  GLLRVAGDR         0.4339        457.1         WB    32.00   Rv2711, TB
   DRB1_1501   48  ERDGLLRVAGDRHLE  GLLRVAGDR         0.4324        464.7         WB    32.00   Rv2711, TB
   DRB1_1501   61  LELTEKGRALAIAVM  LTEKGRALA         0.4320        466.6         WB    32.00   Rv2711, TB
   DRB1_1501   46  RMERDGLLRVAGDRH  GLLRVAGDR         0.4314        469.6         WB    32.00   Rv2711, TB
   DRB1_1501   47  MERDGLLRVAGDRHL  GLLRVAGDR         0.4308        472.8         WB    32.00   Rv2711, TB
   DRB1_1501   51  GLLRVAGDRHLELTE  GLLRVAGDR         0.4203        529.5               32.00   Rv2711, TB
   DRB1_1501    6  TTEMYLRTIYDLEEE  TEMYLRTIY         0.4125        576.0               32.00   Rv2711, TB
   DRB1_1501  108  SEDVERRLVKVLNNP  RLVKVLNNP         0.4111        585.1               32.00   Rv2711, TB
   DRB1_1501  147  DANLVRLTELPAGSP  LVRLTELPA         0.4097        593.8               32.00   Rv2711, TB
   DRB1_1501  148  ANLVRLTELPAGSPV  LVRLTELPA         0.4071        610.8               32.00   Rv2711, TB
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DRB1_1501  146  DDANLVRLTELPAGS  LVRLTELPA        0.4029        639.1               32.00   Rv2711, TB
DRB1_1501  158  AGSPVAVVVRQLTEH  VVVRQLTEH        0.4018        647.3               32.00   Rv2711, TB
DRB1_1501   74  VMRKHRLAERLLVDV  VMRKHRLAE        0.4012        651.5               32.00   Rv2711, TB
DRB1_1501  173  VQGDIDLITRLKDAG  LITRLKDAG        0.3985        670.8               32.00   Rv2711, TB
DRB1_1501  145  ADDANLVRLTELPAG  NLVRLTELP        0.3873        756.7               32.00   Rv2711, TB
DRB1_1501   22  VTPLRARIAERLDQS  PLRARIAER        0.3811        809.8               50.00   Rv2711, TB
DRB1_1501    3  LVDTTEMYLRTIYDL  TEMYLRTIY        0.3791        827.3               50.00   Rv2711, TB
DRB1_1501  149  NLVRLTELPAGSPVA  LVRLTELPA        0.3761        854.7               50.00   Rv2711, TB
DRB1_1501    7  TEMYLRTIYDLEEEG  TEMYLRTIY        0.3677        935.7               50.00   Rv2711, TB
DRB1_1501    2  ELVDTTEMYLRTIYD  TEMYLRTIY        0.3560       1062.2               50.00   Rv2711, TB
DRB1_1501   79  RLAERLLVDVIGLPW  LVDVIGLPW        0.3539       1086.0               50.00   Rv2711, TB
DRB1_1501  179  LITRLKDAGVVPNAR  LITRLKDAG        0.3519       1110.5               50.00   Rv2711, TB
DRB1_1501   80  LAERLLVDVIGLPWE  LVDVIGLPW        0.3511       1120.2               50.00   Rv2711, TB
DRB1_1501   59  RHLELTEKGRALAIA  LTEKGRALA        0.3486       1150.9               50.00   Rv2711, TB
DRB1_1501  144  GADDANLVRLTELPA  NLVRLTELP        0.3484       1153.5               50.00   Rv2711, TB
DRB1_1501  205  TIVIPGHENVTLPHE  VIPGHENVT        0.3479       1159.5               50.00   Rv2711, TB
DRB1_1501  202  GGVTIVIPGHENVTL  VIPGHENVT        0.3444       1204.4               50.00   Rv2711, TB
DRB1_1501  203  GVTIVIPGHENVTLP  IVIPGHENV        0.3438       1211.3               50.00   Rv2711, TB
DRB1_1501   81  AERLLVDVIGLPWEE  LVDVIGLPW        0.3402       1259.9               50.00   Rv2711, TB
DRB1_1501  204  VTIVIPGHENVTLPH  VIPGHENVT        0.3394       1271.1               50.00   Rv2711, TB
DRB1_1501  206  IVIPGHENVTLPHEM  VIPGHENVT        0.3374       1298.8               50.00   Rv2711, TB
DRB1_1501   45  SRMERDGLLRVAGDR  RMERDGLLR        0.3335       1354.2               50.00   Rv2711, TB
DRB1_1501  150  LVRLTELPAGSPVAV  LVRLTELPA        0.3334       1355.8               50.00   Rv2711, TB
DRB1_1501   83  RLLVDVIGLPWEEVH  LVDVIGLPW        0.3322       1374.4               50.00   Rv2711, TB
DRB1_1501   84  LLVDVIGLPWEEVHA  LVDVIGLPW        0.3316       1382.9               50.00   Rv2711, TB
DRB1_1501  106  VMSEDVERRLVKVLN  DVERRLVKV        0.3266       1459.0               50.00   Rv2711, TB
DRB1_1501   75  MRKHRLAERLLVDVI  MRKHRLAER        0.3265       1460.8               50.00   Rv2711, TB
DRB1_1501   43  TVSRMERDGLLRVAG  RMERDGLLR        0.3245       1492.5               50.00   Rv2711, TB
DRB1_1501   82  ERLLVDVIGLPWEEV  LVDVIGLPW        0.3227       1523.3               50.00   Rv2711, TB
DRB1_1501   52  LLRVAGDRHLELTEK  LLRVAGDRH        0.3206       1558.1               50.00   Rv2711, TB
DRB1_1501   41  SQTVSRMERDGLLRV  RMERDGLLR        0.3200       1568.4               50.00   Rv2711, TB
DRB1_1501  107  MSEDVERRLVKVLNN  DVERRLVKV        0.3193       1579.2               50.00   Rv2711, TB
DRB1_1501   58  DRHLELTEKGRALAI  LTEKGRALA        0.3180       1602.7               50.00   Rv2711, TB
DRB1_1501  131  IPGLVELGVGPEPGA  GLVELGVGP        0.3175       1610.4               50.00   Rv2711, TB
DRB1_1501   44  VSRMERDGLLRVAGD  RMERDGLLR        0.3131       1688.8               50.00   Rv2711, TB
DRB1_1501   42  QTVSRMERDGLLRVA  RMERDGLLR        0.3124       1701.8               50.00   Rv2711, TB
DRB1_1501   78  HRLAERLLVDVIGLP  AERLLVDVI        0.3113       1722.0               50.00   Rv2711, TB
DRB1_1501  130  PIPGLVELGVGPEPG  GLVELGVGP        0.3078       1788.4               50.00   Rv2711, TB
DRB1_1501    1  NELVDTTEMYLRTIY  TEMYLRTIY        0.3058       1828.2               50.00   Rv2711, TB
DRB1_1501  172  HVQGDIDLITRLKDA  DLITRLKDA        0.3025       1895.0               50.00   Rv2711, TB
DRB1_1501  105  HVMSEDVERRLVKVL  DVERRLVKV        0.2987       1974.8               50.00   Rv2711, TB
DRB1_1501  132  PGLVELGVGPEPGAD  GLVELGVGP        0.2949       2057.9               50.00   Rv2711, TB
DRB1_1501   24  PLRARIAERLDQSGP  PLRARIAER        0.2931       2097.3               50.00   Rv2711, TB
DRB1_1501  151  VRLTELPAGSPVAVV  ELPAGSPVA        0.2903       2161.5               50.00   Rv2711, TB
DRB1_1501  129  NPIPGLVELGVGPEP  GLVELGVGP        0.2903       2162.7               50.00   Rv2711, TB
DRB1_1501   77  KHRLAERLLVDVIGL  AERLLVDVI        0.2894       2183.3               50.00   Rv2711, TB
DRB1_1501  116  VKVLNNPTTSPFGNP  VKVLNNPTT        0.2887       2200.0               50.00   Rv2711, TB
DRB1_1501    8  EMYLRTIYDLEEEGV  YLRTIYDLE        0.2886       2201.8               50.00   Rv2711, TB
DRB1_1501   23  TPLRARIAERLDQSG  PLRARIAER        0.2875       2229.2               50.00   Rv2711, TB
DRB1_1501  133  GLVELGVGPEPGADD  GLVELGVGP        0.2840       2313.3               50.00   Rv2711, TB
DRB1_1501   76  RKHRLAERLLVDVIG  HRLAERLLV        0.2759       2526.0               50.00   Rv2711, TB
DRB1_1501   85  LVDVIGLPWEEVHAE  LVDVIGLPW        0.2729       2608.6               50.00   Rv2711, TB
DRB1_1501  118  VLNNPTTSPFGNPIP  TTSPFGNPI        0.2686       2733.1               50.00   Rv2711, TB
DRB1_1501   40  VSQTVSRMERDGLLR  RMERDGLLR        0.2666       2793.0               50.00   Rv2711, TB
DRB1_1501  143  PGADDANLVRLTELP  NLVRLTELP        0.2647       2850.8               50.00   Rv2711, TB
DRB1_1501  207  VIPGHENVTLPHEMA  VIPGHENVT        0.2642       2868.9               50.00   Rv2711, TB
DRB1_1501  128  GNPIPGLVELGVGPE  GLVELGVGP        0.2617       2945.2               50.00   Rv2711, TB
DRB1_1501  152  RLTELPAGSPVAVVV  LTELPAGSP        0.2612       2962.3               50.00   Rv2711, TB
DRB1_1501   57  GDRHLELTEKGRALA  LTEKGRALA        0.2610       2967.2               50.00   Rv2711, TB
DRB1_1501  201  GGGVTIVIPGHENVT  VIPGHENVT        0.2604       2988.1               50.00   Rv2711, TB
DRB1_1501  117  KVLNNPTTSPFGNPI  VLNNPTTSP        0.2558       3138.8               50.00   Rv2711, TB
DRB1_1501  104  EHVMSEDVERRLVKV  DVERRLVKV        0.2537       3212.7               50.00   Rv2711, TB
DRB1_1501   38  PTVSQTVSRMERDGL  PTVSQTVSR        0.2459       3495.3               50.00   Rv2711, TB
DRB1_1501   28  RIAERLDQSGPTVSQ  RLDQSGPTV        0.2456       3505.6               50.00   Rv2711, TB
DRB1_1501   27  ARIAERLDQSGPTVS  RLDQSGPTV        0.2445       3550.4               50.00   Rv2711, TB
DRB1_1501  171  EHVQGDIDLITRLKD  HVQGDIDLI        0.2393       3756.0               50.00   Rv2711, TB
DRB1_1501   29  IAERLDQSGPTVSQT  RLDQSGPTV        0.2393       3756.1               50.00   Rv2711, TB
DRB1_1501   26  RARIAERLDQSGPTV  RLDQSGPTV        0.2390       3764.4               50.00   Rv2711, TB
DRB1_1501  170  TEHVQGDIDLITRLK  HVQGDIDLI        0.2380       3805.9               50.00   Rv2711, TB
DRB1_1501   30  AERLDQSGPTVSQTV  RLDQSGPTV        0.2364       3873.0               50.00   Rv2711, TB
DRB1_1501   14  IYDLEEEGVTPLRAR  EGVTPLRAR        0.2353       3921.3               50.00   Rv2711, TB
DRB1_1501  165  VVRQLTEHVQGDIDL  VVRQLTEHV        0.2343       3963.3               50.00   Rv2711, TB
DRB1_1501  120  NNPTTSPFGNPIPGL  TTSPFGNPI        0.2330       4018.5               50.00   Rv2711, TB
DRB1_1501  121  NPTTSPFGNPIPGLV  TTSPFGNPI        0.2300       4152.1               50.00   Rv2711, TB
DRB1_1501    9  MYLRTIYDLEEEGVT  YLRTIYDLE        0.2290       4196.7               50.00   Rv2711, TB
DRB1_1501  188  VVPNARVTVETTPGG  VVPNARVTV        0.2288       4206.3               50.00   Rv2711, TB
DRB1_1501    0  MNELVDTTEMYLRTI  TTEMYLRTI        0.2277       4255.1               50.00   Rv2711, TB
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   DRB1_1501   31  ERLDQSGPTVSQTVS  RLDQSGPTV         0.2247       4395.7                 50.00   Rv2711, TB
   DRB1_1501  213  NVTLPHEMAHAVKVE  TLPHEMAHA         0.2241       4424.9                 50.00   Rv2711, TB
   DRB1_1501  157  PAGSPVAVVVRQLTE  PVAVVVRQL         0.2231       4474.8                 50.00   Rv2711, TB
   DRB1_1501   39  TVSQTVSRMERDGLL  TVSQTVSRM         0.2215       4553.0                 50.00   Rv2711, TB
   DRB1_1501   10  YLRTIYDLEEEGVTP  YLRTIYDLE         0.2198       4635.3                 50.00   Rv2711, TB
   DRB1_1501  200  PGGGVTIVIPGHENV  IVIPGHENV         0.2184       4704.9                 50.00   Rv2711, TB
   DRB1_1501  103  WEHVMSEDVERRLVK  VMSEDVERR         0.2184       4708.6                 50.00   Rv2711, TB
   DRB1_1501  119  LNNPTTSPFGNPIPG  TTSPFGNPI         0.2174       4756.4                 50.00   Rv2711, TB
   DRB1_1501  212  ENVTLPHEMAHAVKV  TLPHEMAHA         0.2160       4828.2                 50.00   Rv2711, TB
   DRB1_1501  182  RLKDAGVVPNARVTV  RLKDAGVVP         0.2153       4867.0                 50.00   Rv2711, TB
   DRB1_1501   32  RLDQSGPTVSQTVSR  RLDQSGPTV         0.2152       4870.4                 50.00   Rv2711, TB
   DRB1_1501  187  GVVPNARVTVETTPG  VVPNARVTV         0.2148       4895.7                 50.00   Rv2711, TB
   DRB1_1501  192  ARVTVETTPGGGVTI  RVTVETTPG         0.2145       4908.7                 50.00   Rv2711, TB
   DRB1_1501  214  VTLPHEMAHAVKVEK  TLPHEMAHA         0.2137       4951.5                 50.00   Rv2711, TB
   DRB1_1501  127  FGNPIPGLVELGVGP  GLVELGVGP         0.2132       4979.1                 50.00   Rv2711, TB
   DRB1_1501  122  PTTSPFGNPIPGLVE  TTSPFGNPI         0.2129       4993.7                 50.00   Rv2711, TB
   DRB1_1501  102  RWEHVMSEDVERRLV  VMSEDVERR         0.2125       5016.3                 50.00   Rv2711, TB
   DRB1_1501  153  LTELPAGSPVAVVVR  LTELPAGSP         0.2105       5125.4                 50.00   Rv2711, TB
   DRB1_1501  169  LTEHVQGDIDLITRL  HVQGDIDLI         0.2102       5141.7                 50.00   Rv2711, TB
   DRB1_1501   56  AGDRHLELTEKGRAL  ELTEKGRAL         0.2066       5345.5                 50.00   Rv2711, TB
   DRB1_1501   89  IGLPWEEVHAEACRW  EVHAEACRW         0.2050       5438.9                 50.00   Rv2711, TB
   DRB1_1501  100  ACRWEHVMSEDVERR  WEHVMSEDV         0.2039       5504.0                 50.00   Rv2711, TB
   DRB1_1501  180  ITRLKDAGVVPNARV  RLKDAGVVP         0.2021       5613.6                 50.00   Rv2711, TB
   DRB1_1501   90  GLPWEEVHAEACRWE  EVHAEACRW         0.2011       5676.2                 50.00   Rv2711, TB
   DRB1_1501  101  CRWEHVMSEDVERRL  VMSEDVERR         0.2007       5701.2                 50.00   Rv2711, TB
   DRB1_1501  190  PNARVTVETTPGGGV  RVTVETTPG         0.1981       5863.1                 50.00   Rv2711, TB
   DRB1_1501  191  NARVTVETTPGGGVT  RVTVETTPG         0.1975       5899.5                 50.00   Rv2711, TB
   DRB1_1501   37  GPTVSQTVSRMERDG  TVSQTVSRM         0.1968       5948.9                 50.00   Rv2711, TB
   DRB1_1501   36  SGPTVSQTVSRMERD  TVSQTVSRM         0.1967       5949.6                 50.00   Rv2711, TB
   DRB1_1501  208  IPGHENVTLPHEMAH  VTLPHEMAH         0.1957       6016.7                 50.00   Rv2711, TB
   DRB1_1501   92  PWEEVHAEACRWEHV  EVHAEACRW         0.1954       6039.5                 50.00   Rv2711, TB
   DRB1_1501  185  DAGVVPNARVTVETT  VVPNARVTV         0.1952       6049.5                 50.00   Rv2711, TB
   DRB1_1501  186  AGVVPNARVTVETTP  VVPNARVTV         0.1934       6165.9                 50.00   Rv2711, TB
   DRB1_1501   86  VDVIGLPWEEVHAEA  VIGLPWEEV         0.1934       6166.2                 50.00   Rv2711, TB
   DRB1_1501  211  HENVTLPHEMAHAVK  TLPHEMAHA         0.1930       6193.6                 50.00   Rv2711, TB
   DRB1_1501  210  GHENVTLPHEMAHAV  VTLPHEMAH         0.1923       6243.6                 50.00   Rv2711, TB
   DRB1_1501   91  LPWEEVHAEACRWEH  EVHAEACRW         0.1908       6343.4                 50.00   Rv2711, TB
   DRB1_1501   93  WEEVHAEACRWEHVM  EVHAEACRW         0.1899       6409.8                 50.00   Rv2711, TB
   DRB1_1501  184  KDAGVVPNARVTVET  VVPNARVTV         0.1891       6463.5                 50.00   Rv2711, TB
   DRB1_1501  155  ELPAGSPVAVVVRQL  ELPAGSPVA         0.1887       6493.9                 50.00   Rv2711, TB
   DRB1_1501  123  TTSPFGNPIPGLVEL  TTSPFGNPI         0.1879       6548.1                 50.00   Rv2711, TB
   DRB1_1501   35  QSGPTVSQTVSRMER  PTVSQTVSR         0.1874       6583.4                 50.00   Rv2711, TB
   DRB1_1501  193  RVTVETTPGGGVTIV  RVTVETTPG         0.1860       6682.5                 50.00   Rv2711, TB
   DRB1_1501  181  TRLKDAGVVPNARVT  RLKDAGVVP         0.1854       6727.3                 50.00   Rv2711, TB
   DRB1_1501   94  EEVHAEACRWEHVMS  EVHAEACRW         0.1826       6929.5                 50.00   Rv2711, TB
   DRB1_1501  183  LKDAGVVPNARVTVE  VVPNARVTV         0.1812       7038.9                 50.00   Rv2711, TB
   DRB1_1501   25  LRARIAERLDQSGPT  LRARIAERL         0.1804       7103.3                 50.00   Rv2711, TB
   DRB1_1501   87  DVIGLPWEEVHAEAC  VIGLPWEEV         0.1803       7109.0                 50.00   Rv2711, TB
   DRB1_1501  215  TLPHEMAHAVKVEKV  TLPHEMAHA         0.1780       7287.5                 50.00   Rv2711, TB
   DRB1_1501  156  LPAGSPVAVVVRQLT  PVAVVVRQL         0.1776       7315.8                 50.00   Rv2711, TB
   DRB1_1501   34  DQSGPTVSQTVSRME  TVSQTVSRM         0.1770       7369.8                 50.00   Rv2711, TB
   DRB1_1501  154  TELPAGSPVAVVVRQ  ELPAGSPVA         0.1768       7380.7                 50.00   Rv2711, TB
   DRB1_1501  197  ETTPGGGVTIVIPGH  GGVTIVIPG         0.1742       7595.1                 50.00   Rv2711, TB
   DRB1_1501  209  PGHENVTLPHEMAHA  VTLPHEMAH         0.1733       7668.4                 50.00   Rv2711, TB
   DRB1_1501   99  EACRWEHVMSEDVER  ACRWEHVMS         0.1730       7695.7                 50.00   Rv2711, TB
   DRB1_1501   88  VIGLPWEEVHAEACR  GLPWEEVHA         0.1721       7767.7                 50.00   Rv2711, TB
   DRB1_1501  189  VPNARVTVETTPGGG  RVTVETTPG         0.1719       7783.8                 50.00   Rv2711, TB
   DRB1_1501  198  TTPGGGVTIVIPGHE  GVTIVIPGH         0.1712       7846.7                 50.00   Rv2711, TB
   DRB1_1501   95  EVHAEACRWEHVMSE  ACRWEHVMS         0.1693       8008.4                 50.00   Rv2711, TB
   DRB1_1501  168  QLTEHVQGDIDLITR  HVQGDIDLI         0.1688       8050.0                 50.00   Rv2711, TB
   DRB1_1501  199  TPGGGVTIVIPGHEN  GVTIVIPGH         0.1682       8102.6                 50.00   Rv2711, TB
   DRB1_1501  134  LVELGVGPEPGADDA  LVELGVGPE         0.1626       8609.7                 50.00   Rv2711, TB
   DRB1_1501   33  LDQSGPTVSQTVSRM  TVSQTVSRM         0.1616       8702.3                 50.00   Rv2711, TB
   DRB1_1501   55  VAGDRHLELTEKGRA  RHLELTEKG         0.1602       8834.8                 50.00   Rv2711, TB
   DRB1_1501  126  PFGNPIPGLVELGVG  PIPGLVELG         0.1600       8853.1                 50.00   Rv2711, TB
   DRB1_1501   98  AEACRWEHVMSEDVE  ACRWEHVMS         0.1592       8928.5                 50.00   Rv2711, TB
   DRB1_1501   53  LRVAGDRHLELTEKG  AGDRHLELT         0.1586       8989.2                 50.00   Rv2711, TB
   DRB1_1501   97  HAEACRWEHVMSEDV  ACRWEHVMS         0.1577       9077.9                 50.00   Rv2711, TB
   DRB1_1501   54  RVAGDRHLELTEKGR  AGDRHLELT         0.1459      10315.9                 50.00   Rv2711, TB
   DRB1_1501  196  VETTPGGGVTIVIPG  TTPGGGVTI         0.1432      10613.7                 50.00   Rv2711, TB
   DRB1_1501  125  SPFGNPIPGLVELGV  PIPGLVELG         0.1424      10708.8                 50.00   Rv2711, TB
   DRB1_1501  167  RQLTEHVQGDIDLIT  HVQGDIDLI         0.1418      10783.0                 50.00   Rv2711, TB
   DRB1_1501  166  VRQLTEHVQGDIDLI  HVQGDIDLI         0.1363      11446.8                 50.00   Rv2711, TB
   DRB1_1501   11  LRTIYDLEEEGVTPL  TIYDLEEEG         0.1208      13524.1                 50.00   Rv2711, TB
   DRB1_1501   12  RTIYDLEEEGVTPLR  DLEEEGVTP         0.1205      13575.6                 50.00   Rv2711, TB
   DRB1_1501  124  TSPFGNPIPGLVELG  PIPGLVELG         0.1195      13729.6                 50.00   Rv2711, TB
   DRB1_1501   96  VHAEACRWEHVMSED  ACRWEHVMS         0.1191      13786.2                 50.00   Rv2711, TB
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   DRB1_1501  195  TVETTPGGGVTIVIP  TTPGGGVTI        0.1184      13890.4               50.00   Rv2711, TB
   DRB1_1501   13  TIYDLEEEGVTPLRA  DLEEEGVTP        0.1158      14277.1               50.00   Rv2711, TB
   DRB1_1501  142  EPGADDANLVRLTEL  ANLVRLTEL        0.1124      14820.3               50.00   Rv2711, TB
   DRB1_1501  194  VTVETTPGGGVTIVI  TTPGGGVTI        0.1103      15154.8               50.00   Rv2711, TB
   DRB1_1501  135  VELGVGPEPGADDAN  ELGVGPEPG        0.1096      15267.4               50.00   Rv2711, TB
   DRB1_1501  136  ELGVGPEPGADDANL  ELGVGPEPG        0.0903      18815.8               50.00   Rv2711, TB
   DRB1_1501  137  LGVGPEPGADDANLV  LGVGPEPGA        0.0614      25727.2               50.00   Rv2711, TB
   DRB1_1501  140  GPEPGADDANLVRLT  DDANLVRLT        0.0612      25784.3               50.00   Rv2711, TB
   DRB1_1501  139  VGPEPGADDANLVRL  ADDANLVRL        0.0555      27433.7               50.00   Rv2711, TB
   DRB1_1501  138  GVGPEPGADDANLVR  GADDANLVR        0.0534      28059.4               50.00   Rv2711, TB
   DRB1_1501  141  PEPGADDANLVRLTE  DDANLVRLT        0.0531      28149.1               50.00   Rv2711, TB
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Allele: DRB1_1501. Number of high binders 12. Number of weak binders 34. Number of peptides 216

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB3_0101  121  NPTTSPFGNPIPGLV  FGNPIPGLV        0.4869        257.7          WB     4.00   Rv2711, TB
   DRB3_0101  122  PTTSPFGNPIPGLVE  FGNPIPGLV        0.4699        309.7          WB     4.00   Rv2711, TB
   DRB3_0101  123  TTSPFGNPIPGLVEL  FGNPIPGLV        0.4605        343.0          WB     4.00   Rv2711, TB
   DRB3_0101  169  LTEHVQGDIDLITRL  VQGDIDLIT        0.4386        434.6          WB     8.00   Rv2711, TB
   DRB3_0101  124  TSPFGNPIPGLVELG  FGNPIPGLV        0.4243        507.3                 8.00   Rv2711, TB
   DRB3_0101  167  RQLTEHVQGDIDLIT  VQGDIDLIT        0.4211        525.3                 8.00   Rv2711, TB
   DRB3_0101  170  TEHVQGDIDLITRLK  VQGDIDLIT        0.4131        572.5                 8.00   Rv2711, TB
   DRB3_0101  168  QLTEHVQGDIDLITR  VQGDIDLIT        0.4055        621.8                 8.00   Rv2711, TB
   DRB3_0101  125  SPFGNPIPGLVELGV  FGNPIPGLV        0.4033        636.4                 8.00   Rv2711, TB
   DRB3_0101    0  MNELVDTTEMYLRTI  ELVDTTEMY        0.3977        676.2                 8.00   Rv2711, TB
   DRB3_0101  171  EHVQGDIDLITRLKD  VQGDIDLIT        0.3893        740.8                 8.00   Rv2711, TB
   DRB3_0101  126  PFGNPIPGLVELGVG  FGNPIPGLV        0.3833        790.0                 8.00   Rv2711, TB
   DRB3_0101    9  MYLRTIYDLEEEGVT  YDLEEEGVT        0.3818        803.1                 8.00   Rv2711, TB
   DRB3_0101    1  NELVDTTEMYLRTIY  ELVDTTEMY        0.3768        847.8                16.00   Rv2711, TB
   DRB3_0101  172  HVQGDIDLITRLKDA  VQGDIDLIT        0.3707        905.7                16.00   Rv2711, TB
   DRB3_0101  127  FGNPIPGLVELGVGP  FGNPIPGLV        0.3643        970.8                16.00   Rv2711, TB
   DRB3_0101   78  HRLAERLLVDVIGLP  LLVDVIGLP        0.3582       1037.4                16.00   Rv2711, TB
   DRB3_0101    2  ELVDTTEMYLRTIYD  ELVDTTEMY        0.3519       1110.1                16.00   Rv2711, TB
   DRB3_0101    3  LVDTTEMYLRTIYDL  MYLRTIYDL        0.3461       1181.9                16.00   Rv2711, TB
   DRB3_0101    4  VDTTEMYLRTIYDLE  MYLRTIYDL        0.3338       1350.2                16.00   Rv2711, TB
   DRB3_0101   41  SQTVSRMERDGLLRV  MERDGLLRV        0.3125       1700.3                16.00   Rv2711, TB
   DRB3_0101    5  DTTEMYLRTIYDLEE  MYLRTIYDL        0.3054       1835.2                16.00   Rv2711, TB
   DRB3_0101   42  QTVSRMERDGLLRVA  MERDGLLRV        0.3039       1865.6                16.00   Rv2711, TB
   DRB3_0101   79  RLAERLLVDVIGLPW  LLVDVIGLP        0.3033       1877.5                16.00   Rv2711, TB
   DRB3_0101   10  YLRTIYDLEEEGVTP  YDLEEEGVT        0.2983       1982.6                16.00   Rv2711, TB
   DRB3_0101  166  VRQLTEHVQGDIDLI  HVQGDIDLI        0.2927       2107.0                32.00   Rv2711, TB
   DRB3_0101   43  TVSRMERDGLLRVAG  MERDGLLRV        0.2902       2165.0                32.00   Rv2711, TB
   DRB3_0101    6  TTEMYLRTIYDLEEE  MYLRTIYDL        0.2867       2248.3                32.00   Rv2711, TB
   DRB3_0101   11  LRTIYDLEEEGVTPL  YDLEEEGVT        0.2860       2266.2                32.00   Rv2711, TB
   DRB3_0101    7  TEMYLRTIYDLEEEG  MYLRTIYDL        0.2853       2281.6                32.00   Rv2711, TB
   DRB3_0101   44  VSRMERDGLLRVAGD  MERDGLLRV        0.2843       2308.0                32.00   Rv2711, TB
   DRB3_0101  173  VQGDIDLITRLKDAG  VQGDIDLIT        0.2794       2433.5                32.00   Rv2711, TB
   DRB3_0101   80  LAERLLVDVIGLPWE  LLVDVIGLP        0.2771       2494.4                32.00   Rv2711, TB
   DRB3_0101  139  VGPEPGADDANLVRL  PGADDANLV        0.2749       2555.3                32.00   Rv2711, TB
   DRB3_0101  140  GPEPGADDANLVRLT  PGADDANLV        0.2744       2568.1                32.00   Rv2711, TB
   DRB3_0101    8  EMYLRTIYDLEEEGV  MYLRTIYDL        0.2713       2656.2                32.00   Rv2711, TB
   DRB3_0101  141  PEPGADDANLVRLTE  PGADDANLV        0.2706       2674.8                32.00   Rv2711, TB
   DRB3_0101  137  LGVGPEPGADDANLV  PGADDANLV        0.2692       2715.5                32.00   Rv2711, TB
   DRB3_0101  142  EPGADDANLVRLTEL  PGADDANLV        0.2678       2757.6                32.00   Rv2711, TB
   DRB3_0101  143  PGADDANLVRLTELP  PGADDANLV        0.2674       2769.5                32.00   Rv2711, TB
   DRB3_0101   72  IAVMRKHRLAERLLV  HRLAERLLV        0.2640       2873.2                32.00   Rv2711, TB
   DRB3_0101  138  GVGPEPGADDANLVR  PGADDANLV        0.2637       2882.3                32.00   Rv2711, TB
   DRB3_0101   45  SRMERDGLLRVAGDR  MERDGLLRV        0.2607       2977.1                32.00   Rv2711, TB
   DRB3_0101   12  RTIYDLEEEGVTPLR  YDLEEEGVT        0.2579       3070.8                32.00   Rv2711, TB
   DRB3_0101  101  CRWEHVMSEDVERRL  MSEDVERRL        0.2500       3343.4                32.00   Rv2711, TB
   DRB3_0101   47  MERDGLLRVAGDRHL  MERDGLLRV        0.2476       3430.1                32.00   Rv2711, TB
   DRB3_0101   81  AERLLVDVIGLPWEE  LLVDVIGLP        0.2448       3537.1                32.00   Rv2711, TB
   DRB3_0101   46  RMERDGLLRVAGDRH  MERDGLLRV        0.2420       3647.7                32.00   Rv2711, TB
   DRB3_0101   13  TIYDLEEEGVTPLRA  YDLEEEGVT        0.2370       3846.7                32.00   Rv2711, TB
   DRB3_0101  210  GHENVTLPHEMAHAV  LPHEMAHAV        0.2363       3877.8                32.00   Rv2711, TB
   DRB3_0101  102  RWEHVMSEDVERRLV  MSEDVERRL        0.2359       3895.0                32.00   Rv2711, TB
   DRB3_0101   73  AVMRKHRLAERLLVD  HRLAERLLV        0.2346       3949.1                32.00   Rv2711, TB
   DRB3_0101  212  ENVTLPHEMAHAVKV  LPHEMAHAV        0.2333       4004.8                32.00   Rv2711, TB
   DRB3_0101   77  KHRLAERLLVDVIGL  HRLAERLLV        0.2307       4121.4                32.00   Rv2711, TB
   DRB3_0101   97  HAEACRWEHVMSEDV  WEHVMSEDV        0.2297       4165.9                32.00   Rv2711, TB
   DRB3_0101   74  VMRKHRLAERLLVDV  HRLAERLLV        0.2256       4353.5                32.00   Rv2711, TB
   DRB3_0101  211  HENVTLPHEMAHAVK  LPHEMAHAV        0.2255       4359.3                32.00   Rv2711, TB
   DRB3_0101  103  WEHVMSEDVERRLVK  MSEDVERRL        0.2255       4360.4                32.00   Rv2711, TB
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DRB3_0101   83  RLLVDVIGLPWEEVH  LLVDVIGLP         0.2249       4385.7                 32.00   Rv2711, TB
DRB3_0101   75  MRKHRLAERLLVDVI  HRLAERLLV         0.2204       4606.5                 32.00   Rv2711, TB
DRB3_0101   82  ERLLVDVIGLPWEEV  LLVDVIGLP         0.2203       4613.4                 32.00   Rv2711, TB
DRB3_0101   98  AEACRWEHVMSEDVE  WEHVMSEDV         0.2167       4795.7                 32.00   Rv2711, TB
DRB3_0101   14  IYDLEEEGVTPLRAR  YDLEEEGVT         0.2156       4850.7                 32.00   Rv2711, TB
DRB3_0101  213  NVTLPHEMAHAVKVE  LPHEMAHAV         0.2120       5043.6                 32.00   Rv2711, TB
DRB3_0101  104  EHVMSEDVERRLVKV  MSEDVERRL         0.2097       5168.8                 32.00   Rv2711, TB
DRB3_0101  105  HVMSEDVERRLVKVL  MSEDVERRL         0.2064       5359.0                 50.00   Rv2711, TB
DRB3_0101   99  EACRWEHVMSEDVER  WEHVMSEDV         0.2055       5412.7                 50.00   Rv2711, TB
DRB3_0101   76  RKHRLAERLLVDVIG  HRLAERLLV         0.2051       5434.6                 50.00   Rv2711, TB
DRB3_0101   49  RDGLLRVAGDRHLEL  VAGDRHLEL         0.2036       5523.9                 50.00   Rv2711, TB
DRB3_0101  106  VMSEDVERRLVKVLN  MSEDVERRL         0.1995       5772.0                 50.00   Rv2711, TB
DRB3_0101   50  DGLLRVAGDRHLELT  VAGDRHLEL         0.1960       5999.1                 50.00   Rv2711, TB
DRB3_0101   84  LLVDVIGLPWEEVHA  LLVDVIGLP         0.1939       6138.3                 50.00   Rv2711, TB
DRB3_0101  100  ACRWEHVMSEDVERR  CRWEHVMSE         0.1931       6187.3                 50.00   Rv2711, TB
DRB3_0101  214  VTLPHEMAHAVKVEK  LPHEMAHAV         0.1916       6290.2                 50.00   Rv2711, TB
DRB3_0101   51  GLLRVAGDRHLELTE  VAGDRHLEL         0.1838       6843.2                 50.00   Rv2711, TB
DRB3_0101   15  YDLEEEGVTPLRARI  YDLEEEGVT         0.1832       6884.8                 50.00   Rv2711, TB
DRB3_0101  107  MSEDVERRLVKVLNN  MSEDVERRL         0.1810       7054.6                 50.00   Rv2711, TB
DRB3_0101  215  TLPHEMAHAVKVEKV  LPHEMAHAV         0.1805       7095.8                 50.00   Rv2711, TB
DRB3_0101   39  TVSQTVSRMERDGLL  SRMERDGLL         0.1756       7480.6                 50.00   Rv2711, TB
DRB3_0101   95  EVHAEACRWEHVMSE  CRWEHVMSE         0.1720       7773.6                 50.00   Rv2711, TB
DRB3_0101   40  VSQTVSRMERDGLLR  SRMERDGLL         0.1705       7907.3                 50.00   Rv2711, TB
DRB3_0101   96  VHAEACRWEHVMSED  CRWEHVMSE         0.1690       8031.6                 50.00   Rv2711, TB
DRB3_0101   52  LLRVAGDRHLELTEK  VAGDRHLEL         0.1677       8142.7                 50.00   Rv2711, TB
DRB3_0101  175  GDIDLITRLKDAGVV  GDIDLITRL         0.1633       8540.6                 50.00   Rv2711, TB
DRB3_0101  174  QGDIDLITRLKDAGV  GDIDLITRL         0.1591       8936.1                 50.00   Rv2711, TB
DRB3_0101   53  LRVAGDRHLELTEKG  VAGDRHLEL         0.1477      10113.2                 50.00   Rv2711, TB
DRB3_0101  206  IVIPGHENVTLPHEM  VIPGHENVT         0.1354      11558.4                 50.00   Rv2711, TB
DRB3_0101  113  RRLVKVLNNPTTSPF  LNNPTTSPF         0.1350      11601.3                 50.00   Rv2711, TB
DRB3_0101   54  RVAGDRHLELTEKGR  VAGDRHLEL         0.1312      12094.9                 50.00   Rv2711, TB
DRB3_0101  156  LPAGSPVAVVVRQLT  VAVVVRQLT         0.1289      12394.9                 50.00   Rv2711, TB
DRB3_0101  207  VIPGHENVTLPHEMA  VIPGHENVT         0.1273      12614.0                 50.00   Rv2711, TB
DRB3_0101   55  VAGDRHLELTEKGRA  VAGDRHLEL         0.1273      12615.1                 50.00   Rv2711, TB
DRB3_0101  159  GSPVAVVVRQLTEHV  VAVVVRQLT         0.1261      12782.8                 50.00   Rv2711, TB
DRB3_0101  114  RLVKVLNNPTTSPFG  LNNPTTSPF         0.1234      13161.8                 50.00   Rv2711, TB
DRB3_0101  190  PNARVTVETTPGGGV  VETTPGGGV         0.1194      13742.9                 50.00   Rv2711, TB
DRB3_0101  182  RLKDAGVVPNARVTV  VVPNARVTV         0.1192      13768.8                 50.00   Rv2711, TB
DRB3_0101  160  SPVAVVVRQLTEHVQ  VAVVVRQLT         0.1189      13815.5                 50.00   Rv2711, TB
DRB3_0101  158  AGSPVAVVVRQLTEH  VAVVVRQLT         0.1186      13858.1                 50.00   Rv2711, TB
DRB3_0101   27  ARIAERLDQSGPTVS  ERLDQSGPT         0.1179      13969.8                 50.00   Rv2711, TB
DRB3_0101   94  EEVHAEACRWEHVMS  HAEACRWEH         0.1166      14167.3                 50.00   Rv2711, TB
DRB3_0101   66  KGRALAIAVMRKHRL  LAIAVMRKH         0.1151      14396.7                 50.00   Rv2711, TB
DRB3_0101  115  LVKVLNNPTTSPFGN  LNNPTTSPF         0.1149      14430.6                 50.00   Rv2711, TB
DRB3_0101  157  PAGSPVAVVVRQLTE  VAVVVRQLT         0.1146      14475.9                 50.00   Rv2711, TB
DRB3_0101   26  RARIAERLDQSGPTV  ERLDQSGPT         0.1138      14592.9                 50.00   Rv2711, TB
DRB3_0101   25  LRARIAERLDQSGPT  ERLDQSGPT         0.1137      14613.2                 50.00   Rv2711, TB
DRB3_0101   85  LVDVIGLPWEEVHAE  IGLPWEEVH         0.1130      14725.7                 50.00   Rv2711, TB
DRB3_0101   87  DVIGLPWEEVHAEAC  LPWEEVHAE         0.1121      14868.0                 50.00   Rv2711, TB
DRB3_0101  161  PVAVVVRQLTEHVQG  VAVVVRQLT         0.1120      14883.6                 50.00   Rv2711, TB
DRB3_0101   64  TEKGRALAIAVMRKH  LAIAVMRKH         0.1119      14894.3                 50.00   Rv2711, TB
DRB3_0101  202  GGVTIVIPGHENVTL  VIPGHENVT         0.1112      15007.2                 50.00   Rv2711, TB
DRB3_0101  183  LKDAGVVPNARVTVE  VVPNARVTV         0.1110      15040.8                 50.00   Rv2711, TB
DRB3_0101   28  RIAERLDQSGPTVSQ  ERLDQSGPT         0.1093      15329.7                 50.00   Rv2711, TB
DRB3_0101   93  WEEVHAEACRWEHVM  EACRWEHVM         0.1092      15338.9                 50.00   Rv2711, TB
DRB3_0101  201  GGGVTIVIPGHENVT  VIPGHENVT         0.1092      15346.2                 50.00   Rv2711, TB
DRB3_0101  191  NARVTVETTPGGGVT  VETTPGGGV         0.1077      15591.8                 50.00   Rv2711, TB
DRB3_0101  162  VAVVVRQLTEHVQGD  VAVVVRQLT         0.1075      15626.1                 50.00   Rv2711, TB
DRB3_0101   86  VDVIGLPWEEVHAEA  LPWEEVHAE         0.1071      15684.8                 50.00   Rv2711, TB
DRB3_0101  203  GVTIVIPGHENVTLP  VIPGHENVT         0.1062      15852.7                 50.00   Rv2711, TB
DRB3_0101   88  VIGLPWEEVHAEACR  IGLPWEEVH         0.1061      15868.9                 50.00   Rv2711, TB
DRB3_0101  184  KDAGVVPNARVTVET  VVPNARVTV         0.1058      15912.2                 50.00   Rv2711, TB
DRB3_0101   48  ERDGLLRVAGDRHLE  LRVAGDRHL         0.1053      15996.2                 50.00   Rv2711, TB
DRB3_0101   67  GRALAIAVMRKHRLA  LAIAVMRKH         0.1045      16135.7                 50.00   Rv2711, TB
DRB3_0101  208  IPGHENVTLPHEMAH  ENVTLPHEM         0.1041      16219.1                 50.00   Rv2711, TB
DRB3_0101  204  VTIVIPGHENVTLPH  VIPGHENVT         0.1040      16226.3                 50.00   Rv2711, TB
DRB3_0101  116  VKVLNNPTTSPFGNP  LNNPTTSPF         0.1035      16321.1                 50.00   Rv2711, TB
DRB3_0101  165  VVRQLTEHVQGDIDL  LTEHVQGDI         0.1026      16481.1                 50.00   Rv2711, TB
DRB3_0101   69  ALAIAVMRKHRLAER  LAIAVMRKH         0.1024      16508.4                 50.00   Rv2711, TB
DRB3_0101  185  DAGVVPNARVTVETT  VVPNARVTV         0.1018      16621.7                 50.00   Rv2711, TB
DRB3_0101  164  VVVRQLTEHVQGDID  LTEHVQGDI         0.1013      16702.1                 50.00   Rv2711, TB
DRB3_0101  163  AVVVRQLTEHVQGDI  LTEHVQGDI         0.1008      16798.9                 50.00   Rv2711, TB
DRB3_0101  117  KVLNNPTTSPFGNPI  LNNPTTSPF         0.1007      16812.5                 50.00   Rv2711, TB
DRB3_0101  205  TIVIPGHENVTLPHE  VIPGHENVT         0.1002      16904.7                 50.00   Rv2711, TB
DRB3_0101   91  LPWEEVHAEACRWEH  LPWEEVHAE         0.1000      16946.8                 50.00   Rv2711, TB
DRB3_0101   89  IGLPWEEVHAEACRW  IGLPWEEVH         0.1000      16955.2                 50.00   Rv2711, TB
DRB3_0101   70  LAIAVMRKHRLAERL  LAIAVMRKH         0.0998      16990.1                 50.00   Rv2711, TB
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DRB3_0101  188  VVPNARVTVETTPGG  VVPNARVTV         0.0995       17042.2                 50.00   Rv2711, TB
DRB3_0101   65  EKGRALAIAVMRKHR  LAIAVMRKH         0.0994       17054.4                 50.00   Rv2711, TB
DRB3_0101   68  RALAIAVMRKHRLAE  LAIAVMRKH         0.0987       17182.9                 50.00   Rv2711, TB
DRB3_0101  186  AGVVPNARVTVETTP  VVPNARVTV         0.0987       17193.2                 50.00   Rv2711, TB
DRB3_0101  118  VLNNPTTSPFGNPIP  LNNPTTSPF         0.0965       17592.1                 50.00   Rv2711, TB
DRB3_0101  176  DIDLITRLKDAGVVP  TRLKDAGVV         0.0963       17635.4                 50.00   Rv2711, TB
DRB3_0101   92  PWEEVHAEACRWEHV  VHAEACRWE         0.0961       17676.2                 50.00   Rv2711, TB
DRB3_0101  193  RVTVETTPGGGVTIV  VETTPGGGV         0.0960       17695.5                 50.00   Rv2711, TB
DRB3_0101  192  ARVTVETTPGGGVTI  VETTPGGGV         0.0949       17907.8                 50.00   Rv2711, TB
DRB3_0101   60  HLELTEKGRALAIAV  KGRALAIAV         0.0948       17932.6                 50.00   Rv2711, TB
DRB3_0101  194  VTVETTPGGGVTIVI  VETTPGGGV         0.0947       17939.0                 50.00   Rv2711, TB
DRB3_0101  177  IDLITRLKDAGVVPN  TRLKDAGVV         0.0947       17945.2                 50.00   Rv2711, TB
DRB3_0101   30  AERLDQSGPTVSQTV  ERLDQSGPT         0.0942       18041.0                 50.00   Rv2711, TB
DRB3_0101  178  DLITRLKDAGVVPNA  TRLKDAGVV         0.0939       18108.9                 50.00   Rv2711, TB
DRB3_0101  119  LNNPTTSPFGNPIPG  LNNPTTSPF         0.0928       18324.7                 50.00   Rv2711, TB
DRB3_0101   61  LELTEKGRALAIAVM  KGRALAIAV         0.0924       18389.5                 50.00   Rv2711, TB
DRB3_0101  209  PGHENVTLPHEMAHA  ENVTLPHEM         0.0923       18420.9                 50.00   Rv2711, TB
DRB3_0101   29  IAERLDQSGPTVSQT  ERLDQSGPT         0.0913       18623.5                 50.00   Rv2711, TB
DRB3_0101  187  GVVPNARVTVETTPG  VVPNARVTV         0.0907       18735.3                 50.00   Rv2711, TB
DRB3_0101   90  GLPWEEVHAEACRWE  VHAEACRWE         0.0895       18991.4                 50.00   Rv2711, TB
DRB3_0101  179  LITRLKDAGVVPNAR  TRLKDAGVV         0.0889       19102.9                 50.00   Rv2711, TB
DRB3_0101  151  VRLTELPAGSPVAVV  LPAGSPVAV         0.0886       19163.2                 50.00   Rv2711, TB
DRB3_0101  144  GADDANLVRLTELPA  GADDANLVR         0.0868       19543.2                 50.00   Rv2711, TB
DRB3_0101  146  DDANLVRLTELPAGS  VRLTELPAG         0.0865       19620.8                 50.00   Rv2711, TB
DRB3_0101  180  ITRLKDAGVVPNARV  TRLKDAGVV         0.0856       19813.0                 50.00   Rv2711, TB
DRB3_0101  145  ADDANLVRLTELPAG  VRLTELPAG         0.0849       19955.4                 50.00   Rv2711, TB
DRB3_0101  195  TVETTPGGGVTIVIP  VETTPGGGV         0.0836       20226.5                 50.00   Rv2711, TB
DRB3_0101   31  ERLDQSGPTVSQTVS  ERLDQSGPT         0.0835       20260.0                 50.00   Rv2711, TB
DRB3_0101   62  ELTEKGRALAIAVMR  KGRALAIAV         0.0825       20470.4                 50.00   Rv2711, TB
DRB3_0101   71  AIAVMRKHRLAERLL  IAVMRKHRL         0.0824       20494.3                 50.00   Rv2711, TB
DRB3_0101  150  LVRLTELPAGSPVAV  LPAGSPVAV         0.0818       20639.2                 50.00   Rv2711, TB
DRB3_0101  196  VETTPGGGVTIVIPG  VETTPGGGV         0.0815       20708.8                 50.00   Rv2711, TB
DRB3_0101  109  EDVERRLVKVLNNPT  LVKVLNNPT         0.0791       21246.0                 50.00   Rv2711, TB
DRB3_0101  110  DVERRLVKVLNNPTT  LVKVLNNPT         0.0788       21324.7                 50.00   Rv2711, TB
DRB3_0101  111  VERRLVKVLNNPTTS  LVKVLNNPT         0.0781       21475.0                 50.00   Rv2711, TB
DRB3_0101  112  ERRLVKVLNNPTTSP  LVKVLNNPT         0.0779       21520.8                 50.00   Rv2711, TB
DRB3_0101  181  TRLKDAGVVPNARVT  TRLKDAGVV         0.0777       21567.0                 50.00   Rv2711, TB
DRB3_0101  148  ANLVRLTELPAGSPV  VRLTELPAG         0.0771       21702.3                 50.00   Rv2711, TB
DRB3_0101  152  RLTELPAGSPVAVVV  PAGSPVAVV         0.0771       21714.3                 50.00   Rv2711, TB
DRB3_0101   63  LTEKGRALAIAVMRK  KGRALAIAV         0.0765       21852.6                 50.00   Rv2711, TB
DRB3_0101  147  DANLVRLTELPAGSP  VRLTELPAG         0.0754       22113.5                 50.00   Rv2711, TB
DRB3_0101   58  DRHLELTEKGRALAI  TEKGRALAI         0.0731       22670.8                 50.00   Rv2711, TB
DRB3_0101  133  GLVELGVGPEPGADD  LGVGPEPGA         0.0707       23274.5                 50.00   Rv2711, TB
DRB3_0101  153  LTELPAGSPVAVVVR  PAGSPVAVV         0.0705       23318.8                 50.00   Rv2711, TB
DRB3_0101  200  PGGGVTIVIPGHENV  TIVIPGHEN         0.0702       23385.8                 50.00   Rv2711, TB
DRB3_0101   59  RHLELTEKGRALAIA  TEKGRALAI         0.0688       23751.7                 50.00   Rv2711, TB
DRB3_0101  149  NLVRLTELPAGSPVA  VRLTELPAG         0.0686       23800.1                 50.00   Rv2711, TB
DRB3_0101  131  IPGLVELGVGPEPGA  LGVGPEPGA         0.0686       23800.6                 50.00   Rv2711, TB
DRB3_0101  155  ELPAGSPVAVVVRQL  PAGSPVAVV         0.0666       24315.7                 50.00   Rv2711, TB
DRB3_0101  199  TPGGGVTIVIPGHEN  TIVIPGHEN         0.0658       24525.5                 50.00   Rv2711, TB
DRB3_0101  189  VPNARVTVETTPGGG  VTVETTPGG         0.0658       24533.7                 50.00   Rv2711, TB
DRB3_0101   22  VTPLRARIAERLDQS  RIAERLDQS         0.0657       24566.7                 50.00   Rv2711, TB
DRB3_0101  134  LVELGVGPEPGADDA  LGVGPEPGA         0.0655       24602.6                 50.00   Rv2711, TB
DRB3_0101  154  TELPAGSPVAVVVRQ  LPAGSPVAV         0.0652       24706.1                 50.00   Rv2711, TB
DRB3_0101   33  LDQSGPTVSQTVSRM  SGPTVSQTV         0.0643       24945.1                 50.00   Rv2711, TB
DRB3_0101   23  TPLRARIAERLDQSG  RIAERLDQS         0.0640       25027.3                 50.00   Rv2711, TB
DRB3_0101   32  RLDQSGPTVSQTVSR  SGPTVSQTV         0.0638       25073.7                 50.00   Rv2711, TB
DRB3_0101  132  PGLVELGVGPEPGAD  LGVGPEPGA         0.0635       25154.6                 50.00   Rv2711, TB
DRB3_0101   24  PLRARIAERLDQSGP  RIAERLDQS         0.0630       25287.0                 50.00   Rv2711, TB
DRB3_0101  108  SEDVERRLVKVLNNP  VERRLVKVL         0.0625       25428.0                 50.00   Rv2711, TB
DRB3_0101  135  VELGVGPEPGADDAN  LGVGPEPGA         0.0612       25798.0                 50.00   Rv2711, TB
DRB3_0101   56  AGDRHLELTEKGRAL  LELTEKGRA         0.0609       25875.1                 50.00   Rv2711, TB
DRB3_0101  136  ELGVGPEPGADDANL  LGVGPEPGA         0.0605       25971.6                 50.00   Rv2711, TB
DRB3_0101   34  DQSGPTVSQTVSRME  SGPTVSQTV         0.0589       26435.7                 50.00   Rv2711, TB
DRB3_0101   35  QSGPTVSQTVSRMER  SGPTVSQTV         0.0551       27550.4                 50.00   Rv2711, TB
DRB3_0101   57  GDRHLELTEKGRALA  LELTEKGRA         0.0550       27581.1                 50.00   Rv2711, TB
DRB3_0101   38  PTVSQTVSRMERDGL  VSRMERDGL         0.0530       28172.8                 50.00   Rv2711, TB
DRB3_0101   36  SGPTVSQTVSRMERD  SGPTVSQTV         0.0517       28569.7                 50.00   Rv2711, TB
DRB3_0101   16  DLEEEGVTPLRARIA  LEEEGVTPL         0.0500       29103.9                 50.00   Rv2711, TB
DRB3_0101   19  EEGVTPLRARIAERL  LRARIAERL         0.0498       29162.2                 50.00   Rv2711, TB
DRB3_0101   20  EGVTPLRARIAERLD  LRARIAERL         0.0479       29790.8                 50.00   Rv2711, TB
DRB3_0101   17  LEEEGVTPLRARIAE  LEEEGVTPL         0.0468       30143.9                 50.00   Rv2711, TB
DRB3_0101   21  GVTPLRARIAERLDQ  LRARIAERL         0.0438       31118.5                 50.00   Rv2711, TB
DRB3_0101  129  NPIPGLVELGVGPEP  VELGVGPEP         0.0423       31623.9                 50.00   Rv2711, TB
DRB3_0101   37  GPTVSQTVSRMERDG  TVSQTVSRM         0.0404       32311.9                 50.00   Rv2711, TB
DRB3_0101  197  ETTPGGGVTIVIPGH  PGGGVTIVI         0.0403       32321.3                 50.00   Rv2711, TB
DRB3_0101  198  TTPGGGVTIVIPGHE  PGGGVTIVI         0.0403       32344.4                 50.00   Rv2711, TB
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   DRB3_0101   18  EEEGVTPLRARIAER  EGVTPLRAR        0.0402      32354.5               50.00   Rv2711, TB
   DRB3_0101  128  GNPIPGLVELGVGPE  IPGLVELGV        0.0388      32856.9               50.00   Rv2711, TB
   DRB3_0101  130  PIPGLVELGVGPEPG  VELGVGPEP        0.0382      33072.0               50.00   Rv2711, TB
   DRB3_0101  120  NNPTTSPFGNPIPGL  PFGNPIPGL        0.0369      33533.5               50.00   Rv2711, TB
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Allele: DRB3_0101. Number of high binders 0. Number of weak binders 4. Number of peptides 216

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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   DRB4_0101  161  PVAVVVRQLTEHVQG  VAVVVRQLT        0.7207         20.5         SB     1.00   Rv2711, TB
   DRB4_0101  160  SPVAVVVRQLTEHVQ  VAVVVRQLT        0.7111         22.8         SB     2.00   Rv2711, TB
   DRB4_0101  162  VAVVVRQLTEHVQGD  VAVVVRQLT        0.7064         24.0         SB     2.00   Rv2711, TB
   DRB4_0101  159  GSPVAVVVRQLTEHV  VAVVVRQLT        0.6945         27.3         SB     2.00   Rv2711, TB
   DRB4_0101  158  AGSPVAVVVRQLTEH  VAVVVRQLT        0.6606         39.4         SB     4.00   Rv2711, TB
   DRB4_0101  157  PAGSPVAVVVRQLTE  VAVVVRQLT        0.6169         63.1         WB     8.00   Rv2711, TB
   DRB4_0101   67  GRALAIAVMRKHRLA  LAIAVMRKH        0.6056         71.3         WB     8.00   Rv2711, TB
   DRB4_0101   66  KGRALAIAVMRKHRL  LAIAVMRKH        0.5963         78.9         WB     8.00   Rv2711, TB
   DRB4_0101   68  RALAIAVMRKHRLAE  LAIAVMRKH        0.5811         93.0         WB     8.00   Rv2711, TB
   DRB4_0101  156  LPAGSPVAVVVRQLT  VAVVVRQLT        0.5738        100.6         WB     8.00   Rv2711, TB
   DRB4_0101   69  ALAIAVMRKHRLAER  LAIAVMRKH        0.5737        100.7         WB     8.00   Rv2711, TB
   DRB4_0101  163  AVVVRQLTEHVQGDI  AVVVRQLTE        0.5675        107.7         WB    16.00   Rv2711, TB
   DRB4_0101   70  LAIAVMRKHRLAERL  LAIAVMRKH        0.5633        112.8         WB    16.00   Rv2711, TB
   DRB4_0101   65  EKGRALAIAVMRKHR  LAIAVMRKH        0.5561        121.9         WB    16.00   Rv2711, TB
   DRB4_0101   71  AIAVMRKHRLAERLL  IAVMRKHRL        0.5539        124.8         WB    16.00   Rv2711, TB
   DRB4_0101  111  VERRLVKVLNNPTTS  RRLVKVLNN        0.5344        154.2         WB    16.00   Rv2711, TB
   DRB4_0101  164  VVVRQLTEHVQGDID  VRQLTEHVQ        0.5338        155.0         WB    16.00   Rv2711, TB
   DRB4_0101  110  DVERRLVKVLNNPTT  RRLVKVLNN        0.5251        170.4         WB    16.00   Rv2711, TB
   DRB4_0101  112  ERRLVKVLNNPTTSP  RRLVKVLNN        0.5250        170.5         WB    16.00   Rv2711, TB
   DRB4_0101   72  IAVMRKHRLAERLLV  IAVMRKHRL        0.5244        171.8         WB    16.00   Rv2711, TB
   DRB4_0101  113  RRLVKVLNNPTTSPF  RRLVKVLNN        0.5147        190.7         WB    16.00   Rv2711, TB
   DRB4_0101   64  TEKGRALAIAVMRKH  LAIAVMRKH        0.5145        191.1         WB    16.00   Rv2711, TB
   DRB4_0101   51  GLLRVAGDRHLELTE  LLRVAGDRH        0.5101        200.5         WB    16.00   Rv2711, TB
   DRB4_0101   50  DGLLRVAGDRHLELT  LLRVAGDRH        0.5017        219.4         WB    16.00   Rv2711, TB
   DRB4_0101  175  GDIDLITRLKDAGVV  IDLITRLKD        0.5016        219.7         WB    16.00   Rv2711, TB
   DRB4_0101  109  EDVERRLVKVLNNPT  RRLVKVLNN        0.4979        228.7         WB    32.00   Rv2711, TB
   DRB4_0101  176  DIDLITRLKDAGVVP  IDLITRLKD        0.4975        229.7         WB    32.00   Rv2711, TB
   DRB4_0101  174  QGDIDLITRLKDAGV  IDLITRLKD        0.4904        247.9         WB    32.00   Rv2711, TB
   DRB4_0101   49  RDGLLRVAGDRHLEL  LLRVAGDRH        0.4882        254.1         WB    32.00   Rv2711, TB
   DRB4_0101    7  TEMYLRTIYDLEEEG  MYLRTIYDL        0.4850        263.0         WB    32.00   Rv2711, TB
   DRB4_0101   48  ERDGLLRVAGDRHLE  LLRVAGDRH        0.4844        264.8         WB    32.00   Rv2711, TB
   DRB4_0101  172  HVQGDIDLITRLKDA  IDLITRLKD        0.4843        265.0         WB    32.00   Rv2711, TB
   DRB4_0101  173  VQGDIDLITRLKDAG  IDLITRLKD        0.4781        283.3         WB    32.00   Rv2711, TB
   DRB4_0101    6  TTEMYLRTIYDLEEE  MYLRTIYDL        0.4773        285.9         WB    32.00   Rv2711, TB
   DRB4_0101   47  MERDGLLRVAGDRHL  LLRVAGDRH        0.4756        291.3         WB    32.00   Rv2711, TB
   DRB4_0101    5  DTTEMYLRTIYDLEE  TEMYLRTIY        0.4727        300.4         WB    32.00   Rv2711, TB
   DRB4_0101  177  IDLITRLKDAGVVPN  IDLITRLKD        0.4684        314.7         WB    32.00   Rv2711, TB
   DRB4_0101  108  SEDVERRLVKVLNNP  RRLVKVLNN        0.4655        325.0         WB    32.00   Rv2711, TB
   DRB4_0101  171  EHVQGDIDLITRLKD  IDLITRLKD        0.4601        344.3         WB    32.00   Rv2711, TB
   DRB4_0101  165  VVRQLTEHVQGDIDL  VRQLTEHVQ        0.4562        359.2         WB    32.00   Rv2711, TB
   DRB4_0101    4  VDTTEMYLRTIYDLE  MYLRTIYDL        0.4526        373.4         WB    32.00   Rv2711, TB
   DRB4_0101  146  DDANLVRLTELPAGS  NLVRLTELP        0.4514        378.4         WB    32.00   Rv2711, TB
   DRB4_0101  148  ANLVRLTELPAGSPV  NLVRLTELP        0.4486        389.8         WB    32.00   Rv2711, TB
   DRB4_0101   46  RMERDGLLRVAGDRH  LLRVAGDRH        0.4451        405.1         WB    32.00   Rv2711, TB
   DRB4_0101   63  LTEKGRALAIAVMRK  GRALAIAVM        0.4450        405.2         WB    32.00   Rv2711, TB
   DRB4_0101  107  MSEDVERRLVKVLNN  RRLVKVLNN        0.4421        418.3         WB    32.00   Rv2711, TB
   DRB4_0101  145  ADDANLVRLTELPAG  NLVRLTELP        0.4397        429.4         WB    32.00   Rv2711, TB
   DRB4_0101  147  DANLVRLTELPAGSP  NLVRLTELP        0.4387        433.8         WB    32.00   Rv2711, TB
   DRB4_0101   77  KHRLAERLLVDVIGL  RLLVDVIGL        0.4375        439.8         WB    32.00   Rv2711, TB
   DRB4_0101   52  LLRVAGDRHLELTEK  LLRVAGDRH        0.4331        461.0         WB    32.00   Rv2711, TB
   DRB4_0101    3  LVDTTEMYLRTIYDL  MYLRTIYDL        0.4300        476.7         WB    32.00   Rv2711, TB
   DRB4_0101  144  GADDANLVRLTELPA  NLVRLTELP        0.4288        483.3         WB    32.00   Rv2711, TB
   DRB4_0101   73  AVMRKHRLAERLLVD  AVMRKHRLA        0.4261        497.5         WB    32.00   Rv2711, TB
   DRB4_0101   78  HRLAERLLVDVIGLP  RLLVDVIGL        0.4161        554.2               32.00   Rv2711, TB
   DRB4_0101   81  AERLLVDVIGLPWEE  RLLVDVIGL        0.4160        555.0               32.00   Rv2711, TB
   DRB4_0101   80  LAERLLVDVIGLPWE  RLLVDVIGL        0.4121        578.8               32.00   Rv2711, TB
   DRB4_0101   82  ERLLVDVIGLPWEEV  RLLVDVIGL        0.4089        599.3               32.00   Rv2711, TB
   DRB4_0101  114  RLVKVLNNPTTSPFG  RLVKVLNNP        0.4084        602.3               32.00   Rv2711, TB
   DRB4_0101    8  EMYLRTIYDLEEEGV  MYLRTIYDL        0.4081        604.1               32.00   Rv2711, TB
   DRB4_0101   62  ELTEKGRALAIAVMR  GRALAIAVM        0.4077        606.7               32.00   Rv2711, TB
   DRB4_0101   83  RLLVDVIGLPWEEVH  RLLVDVIGL        0.4054        622.5               32.00   Rv2711, TB
   DRB4_0101   97  HAEACRWEHVMSEDV  CRWEHVMSE        0.4053        623.2               32.00   Rv2711, TB
   DRB4_0101   79  RLAERLLVDVIGLPW  RLLVDVIGL        0.4050        625.3               32.00   Rv2711, TB
   DRB4_0101   40  VSQTVSRMERDGLLR  VSRMERDGL        0.3960        689.1               50.00   Rv2711, TB
   DRB4_0101  143  PGADDANLVRLTELP  NLVRLTELP        0.3921        718.8               50.00   Rv2711, TB
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DRB4_0101   39  TVSQTVSRMERDGLL  VSRMERDGL        0.3901       734.3              50.00  Rv2711, TB
DRB4_0101   76  RKHRLAERLLVDVIG  KHRLAERLL        0.3883       748.8              50.00  Rv2711, TB
DRB4_0101   25  LRARIAERLDQSGPT  LRARIAERL        0.3860       767.4              50.00  Rv2711, TB
DRB4_0101   38  PTVSQTVSRMERDGL  VSRMERDGL        0.3846       779.0              50.00  Rv2711, TB
DRB4_0101  212  ENVTLPHEMAHAVKV  VTLPHEMAH        0.3831       792.1              50.00  Rv2711, TB
DRB4_0101  200  PGGGVTIVIPGHENV  VTIVIPGHE        0.3824       797.8              50.00  Rv2711, TB
DRB4_0101  210  GHENVTLPHEMAHAV  NVTLPHEMA        0.3802       817.1              50.00  Rv2711, TB
DRB4_0101   85  LVDVIGLPWEEVHAE  LVDVIGLPW        0.3800       819.4              50.00  Rv2711, TB
DRB4_0101   99  EACRWEHVMSEDVER  CRWEHVMSE        0.3792       826.7              50.00  Rv2711, TB
DRB4_0101  213  NVTLPHEMAHAVKVE  VTLPHEMAH        0.3789       828.5              50.00  Rv2711, TB
DRB4_0101   41  SQTVSRMERDGLLRV  QTVSRMERD        0.3776       840.6              50.00  Rv2711, TB
DRB4_0101   24  PLRARIAERLDQSGP  LRARIAERL        0.3776       840.8              50.00  Rv2711, TB
DRB4_0101  166  VRQLTEHVQGDIDLI  VRQLTEHVQ        0.3772       844.4              50.00  Rv2711, TB
DRB4_0101   98  AEACRWEHVMSEDVE  CRWEHVMSE        0.3769       847.5              50.00  Rv2711, TB
DRB4_0101    9  MYLRTIYDLEEEGVT  MYLRTIYDL        0.3757       858.5              50.00  Rv2711, TB
DRB4_0101  211  HENVTLPHEMAHAVK  ENVTLPHEM        0.3743       871.4              50.00  Rv2711, TB
DRB4_0101   84  LLVDVIGLPWEEVHA  LVDVIGLPW        0.3736       877.9              50.00  Rv2711, TB
DRB4_0101   75  MRKHRLAERLLVDVI  HRLAERLLV        0.3720       893.6              50.00  Rv2711, TB
DRB4_0101   53  LRVAGDRHLELTEKG  LRVAGDRHL        0.3714       899.0              50.00  Rv2711, TB
DRB4_0101  201  GGGVTIVIPGHENVT  VTIVIPGHE        0.3713       900.3              50.00  Rv2711, TB
DRB4_0101  214  VTLPHEMAHAVKVEK  VTLPHEMAH        0.3703       909.8              50.00  Rv2711, TB
DRB4_0101   19  EEGVTPLRARIAERL  LRARIAERL        0.3701       911.9              50.00  Rv2711, TB
DRB4_0101  100  ACRWEHVMSEDVERR  CRWEHVMSE        0.3669       944.2              50.00  Rv2711, TB
DRB4_0101  202  GGVTIVIPGHENVTL  VTIVIPGHE        0.3657       956.2              50.00  Rv2711, TB
DRB4_0101  170  TEHVQGDIDLITRLK  EHVQGDIDL        0.3655       958.7              50.00  Rv2711, TB
DRB4_0101   74  VMRKHRLAERLLVDV  KHRLAERLL        0.3643       971.2              50.00  Rv2711, TB
DRB4_0101   21  GVTPLRARIAERLDQ  LRARIAERL        0.3641       972.5              50.00  Rv2711, TB
DRB4_0101   87  DVIGLPWEEVHAEAC  DVIGLPWEE        0.3634       980.3              50.00  Rv2711, TB
DRB4_0101  209  PGHENVTLPHEMAHA  NVTLPHEMA        0.3628       986.2              50.00  Rv2711, TB
DRB4_0101  101  CRWEHVMSEDVERRL  CRWEHVMSE        0.3612      1004.4              50.00  Rv2711, TB
DRB4_0101   86  VDVIGLPWEEVHAEA  DVIGLPWEE        0.3586      1032.8              50.00  Rv2711, TB
DRB4_0101   22  VTPLRARIAERLDQS  LRARIAERL        0.3514      1116.4              50.00  Rv2711, TB
DRB4_0101   96  VHAEACRWEHVMSED  CRWEHVMSE        0.3509      1122.5              50.00  Rv2711, TB
DRB4_0101    2  ELVDTTEMYLRTIYD  ELVDTTEMY        0.3505      1127.2              50.00  Rv2711, TB
DRB4_0101   23  TPLRARIAERLDQSG  LRARIAERL        0.3504      1128.9              50.00  Rv2711, TB
DRB4_0101   20  EGVTPLRARIAERLD  LRARIAERL        0.3486      1150.8              50.00  Rv2711, TB
DRB4_0101  203  GVTIVIPGHENVTLP  GVTIVIPGH        0.3446      1201.4              50.00  Rv2711, TB
DRB4_0101  149  NLVRLTELPAGSPVA  NLVRLTELP        0.3440      1209.4              50.00  Rv2711, TB
DRB4_0101  199  TPGGGVTIVIPGHEN  VTIVIPGHE        0.3427      1225.8              50.00  Rv2711, TB
DRB4_0101   42  QTVSRMERDGLLRVA  VSRMERDGL        0.3395      1269.7              50.00  Rv2711, TB
DRB4_0101   61  LELTEKGRALAIAVM  GRALAIAVM        0.3389      1277.5              50.00  Rv2711, TB
DRB4_0101   55  VAGDRHLELTEKGRA  RHLELTEKG        0.3389      1278.3              50.00  Rv2711, TB
DRB4_0101   54  RVAGDRHLELTEKGR  RHLELTEKG        0.3357      1323.4              50.00  Rv2711, TB
DRB4_0101  208  IPGHENVTLPHEMAH  NVTLPHEMA        0.3346      1338.5              50.00  Rv2711, TB
DRB4_0101  198  TTPGGGVTIVIPGHE  VTIVIPGHE        0.3330      1362.8              50.00  Rv2711, TB
DRB4_0101  178  DLITRLKDAGVVPNA  DLITRLKDA        0.3328      1364.9              50.00  Rv2711, TB
DRB4_0101   95  EVHAEACRWEHVMSE  CRWEHVMSE        0.3316      1382.2              50.00  Rv2711, TB
DRB4_0101   27  ARIAERLDQSGPTVS  ARIAERLDQ        0.3270      1453.7              50.00  Rv2711, TB
DRB4_0101  169  LTEHVQGDIDLITRL  EHVQGDIDL        0.3254      1479.2              50.00  Rv2711, TB
DRB4_0101    1  NELVDTTEMYLRTIY  ELVDTTEMY        0.3245      1493.6              50.00  Rv2711, TB
DRB4_0101   88  VIGLPWEEVHAEACR  IGLPWEEVH        0.3242      1498.5              50.00  Rv2711, TB
DRB4_0101   26  RARIAERLDQSGPTV  ARIAERLDQ        0.3182      1599.1              50.00  Rv2711, TB
DRB4_0101   56  AGDRHLELTEKGRAL  RHLELTEKG        0.3168      1622.4              50.00  Rv2711, TB
DRB4_0101  115  LVKVLNNPTTSPFGN  LVKVLNNPT        0.3137      1679.1              50.00  Rv2711, TB
DRB4_0101   45  SRMERDGLLRVAGDR  GLLRVAGDR        0.3135      1682.4              50.00  Rv2711, TB
DRB4_0101   37  GPTVSQTVSRMERDG  VSQTVSRME        0.3123      1704.4              50.00  Rv2711, TB
DRB4_0101  130  PIPGLVELGVGPEPG  IPGLVELGV        0.3111      1726.1              50.00  Rv2711, TB
DRB4_0101   57  GDRHLELTEKGRALA  RHLELTEKG        0.3111      1726.2              50.00  Rv2711, TB
DRB4_0101  102  RWEHVMSEDVERRLV  WEHVMSEDV        0.3103      1742.2              50.00  Rv2711, TB
DRB4_0101   18  EEEGVTPLRARIAER  VTPLRARIA        0.3097      1752.8              50.00  Rv2711, TB
DRB4_0101  204  VTIVIPGHENVTLPH  IVIPGHENV        0.3066      1812.5              50.00  Rv2711, TB
DRB4_0101  142  EPGADDANLVRLTEL  ANLVRLTEL        0.3065      1815.0              50.00  Rv2711, TB
DRB4_0101  168  QLTEHVQGDIDLITR  EHVQGDIDL        0.3064      1816.6              50.00  Rv2711, TB
DRB4_0101  167  RQLTEHVQGDIDLIT  EHVQGDIDL        0.3027      1890.5              50.00  Rv2711, TB
DRB4_0101  215  TLPHEMAHAVKVEKV  AHAVKVEKV        0.2986      1975.5              50.00  Rv2711, TB
DRB4_0101   43  TVSRMERDGLLRVAG  VSRMERDGL        0.2979      1990.7              50.00  Rv2711, TB
DRB4_0101  106  VMSEDVERRLVKVLN  ERRLVKVLN        0.2962      2027.2              50.00  Rv2711, TB
DRB4_0101  155  ELPAGSPVAVVVRQL  PVAVVVRQL        0.2961      2030.6              50.00  Rv2711, TB
DRB4_0101  131  IPGLVELGVGPEPGA  IPGLVELGV        0.2941      2073.9              50.00  Rv2711, TB
DRB4_0101  103  WEHVMSEDVERRLVK  WEHVMSEDV        0.2911      2143.0              50.00  Rv2711, TB
DRB4_0101   36  SGPTVSQTVSRMERD  TVSQTVSRM        0.2895      2180.3              50.00  Rv2711, TB
DRB4_0101  129  NPIPGLVELGVGPEP  IPGLVELGV        0.2890      2193.4              50.00  Rv2711, TB
DRB4_0101   17  LEEEGVTPLRARIAE  VTPLRARIA        0.2862      2260.8              50.00  Rv2711, TB
DRB4_0101   89  IGLPWEEVHAEACRW  GLPWEEVHA        0.2859      2268.3              50.00  Rv2711, TB
DRB4_0101   44  VSRMERDGLLRVAGD  VSRMERDGL        0.2858      2270.1              50.00  Rv2711, TB
DRB4_0101    0  MNELVDTTEMYLRTI  ELVDTTEMY        0.2852      2284.0              50.00  Rv2711, TB
DRB4_0101  128  GNPIPGLVELGVGPE  IPGLVELGV        0.2824      2355.1              50.00  Rv2711, TB
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    DRB4_0101   16  DLEEEGVTPLRARIA  VTPLRARIA        0.2789       2446.3                50.00   Rv2711, TB
    DRB4_0101  127  FGNPIPGLVELGVGP  IPGLVELGV        0.2788       2447.8                50.00   Rv2711, TB
    DRB4_0101  206  IVIPGHENVTLPHEM  IVIPGHENV        0.2742       2572.9                50.00   Rv2711, TB
    DRB4_0101   28  RIAERLDQSGPTVSQ  IAERLDQSG        0.2740       2579.6                50.00   Rv2711, TB
    DRB4_0101   58  DRHLELTEKGRALAI  RHLELTEKG        0.2724       2625.4                50.00   Rv2711, TB
    DRB4_0101  105  HVMSEDVERRLVKVL  VERRLVKVL        0.2711       2661.1                50.00   Rv2711, TB
    DRB4_0101  186  AGVVPNARVTVETTP  AGVVPNARV        0.2688       2727.1                50.00   Rv2711, TB
    DRB4_0101  207  VIPGHENVTLPHEMA  NVTLPHEMA        0.2662       2806.7                50.00   Rv2711, TB
    DRB4_0101  125  SPFGNPIPGLVELGV  IPGLVELGV        0.2625       2922.1                50.00   Rv2711, TB
    DRB4_0101   10  YLRTIYDLEEEGVTP  LRTIYDLEE        0.2592       3027.9                50.00   Rv2711, TB
    DRB4_0101   35  QSGPTVSQTVSRMER  PTVSQTVSR        0.2547       3178.3                50.00   Rv2711, TB
    DRB4_0101  126  PFGNPIPGLVELGVG  IPGLVELGV        0.2539       3206.1                50.00   Rv2711, TB
    DRB4_0101  185  DAGVVPNARVTVETT  AGVVPNARV        0.2527       3248.9                50.00   Rv2711, TB
    DRB4_0101   59  RHLELTEKGRALAIA  RHLELTEKG        0.2507       3319.2                50.00   Rv2711, TB
    DRB4_0101  197  ETTPGGGVTIVIPGH  GVTIVIPGH        0.2469       3456.9                50.00   Rv2711, TB
    DRB4_0101  205  TIVIPGHENVTLPHE  IVIPGHENV        0.2395       3745.3                50.00   Rv2711, TB
    DRB4_0101  184  KDAGVVPNARVTVET  AGVVPNARV        0.2377       3819.3                50.00   Rv2711, TB
    DRB4_0101   29  IAERLDQSGPTVSQT  IAERLDQSG        0.2361       3885.5                50.00   Rv2711, TB
    DRB4_0101   11  LRTIYDLEEEGVTPL  LRTIYDLEE        0.2346       3949.0                50.00   Rv2711, TB
    DRB4_0101   60  HLELTEKGRALAIAV  EKGRALAIA        0.2317       4076.0                50.00   Rv2711, TB
    DRB4_0101  104  EHVMSEDVERRLVKV  EHVMSEDVE        0.2317       4077.4                50.00   Rv2711, TB
    DRB4_0101  116  VKVLNNPTTSPFGNP  VKVLNNPTT        0.2315       4083.8                50.00   Rv2711, TB
    DRB4_0101  179  LITRLKDAGVVPNAR  LITRLKDAG        0.2306       4122.7                50.00   Rv2711, TB
    DRB4_0101  132  PGLVELGVGPEPGAD  VELGVGPEP        0.2270       4288.9                50.00   Rv2711, TB
    DRB4_0101   90  GLPWEEVHAEACRWE  GLPWEEVHA        0.2247       4397.1                50.00   Rv2711, TB
    DRB4_0101  183  LKDAGVVPNARVTVE  AGVVPNARV        0.2203       4611.2                50.00   Rv2711, TB
    DRB4_0101  181  TRLKDAGVVPNARVT  AGVVPNARV        0.2191       4672.6                50.00   Rv2711, TB
    DRB4_0101  180  ITRLKDAGVVPNARV  ITRLKDAGV        0.2185       4702.0                50.00   Rv2711, TB
    DRB4_0101   34  DQSGPTVSQTVSRME  VSQTVSRME        0.2176       4747.9                50.00   Rv2711, TB
    DRB4_0101  133  GLVELGVGPEPGADD  VELGVGPEP        0.2175       4754.4                50.00   Rv2711, TB
    DRB4_0101  135  VELGVGPEPGADDAN  VELGVGPEP        0.2160       4831.1                50.00   Rv2711, TB
    DRB4_0101  182  RLKDAGVVPNARVTV  AGVVPNARV        0.2146       4902.5                50.00   Rv2711, TB
    DRB4_0101  190  PNARVTVETTPGGGV  ARVTVETTP        0.2145       4910.3                50.00   Rv2711, TB
    DRB4_0101  150  LVRLTELPAGSPVAV  LVRLTELPA        0.2125       5014.5                50.00   Rv2711, TB
    DRB4_0101   94  EEVHAEACRWEHVMS  ACRWEHVMS        0.2078       5277.9                50.00   Rv2711, TB
    DRB4_0101  189  VPNARVTVETTPGGG  ARVTVETTP        0.2077       5286.0                50.00   Rv2711, TB
    DRB4_0101  134  LVELGVGPEPGADDA  VELGVGPEP        0.2009       5686.9                50.00   Rv2711, TB
    DRB4_0101  187  GVVPNARVTVETTPG  ARVTVETTP        0.2002       5729.6                50.00   Rv2711, TB
    DRB4_0101   33  LDQSGPTVSQTVSRM  GPTVSQTVS        0.1993       5790.0                50.00   Rv2711, TB
    DRB4_0101   15  YDLEEEGVTPLRARI  EEGVTPLRA        0.1978       5881.9                50.00   Rv2711, TB
    DRB4_0101   93  WEEVHAEACRWEHVM  HAEACRWEH        0.1941       6120.8                50.00   Rv2711, TB
    DRB4_0101  191  NARVTVETTPGGGVT  ARVTVETTP        0.1939       6133.1                50.00   Rv2711, TB
    DRB4_0101  188  VVPNARVTVETTPGG  ARVTVETTP        0.1930       6192.3                50.00   Rv2711, TB
    DRB4_0101  124  TSPFGNPIPGLVELG  SPFGNPIPG        0.1896       6427.5                50.00   Rv2711, TB
    DRB4_0101   31  ERLDQSGPTVSQTVS  ERLDQSGPT        0.1889       6473.7                50.00   Rv2711, TB
    DRB4_0101  136  ELGVGPEPGADDANL  LGVGPEPGA        0.1844       6797.0                50.00   Rv2711, TB
    DRB4_0101   92  PWEEVHAEACRWEHV  HAEACRWEH        0.1820       6975.9                50.00   Rv2711, TB
    DRB4_0101   32  RLDQSGPTVSQTVSR  GPTVSQTVS        0.1819       6988.0                50.00   Rv2711, TB
    DRB4_0101   30  AERLDQSGPTVSQTV  ERLDQSGPT        0.1805       7092.5                50.00   Rv2711, TB
    DRB4_0101   91  LPWEEVHAEACRWEH  HAEACRWEH        0.1782       7271.5                50.00   Rv2711, TB
    DRB4_0101  192  ARVTVETTPGGGVTI  ARVTVETTP        0.1730       7691.9                50.00   Rv2711, TB
    DRB4_0101  196  VETTPGGGVTIVIPG  GGVTIVIPG        0.1706       7890.4                50.00   Rv2711, TB
    DRB4_0101   12  RTIYDLEEEGVTPLR  RTIYDLEEE        0.1688       8052.7                50.00   Rv2711, TB
    DRB4_0101   13  TIYDLEEEGVTPLRA  EEGVTPLRA        0.1643       8452.3                50.00   Rv2711, TB
    DRB4_0101  151  VRLTELPAGSPVAVV  VRLTELPAG        0.1594       8916.0                50.00   Rv2711, TB
    DRB4_0101  154  TELPAGSPVAVVVRQ  SPVAVVVRQ        0.1568       9165.5                50.00   Rv2711, TB
    DRB4_0101  141  PEPGADDANLVRLTE  ADDANLVRL        0.1495       9922.7                50.00   Rv2711, TB
    DRB4_0101  152  RLTELPAGSPVAVVV  RLTELPAGS        0.1480      10076.5                50.00   Rv2711, TB
    DRB4_0101   14  IYDLEEEGVTPLRAR  EEGVTPLRA        0.1476      10121.5                50.00   Rv2711, TB
    DRB4_0101  123  TTSPFGNPIPGLVEL  SPFGNPIPG        0.1434      10598.5                50.00   Rv2711, TB
    DRB4_0101  140  GPEPGADDANLVRLT  ADDANLVRL        0.1381      11221.8                50.00   Rv2711, TB
    DRB4_0101  153  LTELPAGSPVAVVVR  ELPAGSPVA        0.1372      11332.1                50.00   Rv2711, TB
    DRB4_0101  137  LGVGPEPGADDANLV  LGVGPEPGA        0.1279      12537.1                50.00   Rv2711, TB
    DRB4_0101  122  PTTSPFGNPIPGLVE  SPFGNPIPG        0.1234      13162.1                50.00   Rv2711, TB
    DRB4_0101  117  KVLNNPTTSPFGNPI  KVLNNPTTS        0.1218      13392.3                50.00   Rv2711, TB
    DRB4_0101  193  RVTVETTPGGGVTIV  RVTVETTPG        0.1136      14634.0                50.00   Rv2711, TB
    DRB4_0101  195  TVETTPGGGVTIVIP  GGGVTIVIP        0.1105      15124.7                50.00   Rv2711, TB
    DRB4_0101  121  NPTTSPFGNPIPGLV  SPFGNPIPG        0.1094      15300.0                50.00   Rv2711, TB
    DRB4_0101  119  LNNPTTSPFGNPIPG  LNNPTTSPF        0.0984      17246.1                50.00   Rv2711, TB
    DRB4_0101  120  NNPTTSPFGNPIPGL  SPFGNPIPG        0.0926      18365.0                50.00   Rv2711, TB
    DRB4_0101  118  VLNNPTTSPFGNPIP  LNNPTTSPF        0.0911      18663.5                50.00   Rv2711, TB
    DRB4_0101  194  VTVETTPGGGVTIVI  VTVETTPGG        0.0880      19294.7                50.00   Rv2711, TB
    DRB4_0101  139  VGPEPGADDANLVRL  ADDANLVRL        0.0862      19677.9                50.00   Rv2711, TB
    DRB4_0101  138  GVGPEPGADDANLVR  GPEPGADDA        0.0647      24837.4                50.00   Rv2711, TB
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  Allele: DRB4_0101. Number of high binders 5. Number of weak binders 48. Number of peptides 216
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     Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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  DRB5_0101   67  GRALAIAVMRKHRLA  AIAVMRKHR         0.7447          15.8        SB     2.00   Rv2711, TB
  DRB5_0101   68  RALAIAVMRKHRLAE  AIAVMRKHR         0.7413          16.4        SB     2.00   Rv2711, TB
  DRB5_0101   66  KGRALAIAVMRKHRL  AIAVMRKHR         0.7316          18.2        SB     2.00   Rv2711, TB
  DRB5_0101  113  RRLVKVLNNPTTSPF  LVKVLNNPT         0.7123          22.5        SB     4.00   Rv2711, TB
  DRB5_0101   69  ALAIAVMRKHRLAER  AIAVMRKHR         0.7096          23.2        SB     4.00   Rv2711, TB
  DRB5_0101  112  ERRLVKVLNNPTTSP  LVKVLNNPT         0.6997          25.8        SB     4.00   Rv2711, TB
  DRB5_0101   70  LAIAVMRKHRLAERL  AIAVMRKHR         0.6941          27.4        SB     4.00   Rv2711, TB
  DRB5_0101  111  VERRLVKVLNNPTTS  LVKVLNNPT         0.6871          29.5        SB     4.00   Rv2711, TB
  DRB5_0101   65  EKGRALAIAVMRKHR  RALAIAVMR         0.6858          29.9        SB     4.00   Rv2711, TB
  DRB5_0101  114  RLVKVLNNPTTSPFG  LVKVLNNPT         0.6734          34.2        SB     4.00   Rv2711, TB
  DRB5_0101   71  AIAVMRKHRLAERLL  AIAVMRKHR         0.6615          39.0        SB     8.00   Rv2711, TB
  DRB5_0101  110  DVERRLVKVLNNPTT  RRLVKVLNN         0.6601          39.6        SB     8.00   Rv2711, TB
  DRB5_0101  109  EDVERRLVKVLNNPT  RRLVKVLNN         0.5869          87.4        WB    16.00   Rv2711, TB
  DRB5_0101  115  LVKVLNNPTTSPFGN  LVKVLNNPT         0.5832          90.9        WB    16.00   Rv2711, TB
  DRB5_0101   72  IAVMRKHRLAERLLV  IAVMRKHRL         0.5731         101.4        WB    16.00   Rv2711, TB
  DRB5_0101   64  TEKGRALAIAVMRKH  RALAIAVMR         0.5633         112.7        WB    16.00   Rv2711, TB
  DRB5_0101   19  EEGVTPLRARIAERL  GVTPLRARI         0.5603         116.5        WB    16.00   Rv2711, TB
  DRB5_0101   49  RDGLLRVAGDRHLEL  LLRVAGDRH         0.5562         121.8        WB    16.00   Rv2711, TB
  DRB5_0101   50  DGLLRVAGDRHLELT  LLRVAGDRH         0.5498         130.5        WB    16.00   Rv2711, TB
  DRB5_0101   18  EEEGVTPLRARIAER  GVTPLRARI         0.5472         134.2        WB    16.00   Rv2711, TB
  DRB5_0101   20  EGVTPLRARIAERLD  GVTPLRARI         0.5467         134.9        WB    16.00   Rv2711, TB
  DRB5_0101   51  GLLRVAGDRHLELTE  LRVAGDRHL         0.5393         146.2        WB    16.00   Rv2711, TB
  DRB5_0101   17  LEEEGVTPLRARIAE  GVTPLRARI         0.5324         157.5        WB    16.00   Rv2711, TB
  DRB5_0101   48  ERDGLLRVAGDRHLE  LLRVAGDRH         0.5157         188.6        WB    32.00   Rv2711, TB
  DRB5_0101   16  DLEEEGVTPLRARIA  GVTPLRARI         0.5126         195.1        WB    32.00   Rv2711, TB
  DRB5_0101   21  GVTPLRARIAERLDQ  GVTPLRARI         0.5109         198.7        WB    32.00   Rv2711, TB
  DRB5_0101  215  TLPHEMAHAVKVEKV  LPHEMAHAV         0.5066         208.2        WB    32.00   Rv2711, TB
  DRB5_0101   73  AVMRKHRLAERLLVD  RKHRLAERL         0.5047         212.5        WB    32.00   Rv2711, TB
  DRB5_0101  214  VTLPHEMAHAVKVEK  LPHEMAHAV         0.5035         215.3        WB    32.00   Rv2711, TB
  DRB5_0101  212  ENVTLPHEMAHAVKV  LPHEMAHAV         0.5028         217.0        WB    32.00   Rv2711, TB
  DRB5_0101   75  MRKHRLAERLLVDVI  HRLAERLLV         0.5014         220.2        WB    32.00   Rv2711, TB
  DRB5_0101   74  VMRKHRLAERLLVDV  HRLAERLLV         0.5007         222.0        WB    32.00   Rv2711, TB
  DRB5_0101   63  LTEKGRALAIAVMRK  RALAIAVMR         0.4970         231.0        WB    32.00   Rv2711, TB
  DRB5_0101    4  VDTTEMYLRTIYDLE  EMYLRTIYD         0.4869         257.7        WB    32.00   Rv2711, TB
  DRB5_0101  213  NVTLPHEMAHAVKVE  LPHEMAHAV         0.4865         258.9        WB    32.00   Rv2711, TB
  DRB5_0101   52  LLRVAGDRHLELTEK  LLRVAGDRH         0.4857         261.0        WB    32.00   Rv2711, TB
  DRB5_0101   47  MERDGLLRVAGDRHL  LLRVAGDRH         0.4843         264.9        WB    32.00   Rv2711, TB
  DRB5_0101   15  YDLEEEGVTPLRARI  GVTPLRARI         0.4610         341.1        WB    32.00   Rv2711, TB
  DRB5_0101    3  LVDTTEMYLRTIYDL  VDTTEMYLR         0.4609         341.4        WB    32.00   Rv2711, TB
  DRB5_0101  116  VKVLNNPTTSPFGNP  VKVLNNPTT         0.4537         368.9        WB    32.00   Rv2711, TB
  DRB5_0101  108  SEDVERRLVKVLNNP  RRLVKVLNN         0.4512         379.2        WB    32.00   Rv2711, TB
  DRB5_0101   76  RKHRLAERLLVDVIG  RKHRLAERL         0.4498         384.9        WB    32.00   Rv2711, TB
  DRB5_0101  100  ACRWEHVMSEDVERR  WEHVMSEDV         0.4450         405.4        WB    32.00   Rv2711, TB
  DRB5_0101    5  DTTEMYLRTIYDLEE  EMYLRTIYD         0.4450         405.6        WB    32.00   Rv2711, TB
  DRB5_0101  211  HENVTLPHEMAHAVK  LPHEMAHAV         0.4398         428.8        WB    32.00   Rv2711, TB
  DRB5_0101  102  RWEHVMSEDVERRLV  HVMSEDVER         0.4381         436.7        WB    32.00   Rv2711, TB
  DRB5_0101    6  TTEMYLRTIYDLEEE  EMYLRTIYD         0.4340         456.6        WB    32.00   Rv2711, TB
  DRB5_0101  101  CRWEHVMSEDVERRL  HVMSEDVER         0.4310         471.7        WB    32.00   Rv2711, TB
  DRB5_0101  160  SPVAVVVRQLTEHVQ  VVRQLTEHV         0.4258         499.1        WB    32.00   Rv2711, TB
  DRB5_0101  103  WEHVMSEDVERRLVK  VMSEDVERR         0.4257         499.6        WB    32.00   Rv2711, TB
  DRB5_0101  159  GSPVAVVVRQLTEHV  VVRQLTEHV         0.4249         503.8              32.00   Rv2711, TB
  DRB5_0101    2  ELVDTTEMYLRTIYD  VDTTEMYLR         0.4216         522.1              32.00   Rv2711, TB
  DRB5_0101   36  SGPTVSQTVSRMERD  PTVSQTVSR         0.4182         541.8              32.00   Rv2711, TB
  DRB5_0101   46  RMERDGLLRVAGDRH  LLRVAGDRH         0.4136         569.4              32.00   Rv2711, TB
  DRB5_0101    7  TEMYLRTIYDLEEEG  EMYLRTIYD         0.4119         580.4              50.00   Rv2711, TB
  DRB5_0101   37  GPTVSQTVSRMERDG  PTVSQTVSR         0.4079         605.5              50.00   Rv2711, TB
  DRB5_0101   35  QSGPTVSQTVSRMER  PTVSQTVSR         0.4076         607.5              50.00   Rv2711, TB
  DRB5_0101  210  GHENVTLPHEMAHAV  LPHEMAHAV         0.4069         612.1              50.00   Rv2711, TB
  DRB5_0101  162  VAVVVRQLTEHVQGD  VVRQLTEHV         0.4028         640.0              50.00   Rv2711, TB
  DRB5_0101  161  PVAVVVRQLTEHVQG  VVRQLTEHV         0.3995         663.1              50.00   Rv2711, TB
  DRB5_0101    8  EMYLRTIYDLEEEGV  EMYLRTIYD         0.3968         682.7              50.00   Rv2711, TB
  DRB5_0101   38  PTVSQTVSRMERDGL  PTVSQTVSR         0.3944         700.8              50.00   Rv2711, TB
  DRB5_0101  150  LVRLTELPAGSPVAV  RLTELPAGS         0.3879         752.1              50.00   Rv2711, TB
  DRB5_0101   62  ELTEKGRALAIAVMR  RALAIAVMR         0.3873         757.3              50.00   Rv2711, TB
  DRB5_0101   22  VTPLRARIAERLDQS  PLRARIAER         0.3826         796.6              50.00   Rv2711, TB
  DRB5_0101    1  NELVDTTEMYLRTIY  VDTTEMYLR         0.3801         817.9              50.00   Rv2711, TB
  DRB5_0101  149  NLVRLTELPAGSPVA  RLTELPAGS         0.3798         821.2              50.00   Rv2711, TB
  DRB5_0101   99  EACRWEHVMSEDVER  WEHVMSEDV         0.3769         846.9              50.00   Rv2711, TB
  DRB5_0101  107  MSEDVERRLVKVLNN  RRLVKVLNN         0.3764         851.5              50.00   Rv2711, TB
  DRB5_0101   58  DRHLELTEKGRALAI  LELTEKGRA         0.3758         857.5              50.00   Rv2711, TB
  DRB5_0101  163  AVVVRQLTEHVQGDI  VVRQLTEHV         0.3727         886.1              50.00   Rv2711, TB
  DRB5_0101  104  EHVMSEDVERRLVKV  VMSEDVERR         0.3714         899.4              50.00   Rv2711, TB
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DRB5_0101  151  VRLTELPAGSPVAVV  RLTELPAGS        0.3708        904.5                 50.00   Rv2711, TB
DRB5_0101   57  GDRHLELTEKGRALA  HLELTEKGR        0.3704        908.6                 50.00   Rv2711, TB
DRB5_0101  105  HVMSEDVERRLVKVL  VMSEDVERR        0.3700        912.6                 50.00   Rv2711, TB
DRB5_0101   23  TPLRARIAERLDQSG  PLRARIAER        0.3672        940.5                 50.00   Rv2711, TB
DRB5_0101   59  RHLELTEKGRALAIA  LELTEKGRA        0.3584       1034.5                 50.00   Rv2711, TB
DRB5_0101  148  ANLVRLTELPAGSPV  RLTELPAGS        0.3545       1079.7                 50.00   Rv2711, TB
DRB5_0101   77  KHRLAERLLVDVIGL  HRLAERLLV        0.3535       1091.1                 50.00   Rv2711, TB
DRB5_0101    0  MNELVDTTEMYLRTI  VDTTEMYLR        0.3505       1126.5                 50.00   Rv2711, TB
DRB5_0101  164  VVVRQLTEHVQGDID  VVRQLTEHV        0.3498       1136.1                 50.00   Rv2711, TB
DRB5_0101  182  RLKDAGVVPNARVTV  AGVVPNARV        0.3491       1144.0                 50.00   Rv2711, TB
DRB5_0101   34  DQSGPTVSQTVSRME  PTVSQTVSR        0.3481       1157.2                 50.00   Rv2711, TB
DRB5_0101   78  HRLAERLLVDVIGLP  HRLAERLLV        0.3458       1186.1                 50.00   Rv2711, TB
DRB5_0101  158  AGSPVAVVVRQLTEH  SPVAVVVRQ        0.3419       1236.4                 50.00   Rv2711, TB
DRB5_0101   24  PLRARIAERLDQSGP  PLRARIAER        0.3419       1236.6                 50.00   Rv2711, TB
DRB5_0101   56  AGDRHLELTEKGRAL  HLELTEKGR        0.3413       1244.7                 50.00   Rv2711, TB
DRB5_0101   95  EVHAEACRWEHVMSE  EVHAEACRW        0.3379       1292.0                 50.00   Rv2711, TB
DRB5_0101   53  LRVAGDRHLELTEKG  LRVAGDRHL        0.3370       1304.0                 50.00   Rv2711, TB
DRB5_0101  181  TRLKDAGVVPNARVT  AGVVPNARV        0.3289       1424.1                 50.00   Rv2711, TB
DRB5_0101  180  ITRLKDAGVVPNARV  AGVVPNARV        0.3261       1467.5                 50.00   Rv2711, TB
DRB5_0101   98  AEACRWEHVMSEDVE  WEHVMSEDV        0.3243       1497.0                 50.00   Rv2711, TB
DRB5_0101   94  EEVHAEACRWEHVMS  EVHAEACRW        0.3207       1555.2                 50.00   Rv2711, TB
DRB5_0101  147  DANLVRLTELPAGSP  RLTELPAGS        0.3202       1563.6                 50.00   Rv2711, TB
DRB5_0101   60  HLELTEKGRALAIAV  LELTEKGRA        0.3137       1678.0                 50.00   Rv2711, TB
DRB5_0101  157  PAGSPVAVVVRQLTE  SPVAVVVRQ        0.3123       1703.6                 50.00   Rv2711, TB
DRB5_0101  183  LKDAGVVPNARVTVE  AGVVPNARV        0.3122       1705.9                 50.00   Rv2711, TB
DRB5_0101  209  PGHENVTLPHEMAHA  ENVTLPHEM        0.3090       1765.5                 50.00   Rv2711, TB
DRB5_0101   97  HAEACRWEHVMSEDV  WEHVMSEDV        0.3085       1774.9                 50.00   Rv2711, TB
DRB5_0101   33  LDQSGPTVSQTVSRM  PTVSQTVSR        0.3055       1834.7                 50.00   Rv2711, TB
DRB5_0101   93  WEEVHAEACRWEHVM  EVHAEACRW        0.3017       1911.1                 50.00   Rv2711, TB
DRB5_0101  106  VMSEDVERRLVKVLN  VMSEDVERR        0.2993       1961.4                 50.00   Rv2711, TB
DRB5_0101  179  LITRLKDAGVVPNAR  ITRLKDAGV        0.2983       1983.2                 50.00   Rv2711, TB
DRB5_0101  152  RLTELPAGSPVAVVV  RLTELPAGS        0.2983       1983.7                 50.00   Rv2711, TB
DRB5_0101   45  SRMERDGLLRVAGDR  RMERDGLLR        0.2977       1994.6                 50.00   Rv2711, TB
DRB5_0101  203  GVTIVIPGHENVTLP  VTIVIPGHE        0.2972       2005.8                 50.00   Rv2711, TB
DRB5_0101  202  GGVTIVIPGHENVTL  VTIVIPGHE        0.2971       2008.2                 50.00   Rv2711, TB
DRB5_0101  184  KDAGVVPNARVTVET  AGVVPNARV        0.2961       2029.6                 50.00   Rv2711, TB
DRB5_0101   92  PWEEVHAEACRWEHV  EVHAEACRW        0.2952       2050.8                 50.00   Rv2711, TB
DRB5_0101   55  VAGDRHLELTEKGRA  LELTEKGRA        0.2944       2068.0                 50.00   Rv2711, TB
DRB5_0101  146  DDANLVRLTELPAGS  RLTELPAGS        0.2904       2160.6                 50.00   Rv2711, TB
DRB5_0101    9  MYLRTIYDLEEEGVT  LRTIYDLEE        0.2883       2209.9                 50.00   Rv2711, TB
DRB5_0101  177  IDLITRLKDAGVVPN  LITRLKDAG        0.2878       2220.1                 50.00   Rv2711, TB
DRB5_0101  185  DAGVVPNARVTVETT  AGVVPNARV        0.2853       2282.3                 50.00   Rv2711, TB
DRB5_0101  117  KVLNNPTTSPFGNPI  KVLNNPTTS        0.2850       2289.1                 50.00   Rv2711, TB
DRB5_0101   91  LPWEEVHAEACRWEH  EVHAEACRW        0.2841       2312.5                 50.00   Rv2711, TB
DRB5_0101  124  TSPFGNPIPGLVELG  FGNPIPGLV        0.2827       2347.8                 50.00   Rv2711, TB
DRB5_0101  178  DLITRLKDAGVVPNA  ITRLKDAGV        0.2826       2349.8                 50.00   Rv2711, TB
DRB5_0101  175  GDIDLITRLKDAGVV  ITRLKDAGV        0.2821       2361.9                 50.00   Rv2711, TB
DRB5_0101  201  GGGVTIVIPGHENVT  VTIVIPGHE        0.2789       2445.9                 50.00   Rv2711, TB
DRB5_0101  156  LPAGSPVAVVVRQLT  SPVAVVVRQ        0.2782       2464.5                 50.00   Rv2711, TB
DRB5_0101  123  TTSPFGNPIPGLVEL  FGNPIPGLV        0.2781       2466.7                 50.00   Rv2711, TB
DRB5_0101  174  QGDIDLITRLKDAGV  IDLITRLKD        0.2763       2514.3                 50.00   Rv2711, TB
DRB5_0101   14  IYDLEEEGVTPLRAR  EEGVTPLRA        0.2729       2610.8                 50.00   Rv2711, TB
DRB5_0101  165  VVRQLTEHVQGDIDL  VVRQLTEHV        0.2725       2622.2                 50.00   Rv2711, TB
DRB5_0101   39  TVSQTVSRMERDGLL  TVSQTVSRM        0.2700       2694.2                 50.00   Rv2711, TB
DRB5_0101  125  SPFGNPIPGLVELGV  FGNPIPGLV        0.2698       2697.5                 50.00   Rv2711, TB
DRB5_0101   90  GLPWEEVHAEACRWE  EVHAEACRW        0.2659       2816.8                 50.00   Rv2711, TB
DRB5_0101   61  LELTEKGRALAIAVM  LELTEKGRA        0.2655       2826.2                 50.00   Rv2711, TB
DRB5_0101   43  TVSRMERDGLLRVAG  RMERDGLLR        0.2634       2893.1                 50.00   Rv2711, TB
DRB5_0101  204  VTIVIPGHENVTLPH  VTIVIPGHE        0.2621       2934.2                 50.00   Rv2711, TB
DRB5_0101   44  VSRMERDGLLRVAGD  RMERDGLLR        0.2596       3013.6                 50.00   Rv2711, TB
DRB5_0101   25  LRARIAERLDQSGPT  LRARIAERL        0.2576       3078.7                 50.00   Rv2711, TB
DRB5_0101  122  PTTSPFGNPIPGLVE  FGNPIPGLV        0.2573       3090.0                 50.00   Rv2711, TB
DRB5_0101  208  IPGHENVTLPHEMAH  ENVTLPHEM        0.2571       3098.0                 50.00   Rv2711, TB
DRB5_0101  176  DIDLITRLKDAGVVP  ITRLKDAGV        0.2550       3167.4                 50.00   Rv2711, TB
DRB5_0101  186  AGVVPNARVTVETTP  AGVVPNARV        0.2545       3184.3                 50.00   Rv2711, TB
DRB5_0101   79  RLAERLLVDVIGLPW  RLLVDVIGL        0.2517       3281.8                 50.00   Rv2711, TB
DRB5_0101  200  PGGGVTIVIPGHENV  VTIVIPGHE        0.2490       3378.9                 50.00   Rv2711, TB
DRB5_0101   42  QTVSRMERDGLLRVA  RMERDGLLR        0.2441       3565.8                 50.00   Rv2711, TB
DRB5_0101   80  LAERLLVDVIGLPWE  RLLVDVIGL        0.2438       3575.8                 50.00   Rv2711, TB
DRB5_0101   41  SQTVSRMERDGLLRV  RMERDGLLR        0.2429       3612.1                 50.00   Rv2711, TB
DRB5_0101  155  ELPAGSPVAVVVRQL  GSPVAVVVR        0.2419       3648.5                 50.00   Rv2711, TB
DRB5_0101  126  PFGNPIPGLVELGVG  FGNPIPGLV        0.2401       3723.4                 50.00   Rv2711, TB
DRB5_0101  173  VQGDIDLITRLKDAG  DIDLITRLK        0.2381       3804.2                 50.00   Rv2711, TB
DRB5_0101  127  FGNPIPGLVELGVGP  FGNPIPGLV        0.2368       3856.0                 50.00   Rv2711, TB
DRB5_0101   10  YLRTIYDLEEEGVTP  YLRTIYDLE        0.2297       4164.6                 50.00   Rv2711, TB
DRB5_0101   81  AERLLVDVIGLPWEE  RLLVDVIGL        0.2285       4221.1                 50.00   Rv2711, TB
DRB5_0101   89  IGLPWEEVHAEACRW  EVHAEACRW        0.2281       4237.2                 50.00   Rv2711, TB
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   DRB5_0101  121  NPTTSPFGNPIPGLV  FGNPIPGLV        0.2244       4409.8                50.00   Rv2711, TB
   DRB5_0101   82  ERLLVDVIGLPWEEV  RLLVDVIGL        0.2234       4456.6                50.00   Rv2711, TB
   DRB5_0101   54  RVAGDRHLELTEKGR  RHLELTEKG        0.2232       4469.4                50.00   Rv2711, TB
   DRB5_0101   40  VSQTVSRMERDGLLR  RMERDGLLR        0.2220       4524.5                50.00   Rv2711, TB
   DRB5_0101  118  VLNNPTTSPFGNPIP  LNNPTTSPF        0.2213       4562.5                50.00   Rv2711, TB
   DRB5_0101  145  ADDANLVRLTELPAG  LVRLTELPA        0.2176       4747.5                50.00   Rv2711, TB
   DRB5_0101  199  TPGGGVTIVIPGHEN  VTIVIPGHE        0.2173       4762.4                50.00   Rv2711, TB
   DRB5_0101  207  VIPGHENVTLPHEMA  ENVTLPHEM        0.2148       4895.7                50.00   Rv2711, TB
   DRB5_0101  172  HVQGDIDLITRLKDA  DIDLITRLK        0.2146       4904.6                50.00   Rv2711, TB
   DRB5_0101   32  RLDQSGPTVSQTVSR  PTVSQTVSR        0.2125       5017.3                50.00   Rv2711, TB
   DRB5_0101   83  RLLVDVIGLPWEEVH  RLLVDVIGL        0.2119       5049.4                50.00   Rv2711, TB
   DRB5_0101   96  VHAEACRWEHVMSED  CRWEHVMSE        0.2114       5078.8                50.00   Rv2711, TB
   DRB5_0101  192  ARVTVETTPGGGVTI  RVTVETTPG        0.2113       5083.2                50.00   Rv2711, TB
   DRB5_0101  191  NARVTVETTPGGGVT  RVTVETTPG        0.2102       5143.5                50.00   Rv2711, TB
   DRB5_0101  154  TELPAGSPVAVVVRQ  GSPVAVVVR        0.2091       5204.4                50.00   Rv2711, TB
   DRB5_0101  187  GVVPNARVTVETTPG  GVVPNARVT        0.2043       5482.2                50.00   Rv2711, TB
   DRB5_0101  190  PNARVTVETTPGGGV  RVTVETTPG        0.2029       5564.3                50.00   Rv2711, TB
   DRB5_0101  193  RVTVETTPGGGVTIV  RVTVETTPG        0.1964       5969.9                50.00   Rv2711, TB
   DRB5_0101  189  VPNARVTVETTPGGG  RVTVETTPG        0.1939       6137.1                50.00   Rv2711, TB
   DRB5_0101  188  VVPNARVTVETTPGG  RVTVETTPG        0.1892       6455.8                50.00   Rv2711, TB
   DRB5_0101  153  LTELPAGSPVAVVVR  GSPVAVVVR        0.1873       6588.4                50.00   Rv2711, TB
   DRB5_0101  144  GADDANLVRLTELPA  LVRLTELPA        0.1852       6743.1                50.00   Rv2711, TB
   DRB5_0101  206  IVIPGHENVTLPHEM  ENVTLPHEM        0.1840       6828.7                50.00   Rv2711, TB
   DRB5_0101  171  EHVQGDIDLITRLKD  DIDLITRLK        0.1803       7107.4                50.00   Rv2711, TB
   DRB5_0101  119  LNNPTTSPFGNPIPG  LNNPTTSPF        0.1797       7156.8                50.00   Rv2711, TB
   DRB5_0101   13  TIYDLEEEGVTPLRA  EEGVTPLRA        0.1784       7256.9                50.00   Rv2711, TB
   DRB5_0101  198  TTPGGGVTIVIPGHE  VTIVIPGHE        0.1749       7533.8                50.00   Rv2711, TB
   DRB5_0101  128  GNPIPGLVELGVGPE  GLVELGVGP        0.1671       8201.5                50.00   Rv2711, TB
   DRB5_0101   84  LLVDVIGLPWEEVHA  DVIGLPWEE        0.1668       8228.4                50.00   Rv2711, TB
   DRB5_0101  205  TIVIPGHENVTLPHE  TIVIPGHEN        0.1623       8634.9                50.00   Rv2711, TB
   DRB5_0101  129  NPIPGLVELGVGPEP  GLVELGVGP        0.1563       9216.0                50.00   Rv2711, TB
   DRB5_0101   85  LVDVIGLPWEEVHAE  LVDVIGLPW        0.1530       9552.6                50.00   Rv2711, TB
   DRB5_0101  170  TEHVQGDIDLITRLK  DIDLITRLK        0.1514       9712.4                50.00   Rv2711, TB
   DRB5_0101   87  DVIGLPWEEVHAEAC  LPWEEVHAE        0.1506       9800.9                50.00   Rv2711, TB
   DRB5_0101   86  VDVIGLPWEEVHAEA  LPWEEVHAE        0.1484      10036.2                50.00   Rv2711, TB
   DRB5_0101   11  LRTIYDLEEEGVTPL  LRTIYDLEE        0.1481      10071.1                50.00   Rv2711, TB
   DRB5_0101  120  NNPTTSPFGNPIPGL  TTSPFGNPI        0.1468      10209.5                50.00   Rv2711, TB
   DRB5_0101  133  GLVELGVGPEPGADD  GLVELGVGP        0.1435      10582.4                50.00   Rv2711, TB
   DRB5_0101  143  PGADDANLVRLTELP  ADDANLVRL        0.1401      10982.8                50.00   Rv2711, TB
   DRB5_0101  132  PGLVELGVGPEPGAD  GLVELGVGP        0.1368      11381.0                50.00   Rv2711, TB
   DRB5_0101   88  VIGLPWEEVHAEACR  LPWEEVHAE        0.1331      11839.5                50.00   Rv2711, TB
   DRB5_0101  130  PIPGLVELGVGPEPG  GLVELGVGP        0.1310      12114.4                50.00   Rv2711, TB
   DRB5_0101  131  IPGLVELGVGPEPGA  GLVELGVGP        0.1308      12149.3                50.00   Rv2711, TB
   DRB5_0101  142  EPGADDANLVRLTEL  ADDANLVRL        0.1249      12940.9                50.00   Rv2711, TB
   DRB5_0101  136  ELGVGPEPGADDANL  GVGPEPGAD        0.1233      13176.2                50.00   Rv2711, TB
   DRB5_0101   27  ARIAERLDQSGPTVS  ARIAERLDQ        0.1198      13685.6                50.00   Rv2711, TB
   DRB5_0101  135  VELGVGPEPGADDAN  GVGPEPGAD        0.1195      13729.5                50.00   Rv2711, TB
   DRB5_0101   26  RARIAERLDQSGPTV  ARIAERLDQ        0.1178      13973.3                50.00   Rv2711, TB
   DRB5_0101  137  LGVGPEPGADDANLV  GVGPEPGAD        0.1178      13984.8                50.00   Rv2711, TB
   DRB5_0101   12  RTIYDLEEEGVTPLR  YDLEEEGVT        0.1152      14372.6                50.00   Rv2711, TB
   DRB5_0101  166  VRQLTEHVQGDIDLI  VRQLTEHVQ        0.1152      14377.3                50.00   Rv2711, TB
   DRB5_0101   28  RIAERLDQSGPTVSQ  RLDQSGPTV        0.1147      14453.7                50.00   Rv2711, TB
   DRB5_0101   29  IAERLDQSGPTVSQT  RLDQSGPTV        0.1101      15192.1                50.00   Rv2711, TB
   DRB5_0101   31  ERLDQSGPTVSQTVS  RLDQSGPTV        0.1093      15326.5                50.00   Rv2711, TB
   DRB5_0101  138  GVGPEPGADDANLVR  GVGPEPGAD        0.1091      15361.7                50.00   Rv2711, TB
   DRB5_0101  134  LVELGVGPEPGADDA  GVGPEPGAD        0.1075      15627.1                50.00   Rv2711, TB
   DRB5_0101   30  AERLDQSGPTVSQTV  RLDQSGPTV        0.1045      16145.1                50.00   Rv2711, TB
   DRB5_0101  194  VTVETTPGGGVTIVI  VTVETTPGG        0.0996      17018.8                50.00   Rv2711, TB
   DRB5_0101  141  PEPGADDANLVRLTE  ADDANLVRL        0.0982      17271.5                50.00   Rv2711, TB
   DRB5_0101  169  LTEHVQGDIDLITRL  GDIDLITRL        0.0879      19325.2                50.00   Rv2711, TB
   DRB5_0101  140  GPEPGADDANLVRLT  ADDANLVRL        0.0823      20528.5                50.00   Rv2711, TB
   DRB5_0101  167  RQLTEHVQGDIDLIT  RQLTEHVQG        0.0797      21109.9                50.00   Rv2711, TB
   DRB5_0101  139  VGPEPGADDANLVRL  ADDANLVRL        0.0763      21897.4                50.00   Rv2711, TB
   DRB5_0101  197  ETTPGGGVTIVIPGH  GVTIVIPGH        0.0731      22663.9                50.00   Rv2711, TB
   DRB5_0101  195  TVETTPGGGVTIVIP  TVETTPGGG        0.0604      26010.4                50.00   Rv2711, TB
   DRB5_0101  168  QLTEHVQGDIDLITR  EHVQGDIDL        0.0581      26665.8                50.00   Rv2711, TB
   DRB5_0101  196  VETTPGGGVTIVIPG  GGVTIVIPG        0.0556      27409.1                50.00   Rv2711, TB
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Allele: DRB5_0101. Number of high binders 12. Number of weak binders 38. Number of peptides 216

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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         IAb  153  LTELPAGSPVAVVVR  LPAGSPVAV        0.6090         68.8         WB     2.00   Rv2711, TB
         IAb  154  TELPAGSPVAVVVRQ  LPAGSPVAV        0.6033         73.1         WB     2.00   Rv2711, TB
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IAb  152  RLTELPAGSPVAVVV  ELPAGSPVA        0.5885          85.8          WB     2.00   Rv2711, TB
IAb  155  ELPAGSPVAVVVRQL  LPAGSPVAV        0.5865          87.7          WB     2.00   Rv2711, TB
IAb  116  VKVLNNPTTSPFGNP  KVLNNPTTS        0.5720         102.5          WB     4.00   Rv2711, TB
IAb  115  LVKVLNNPTTSPFGN  KVLNNPTTS        0.5682         107.0          WB     4.00   Rv2711, TB
IAb  114  RLVKVLNNPTTSPFG  KVLNNPTTS        0.5573         120.3          WB     4.00   Rv2711, TB
IAb  124  TSPFGNPIPGLVELG  SPFGNPIPG        0.5492         131.3          WB     4.00   Rv2711, TB
IAb  123  TTSPFGNPIPGLVEL  SPFGNPIPG        0.5488         131.9          WB     4.00   Rv2711, TB
IAb  122  PTTSPFGNPIPGLVE  SPFGNPIPG        0.5355         152.3          WB     4.00   Rv2711, TB
IAb  151  VRLTELPAGSPVAVV  ELPAGSPVA        0.5311         159.6          WB     4.00   Rv2711, TB
IAb  113  RRLVKVLNNPTTSPF  KVLNNPTTS        0.5277         165.7          WB     4.00   Rv2711, TB
IAb  121  NPTTSPFGNPIPGLV  SPFGNPIPG        0.5084         204.2          WB     8.00   Rv2711, TB
IAb  117  KVLNNPTTSPFGNPI  KVLNNPTTS        0.4871         257.0          WB     8.00   Rv2711, TB
IAb  150  LVRLTELPAGSPVAV  LPAGSPVAV        0.4786         282.0          WB     8.00   Rv2711, TB
IAb  112  ERRLVKVLNNPTTSP  KVLNNPTTS        0.4563         358.6          WB     8.00   Rv2711, TB
IAb  156  LPAGSPVAVVVRQLT  LPAGSPVAV        0.4321         466.0          WB    16.00   Rv2711, TB
IAb   31  ERLDQSGPTVSQTVS  LDQSGPTVS        0.4176         545.2                16.00   Rv2711, TB
IAb  120  NNPTTSPFGNPIPGL  SPFGNPIPG        0.4175         545.8                16.00   Rv2711, TB
IAb   30  AERLDQSGPTVSQTV  LDQSGPTVS        0.4157         556.8                16.00   Rv2711, TB
IAb  125  SPFGNPIPGLVELGV  SPFGNPIPG        0.4104         589.8                16.00   Rv2711, TB
IAb   32  RLDQSGPTVSQTVSR  LDQSGPTVS        0.4052         623.7                16.00   Rv2711, TB
IAb  119  LNNPTTSPFGNPIPG  SPFGNPIPG        0.4043         629.9                16.00   Rv2711, TB
IAb  111  VERRLVKVLNNPTTS  KVLNNPTTS        0.3912         725.6                16.00   Rv2711, TB
IAb   33  LDQSGPTVSQTVSRM  LDQSGPTVS        0.3875         754.9                16.00   Rv2711, TB
IAb  118  VLNNPTTSPFGNPIP  NPTTSPFGN        0.3870         759.8                16.00   Rv2711, TB
IAb   29  IAERLDQSGPTVSQT  LDQSGPTVS        0.3612        1004.4                16.00   Rv2711, TB
IAb  149  NLVRLTELPAGSPVA  ELPAGSPVA        0.3452        1193.5                32.00   Rv2711, TB
IAb   19  EEGVTPLRARIAERL  VTPLRARIA        0.3337        1351.3                32.00   Rv2711, TB
IAb   18  EEEGVTPLRARIAER  VTPLRARIA        0.3185        1594.2                32.00   Rv2711, TB
IAb   17  LEEEGVTPLRARIAE  EEGVTPLRA        0.3173        1614.4                32.00   Rv2711, TB
IAb  203  GVTIVIPGHENVTLP  VTIVIPGHE        0.3146        1662.7                32.00   Rv2711, TB
IAb   28  RIAERLDQSGPTVSQ  LDQSGPTVS        0.3142        1668.7                32.00   Rv2711, TB
IAb  204  VTIVIPGHENVTLPH  VTIVIPGHE        0.3078        1789.3                32.00   Rv2711, TB
IAb   16  DLEEEGVTPLRARIA  EEGVTPLRA        0.3026        1892.8                32.00   Rv2711, TB
IAb   20  EGVTPLRARIAERLD  VTPLRARIA        0.3001        1944.3                32.00   Rv2711, TB
IAb  215  TLPHEMAHAVKVEKV  HEMAHAVKV        0.2999        1948.1                32.00   Rv2711, TB
IAb  202  GGVTIVIPGHENVTL  VTIVIPGHE        0.2994        1959.8                32.00   Rv2711, TB
IAb   22  VTPLRARIAERLDQS  VTPLRARIA        0.2938        2081.0                32.00   Rv2711, TB
IAb  126  PFGNPIPGLVELGVG  GNPIPGLVE        0.2916        2130.9                32.00   Rv2711, TB
IAb   21  GVTPLRARIAERLDQ  VTPLRARIA        0.2878        2222.3                32.00   Rv2711, TB
IAb   64  TEKGRALAIAVMRKH  GRALAIAVM        0.2866        2249.4                32.00   Rv2711, TB
IAb   27  ARIAERLDQSGPTVS  LDQSGPTVS        0.2818        2370.2                32.00   Rv2711, TB
IAb  201  GGGVTIVIPGHENVT  VTIVIPGHE        0.2765        2509.3                32.00   Rv2711, TB
IAb   66  KGRALAIAVMRKHRL  GRALAIAVM        0.2753        2542.4                32.00   Rv2711, TB
IAb  182  RLKDAGVVPNARVTV  LKDAGVVPN        0.2738        2585.0                32.00   Rv2711, TB
IAb   65  EKGRALAIAVMRKHR  GRALAIAVM        0.2712        2659.3                32.00   Rv2711, TB
IAb   63  LTEKGRALAIAVMRK  GRALAIAVM        0.2709        2667.2                32.00   Rv2711, TB
IAb  214  VTLPHEMAHAVKVEK  HEMAHAVKV        0.2705        2679.0                32.00   Rv2711, TB
IAb  213  NVTLPHEMAHAVKVE  HEMAHAVKV        0.2659        2814.6                32.00   Rv2711, TB
IAb  183  LKDAGVVPNARVTVE  LKDAGVVPN        0.2653        2834.6                32.00   Rv2711, TB
IAb  127  FGNPIPGLVELGVGP  GNPIPGLVE        0.2639        2876.5                32.00   Rv2711, TB
IAb   67  GRALAIAVMRKHRLA  RALAIAVMR        0.2622        2930.3                32.00   Rv2711, TB
IAb  205  TIVIPGHENVTLPHE  TIVIPGHEN        0.2620        2936.7                32.00   Rv2711, TB
IAb  181  TRLKDAGVVPNARVT  LKDAGVVPN        0.2620        2938.0                32.00   Rv2711, TB
IAb  212  ENVTLPHEMAHAVKV  HEMAHAVKV        0.2598        3007.7                32.00   Rv2711, TB
IAb   62  ELTEKGRALAIAVMR  GRALAIAVM        0.2595        3016.5                32.00   Rv2711, TB
IAb  180  ITRLKDAGVVPNARV  LKDAGVVPN        0.2433        3593.7                50.00   Rv2711, TB
IAb  134  LVELGVGPEPGADDA  LVELGVGPE        0.2385        3787.0                50.00   Rv2711, TB
IAb  184  KDAGVVPNARVTVET  DAGVVPNAR        0.2379        3810.0                50.00   Rv2711, TB
IAb  185  DAGVVPNARVTVETT  GVVPNARVT        0.2292        4189.8                50.00   Rv2711, TB
IAb   61  LELTEKGRALAIAVM  GRALAIAVM        0.2285        4221.1                50.00   Rv2711, TB
IAb  200  PGGGVTIVIPGHENV  VTIVIPGHE        0.2265        4312.1                50.00   Rv2711, TB
IAb  133  GLVELGVGPEPGADD  LVELGVGPE        0.2253        4369.0                50.00   Rv2711, TB
IAb  148  ANLVRLTELPAGSPV  RLTELPAGS        0.2215        4552.1                50.00   Rv2711, TB
IAb  210  GHENVTLPHEMAHAV  GHENVTLPH        0.2198        4633.5                50.00   Rv2711, TB
IAb  207  VIPGHENVTLPHEMA  VIPGHENVT        0.2176        4746.4                50.00   Rv2711, TB
IAb   15  YDLEEEGVTPLRARI  EEGVTPLRA        0.2154        4861.5                50.00   Rv2711, TB
IAb  179  LITRLKDAGVVPNAR  LKDAGVVPN        0.2150        4884.7                50.00   Rv2711, TB
IAb  132  PGLVELGVGPEPGAD  LVELGVGPE        0.2145        4909.5                50.00   Rv2711, TB
IAb  209  PGHENVTLPHEMAHA  ENVTLPHEM        0.2125        5015.7                50.00   Rv2711, TB
IAb  199  TPGGGVTIVIPGHEN  VTIVIPGHE        0.2078        5278.7                50.00   Rv2711, TB
IAb  135  VELGVGPEPGADDAN  ELGVGPEPG        0.2074        5299.4                50.00   Rv2711, TB
IAb   34  DQSGPTVSQTVSRME  SGPTVSQTV        0.2054        5414.9                50.00   Rv2711, TB
IAb  208  IPGHENVTLPHEMAH  GHENVTLPH        0.2050        5441.1                50.00   Rv2711, TB
IAb  186  AGVVPNARVTVETTP  GVVPNARVT        0.2030        5561.8                50.00   Rv2711, TB
IAb  198  TTPGGGVTIVIPGHE  VTIVIPGHE        0.2020        5618.1                50.00   Rv2711, TB
IAb  211  HENVTLPHEMAHAVK  ENVTLPHEM        0.2016        5647.1                50.00   Rv2711, TB
IAb  187  GVVPNARVTVETTPG  GVVPNARVT        0.1967        5954.5                50.00   Rv2711, TB
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IAb   35  QSGPTVSQTVSRMER  SGPTVSQTV         0.1962       5984.7                 50.00   Rv2711, TB
IAb   23  TPLRARIAERLDQSG  TPLRARIAE         0.1961       5992.8                 50.00   Rv2711, TB
IAb  206  IVIPGHENVTLPHEM  VIPGHENVT         0.1958       6009.5                 50.00   Rv2711, TB
IAb   87  DVIGLPWEEVHAEAC  DVIGLPWEE         0.1955       6031.8                 50.00   Rv2711, TB
IAb   14  IYDLEEEGVTPLRAR  EEGVTPLRA         0.1952       6052.2                 50.00   Rv2711, TB
IAb  110  DVERRLVKVLNNPTT  VKVLNNPTT         0.1922       6245.9                 50.00   Rv2711, TB
IAb   68  RALAIAVMRKHRLAE  RALAIAVMR         0.1886       6496.0                 50.00   Rv2711, TB
IAb   86  VDVIGLPWEEVHAEA  DVIGLPWEE         0.1879       6546.2                 50.00   Rv2711, TB
IAb   90  GLPWEEVHAEACRWE  LPWEEVHAE         0.1858       6700.2                 50.00   Rv2711, TB
IAb   88  VIGLPWEEVHAEACR  LPWEEVHAE         0.1835       6867.3                 50.00   Rv2711, TB
IAb   36  SGPTVSQTVSRMERD  SGPTVSQTV         0.1824       6949.3                 50.00   Rv2711, TB
IAb  136  ELGVGPEPGADDANL  ELGVGPEPG         0.1813       7027.8                 50.00   Rv2711, TB
IAb  147  DANLVRLTELPAGSP  LVRLTELPA         0.1801       7122.5                 50.00   Rv2711, TB
IAb  131  IPGLVELGVGPEPGA  LVELGVGPE         0.1788       7220.4                 50.00   Rv2711, TB
IAb   60  HLELTEKGRALAIAV  KGRALAIAV         0.1787       7229.7                 50.00   Rv2711, TB
IAb   89  IGLPWEEVHAEACRW  LPWEEVHAE         0.1787       7233.0                 50.00   Rv2711, TB
IAb   85  LVDVIGLPWEEVHAE  DVIGLPWEE         0.1764       7413.6                 50.00   Rv2711, TB
IAb  157  PAGSPVAVVVRQLTE  PAGSPVAVV         0.1730       7688.7                 50.00   Rv2711, TB
IAb  128  GNPIPGLVELGVGPE  GNPIPGLVE         0.1706       7895.1                 50.00   Rv2711, TB
IAb  188  VVPNARVTVETTPGG  VVPNARVTV         0.1680       8116.1                 50.00   Rv2711, TB
IAb  178  DLITRLKDAGVVPNA  LKDAGVVPN         0.1648       8402.1                 50.00   Rv2711, TB
IAb  197  ETTPGGGVTIVIPGH  TTPGGGVTI         0.1602       8830.4                 50.00   Rv2711, TB
IAb   84  LLVDVIGLPWEEVHA  DVIGLPWEE         0.1598       8874.6                 50.00   Rv2711, TB
IAb   91  LPWEEVHAEACRWEH  LPWEEVHAE         0.1587       8984.0                 50.00   Rv2711, TB
IAb  192  ARVTVETTPGGGVTI  TTPGGGVTI         0.1561       9232.3                 50.00   Rv2711, TB
IAb  189  VPNARVTVETTPGGG  NARVTVETT         0.1530       9552.1                 50.00   Rv2711, TB
IAb   13  TIYDLEEEGVTPLRA  EEGVTPLRA         0.1513       9728.1                 50.00   Rv2711, TB
IAb  196  VETTPGGGVTIVIPG  TTPGGGVTI         0.1472      10169.5                 50.00   Rv2711, TB
IAb  190  PNARVTVETTPGGGV  NARVTVETT         0.1459      10309.9                 50.00   Rv2711, TB
IAb  193  RVTVETTPGGGVTIV  TTPGGGVTI         0.1442      10503.0                 50.00   Rv2711, TB
IAb   37  GPTVSQTVSRMERDG  TVSQTVSRM         0.1420      10760.1                 50.00   Rv2711, TB
IAb  146  DDANLVRLTELPAGS  LVRLTELPA         0.1410      10877.7                 50.00   Rv2711, TB
IAb  130  PIPGLVELGVGPEPG  LVELGVGPE         0.1389      11130.2                 50.00   Rv2711, TB
IAb  195  TVETTPGGGVTIVIP  TTPGGGVTI         0.1358      11507.9                 50.00   Rv2711, TB
IAb  137  LGVGPEPGADDANLV  GVGPEPGAD         0.1346      11659.9                 50.00   Rv2711, TB
IAb   59  RHLELTEKGRALAIA  ELTEKGRAL         0.1345      11666.7                 50.00   Rv2711, TB
IAb   26  RARIAERLDQSGPTV  RLDQSGPTV         0.1334      11812.4                 50.00   Rv2711, TB
IAb  191  NARVTVETTPGGGVT  RVTVETTPG         0.1318      12017.1                 50.00   Rv2711, TB
IAb  194  VTVETTPGGGVTIVI  TTPGGGVTI         0.1307      12155.9                 50.00   Rv2711, TB
IAb  159  GSPVAVVVRQLTEHV  GSPVAVVVR         0.1292      12351.7                 50.00   Rv2711, TB
IAb   24  PLRARIAERLDQSGP  LRARIAERL         0.1286      12440.1                 50.00   Rv2711, TB
IAb  177  IDLITRLKDAGVVPN  LKDAGVVPN         0.1276      12564.8                 50.00   Rv2711, TB
IAb   25  LRARIAERLDQSGPT  LRARIAERL         0.1274      12604.4                 50.00   Rv2711, TB
IAb  158  AGSPVAVVVRQLTEH  GSPVAVVVR         0.1241      13050.3                 50.00   Rv2711, TB
IAb   83  RLLVDVIGLPWEEVH  DVIGLPWEE         0.1228      13241.8                 50.00   Rv2711, TB
IAb  129  NPIPGLVELGVGPEP  LVELGVGPE         0.1185      13873.7                 50.00   Rv2711, TB
IAb  160  SPVAVVVRQLTEHVQ  VVRQLTEHV         0.1167      14149.7                 50.00   Rv2711, TB
IAb   82  ERLLVDVIGLPWEEV  DVIGLPWEE         0.1157      14293.1                 50.00   Rv2711, TB
IAb   73  AVMRKHRLAERLLVD  VMRKHRLAE         0.1153      14366.9                 50.00   Rv2711, TB
IAb   74  VMRKHRLAERLLVDV  VMRKHRLAE         0.1150      14408.6                 50.00   Rv2711, TB
IAb   58  DRHLELTEKGRALAI  ELTEKGRAL         0.1144      14494.3                 50.00   Rv2711, TB
IAb  161  PVAVVVRQLTEHVQG  VVRQLTEHV         0.1126      14788.8                 50.00   Rv2711, TB
IAb   51  GLLRVAGDRHLELTE  LRVAGDRHL         0.1118      14914.1                 50.00   Rv2711, TB
IAb   38  PTVSQTVSRMERDGL  TVSQTVSRM         0.1095      15284.8                 50.00   Rv2711, TB
IAb   50  DGLLRVAGDRHLELT  LRVAGDRHL         0.1093      15331.3                 50.00   Rv2711, TB
IAb   72  IAVMRKHRLAERLLV  VMRKHRLAE         0.1088      15404.1                 50.00   Rv2711, TB
IAb   92  PWEEVHAEACRWEHV  WEEVHAEAC         0.1081      15526.5                 50.00   Rv2711, TB
IAb  138  GVGPEPGADDANLVR  GVGPEPGAD         0.1078      15581.2                 50.00   Rv2711, TB
IAb  162  VAVVVRQLTEHVQGD  VVRQLTEHV         0.1071      15684.8                 50.00   Rv2711, TB
IAb  100  ACRWEHVMSEDVERR  CRWEHVMSE         0.1069      15735.0                 50.00   Rv2711, TB
IAb   93  WEEVHAEACRWEHVM  WEEVHAEAC         0.1056      15956.8                 50.00   Rv2711, TB
IAb   52  LLRVAGDRHLELTEK  LRVAGDRHL         0.1054      15979.0                 50.00   Rv2711, TB
IAb   69  ALAIAVMRKHRLAER  LAIAVMRKH         0.1040      16231.8                 50.00   Rv2711, TB
IAb  163  AVVVRQLTEHVQGDI  VVRQLTEHV         0.1028      16435.9                 50.00   Rv2711, TB
IAb  101  CRWEHVMSEDVERRL  CRWEHVMSE         0.1028      16441.2                 50.00   Rv2711, TB
IAb   49  RDGLLRVAGDRHLEL  LRVAGDRHL         0.1006      16831.3                 50.00   Rv2711, TB
IAb   97  HAEACRWEHVMSEDV  CRWEHVMSE         0.1006      16841.7                 50.00   Rv2711, TB
IAb  145  ADDANLVRLTELPAG  LVRLTELPA         0.0999      16971.9                 50.00   Rv2711, TB
IAb   99  EACRWEHVMSEDVER  CRWEHVMSE         0.0988      17172.1                 50.00   Rv2711, TB
IAb   98  AEACRWEHVMSEDVE  CRWEHVMSE         0.0982      17279.7                 50.00   Rv2711, TB
IAb   53  LRVAGDRHLELTEKG  LRVAGDRHL         0.0981      17299.0                 50.00   Rv2711, TB
IAb   70  LAIAVMRKHRLAERL  LAIAVMRKH         0.0968      17545.5                 50.00   Rv2711, TB
IAb   75  MRKHRLAERLLVDVI  KHRLAERLL         0.0935      18172.5                 50.00   Rv2711, TB
IAb  164  VVVRQLTEHVQGDID  VVVRQLTEH         0.0921      18466.2                 50.00   Rv2711, TB
IAb   48  ERDGLLRVAGDRHLE  LRVAGDRHL         0.0902      18839.6                 50.00   Rv2711, TB
IAb   11  LRTIYDLEEEGVTPL  LEEEGVTPL         0.0889      19104.4                 50.00   Rv2711, TB
IAb  109  EDVERRLVKVLNNPT  RRLVKVLNN         0.0888      19131.9                 50.00   Rv2711, TB
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         IAb   95  EVHAEACRWEHVMSE  CRWEHVMSE         0.0886      19164.6                  50.00  Rv2711, TB
         IAb   71  AIAVMRKHRLAERLL  VMRKHRLAE         0.0869      19522.7                  50.00  Rv2711, TB
         IAb   96  VHAEACRWEHVMSED  CRWEHVMSE         0.0863      19653.1                  50.00  Rv2711, TB
         IAb   81  AERLLVDVIGLPWEE  DVIGLPWEE         0.0861      19689.5                  50.00  Rv2711, TB
         IAb   76  RKHRLAERLLVDVIG  HRLAERLLV         0.0830      20360.8                  50.00  Rv2711, TB
         IAb  139  VGPEPGADDANLVRL  VGPEPGADD         0.0822      20551.8                  50.00  Rv2711, TB
         IAb   94  EEVHAEACRWEHVMS  EEVHAEACR         0.0802      20993.7                  50.00  Rv2711, TB
         IAb   47  MERDGLLRVAGDRHL  LRVAGDRHL         0.0799      21066.5                  50.00  Rv2711, TB
         IAb   39  TVSQTVSRMERDGLL  TVSQTVSRM         0.0798      21096.6                  50.00  Rv2711, TB
         IAb  144  GADDANLVRLTELPA  LVRLTELPA         0.0792      21216.6                  50.00  Rv2711, TB
         IAb   12  RTIYDLEEEGVTPLR  LEEEGVTPL         0.0762      21917.0                  50.00  Rv2711, TB
         IAb   10  YLRTIYDLEEEGVTP  LRTIYDLEE         0.0759      21983.0                  50.00  Rv2711, TB
         IAb    8  EMYLRTIYDLEEEGV  EMYLRTIYD         0.0752      22164.8                  50.00  Rv2711, TB
         IAb    9  MYLRTIYDLEEEGVT  LRTIYDLEE         0.0744      22347.6                  50.00  Rv2711, TB
         IAb    0  MNELVDTTEMYLRTI  NELVDTTEM         0.0740      22440.1                  50.00  Rv2711, TB
         IAb   77  KHRLAERLLVDVIGL  KHRLAERLL         0.0722      22891.6                  50.00  Rv2711, TB
         IAb    1  NELVDTTEMYLRTIY  NELVDTTEM         0.0679      23991.7                  50.00  Rv2711, TB
         IAb  165  VVRQLTEHVQGDIDL  VVRQLTEHV         0.0665      24357.1                  50.00  Rv2711, TB
         IAb  176  DIDLITRLKDAGVVP  TRLKDAGVV         0.0661      24459.0                  50.00  Rv2711, TB
         IAb    6  TTEMYLRTIYDLEEE  EMYLRTIYD         0.0657      24563.2                  50.00  Rv2711, TB
         IAb  108  SEDVERRLVKVLNNP  RRLVKVLNN         0.0633      25209.1                  50.00  Rv2711, TB
         IAb   78  HRLAERLLVDVIGLP  HRLAERLLV         0.0628      25340.4                  50.00  Rv2711, TB
         IAb    7  TEMYLRTIYDLEEEG  EMYLRTIYD         0.0628      25351.7                  50.00  Rv2711, TB
         IAb   57  GDRHLELTEKGRALA  ELTEKGRAL         0.0572      26918.6                  50.00  Rv2711, TB
         IAb  141  PEPGADDANLVRLTE  PEPGADDAN         0.0570      26990.1                  50.00  Rv2711, TB
         IAb  166  VRQLTEHVQGDIDLI  VRQLTEHVQ         0.0569      27019.3                  50.00  Rv2711, TB
         IAb  140  GPEPGADDANLVRLT  PEPGADDAN         0.0564      27150.3                  50.00  Rv2711, TB
         IAb    5  DTTEMYLRTIYDLEE  EMYLRTIYD         0.0560      27277.2                  50.00  Rv2711, TB
         IAb  102  RWEHVMSEDVERRLV  WEHVMSEDV         0.0539      27908.3                  50.00  Rv2711, TB
         IAb   80  LAERLLVDVIGLPWE  RLLVDVIGL         0.0534      28063.6                  50.00  Rv2711, TB
         IAb  175  GDIDLITRLKDAGVV  TRLKDAGVV         0.0529      28194.5                  50.00  Rv2711, TB
         IAb    4  VDTTEMYLRTIYDLE  EMYLRTIYD         0.0526      28289.5                  50.00  Rv2711, TB
         IAb  103  WEHVMSEDVERRLVK  WEHVMSEDV         0.0497      29208.9                  50.00  Rv2711, TB
         IAb    3  LVDTTEMYLRTIYDL  EMYLRTIYD         0.0488      29498.0                  50.00  Rv2711, TB
         IAb   40  VSQTVSRMERDGLLR  VSQTVSRME         0.0477      29844.7                  50.00  Rv2711, TB
         IAb  168  QLTEHVQGDIDLITR  TEHVQGDID         0.0472      29999.7                  50.00  Rv2711, TB
         IAb    2  ELVDTTEMYLRTIYD  TTEMYLRTI         0.0462      30334.3                  50.00  Rv2711, TB
         IAb  142  EPGADDANLVRLTEL  PGADDANLV         0.0454      30596.7                  50.00  Rv2711, TB
         IAb  167  RQLTEHVQGDIDLIT  TEHVQGDID         0.0450      30710.4                  50.00  Rv2711, TB
         IAb   79  RLAERLLVDVIGLPW  RLAERLLVD         0.0448      30791.3                  50.00  Rv2711, TB
         IAb  107  MSEDVERRLVKVLNN  RRLVKVLNN         0.0447      30833.3                  50.00  Rv2711, TB
         IAb  143  PGADDANLVRLTELP  PGADDANLV         0.0440      31053.3                  50.00  Rv2711, TB
         IAb   56  AGDRHLELTEKGRAL  ELTEKGRAL         0.0436      31186.9                  50.00  Rv2711, TB
         IAb  169  LTEHVQGDIDLITRL  HVQGDIDLI         0.0434      31270.1                  50.00  Rv2711, TB
         IAb   46  RMERDGLLRVAGDRH  MERDGLLRV         0.0427      31509.2                  50.00  Rv2711, TB
         IAb  170  TEHVQGDIDLITRLK  TEHVQGDID         0.0411      32064.9                  50.00  Rv2711, TB
         IAb  174  QGDIDLITRLKDAGV  IDLITRLKD         0.0410      32090.3                  50.00  Rv2711, TB
         IAb   45  SRMERDGLLRVAGDR  MERDGLLRV         0.0382      33080.2                  50.00  Rv2711, TB
         IAb  171  EHVQGDIDLITRLKD  EHVQGDIDL         0.0379      33195.6                  50.00  Rv2711, TB
         IAb   54  RVAGDRHLELTEKGR  RVAGDRHLE         0.0374      33367.4                  50.00  Rv2711, TB
         IAb  172  HVQGDIDLITRLKDA  IDLITRLKD         0.0364      33712.9                  50.00  Rv2711, TB
         IAb   44  VSRMERDGLLRVAGD  MERDGLLRV         0.0338      34692.0                  50.00  Rv2711, TB
         IAb   55  VAGDRHLELTEKGRA  RHLELTEKG         0.0332      34927.8                  50.00  Rv2711, TB
         IAb  173  VQGDIDLITRLKDAG  IDLITRLKD         0.0329      35009.1                  50.00  Rv2711, TB
         IAb   43  TVSRMERDGLLRVAG  MERDGLLRV         0.0322      35273.4                  50.00  Rv2711, TB
         IAb   42  QTVSRMERDGLLRVA  MERDGLLRV         0.0319      35388.8                  50.00  Rv2711, TB
         IAb  104  EHVMSEDVERRLVKV  HVMSEDVER         0.0306      35904.9                  50.00  Rv2711, TB
         IAb   41  SQTVSRMERDGLLRV  MERDGLLRV         0.0276      37076.2                  50.00  Rv2711, TB
         IAb  105  HVMSEDVERRLVKVL  HVMSEDVER         0.0231      38929.4                  50.00  Rv2711, TB
         IAb  106  VMSEDVERRLVKVLN  VERRLVKVL         0.0197      40395.6                  50.00  Rv2711, TB
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Allele: IAb. Number of high binders 0. Number of weak binders 17. Number of peptides 216

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      Allele  pos          peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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         IAd   65  EKGRALAIAVMRKHR  RALAIAVMR         0.4726        300.7          WB     0.80  Rv2711, TB
         IAd   66  KGRALAIAVMRKHRL  RALAIAVMR         0.4706        307.4          WB     0.80  Rv2711, TB
         IAd   64  TEKGRALAIAVMRKH  RALAIAVMR         0.4693        311.7          WB     0.80  Rv2711, TB
         IAd   67  GRALAIAVMRKHRLA  RALAIAVMR         0.4497        385.4          WB     1.00  Rv2711, TB
         IAd   63  LTEKGRALAIAVMRK  RALAIAVMR         0.4183        541.3                 2.00  Rv2711, TB
         IAd  215  TLPHEMAHAVKVEKV  AHAVKVEKV         0.4162        553.8                 2.00  Rv2711, TB
         IAd   68  RALAIAVMRKHRLAE  RALAIAVMR         0.3921        718.8                 4.00  Rv2711, TB
         IAd  180  ITRLKDAGVVPNARV  LKDAGVVPN         0.3763        852.4                 4.00  Rv2711, TB
         IAd  147  DANLVRLTELPAGSP  LVRLTELPA         0.3735        878.6                 4.00  Rv2711, TB
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IAd  148  ANLVRLTELPAGSPV  LVRLTELPA         0.3726         887.8                4.00   Rv2711, TB
IAd  179  LITRLKDAGVVPNAR  LKDAGVVPN         0.3673         940.1                4.00   Rv2711, TB
IAd  145  ADDANLVRLTELPAG  LVRLTELPA         0.3670         942.5                4.00   Rv2711, TB
IAd  146  DDANLVRLTELPAGS  LVRLTELPA         0.3609        1007.3                4.00   Rv2711, TB
IAd   42  QTVSRMERDGLLRVA  MERDGLLRV         0.3596        1021.2                4.00   Rv2711, TB
IAd  178  DLITRLKDAGVVPNA  LKDAGVVPN         0.3591        1026.7                4.00   Rv2711, TB
IAd   43  TVSRMERDGLLRVAG  MERDGLLRV         0.3418        1238.5                8.00   Rv2711, TB
IAd   44  VSRMERDGLLRVAGD  MERDGLLRV         0.3372        1301.1                8.00   Rv2711, TB
IAd  150  LVRLTELPAGSPVAV  LVRLTELPA         0.3333        1358.4                8.00   Rv2711, TB
IAd  181  TRLKDAGVVPNARVT  LKDAGVVPN         0.3311        1390.8                8.00   Rv2711, TB
IAd   69  ALAIAVMRKHRLAER  ALAIAVMRK         0.3211        1550.1                8.00   Rv2711, TB
IAd   62  ELTEKGRALAIAVMR  RALAIAVMR         0.3208        1554.1                8.00   Rv2711, TB
IAd  149  NLVRLTELPAGSPVA  LVRLTELPA         0.3127        1697.4                8.00   Rv2711, TB
IAd  144  GADDANLVRLTELPA  LVRLTELPA         0.2983        1982.7               16.00   Rv2711, TB
IAd   45  SRMERDGLLRVAGDR  MERDGLLRV         0.2979        1991.1               16.00   Rv2711, TB
IAd  182  RLKDAGVVPNARVTV  LKDAGVVPN         0.2919        2124.4               16.00   Rv2711, TB
IAd   41  SQTVSRMERDGLLRV  MERDGLLRV         0.2895        2179.9               16.00   Rv2711, TB
IAd  101  CRWEHVMSEDVERRL  VMSEDVERR         0.2877        2223.9               16.00   Rv2711, TB
IAd   75  MRKHRLAERLLVDVI  MRKHRLAER         0.2859        2268.5               16.00   Rv2711, TB
IAd  183  LKDAGVVPNARVTVE  LKDAGVVPN         0.2798        2421.7               16.00   Rv2711, TB
IAd   79  RLAERLLVDVIGLPW  AERLLVDVI         0.2794        2431.3               16.00   Rv2711, TB
IAd  100  ACRWEHVMSEDVERR  VMSEDVERR         0.2744        2567.1               16.00   Rv2711, TB
IAd  155  ELPAGSPVAVVVRQL  PVAVVVRQL         0.2665        2795.9               16.00   Rv2711, TB
IAd   80  LAERLLVDVIGLPWE  AERLLVDVI         0.2654        2831.1               16.00   Rv2711, TB
IAd   47  MERDGLLRVAGDRHL  ERDGLLRVA         0.2639        2877.9               16.00   Rv2711, TB
IAd   70  LAIAVMRKHRLAERL  MRKHRLAER         0.2636        2887.1               16.00   Rv2711, TB
IAd   78  HRLAERLLVDVIGLP  AERLLVDVI         0.2630        2905.7               16.00   Rv2711, TB
IAd  156  LPAGSPVAVVVRQLT  GSPVAVVVR         0.2627        2915.5               16.00   Rv2711, TB
IAd   77  KHRLAERLLVDVIGL  AERLLVDVI         0.2601        2996.0               16.00   Rv2711, TB
IAd   46  RMERDGLLRVAGDRH  MERDGLLRV         0.2597        3009.2               16.00   Rv2711, TB
IAd   76  RKHRLAERLLVDVIG  RKHRLAERL         0.2498        3352.0               16.00   Rv2711, TB
IAd  154  TELPAGSPVAVVVRQ  SPVAVVVRQ         0.2425        3626.4               32.00   Rv2711, TB
IAd  151  VRLTELPAGSPVAVV  VRLTELPAG         0.2401        3723.6               32.00   Rv2711, TB
IAd   19  EEGVTPLRARIAERL  LRARIAERL         0.2378        3814.7               32.00   Rv2711, TB
IAd  102  RWEHVMSEDVERRLV  VMSEDVERR         0.2375        3828.1               32.00   Rv2711, TB
IAd   72  IAVMRKHRLAERLLV  MRKHRLAER         0.2372        3838.4               32.00   Rv2711, TB
IAd   74  VMRKHRLAERLLVDV  MRKHRLAER         0.2363        3879.7               32.00   Rv2711, TB
IAd  177  IDLITRLKDAGVVPN  LKDAGVVPN         0.2358        3900.3               32.00   Rv2711, TB
IAd  214  VTLPHEMAHAVKVEK  HEMAHAVKV         0.2267        4302.2               32.00   Rv2711, TB
IAd   71  AIAVMRKHRLAERLL  MRKHRLAER         0.2252        4374.6               32.00   Rv2711, TB
IAd   81  AERLLVDVIGLPWEE  AERLLVDVI         0.2237        4446.0               32.00   Rv2711, TB
IAd   48  ERDGLLRVAGDRHLE  ERDGLLRVA         0.2214        4557.6               32.00   Rv2711, TB
IAd  103  WEHVMSEDVERRLVK  VMSEDVERR         0.2207        4591.1               32.00   Rv2711, TB
IAd   16  DLEEEGVTPLRARIA  LEEEGVTPL         0.2206        4596.4               32.00   Rv2711, TB
IAd   73  AVMRKHRLAERLLVD  MRKHRLAER         0.2171        4772.5               32.00   Rv2711, TB
IAd  169  LTEHVQGDIDLITRL  VQGDIDLIT         0.2112        5085.7               32.00   Rv2711, TB
IAd  157  PAGSPVAVVVRQLTE  SPVAVVVRQ         0.2103        5137.8               32.00   Rv2711, TB
IAd  153  LTELPAGSPVAVVVR  LPAGSPVAV         0.2053        5424.2               32.00   Rv2711, TB
IAd  159  GSPVAVVVRQLTEHV  SPVAVVVRQ         0.2027        5580.1               32.00   Rv2711, TB
IAd   17  LEEEGVTPLRARIAE  LEEEGVTPL         0.2014        5656.3               32.00   Rv2711, TB
IAd  170  TEHVQGDIDLITRLK  VQGDIDLIT         0.2013        5666.3               32.00   Rv2711, TB
IAd  171  EHVQGDIDLITRLKD  HVQGDIDLI         0.2000        5743.1               32.00   Rv2711, TB
IAd   15  YDLEEEGVTPLRARI  LEEEGVTPL         0.1946        6091.7               32.00   Rv2711, TB
IAd   14  IYDLEEEGVTPLRAR  LEEEGVTPL         0.1901        6394.0               32.00   Rv2711, TB
IAd  160  SPVAVVVRQLTEHVQ  PVAVVVRQL         0.1882        6528.8               32.00   Rv2711, TB
IAd   99  EACRWEHVMSEDVER  WEHVMSEDV         0.1875        6577.4               32.00   Rv2711, TB
IAd  143  PGADDANLVRLTELP  ANLVRLTEL         0.1842        6811.5               32.00   Rv2711, TB
IAd   18  EEEGVTPLRARIAER  EEGVTPLRA         0.1816        7009.4               32.00   Rv2711, TB
IAd  106  VMSEDVERRLVKVLN  VMSEDVERR         0.1807        7078.6               32.00   Rv2711, TB
IAd   13  TIYDLEEEGVTPLRA  LEEEGVTPL         0.1795        7170.3               32.00   Rv2711, TB
IAd   21  GVTPLRARIAERLDQ  LRARIAERL         0.1767        7387.4               50.00   Rv2711, TB
IAd  168  QLTEHVQGDIDLITR  QGDIDLITR         0.1764        7411.0               50.00   Rv2711, TB
IAd   20  EGVTPLRARIAERLD  LRARIAERL         0.1764        7412.2               50.00   Rv2711, TB
IAd   98  AEACRWEHVMSEDVE  CRWEHVMSE         0.1755        7487.0               50.00   Rv2711, TB
IAd  158  AGSPVAVVVRQLTEH  SPVAVVVRQ         0.1735        7647.4               50.00   Rv2711, TB
IAd   61  LELTEKGRALAIAVM  GRALAIAVM         0.1729        7702.8               50.00   Rv2711, TB
IAd  152  RLTELPAGSPVAVVV  LPAGSPVAV         0.1695        7989.1               50.00   Rv2711, TB
IAd  210  GHENVTLPHEMAHAV  GHENVTLPH         0.1695        7990.8               50.00   Rv2711, TB
IAd  104  EHVMSEDVERRLVKV  VMSEDVERR         0.1687        8059.5               50.00   Rv2711, TB
IAd   22  VTPLRARIAERLDQS  LRARIAERL         0.1675        8162.7               50.00   Rv2711, TB
IAd  184  KDAGVVPNARVTVET  KDAGVVPNA         0.1664        8259.6               50.00   Rv2711, TB
IAd  105  HVMSEDVERRLVKVL  VMSEDVERR         0.1648        8402.0               50.00   Rv2711, TB
IAd  172  HVQGDIDLITRLKDA  HVQGDIDLI         0.1641        8471.9               50.00   Rv2711, TB
IAd  161  PVAVVVRQLTEHVQG  PVAVVVRQL         0.1636        8515.8               50.00   Rv2711, TB
IAd   40  VSQTVSRMERDGLLR  RMERDGLLR         0.1632        8549.6               50.00   Rv2711, TB
IAd   97  HAEACRWEHVMSEDV  CRWEHVMSE         0.1584        9008.2               50.00   Rv2711, TB
IAd  212  ENVTLPHEMAHAVKV  HEMAHAVKV         0.1577        9076.0               50.00   Rv2711, TB
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IAd  209  PGHENVTLPHEMAHA  GHENVTLPH          0.1564       9207.4                 50.00   Rv2711, TB
IAd  213  NVTLPHEMAHAVKVE  HEMAHAVKV          0.1559       9256.0                 50.00   Rv2711, TB
IAd   24  PLRARIAERLDQSGP  LRARIAERL          0.1558       9270.3                 50.00   Rv2711, TB
IAd  107  MSEDVERRLVKVLNN  RRLVKVLNN          0.1545       9395.4                 50.00   Rv2711, TB
IAd  189  VPNARVTVETTPGGG  NARVTVETT          0.1529       9557.0                 50.00   Rv2711, TB
IAd   23  TPLRARIAERLDQSG  LRARIAERL          0.1528       9566.7                 50.00   Rv2711, TB
IAd  109  EDVERRLVKVLNNPT  RRLVKVLNN          0.1527       9582.3                 50.00   Rv2711, TB
IAd  208  IPGHENVTLPHEMAH  GHENVTLPH          0.1508       9776.9                 50.00   Rv2711, TB
IAd  110  DVERRLVKVLNNPTT  RRLVKVLNN          0.1504       9827.8                 50.00   Rv2711, TB
IAd  190  PNARVTVETTPGGGV  NARVTVETT          0.1480      10077.2                 50.00   Rv2711, TB
IAd  188  VVPNARVTVETTPGG  NARVTVETT          0.1473      10158.0                 50.00   Rv2711, TB
IAd   95  EVHAEACRWEHVMSE  AEACRWEHV          0.1470      10196.3                 50.00   Rv2711, TB
IAd  142  EPGADDANLVRLTEL  ANLVRLTEL          0.1464      10262.6                 50.00   Rv2711, TB
IAd  207  VIPGHENVTLPHEMA  GHENVTLPH          0.1440      10527.8                 50.00   Rv2711, TB
IAd  111  VERRLVKVLNNPTTS  RRLVKVLNN          0.1433      10609.5                 50.00   Rv2711, TB
IAd  108  SEDVERRLVKVLNNP  RRLVKVLNN          0.1412      10855.2                 50.00   Rv2711, TB
IAd   96  VHAEACRWEHVMSED  AEACRWEHV          0.1407      10906.2                 50.00   Rv2711, TB
IAd   82  ERLLVDVIGLPWEEV  RLLVDVIGL          0.1403      10961.7                 50.00   Rv2711, TB
IAd   12  RTIYDLEEEGVTPLR  LEEEGVTPL          0.1401      10975.8                 50.00   Rv2711, TB
IAd  211  HENVTLPHEMAHAVK  LPHEMAHAV          0.1385      11173.1                 50.00   Rv2711, TB
IAd   94  EEVHAEACRWEHVMS  AEACRWEHV          0.1345      11668.9                 50.00   Rv2711, TB
IAd   39  TVSQTVSRMERDGLL  TVSQTVSRM          0.1323      11952.8                 50.00   Rv2711, TB
IAd   11  LRTIYDLEEEGVTPL  LEEEGVTPL          0.1315      12057.5                 50.00   Rv2711, TB
IAd  173  VQGDIDLITRLKDAG  GDIDLITRL          0.1314      12069.1                 50.00   Rv2711, TB
IAd   49  RDGLLRVAGDRHLEL  LRVAGDRHL          0.1313      12074.1                 50.00   Rv2711, TB
IAd  187  GVVPNARVTVETTPG  NARVTVETT          0.1312      12094.4                 50.00   Rv2711, TB
IAd  162  VAVVVRQLTEHVQGD  VAVVVRQLT          0.1295      12313.3                 50.00   Rv2711, TB
IAd    6  TTEMYLRTIYDLEEE  LRTIYDLEE          0.1281      12502.4                 50.00   Rv2711, TB
IAd  167  RQLTEHVQGDIDLIT  HVQGDIDLI          0.1267      12689.5                 50.00   Rv2711, TB
IAd   38  PTVSQTVSRMERDGL  TVSQTVSRM          0.1251      12916.4                 50.00   Rv2711, TB
IAd  206  IVIPGHENVTLPHEM  GHENVTLPH          0.1230      13210.1                 50.00   Rv2711, TB
IAd   25  LRARIAERLDQSGPT  LRARIAERL          0.1220      13355.6                 50.00   Rv2711, TB
IAd   90  GLPWEEVHAEACRWE  LPWEEVHAE          0.1219      13375.2                 50.00   Rv2711, TB
IAd   53  LRVAGDRHLELTEKG  RHLELTEKG          0.1217      13393.2                 50.00   Rv2711, TB
IAd    3  LVDTTEMYLRTIYDL  TTEMYLRTI          0.1212      13465.9                 50.00   Rv2711, TB
IAd   91  LPWEEVHAEACRWEH  HAEACRWEH          0.1204      13588.7                 50.00   Rv2711, TB
IAd    5  DTTEMYLRTIYDLEE  TTEMYLRTI          0.1203      13598.8                 50.00   Rv2711, TB
IAd  191  NARVTVETTPGGGVT  NARVTVETT          0.1201      13640.9                 50.00   Rv2711, TB
IAd   36  SGPTVSQTVSRMERD  VSQTVSRME          0.1176      14015.4                 50.00   Rv2711, TB
IAd   37  GPTVSQTVSRMERDG  TVSQTVSRM          0.1171      14078.9                 50.00   Rv2711, TB
IAd  164  VVVRQLTEHVQGDID  VRQLTEHVQ          0.1168      14125.6                 50.00   Rv2711, TB
IAd    4  VDTTEMYLRTIYDLE  TTEMYLRTI          0.1168      14132.8                 50.00   Rv2711, TB
IAd  165  VVRQLTEHVQGDIDL  VRQLTEHVQ          0.1159      14275.4                 50.00   Rv2711, TB
IAd  163  AVVVRQLTEHVQGDI  VRQLTEHVQ          0.1157      14291.8                 50.00   Rv2711, TB
IAd   92  PWEEVHAEACRWEHV  WEEVHAEAC          0.1154      14341.1                 50.00   Rv2711, TB
IAd   58  DRHLELTEKGRALAI  RHLELTEKG          0.1144      14503.5                 50.00   Rv2711, TB
IAd   50  DGLLRVAGDRHLELT  LRVAGDRHL          0.1142      14534.0                 50.00   Rv2711, TB
IAd  131  IPGLVELGVGPEPGA  PGLVELGVG          0.1138      14598.5                 50.00   Rv2711, TB
IAd   59  RHLELTEKGRALAIA  RHLELTEKG          0.1138      14600.4                 50.00   Rv2711, TB
IAd   55  VAGDRHLELTEKGRA  RHLELTEKG          0.1133      14678.1                 50.00   Rv2711, TB
IAd   57  GDRHLELTEKGRALA  RHLELTEKG          0.1118      14910.6                 50.00   Rv2711, TB
IAd  112  ERRLVKVLNNPTTSP  RRLVKVLNN          0.1117      14931.4                 50.00   Rv2711, TB
IAd  166  VRQLTEHVQGDIDLI  HVQGDIDLI          0.1103      15157.6                 50.00   Rv2711, TB
IAd  205  TIVIPGHENVTLPHE  GHENVTLPH          0.1089      15396.5                 50.00   Rv2711, TB
IAd   93  WEEVHAEACRWEHVM  WEEVHAEAC          0.1086      15445.5                 50.00   Rv2711, TB
IAd   35  QSGPTVSQTVSRMER  VSQTVSRME          0.1076      15613.7                 50.00   Rv2711, TB
IAd  174  QGDIDLITRLKDAGV  QGDIDLITR          0.1072      15669.2                 50.00   Rv2711, TB
IAd    9  MYLRTIYDLEEEGVT  MYLRTIYDL          0.1062      15842.3                 50.00   Rv2711, TB
IAd  186  AGVVPNARVTVETTP  NARVTVETT          0.1056      15955.5                 50.00   Rv2711, TB
IAd   54  RVAGDRHLELTEKGR  RHLELTEKG          0.1035      16313.8                 50.00   Rv2711, TB
IAd   60  HLELTEKGRALAIAV  KGRALAIAV          0.1034      16336.1                 50.00   Rv2711, TB
IAd   30  AERLDQSGPTVSQTV  ERLDQSGPT          0.1031      16384.2                 50.00   Rv2711, TB
IAd  202  GGVTIVIPGHENVTL  GGVTIVIPG          0.1009      16776.9                 50.00   Rv2711, TB
IAd   52  LLRVAGDRHLELTEK  LRVAGDRHL          0.1002      16912.5                 50.00   Rv2711, TB
IAd   34  DQSGPTVSQTVSRME  VSQTVSRME          0.0999      16965.7                 50.00   Rv2711, TB
IAd  185  DAGVVPNARVTVETT  NARVTVETT          0.0998      16988.1                 50.00   Rv2711, TB
IAd   85  LVDVIGLPWEEVHAE  LVDVIGLPW          0.0987      17190.9                 50.00   Rv2711, TB
IAd   89  IGLPWEEVHAEACRW  WEEVHAEAC          0.0981      17297.6                 50.00   Rv2711, TB
IAd   56  AGDRHLELTEKGRAL  RHLELTEKG          0.0980      17315.8                 50.00   Rv2711, TB
IAd  130  PIPGLVELGVGPEPG  PGLVELGVG          0.0980      17317.3                 50.00   Rv2711, TB
IAd  201  GGGVTIVIPGHENVT  GGVTIVIPG          0.0976      17384.5                 50.00   Rv2711, TB
IAd  200  PGGGVTIVIPGHENV  GGVTIVIPG          0.0970      17498.3                 50.00   Rv2711, TB
IAd   29  IAERLDQSGPTVSQT  ERLDQSGPT          0.0966      17578.8                 50.00   Rv2711, TB
IAd  129  NPIPGLVELGVGPEP  PGLVELGVG          0.0966      17586.6                 50.00   Rv2711, TB
IAd   28  RIAERLDQSGPTVSQ  ERLDQSGPT          0.0963      17636.9                 50.00   Rv2711, TB
IAd   33  LDQSGPTVSQTVSRM  PTVSQTVSR          0.0961      17673.2                 50.00   Rv2711, TB
IAd   51  GLLRVAGDRHLELTE  LRVAGDRHL          0.0948      17936.7                 50.00   Rv2711, TB
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         IAd  128  GNPIPGLVELGVGPE  PGLVELGVG         0.0938      18114.0                50.00   Rv2711, TB
         IAd   27  ARIAERLDQSGPTVS  RIAERLDQS         0.0937      18137.3                50.00   Rv2711, TB
         IAd   10  YLRTIYDLEEEGVTP  LRTIYDLEE         0.0933      18221.7                50.00   Rv2711, TB
         IAd    8  EMYLRTIYDLEEEGV  MYLRTIYDL         0.0931      18259.0                50.00   Rv2711, TB
         IAd   88  VIGLPWEEVHAEACR  GLPWEEVHA         0.0931      18264.5                50.00   Rv2711, TB
         IAd  141  PEPGADDANLVRLTE  ADDANLVRL         0.0925      18381.1                50.00   Rv2711, TB
         IAd   83  RLLVDVIGLPWEEVH  RLLVDVIGL         0.0919      18494.4                50.00   Rv2711, TB
         IAd  199  TPGGGVTIVIPGHEN  GGVTIVIPG         0.0915      18580.5                50.00   Rv2711, TB
         IAd   31  ERLDQSGPTVSQTVS  LDQSGPTVS         0.0902      18843.4                50.00   Rv2711, TB
         IAd  140  GPEPGADDANLVRLT  ADDANLVRL         0.0902      18845.1                50.00   Rv2711, TB
         IAd   87  DVIGLPWEEVHAEAC  GLPWEEVHA         0.0897      18942.0                50.00   Rv2711, TB
         IAd  139  VGPEPGADDANLVRL  ADDANLVRL         0.0895      18975.6                50.00   Rv2711, TB
         IAd  132  PGLVELGVGPEPGAD  PGLVELGVG         0.0881      19276.5                50.00   Rv2711, TB
         IAd    7  TEMYLRTIYDLEEEG  MYLRTIYDL         0.0880      19291.5                50.00   Rv2711, TB
         IAd  175  GDIDLITRLKDAGVV  TRLKDAGVV         0.0867      19577.3                50.00   Rv2711, TB
         IAd   32  RLDQSGPTVSQTVSR  PTVSQTVSR         0.0857      19775.7                50.00   Rv2711, TB
         IAd    0  MNELVDTTEMYLRTI  TTEMYLRTI         0.0848      19979.2                50.00   Rv2711, TB
         IAd   26  RARIAERLDQSGPTV  ARIAERLDQ         0.0830      20379.1                50.00   Rv2711, TB
         IAd  176  DIDLITRLKDAGVVP  TRLKDAGVV         0.0824      20490.8                50.00   Rv2711, TB
         IAd  113  RRLVKVLNNPTTSPF  RRLVKVLNN         0.0794      21183.3                50.00   Rv2711, TB
         IAd  198  TTPGGGVTIVIPGHE  GGVTIVIPG         0.0787      21345.5                50.00   Rv2711, TB
         IAd   86  VDVIGLPWEEVHAEA  VIGLPWEEV         0.0777      21559.1                50.00   Rv2711, TB
         IAd   84  LLVDVIGLPWEEVHA  LVDVIGLPW         0.0777      21581.5                50.00   Rv2711, TB
         IAd  127  FGNPIPGLVELGVGP  PGLVELGVG         0.0765      21854.0                50.00   Rv2711, TB
         IAd    2  ELVDTTEMYLRTIYD  TTEMYLRTI         0.0751      22180.6                50.00   Rv2711, TB
         IAd  204  VTIVIPGHENVTLPH  GHENVTLPH         0.0731      22661.4                50.00   Rv2711, TB
         IAd  126  PFGNPIPGLVELGVG  PGLVELGVG         0.0688      23742.2                50.00   Rv2711, TB
         IAd    1  NELVDTTEMYLRTIY  TTEMYLRTI         0.0672      24159.7                50.00   Rv2711, TB
         IAd  192  ARVTVETTPGGGVTI  RVTVETTPG         0.0628      25338.2                50.00   Rv2711, TB
         IAd  197  ETTPGGGVTIVIPGH  GGVTIVIPG         0.0618      25613.0                50.00   Rv2711, TB
         IAd  203  GVTIVIPGHENVTLP  GVTIVIPGH         0.0566      27091.9                50.00   Rv2711, TB
         IAd  133  GLVELGVGPEPGADD  LVELGVGPE         0.0461      30373.1                50.00   Rv2711, TB
         IAd  114  RLVKVLNNPTTSPFG  RLVKVLNNP         0.0459      30429.0                50.00   Rv2711, TB
         IAd  125  SPFGNPIPGLVELGV  IPGLVELGV         0.0437      31152.5                50.00   Rv2711, TB
         IAd  134  LVELGVGPEPGADDA  LVELGVGPE         0.0423      31638.0                50.00   Rv2711, TB
         IAd  115  LVKVLNNPTTSPFGN  VKVLNNPTT         0.0402      32374.8                50.00   Rv2711, TB
         IAd  193  RVTVETTPGGGVTIV  RVTVETTPG         0.0390      32782.7                50.00   Rv2711, TB
         IAd  138  GVGPEPGADDANLVR  PGADDANLV         0.0349      34273.8                50.00   Rv2711, TB
         IAd  196  VETTPGGGVTIVIPG  GGVTIVIPG         0.0334      34838.7                50.00   Rv2711, TB
         IAd  119  LNNPTTSPFGNPIPG  LNNPTTSPF         0.0332      34904.7                50.00   Rv2711, TB
         IAd  137  LGVGPEPGADDANLV  PGADDANLV         0.0307      35879.2                50.00   Rv2711, TB
         IAd  116  VKVLNNPTTSPFGNP  VKVLNNPTT         0.0301      36096.9                50.00   Rv2711, TB
         IAd  118  VLNNPTTSPFGNPIP  LNNPTTSPF         0.0271      37276.1                50.00   Rv2711, TB
         IAd  135  VELGVGPEPGADDAN  ELGVGPEPG         0.0269      37381.1                50.00   Rv2711, TB
         IAd  117  KVLNNPTTSPFGNPI  LNNPTTSPF         0.0256      37911.4                50.00   Rv2711, TB
         IAd  136  ELGVGPEPGADDANL  ELGVGPEPG         0.0254      37974.7                50.00   Rv2711, TB
         IAd  120  NNPTTSPFGNPIPGL  PTTSPFGNP         0.0128      43550.9                50.00   Rv2711, TB
         IAd  121  NPTTSPFGNPIPGLV  PTTSPFGNP         0.0115      44162.5                50.00   Rv2711, TB
         IAd  124  TSPFGNPIPGLVELG  SPFGNPIPG         0.0106      44599.0                50.00   Rv2711, TB
         IAd  123  TTSPFGNPIPGLVEL  NPIPGLVEL         0.0100      44883.7                50.00   Rv2711, TB
         IAd  122  PTTSPFGNPIPGLVE  SPFGNPIPG         0.0095      45139.9                50.00   Rv2711, TB
         IAd  195  TVETTPGGGVTIVIP  GGGVTIVIP         0.0093      45202.4                50.00   Rv2711, TB
         IAd  194  VTVETTPGGGVTIVI  VTVETTPGG         0.0092      45259.7                50.00   Rv2711, TB
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Allele: IAd. Number of high binders 0. Number of weak binders 4. Number of peptides 216

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      Allele  pos           peptide       core 1-log50k(aff) affinity(nM) Bind Level  %Random     Identity
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         IAs  198  TTPGGGVTIVIPGHE  VTIVIPGHE         0.2835       2327.8                 4.00   Rv2711, TB
         IAs  206  IVIPGHENVTLPHEM  ENVTLPHEM         0.2818       2369.4                 4.00   Rv2711, TB
         IAs  111  VERRLVKVLNNPTTS  KVLNNPTTS         0.2791       2439.7                 4.00   Rv2711, TB
         IAs  199  TPGGGVTIVIPGHEN  VTIVIPGHE         0.2749       2553.7                 4.00   Rv2711, TB
         IAs  112  ERRLVKVLNNPTTSP  KVLNNPTTS         0.2733       2598.4                 4.00   Rv2711, TB
         IAs   62  ELTEKGRALAIAVMR  RALAIAVMR         0.2717       2644.0                 4.00   Rv2711, TB
         IAs  200  PGGGVTIVIPGHENV  VTIVIPGHE         0.2697       2702.6                 4.00   Rv2711, TB
         IAs  201  GGGVTIVIPGHENVT  VTIVIPGHE         0.2686       2732.7                 4.00   Rv2711, TB
         IAs  113  RRLVKVLNNPTTSPF  KVLNNPTTS         0.2684       2740.2                 4.00   Rv2711, TB
         IAs  207  VIPGHENVTLPHEMA  ENVTLPHEM         0.2671       2779.0                 4.00   Rv2711, TB
         IAs   64  TEKGRALAIAVMRKH  RALAIAVMR         0.2637       2882.3                 8.00   Rv2711, TB
         IAs  114  RLVKVLNNPTTSPFG  RLVKVLNNP         0.2634       2891.1                 8.00   Rv2711, TB
         IAs  211  HENVTLPHEMAHAVK  ENVTLPHEM         0.2587       3044.9                 8.00   Rv2711, TB
         IAs   63  LTEKGRALAIAVMRK  RALAIAVMR         0.2577       3075.9                 8.00   Rv2711, TB
         IAs  208  IPGHENVTLPHEMAH  ENVTLPHEM         0.2554       3154.2                 8.00   Rv2711, TB
         IAs   65  EKGRALAIAVMRKHR  RALAIAVMR         0.2553       3155.7                 8.00   Rv2711, TB
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IAs  210  GHENVTLPHEMAHAV  ENVTLPHEM        0.2492       3371.9                 8.00   Rv2711, TB
IAs  209  PGHENVTLPHEMAHA  ENVTLPHEM        0.2476       3430.4                 8.00   Rv2711, TB
IAs  110  DVERRLVKVLNNPTT  RLVKVLNNP        0.2163       4815.8                 8.00   Rv2711, TB
IAs   67  GRALAIAVMRKHRLA  RALAIAVMR        0.2154       4862.0                 8.00   Rv2711, TB
IAs   66  KGRALAIAVMRKHRL  RALAIAVMR        0.2091       5204.8                16.00   Rv2711, TB
IAs  202  GGVTIVIPGHENVTL  VTIVIPGHE        0.2011       5673.1                16.00   Rv2711, TB
IAs  197  ETTPGGGVTIVIPGH  GGGVTIVIP        0.1957       6018.5                16.00   Rv2711, TB
IAs  108  SEDVERRLVKVLNNP  RLVKVLNNP        0.1929       6202.2                16.00   Rv2711, TB
IAs  109  EDVERRLVKVLNNPT  RLVKVLNNP        0.1881       6533.6                16.00   Rv2711, TB
IAs  203  GVTIVIPGHENVTLP  VTIVIPGHE        0.1877       6563.3                16.00   Rv2711, TB
IAs   83  RLLVDVIGLPWEEVH  LLVDVIGLP        0.1666       8239.3                16.00   Rv2711, TB
IAs   84  LLVDVIGLPWEEVHA  LLVDVIGLP        0.1661       8288.6                16.00   Rv2711, TB
IAs   68  RALAIAVMRKHRLAE  RALAIAVMR        0.1631       8559.7                16.00   Rv2711, TB
IAs   81  AERLLVDVIGLPWEE  DVIGLPWEE        0.1597       8884.8                32.00   Rv2711, TB
IAs   22  VTPLRARIAERLDQS  RIAERLDQS        0.1590       8947.9                32.00   Rv2711, TB
IAs   82  ERLLVDVIGLPWEEV  LLVDVIGLP        0.1561       9233.7                32.00   Rv2711, TB
IAs  196  VETTPGGGVTIVIPG  GGGVTIVIP        0.1513       9729.8                32.00   Rv2711, TB
IAs   78  HRLAERLLVDVIGLP  LLVDVIGLP        0.1505       9808.4                32.00   Rv2711, TB
IAs  116  VKVLNNPTTSPFGNP  KVLNNPTTS        0.1499       9878.5                32.00   Rv2711, TB
IAs  212  ENVTLPHEMAHAVKV  ENVTLPHEM        0.1485      10029.0                32.00   Rv2711, TB
IAs   23  TPLRARIAERLDQSG  RIAERLDQS        0.1472      10168.5                32.00   Rv2711, TB
IAs   98  AEACRWEHVMSEDVE  EHVMSEDVE        0.1470      10191.2                32.00   Rv2711, TB
IAs   80  LAERLLVDVIGLPWE  LLVDVIGLP        0.1462      10274.8                32.00   Rv2711, TB
IAs  115  LVKVLNNPTTSPFGN  KVLNNPTTS        0.1456      10344.8                32.00   Rv2711, TB
IAs   79  RLAERLLVDVIGLPW  LLVDVIGLP        0.1439      10537.4                32.00   Rv2711, TB
IAs   24  PLRARIAERLDQSGP  RIAERLDQS        0.1437      10565.3                32.00   Rv2711, TB
IAs  121  NPTTSPFGNPIPGLV  SPFGNPIPG        0.1425      10698.0                32.00   Rv2711, TB
IAs   61  LELTEKGRALAIAVM  EKGRALAIA        0.1423      10725.2                32.00   Rv2711, TB
IAs  122  PTTSPFGNPIPGLVE  SPFGNPIPG        0.1369      11370.0                32.00   Rv2711, TB
IAs   25  LRARIAERLDQSGPT  RIAERLDQS        0.1362      11451.9                32.00   Rv2711, TB
IAs  205  TIVIPGHENVTLPHE  PGHENVTLP        0.1318      12010.2                32.00   Rv2711, TB
IAs   27  ARIAERLDQSGPTVS  RIAERLDQS        0.1310      12116.9                32.00   Rv2711, TB
IAs  119  LNNPTTSPFGNPIPG  SPFGNPIPG        0.1307      12155.4                32.00   Rv2711, TB
IAs   70  LAIAVMRKHRLAERL  LAIAVMRKH        0.1290      12377.8                32.00   Rv2711, TB
IAs  123  TTSPFGNPIPGLVEL  SPFGNPIPG        0.1282      12490.1                32.00   Rv2711, TB
IAs   26  RARIAERLDQSGPTV  RIAERLDQS        0.1279      12531.0                32.00   Rv2711, TB
IAs  187  GVVPNARVTVETTPG  ARVTVETTP        0.1275      12588.9                32.00   Rv2711, TB
IAs  130  PIPGLVELGVGPEPG  VELGVGPEP        0.1267      12696.8                32.00   Rv2711, TB
IAs  188  VVPNARVTVETTPGG  ARVTVETTP        0.1265      12725.8                32.00   Rv2711, TB
IAs  189  VPNARVTVETTPGGG  ARVTVETTP        0.1251      12916.7                32.00   Rv2711, TB
IAs  183  LKDAGVVPNARVTVE  KDAGVVPNA        0.1237      13107.2                32.00   Rv2711, TB
IAs   36  SGPTVSQTVSRMERD  QTVSRMERD        0.1232      13182.0                32.00   Rv2711, TB
IAs  181  TRLKDAGVVPNARVT  KDAGVVPNA        0.1222      13324.8                32.00   Rv2711, TB
IAs   35  QSGPTVSQTVSRMER  VSQTVSRME        0.1217      13405.4                32.00   Rv2711, TB
IAs  135  VELGVGPEPGADDAN  VELGVGPEP        0.1215      13434.7                32.00   Rv2711, TB
IAs  120  NNPTTSPFGNPIPGL  SPFGNPIPG        0.1208      13538.2                32.00   Rv2711, TB
IAs   69  ALAIAVMRKHRLAER  LAIAVMRKH        0.1206      13563.4                32.00   Rv2711, TB
IAs  131  IPGLVELGVGPEPGA  VELGVGPEP        0.1204      13590.4                32.00   Rv2711, TB
IAs   53  LRVAGDRHLELTEKG  RHLELTEKG        0.1204      13592.3                32.00   Rv2711, TB
IAs  184  KDAGVVPNARVTVET  KDAGVVPNA        0.1201      13627.1                32.00   Rv2711, TB
IAs  134  LVELGVGPEPGADDA  VELGVGPEP        0.1201      13636.7                32.00   Rv2711, TB
IAs  117  KVLNNPTTSPFGNPI  KVLNNPTTS        0.1198      13682.5                32.00   Rv2711, TB
IAs  192  ARVTVETTPGGGVTI  ARVTVETTP        0.1194      13735.1                32.00   Rv2711, TB
IAs  136  ELGVGPEPGADDANL  ELGVGPEPG        0.1170      14093.1                32.00   Rv2711, TB
IAs  180  ITRLKDAGVVPNARV  KDAGVVPNA        0.1170      14105.6                32.00   Rv2711, TB
IAs  191  NARVTVETTPGGGVT  ARVTVETTP        0.1165      14174.0                32.00   Rv2711, TB
IAs  182  RLKDAGVVPNARVTV  KDAGVVPNA        0.1164      14194.7                32.00   Rv2711, TB
IAs  132  PGLVELGVGPEPGAD  VELGVGPEP        0.1158      14284.1                32.00   Rv2711, TB
IAs  195  TVETTPGGGVTIVIP  GGGVTIVIP        0.1157      14302.2                32.00   Rv2711, TB
IAs   37  GPTVSQTVSRMERDG  QTVSRMERD        0.1152      14374.8                32.00   Rv2711, TB
IAs  133  GLVELGVGPEPGADD  VELGVGPEP        0.1142      14537.9                32.00   Rv2711, TB
IAs  179  LITRLKDAGVVPNAR  KDAGVVPNA        0.1141      14545.5                32.00   Rv2711, TB
IAs  204  VTIVIPGHENVTLPH  VTIVIPGHE        0.1127      14774.8                32.00   Rv2711, TB
IAs  124  TSPFGNPIPGLVELG  SPFGNPIPG        0.1117      14928.9                32.00   Rv2711, TB
IAs   34  DQSGPTVSQTVSRME  VSQTVSRME        0.1103      15159.9                50.00   Rv2711, TB
IAs  190  PNARVTVETTPGGGV  ARVTVETTP        0.1097      15257.5                50.00   Rv2711, TB
IAs  125  SPFGNPIPGLVELGV  SPFGNPIPG        0.1089      15396.1                50.00   Rv2711, TB
IAs   39  TVSQTVSRMERDGLL  QTVSRMERD        0.1088      15399.5                50.00   Rv2711, TB
IAs   28  RIAERLDQSGPTVSQ  RIAERLDQS        0.1088      15412.5                50.00   Rv2711, TB
IAs   54  RVAGDRHLELTEKGR  RHLELTEKG        0.1069      15721.4                50.00   Rv2711, TB
IAs    1  NELVDTTEMYLRTIY  ELVDTTEMY        0.1067      15755.4                50.00   Rv2711, TB
IAs   59  RHLELTEKGRALAIA  RHLELTEKG        0.1058      15909.4                50.00   Rv2711, TB
IAs   38  PTVSQTVSRMERDGL  QTVSRMERD        0.1050      16062.0                50.00   Rv2711, TB
IAs   99  EACRWEHVMSEDVER  EHVMSEDVE        0.1045      16132.2                50.00   Rv2711, TB
IAs    6  TTEMYLRTIYDLEEE  RTIYDLEEE        0.1037      16286.3                50.00   Rv2711, TB
IAs   40  VSQTVSRMERDGLLR  QTVSRMERD        0.1030      16406.4                50.00   Rv2711, TB
IAs   33  LDQSGPTVSQTVSRM  QSGPTVSQT        0.1006      16841.5                50.00   Rv2711, TB
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IAs  186  AGVVPNARVTVETTP  ARVTVETTP        0.1005      16863.7                  50.00   Rv2711, TB
IAs  149  NLVRLTELPAGSPVA  NLVRLTELP        0.0996      17011.6                  50.00   Rv2711, TB
IAs   32  RLDQSGPTVSQTVSR  GPTVSQTVS        0.0988      17169.5                  50.00   Rv2711, TB
IAs  148  ANLVRLTELPAGSPV  NLVRLTELP        0.0987      17187.9                  50.00   Rv2711, TB
IAs   31  ERLDQSGPTVSQTVS  ERLDQSGPT        0.0977      17380.4                  50.00   Rv2711, TB
IAs   55  VAGDRHLELTEKGRA  RHLELTEKG        0.0974      17423.3                  50.00   Rv2711, TB
IAs   41  SQTVSRMERDGLLRV  QTVSRMERD        0.0974      17425.8                  50.00   Rv2711, TB
IAs    0  MNELVDTTEMYLRTI  ELVDTTEMY        0.0970      17501.7                  50.00   Rv2711, TB
IAs  178  DLITRLKDAGVVPNA  KDAGVVPNA        0.0961      17673.4                  50.00   Rv2711, TB
IAs   58  DRHLELTEKGRALAI  RHLELTEKG        0.0941      18065.6                  50.00   Rv2711, TB
IAs  100  ACRWEHVMSEDVERR  EHVMSEDVE        0.0936      18166.6                  50.00   Rv2711, TB
IAs   73  AVMRKHRLAERLLVD  RLAERLLVD        0.0925      18376.1                  50.00   Rv2711, TB
IAs  215  TLPHEMAHAVKVEKV  AHAVKVEKV        0.0925      18380.3                  50.00   Rv2711, TB
IAs    2  ELVDTTEMYLRTIYD  ELVDTTEMY        0.0924      18404.0                  50.00   Rv2711, TB
IAs  143  PGADDANLVRLTELP  NLVRLTELP        0.0922      18441.5                  50.00   Rv2711, TB
IAs   57  GDRHLELTEKGRALA  RHLELTEKG        0.0918      18527.9                  50.00   Rv2711, TB
IAs   92  PWEEVHAEACRWEHV  AEACRWEHV        0.0908      18721.1                  50.00   Rv2711, TB
IAs  144  GADDANLVRLTELPA  NLVRLTELP        0.0908      18723.8                  50.00   Rv2711, TB
IAs   96  VHAEACRWEHVMSED  VHAEACRWE        0.0903      18812.5                  50.00   Rv2711, TB
IAs   56  AGDRHLELTEKGRAL  RHLELTEKG        0.0902      18849.2                  50.00   Rv2711, TB
IAs   21  GVTPLRARIAERLDQ  LRARIAERL        0.0900      18888.4                  50.00   Rv2711, TB
IAs   42  QTVSRMERDGLLRVA  QTVSRMERD        0.0895      18990.4                  50.00   Rv2711, TB
IAs   93  WEEVHAEACRWEHVM  VHAEACRWE        0.0894      19001.7                  50.00   Rv2711, TB
IAs   30  AERLDQSGPTVSQTV  ERLDQSGPT        0.0891      19069.1                  50.00   Rv2711, TB
IAs  161  PVAVVVRQLTEHVQG  PVAVVVRQL        0.0882      19261.1                  50.00   Rv2711, TB
IAs  214  VTLPHEMAHAVKVEK  EMAHAVKVE        0.0874      19431.0                  50.00   Rv2711, TB
IAs  102  RWEHVMSEDVERRLV  EHVMSEDVE        0.0873      19441.6                  50.00   Rv2711, TB
IAs  147  DANLVRLTELPAGSP  NLVRLTELP        0.0867      19559.7                  50.00   Rv2711, TB
IAs   94  EEVHAEACRWEHVMS  VHAEACRWE        0.0867      19569.5                  50.00   Rv2711, TB
IAs    7  TEMYLRTIYDLEEEG  RTIYDLEEE        0.0864      19638.4                  50.00   Rv2711, TB
IAs  146  DDANLVRLTELPAGS  NLVRLTELP        0.0863      19661.4                  50.00   Rv2711, TB
IAs  158  AGSPVAVVVRQLTEH  VVVRQLTEH        0.0858      19750.0                  50.00   Rv2711, TB
IAs   95  EVHAEACRWEHVMSE  VHAEACRWE        0.0856      19811.0                  50.00   Rv2711, TB
IAs  213  NVTLPHEMAHAVKVE  EMAHAVKVE        0.0853      19857.8                  50.00   Rv2711, TB
IAs  145  ADDANLVRLTELPAG  NLVRLTELP        0.0853      19864.9                  50.00   Rv2711, TB
IAs  103  WEHVMSEDVERRLVK  EHVMSEDVE        0.0852      19883.2                  50.00   Rv2711, TB
IAs  101  CRWEHVMSEDVERRL  EHVMSEDVE        0.0852      19887.5                  50.00   Rv2711, TB
IAs   71  AIAVMRKHRLAERLL  AVMRKHRLA        0.0840      20158.5                  50.00   Rv2711, TB
IAs  150  LVRLTELPAGSPVAV  LPAGSPVAV        0.0819      20618.2                  50.00   Rv2711, TB
IAs  129  NPIPGLVELGVGPEP  VELGVGPEP        0.0803      20974.6                  50.00   Rv2711, TB
IAs  137  LGVGPEPGADDANLV  PGADDANLV        0.0794      21183.5                  50.00   Rv2711, TB
IAs  160  SPVAVVVRQLTEHVQ  SPVAVVVRQ        0.0788      21307.9                  50.00   Rv2711, TB
IAs  159  GSPVAVVVRQLTEHV  VVVRQLTEH        0.0787      21348.1                  50.00   Rv2711, TB
IAs   29  IAERLDQSGPTVSQT  ERLDQSGPT        0.0780      21508.5                  50.00   Rv2711, TB
IAs   85  LVDVIGLPWEEVHAE  VDVIGLPWE        0.0774      21629.6                  50.00   Rv2711, TB
IAs  151  VRLTELPAGSPVAVV  TELPAGSPV        0.0774      21642.7                  50.00   Rv2711, TB
IAs   72  IAVMRKHRLAERLLV  AVMRKHRLA        0.0773      21660.1                  50.00   Rv2711, TB
IAs  104  EHVMSEDVERRLVKV  EHVMSEDVE        0.0771      21716.4                  50.00   Rv2711, TB
IAs  157  PAGSPVAVVVRQLTE  AVVVRQLTE        0.0771      21720.6                  50.00   Rv2711, TB
IAs   97  HAEACRWEHVMSEDV  AEACRWEHV        0.0770      21726.0                  50.00   Rv2711, TB
IAs  152  RLTELPAGSPVAVVV  TELPAGSPV        0.0769      21755.2                  50.00   Rv2711, TB
IAs  153  LTELPAGSPVAVVVR  TELPAGSPV        0.0767      21799.2                  50.00   Rv2711, TB
IAs   86  VDVIGLPWEEVHAEA  VDVIGLPWE        0.0763      21908.5                  50.00   Rv2711, TB
IAs  156  LPAGSPVAVVVRQLT  SPVAVVVRQ        0.0751      22176.1                  50.00   Rv2711, TB
IAs  154  TELPAGSPVAVVVRQ  SPVAVVVRQ        0.0744      22346.1                  50.00   Rv2711, TB
IAs    8  EMYLRTIYDLEEEGV  RTIYDLEEE        0.0744      22348.3                  50.00   Rv2711, TB
IAs   19  EEGVTPLRARIAERL  LRARIAERL        0.0741      22427.0                  50.00   Rv2711, TB
IAs   15  YDLEEEGVTPLRARI  EGVTPLRAR        0.0730      22689.9                  50.00   Rv2711, TB
IAs  185  DAGVVPNARVTVETT  VPNARVTVE        0.0728      22749.1                  50.00   Rv2711, TB
IAs  138  GVGPEPGADDANLVR  PGADDANLV        0.0726      22789.3                  50.00   Rv2711, TB
IAs  142  EPGADDANLVRLTEL  PGADDANLV        0.0726      22802.6                  50.00   Rv2711, TB
IAs  155  ELPAGSPVAVVVRQL  SPVAVVVRQ        0.0715      23060.1                  50.00   Rv2711, TB
IAs  162  VAVVVRQLTEHVQGD  RQLTEHVQG        0.0714      23092.9                  50.00   Rv2711, TB
IAs  140  GPEPGADDANLVRLT  PGADDANLV        0.0706      23301.9                  50.00   Rv2711, TB
IAs  177  IDLITRLKDAGVVPN  TRLKDAGVV        0.0703      23365.0                  50.00   Rv2711, TB
IAs    9  MYLRTIYDLEEEGVT  RTIYDLEEE        0.0701      23425.3                  50.00   Rv2711, TB
IAs  139  VGPEPGADDANLVRL  PGADDANLV        0.0694      23592.2                  50.00   Rv2711, TB
IAs   20  EGVTPLRARIAERLD  LRARIAERL        0.0691      23666.6                  50.00   Rv2711, TB
IAs  127  FGNPIPGLVELGVGP  PGLVELGVG        0.0688      23742.5                  50.00   Rv2711, TB
IAs  193  RVTVETTPGGGVTIV  RVTVETTPG        0.0683      23869.2                  50.00   Rv2711, TB
IAs  126  PFGNPIPGLVELGVG  PGLVELGVG        0.0681      23936.4                  50.00   Rv2711, TB
IAs   10  YLRTIYDLEEEGVTP  RTIYDLEEE        0.0680      23952.2                  50.00   Rv2711, TB
IAs  118  VLNNPTTSPFGNPIP  TSPFGNPIP        0.0679      23993.5                  50.00   Rv2711, TB
IAs   16  DLEEEGVTPLRARIA  EGVTPLRAR        0.0674      24102.0                  50.00   Rv2711, TB
IAs   74  VMRKHRLAERLLVDV  RKHRLAERL        0.0662      24430.7                  50.00   Rv2711, TB
IAs   76  RKHRLAERLLVDVIG  RKHRLAERL        0.0662      24436.8                  50.00   Rv2711, TB
IAs  141  PEPGADDANLVRLTE  PGADDANLV        0.0654      24643.3                  50.00   Rv2711, TB
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         IAs   75  MRKHRLAERLLVDVI  RKHRLAERL        0.0646      24850.0               50.00   Rv2711, TB
         IAs   12  RTIYDLEEEGVTPLR  RTIYDLEEE        0.0646      24858.9               50.00   Rv2711, TB
         IAs   17  LEEEGVTPLRARIAE  EGVTPLRAR        0.0643      24928.7               50.00   Rv2711, TB
         IAs   11  LRTIYDLEEEGVTPL  RTIYDLEEE        0.0632      25234.0               50.00   Rv2711, TB
         IAs  163  AVVVRQLTEHVQGDI  RQLTEHVQG        0.0630      25284.0               50.00   Rv2711, TB
         IAs   87  DVIGLPWEEVHAEAC  VIGLPWEEV        0.0614      25744.4               50.00   Rv2711, TB
         IAs   14  IYDLEEEGVTPLRAR  EGVTPLRAR        0.0612      25794.6               50.00   Rv2711, TB
         IAs   18  EEEGVTPLRARIAER  EGVTPLRAR        0.0611      25824.2               50.00   Rv2711, TB
         IAs  175  GDIDLITRLKDAGVV  TRLKDAGVV        0.0582      26649.4               50.00   Rv2711, TB
         IAs   88  VIGLPWEEVHAEACR  VIGLPWEEV        0.0580      26683.2               50.00   Rv2711, TB
         IAs   60  HLELTEKGRALAIAV  EKGRALAIA        0.0574      26872.0               50.00   Rv2711, TB
         IAs   90  GLPWEEVHAEACRWE  VHAEACRWE        0.0569      27002.6               50.00   Rv2711, TB
         IAs  176  DIDLITRLKDAGVVP  TRLKDAGVV        0.0565      27140.6               50.00   Rv2711, TB
         IAs    3  LVDTTEMYLRTIYDL  VDTTEMYLR        0.0562      27214.1               50.00   Rv2711, TB
         IAs    4  VDTTEMYLRTIYDLE  TTEMYLRTI        0.0556      27406.2               50.00   Rv2711, TB
         IAs   48  ERDGLLRVAGDRHLE  RVAGDRHLE        0.0556      27410.6               50.00   Rv2711, TB
         IAs   77  KHRLAERLLVDVIGL  RLAERLLVD        0.0554      27462.0               50.00   Rv2711, TB
         IAs   91  LPWEEVHAEACRWEH  VHAEACRWE        0.0532      28109.5               50.00   Rv2711, TB
         IAs  107  MSEDVERRLVKVLNN  RRLVKVLNN        0.0503      29022.4               50.00   Rv2711, TB
         IAs   47  MERDGLLRVAGDRHL  LRVAGDRHL        0.0499      29127.5               50.00   Rv2711, TB
         IAs   45  SRMERDGLLRVAGDR  GLLRVAGDR        0.0484      29622.4               50.00   Rv2711, TB
         IAs  164  VVVRQLTEHVQGDID  RQLTEHVQG        0.0473      29975.1               50.00   Rv2711, TB
         IAs   49  RDGLLRVAGDRHLEL  RVAGDRHLE        0.0465      30217.7               50.00   Rv2711, TB
         IAs   89  IGLPWEEVHAEACRW  LPWEEVHAE        0.0457      30484.3               50.00   Rv2711, TB
         IAs  165  VVRQLTEHVQGDIDL  RQLTEHVQG        0.0456      30532.5               50.00   Rv2711, TB
         IAs  128  GNPIPGLVELGVGPE  PGLVELGVG        0.0445      30889.1               50.00   Rv2711, TB
         IAs  166  VRQLTEHVQGDIDLI  RQLTEHVQG        0.0443      30968.0               50.00   Rv2711, TB
         IAs  194  VTVETTPGGGVTIVI  TPGGGVTIV        0.0437      31160.6               50.00   Rv2711, TB
         IAs    5  DTTEMYLRTIYDLEE  TEMYLRTIY        0.0432      31320.5               50.00   Rv2711, TB
         IAs   50  DGLLRVAGDRHLELT  RVAGDRHLE        0.0429      31419.6               50.00   Rv2711, TB
         IAs  167  RQLTEHVQGDIDLIT  RQLTEHVQG        0.0422      31663.3               50.00   Rv2711, TB
         IAs   13  TIYDLEEEGVTPLRA  EEGVTPLRA        0.0417      31835.4               50.00   Rv2711, TB
         IAs   46  RMERDGLLRVAGDRH  GLLRVAGDR        0.0407      32185.9               50.00   Rv2711, TB
         IAs  172  HVQGDIDLITRLKDA  DLITRLKDA        0.0365      33674.6               50.00   Rv2711, TB
         IAs   51  GLLRVAGDRHLELTE  RVAGDRHLE        0.0362      33798.3               50.00   Rv2711, TB
         IAs   44  VSRMERDGLLRVAGD  SRMERDGLL        0.0362      33799.1               50.00   Rv2711, TB
         IAs  169  LTEHVQGDIDLITRL  GDIDLITRL        0.0347      34367.0               50.00   Rv2711, TB
         IAs   43  TVSRMERDGLLRVAG  SRMERDGLL        0.0345      34423.2               50.00   Rv2711, TB
         IAs  170  TEHVQGDIDLITRLK  GDIDLITRL        0.0337      34740.8               50.00   Rv2711, TB
         IAs  171  EHVQGDIDLITRLKD  GDIDLITRL        0.0327      35113.4               50.00   Rv2711, TB
         IAs   52  LLRVAGDRHLELTEK  RVAGDRHLE        0.0324      35229.9               50.00   Rv2711, TB
         IAs  174  QGDIDLITRLKDAGV  DLITRLKDA        0.0304      36003.7               50.00   Rv2711, TB
         IAs  168  QLTEHVQGDIDLITR  EHVQGDIDL        0.0298      36222.1               50.00   Rv2711, TB
         IAs  173  VQGDIDLITRLKDAG  DLITRLKDA        0.0286      36682.4               50.00   Rv2711, TB
         IAs  105  HVMSEDVERRLVKVL  EDVERRLVK        0.0285      36744.7               50.00   Rv2711, TB
         IAs  106  VMSEDVERRLVKVLN  EDVERRLVK        0.0256      37916.8               50.00   Rv2711, TB
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Allele: IAs. Number of high binders 0. Number of weak binders 0. Number of peptides 216

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Explain the output. Go **back**.