

Supplementary Figures

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# NetMHCpan version 4.0

# Input is in FSA format

# Peptide length 8,9,10,11,12

# Make Eluted ligand likelihood predictions

HLA-B44:03: Distance to training data 0.000 (using nearest neighbor HLA-B44:03)

# Rank Threshold for Strong binding peptides 0.500
# Rank Threshold for Weak binding peptides 2.000
-----
Pos      HLA      Peptide      Core Of Gp Gl Ip Il      Icore      Identity Score %Rank BLevel
-----
534 HLA-B*44:03 KEQIERLGY KEQIERLGY 0 0 0 0 0 KEQIERLGY ENSP00000363746 0.906 0.06 <= SB
498 HLA-B*44:03 QEWEVKALL QEWEVKALL 0 0 0 0 0 QEWEVKALL ENSP00000363746 0.835 0.10 <= SB
236 HLA-B*44:03 MEAVRDIRF MEAVRDIRF 0 0 0 0 0 MEAVRDIRF ENSP00000363746 0.829 0.10 <= SB
247 HLA-B*44:03 SEALLAVAQNRW SEALLAQRW 0 4 3 0 0 SEALLAVAQNRW ENSP00000363746 0.779 0.13 <= SB
294 HLA-B*44:03 SETGFLTYL SETGFLTYL 0 0 0 0 0 SETGFLTYL ENSP00000363746 0.741 0.15 <= SB
294 HLA-B*44:03 SETGFLTY SET-GFLTY 0 0 0 3 1 SETGFLTY ENSP00000363746 0.651 0.21 <= SB
522 HLA-B*44:03 AEVVISL AEVVISL 0 0 0 0 6 1 AEVVISL ENSP00000363746 0.625 0.24 <= SB
533 HLA-B*44:03 KKEQIERLGY KEQIERLGY 0 1 1 0 0 KKEQIERLGY ENSP00000363746 0.520 0.33 <= SB
51 HLA-B*44:03 RELRPQRPNAY RELRPQRAY 0 7 3 0 0 RELRPQRPNAY ENSP00000363746 0.415 0.43 <= SB

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Supplementary Figure 1: Output example from NetMHCpan-4.0. The protein sequence for ENSP00000363746 was screened for potential HLA-B*44:03 binders of length 8-12 using the eluted ligand prediction mode of NetMHCpan-4.0. Only strong predictions (SB) are shown. For each peptide the binding core is reported (the peptide sequence predicted to be “seen” by the MHC molecule after accommodating indels), the Icore (the biological fragment predicted to form complex with the MHC including indels), the location and length of gaps, Gp/Gl (deletions) and insertions, Ip/Ii, as well as the prediction score and predicted rank value. The two entries highlighted in red corresponds to eluted ligands contained within the Pearson data set (16).