

## Supplementary material:

**Table 1:** Predicted MHC class II restricted peptides in virulent factors having human homologs using NETMHC 2.2 (affinity score: IC50 < 50).

pos	matched peptide	affinity(nM)	Allele
7	NYLAQTYSVLVTSA	30.3	HLA-DRB10701
81	LLAFTNPTVNSYKRL	28.2	HLA-DRB10101
11	YLQYTSGSTRTYPAGV	38.8	HLA-DRB10401
85	FCLFSSGAALLGSPG	7.5	HLA-DRB10101
68	RNTVQFAAAVQAAME	6.8	HLA-DRB10101
102	RNTVQFAAAVQAAME	35.6	HLA-DRB10701
17	YLQYTSGSTRTYPAGV	38.8	HLA-DRB10401
5	LGHFAAVSAATGLVV	3.7	HLA-DRB10101
8	QLTYRELDALADRLA	20.8	HLA-DRB10401
194	GNTVAMRLRPQSAMS	15.2	HLA-DRB10101
8	YARYLAEHGARRIVL	4.8	HLA-DRB10701
11	RHRLLSDVTRALADE	17.9	HLA-DRB10301
148	ILAELGMDTTTLVAA	34.4	HLA-DRB10101
12	LAELGMDTTTLVAAL	17.9	HLA-DRB10301
6	ERHTAINSLVTATHG	29.1	HLA-DRB10401
20	LDIFAALRSGGAIIV	4.9	HLA-DRB10101
157	LAYVLFTSGSTGEPK	13.4	HLA-DRB10101
109	TLLLADVLAAAPAEF	10.5	HLA-DRB10101
195	VQEALRSAAGHSAYP	15.7	HLA-DRB10101
219	GGHFYLNHDHLDAVAR	17.5	HLA-DRB10101
43	KSLVANDVDTFVVQY	39	HLA-DRB10301
303	AAQRAVRAALNGRTA	28.1	HLA-DRB10101
45	YHDMGLILGICAPLV	12.6	HLA-DRB10101
64	RFDYEQLTAGQARPC	18	HLA-DRB10101
120	LPLYHDMGLILGICA	34.2	HLA-DRB10101
40	AVYRAALAAAGVQPE	5.4	HLA-DRB10101
115	KLMTRIAGAGAMGSV	8.8	HLA-DRB10101
18	VVTGLNNSVASGRIA	16.5	HLA-DRB11302
43	LPFYHDMGLVIGICA	14	HLA-DRB10101
50	VDYRLIPKHSGLMAL	17.8	HLA-DRB10101
6	DSAGGYLALALAQRL	15.7	HLA-DRB10701
2	HAFYLQYKNVKVDFA	5.9	HLA-DRB10101
19	WDYGALEPHISGQIN	10	HLA-DRB11501
31	YGALEPHISGQINEL	15.8	HLA-DRB10101
50	PDLWDYGALEPHIS	38.4	HLA-DRB10101
41	SLRLLQVGGSKLEPE	7.6	HLA-DRB10101
154	EGELLVRGPYTLNGY	40.6	HLA-DRB10101
169	PGDRVLLQLPNGCQF	47.7	HLA-DRB10101
4	QWSRLLAQRALDS	3.8	HLA-DRB10101
111	LLATAAARMVTAWRR	8.8	HLA-DRB10101
163	DSIVALSVVQAARRR	12.2	HLA-DRB10101
165	QAAYVIFTSGTTGTP	12.5	HLA-DRB10101
392	AYVIFTSGTTGTPKG	34.4	HLA-DRB10101
438	GELVTAVAEQTLGAL	42.3	HLA-DRB10101
129	DLDRIRARVAAALPE	10.4	HLA-DRB10101
54	GVDLDRIRARVAAAL	22.9	HLA-DRB10301
390	YLIYTSGTTGLPKGV	41.8	HLA-DRB10101
59	ICVSYRITGDIDLAR	24.4	HLA-DRB10301
111	VDALSANIVSAAVAD	13	HLA-DRB10101
34	RGERFVDALSANIVS	9.8	HLA-DRB10701
41	GERFVDALSANIVSA	30.3	HLA-DRB11302
115	AANRLLDVMAAQLRA	13.4	HLA-DRB10101
263	GHSLGEVAAAYLAGS	40.6	HLA-DRB10101
90	VGHSLGEVAAAYLAG	39.8	HLA-DRB10701
102	LTVDTS CSSALAAFH	39.6	HLA-DRB10101
164	VQFVGPLSVVDSALA	42.6	HLA-DRB10101

103	SFAILHPKKYEEIVR	24.3	HLA-DRB10101
53	GKTTIARVVANILAG	12	HLA-DRB10101
133	TLLLGPPGTGKTSVA	39	HLA-DRB10101

**Table 2:** Predicted MHC class I restricted peptides in virulent factors having human homologs using NETMHC 2.2 (affinity score: IC 50 < 50).

pos	matched peptide	affinity(nM)	Allele
18	ALLSGLLRA	26	A*0201
394	FIDEAYALV	5	A*0201
438	AIINTLLLY	26	A*1101
4	FLITVALAL	9	A*0201
281	LLAEAQAEL	17	A*0201
499	LPRTSSGKL	7	B*0702
332	APAGRPLL	14	B*0702
272	TPATPATPV	20	B*0702
236	YPAVLTSVP	9	B*0702
685	PSDPTALAY	14	A*0101
862	SLVGYVTPA	13	A*0201
218	FYHDMGLVI	42	A2402
166	YLQYKNVKV	9	A*0201
1580	ALAAAILADV	13	A*0201
697	TSGSTGEPK	41	A*1101
16	LPRRLAIAA	33	B*0702

**Table 3:** Human homologs of *M. tuberculosis* virulent factors identified using BLASTP search (cut-off E value < 0.01)

<i>M. tuberculosis</i>		Human		Sequence identity (%)
VFG	GenBank Description	Gene ID	GenBank Description	
1384	Pyrroline-5-carboxylase (proC)	NP_075566	Pyrroline-5-carboxylate reductase 3	32
1387	SAICAR synthetase (purC)	NP_001072993	Multi-functional protein ADE2 isoform 1	21
1393	Fatty acyl-AMP ligase (fadD33)	XP_005257758	Acyl-CoA synthetase family member 2	25
1399	Glutamine synthetase (GlnA1)	NP_057655	Lengsin isoform A	24
1403	Phenyloxazoline synthase MbtB	XP_005265782	Acyl-CoA synthetase isoform X5	27
1408	Myco-cerosic acid synthase (Mas)	NP_004095	Fatty acid synthase	30
1415	Esterase/lipase (LipF)	NP_997248	Aryl acetamide deacetylase-like 2 precursor	34
1811	fbpC2	NP_001975	S-formyl glutathione hydrolase	24
1812	Secreted antigen 85-B FbpB (85B)	XP_005266335	S-formylglutathione hydrolase isoform X1	31
1817	Salicyl-S-ArCP synthetase	NP_001230208	Acyl-CoA synthetase family member 3	27
1820	Peptide synthetase (MbtF)	NP_115890	Acetyl-coenzyme A synthetase 2-like	23
1821	Peptide synthetase (MbtE)	XP_005265781	Acyl-CoA synthetase isoform X4	26
1822	Poly ketide synthetase (MbtD)	NP_004095	Fatty acid synthase	26
1823	Polyketidesynthetase (MbtC)	NP_004095	Fatty acid synthase	33
1826	GTP pyrophosphokinase (RelA)	NP_940929	3'-pyrophos-phohydrolase MESH1	39
2380	ESX-1 type VII secretion protein	XP_005264430	ATPase family AAA domain 2B isoform X2	31
1404	Alkyl hydroperoxidoreductase C (AhpC)	NP_054817	Thio-redoxin-dependent peroxide reductase	37
1407	Fatty-acid-AMP ligase (FadD26)	NP_055789	Disco-interacting protein 2 homolog C	26
1409	Fatty-acid-AMP ligase (FadD28)	XP_005252487	Disco-interacting protein 2 homolog C isoform X5	25
1421	Superoxide dismutase [FE] (SodA)	NP_001019636	Superoxide dismutase [Mn]	52
1825	Sensor histidine kinase (DevS)	NP_001137311	cGMP-dependent 3',5'-cyclic phosphodiesterase	27
2391	Membrane-anchored mycosin (MycP1)	NP_777596	Proprotein convert a ses-ubtilisin	27
2401	ESX conserved EccA5	NP_054828	ATPase family AAA domain-containing protein 2	30
1380	Cu, Zn Superoxide dismutase (sodC)	NP_005116	Copper chaperone for superoxide dismutase	28
1397	Heat shock protein (HspX)	NP_077721	Outer dense fiber protein 1	34

**Table 4:** Predicted B cell epitopes in virulent factors and its corresponding human homologs using BCPRED (cut-off score < 0.9).

VFG	Epitope ( <i>M. tb</i> )	Human AC #	Matched peptide (human)	Domain name
1393	STCAVTVPVPGIGLLADRVI	XP_005257758	NSPVTFAHFPEPTVEQKAES	Malonyl-CoA synthetase

1399	DAISGWWNTGAATEADGSPN	NP_057655	QELVDGLYHTGANVESFSSS	Glutamine synthetase
1403	FAGLGGATETAHVHATIFEVQ	XP_005265782	IFNVYGITEVSSWATIYRIP	Adenylate forming
1403	ADSGDDCPDWVAGELWVSGR	XP_005265782	RDINGFTIQEGSGQVFLGGR	Adenylate forming
1404	IVDPNNEIQFVSATAGSVGR	NP_054817	IIDPNGVIKHLVNDLPVGR	Peroxiredoxin (PRX)
1407	PKQTAQVFDAKLVDPAPAAP	NP_055789	GDESLQSDHFNLSFGDTQ	Adenylate forming
1408	AIVEEAPAEASAPESPFGDA	NP_004095	IILRPNTQPPPAPAPHATLP	polyketide synthases
1409	VHGDNVANGYWQKPDESERT	XP_005252487	VCAVATGTSYYGLSGMTKNT	Adenylate forming
1421	AEYTLPLDWDYGALEPHIS	NP_001019636	KHSLPDLPHYDYGALEPHINA	Fe/Mn superoxide dismutases
1811	MPAWLQANKGVSPGTGNAAVG	NP_001975	LPQLINANFPVDPQRMSIFG	S-formylglutathione hydrolase
1817	LLRAGAIPVMCLPGHRAAEL	NP_001230208	SWMSGGVAVPLYRKHPAAQ	Malonyl-CoA synthetase
1820	RVAEILRQTSAPVVIDEGVF	NP_115890	RVVELKKIVDEAVKHCPTVQ	Malonyl-CoA synthetase
1820	DENALAAINVTEGPATPPQT	NP_115890	MRLLLRKIITSEAQELGDTT	Malonyl-CoA synthetase
1821	TSGTTGLPKGVAVPHRPVAE	XP_005265781	TSGTTGIPKIVRVPHKCIVP	Adenylate forming domain
1821	PKINTTMHLLDDSLQPVPTG	XP_005265781	PLLGTVVEVRDTNGFTIQEG	Adenylate forming
1823	LAGHDVGCYVGASALEYGPA	NP_004095	LRGTHTGWVWGVSGSETSEA	Polyketide synthases
1823	GMVEGHGTATRLGDRTELRS	NP_004095	EYIEAHGTGTVKVGDPQELNG	Polyketide synthases
2380	DEAYALVQERDGRTPFGQE	XP_005264430	DEIDGLAPVRSSRQDQIHSS	ATPase family AAA
2389	SPPPPDVPTLVVPSGTPGT	NP_055853	TPEEPASPAAAVPTPEEPTS	EspG family
2389	PIPGAVPTPITPTGTPVTP	NP_055853	PEEPTSPAAAVPTPEEPTSP	EspG family
2391	DPRGWNNVQTVVTPAWYAPL	NP_777596	APEVITVGATNAQDQPVTLG	Peptidase S8 & S53
2401	HTLHEKGYSQGDPYGNAIN	XP_005264430	DGLAPVRSSRQDQIHSSIVS	ATPase family AAA