Computationally validated SARS-CoV-2 CTL and HTL Multi-Patch Vaccines designed by reverse epitomics approach, shows potential to cover large ethnically distributed human population worldwide

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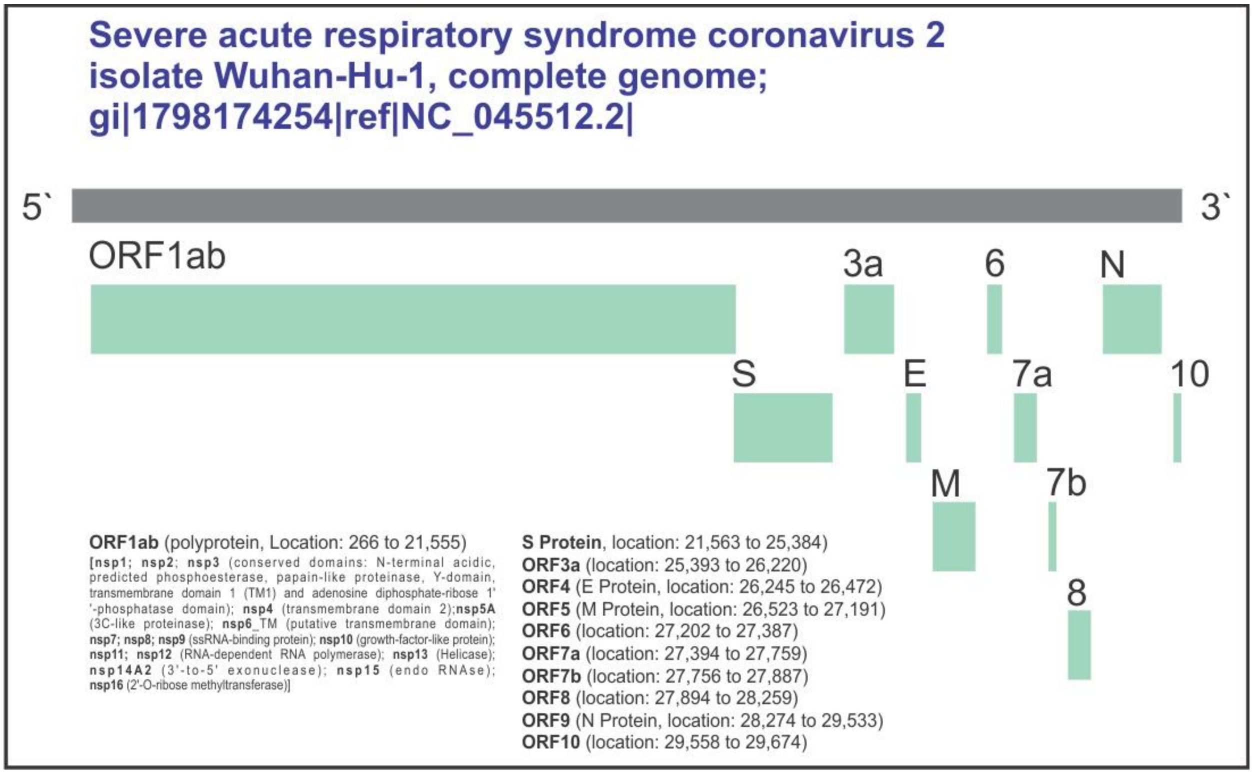


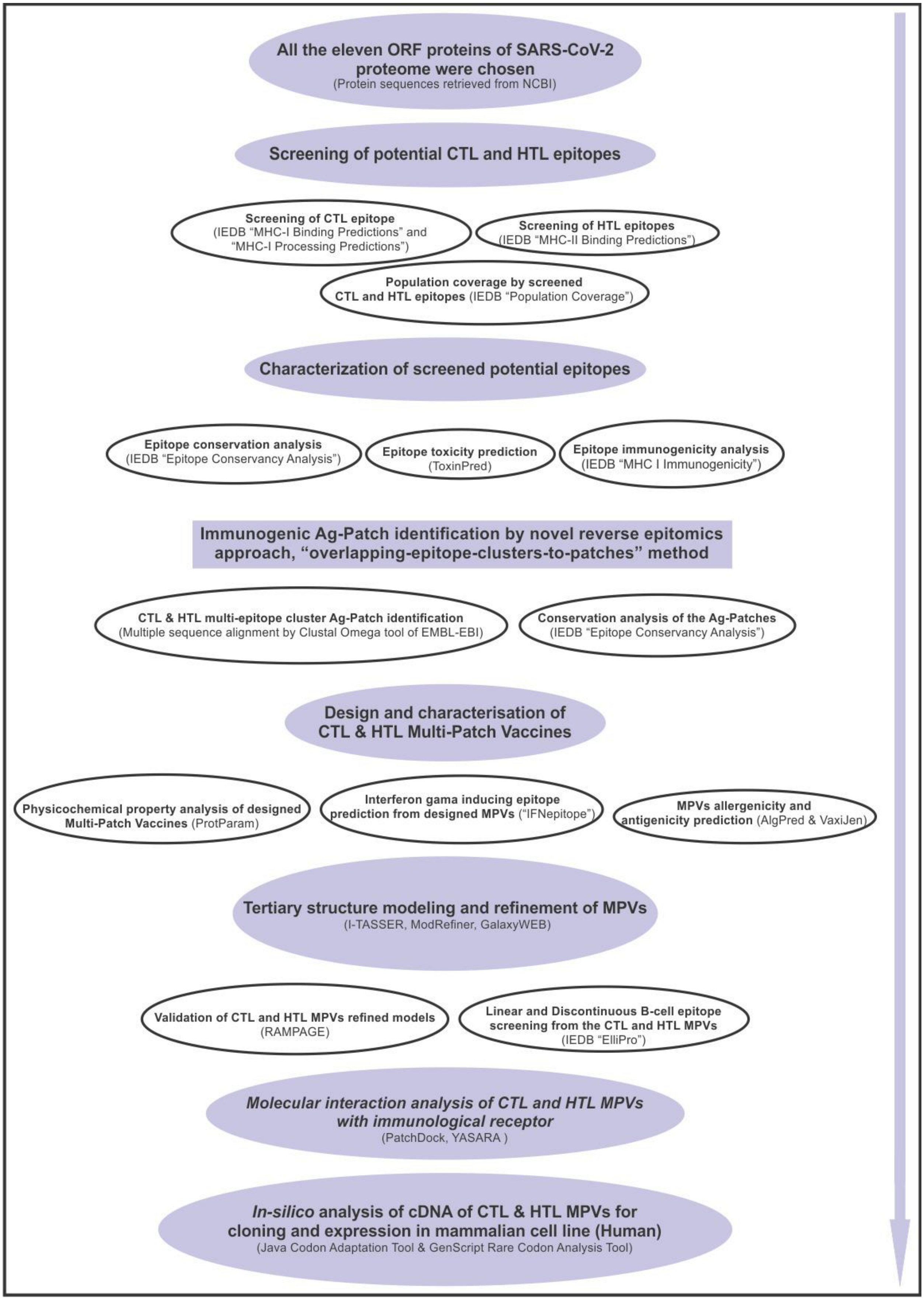
Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1, complete genome; gi|1798174254|ref|NC_045512.2|

ORF1ab (polyprotein, Location: 266 to 21,555)

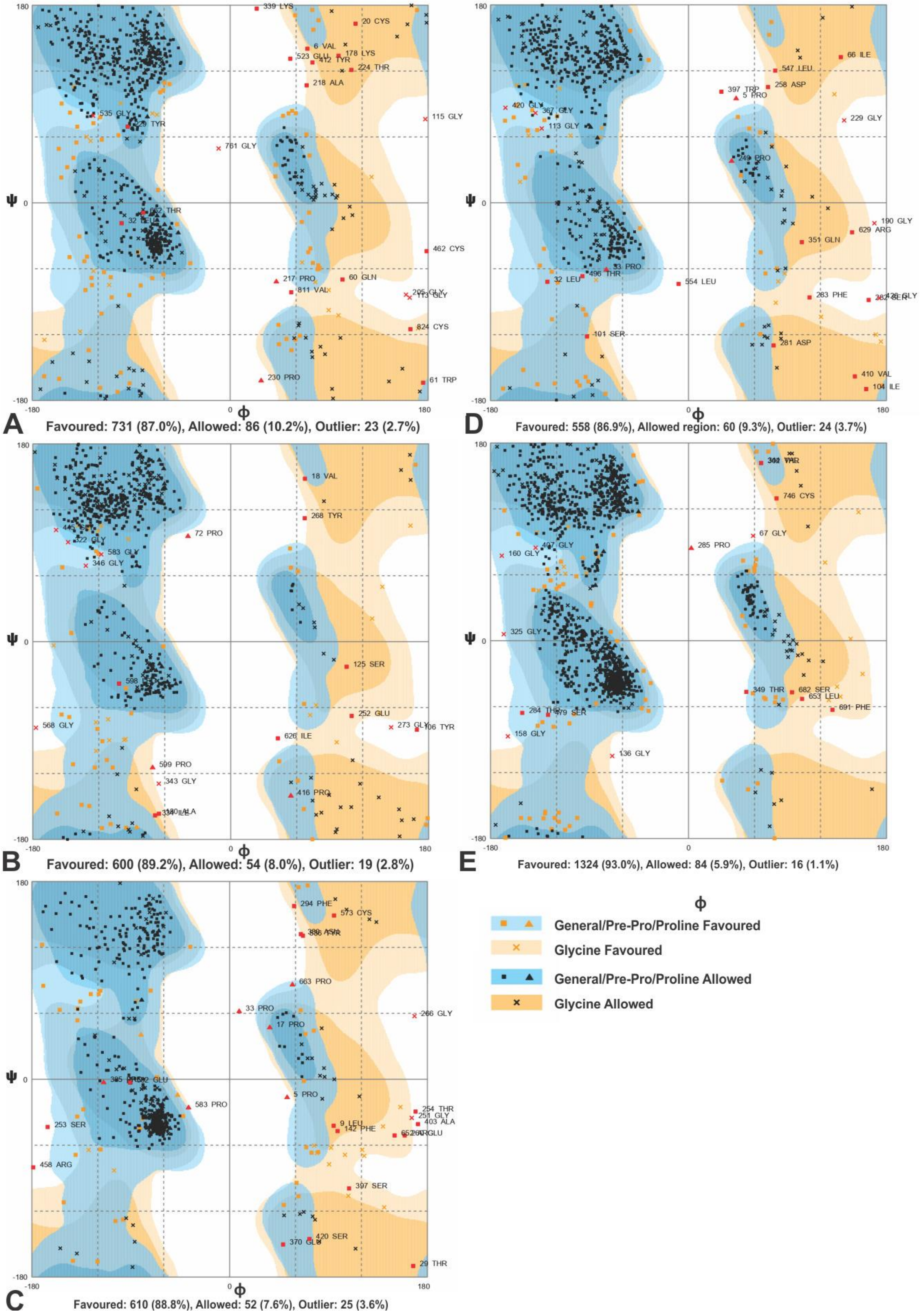
[**nsp1**; **nsp2**; **nsp3** (conserved domains: N-terminal acidic, predicted phosphoesterase, papain-like proteinase, Y-domain, transmembrane domain 1 (TM1) and adenosine diphosphate-ribose 1' '-phosphatase domain); **nsp4** (transmembrane domain 2);**nsp5A** (3C-like proteinase); **nsp6**_TM (putative transmembrane domain); **nsp7; nsp8; nsp9** (ssRNA-binding protein); **nsp10** (growth-factor-like protein); **nsp11; nsp12** (RNA-dependent RNA polymerase); **nsp13** (Helicase); **nsp14A2** (3'-to-5' exonuclease); **nsp15** (endo RNAse); **nsp16** (2'-O-ribose methyltransferase)]

S Protein, location: 21,563 to 25,384)
ORF3a (location: 25,393 to 26,220)
ORF4 (E Protein, location: 26,245 to 26,472)
ORF5 (M Protein, location: 26,523 to 27,191)
ORF6 (location: 27,202 to 27,387)
ORF7a (location: 27,394 to 27,759)
ORF7b (location: 27,756 to 27,887)
ORF8 (location: 27,894 to 28,259)
ORF9 (N Protein, location: 28,274 to 29,533)
ORF10 (location: 29,558 to 29,674)

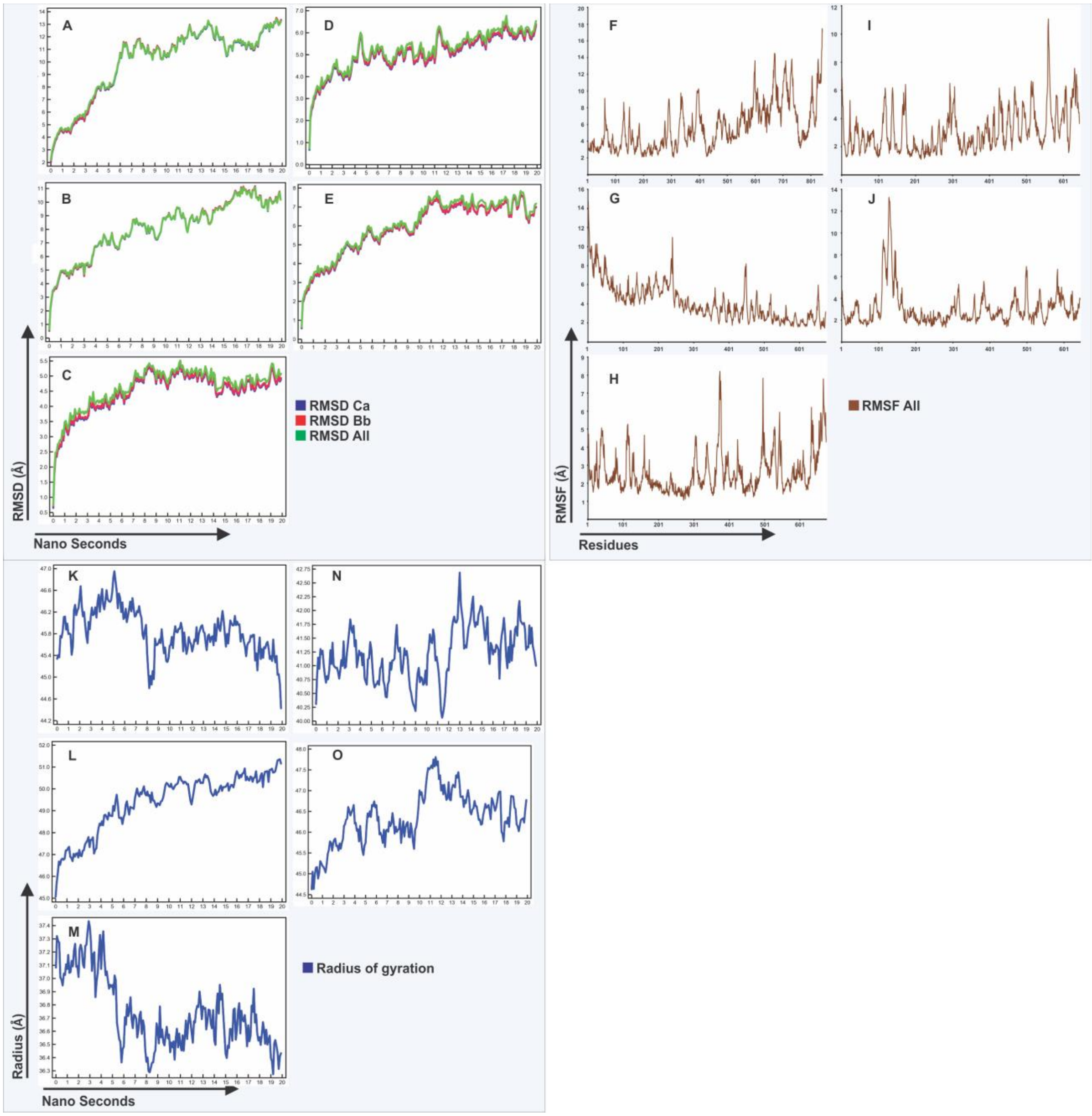
Supplementary Figure S1. Schematic presentation of all the ORF protein expressed by SARS-CoV-2 genome.



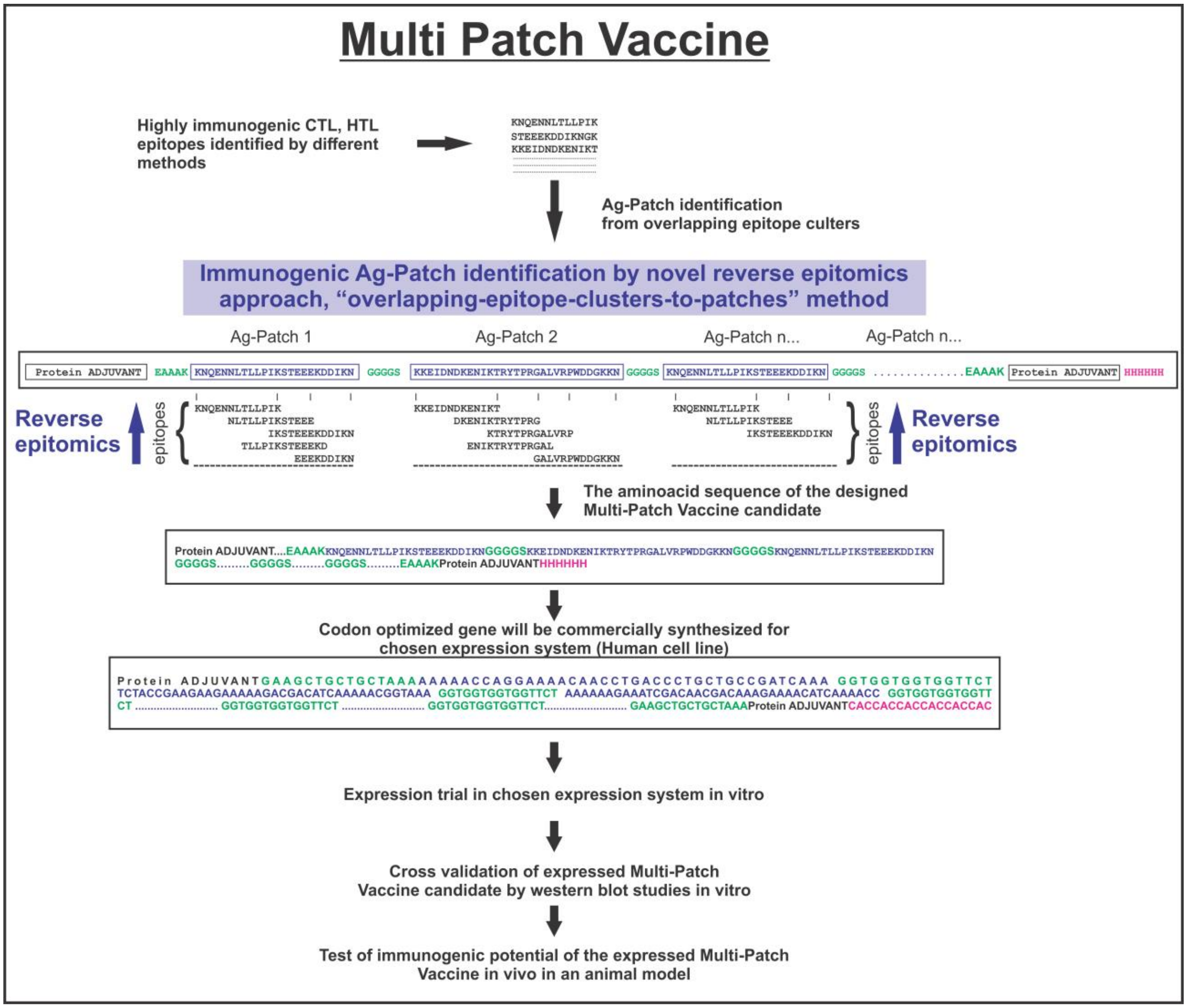
Supplementary Figure S2. Schematic representation of workflow and methodology.



Supplementary Figure S3. RAMPAGE analysis for all the MPVs **(A)** CTL-MPV-1, **(B)** CTL-MPV-2, **(C)** CTL-MPV-3, **(D)** HTL-MPV-1, **(E)** HTL-MPV-2.



Supplementary Figure S4. Molecular Dynamics simulation study of MPVs and TLR3-ECD complexes. (A-E): Root Mean Square Deviation (RMSD) for Cα, Backbone and all atoms (RMSD Ca, RMSD Bb, & RMSD All) respectively for (A) CTL-MPV-1:TLR3-ECD, (B) CTL-MPV-2:TLR3-ECD, (C) CTL-MPV-3:TLR3-ECD, (D) HTL-MPV-1:TLR3-ECD, (E) HTL-MPV-2:TLR3-ECD complexes. (F-J) Root Mean Square Fluctuation (RMSF) in the conformation of residues of the MPVs in complex with TLR3-ECD. RMSF: (F) CTL-MPV-1:TLR3-ECD, (G) CTL-MPV-2:TLR3-ECD, (H) CTL-MPV-3:TLR3-ECD, (I) HTL-MPV-1:TLR3-ECD, (J) HTL-MPV-2:TLR3-ECD. (K-O) Radius of gyration for all the MPVs and TLR3-ECD complexes are shown. Rg: (K) CTL-MPV-1:TLR3-ECD, (L) CTL-MPV-2:TLR3-ECD, (M) CTL-MPV-3:TLR3-ECD, (N) HTL-MPV-1:TLR3-ECD, (O) HTL-MPV-2:TLR3-ECD.



Supplementary Figure S5. Work flow concept chart from Ag-Patch (antigenic patch) identification to in vivo trial for the proposed MPVs against SARS-CoV-2.

Supplementary Table S1: High Percentile Ranking CTL epitopes-HLA allele pairs screened from entire proteome of SARS-CoV-2 by the “MHC-I Processing Predictions” tool of IEDB. These epitopes were further utilized to identify the potentially immunogenic multiple epitope cluster based CTL Ag-Patches from the entire proteome of the SRAS-CoV-2. The epitopes shown in **RED** are the epitope which form Overlapping epitope clusters. The screened epitopes are in consensus with the previous studies [Srivastava et al. 2020a; Srivastava et al., 2020b and Grifoni et al., 2020a].

S.No.	ORF	Allele	Peptide Length	Peptide	Immunogenicity	Conservancy	Toxicity	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]	
1	E Protein	A*02:01	9	FLAFVVFLL	0.30188	100.00% (35/35)	Non-Toxin	1.45	0.41	-0.81	1.86	1.05	6.5	
2	E Protein	A*02:01	9	FLAFVVFLL	0.30188	100.00% (35/35)	Non-Toxin	1.45	0.41	-0.81	1.86	1.05	6.5	
3	E Protein	A*02:03	9	FLAFVVFLL	0.30188	100.00% (35/35)	Non-Toxin	1.45	0.41	-1.17	1.86	0.69	14.9	
4	E Protein	A*02:06	9	FLAFVVFLL	0.30188	100.00% (35/35)	Non-Toxin	1.45	0.41	-1.22	1.86	0.64	16.6	
5	E Protein	A*02:01	9	FLLVTLAIL	0.17608	100.00% (35/35)	Non-Toxin	1.51	0.41	-1.34	1.92	0.59	21.7	
6	E Protein	A*02:06	9	FVVFLLVTL	0.16748	100.00% (35/35)	Non-Toxin	2	0.54	-2.05	2.54	0.48	113.2	
7	E Protein	B*15:01	10	ILTALRLCAY	0.05849	97.14% (34/35)	Non-Toxin	1.42	1.34	-1.77	2.76	0.99	58.4	
8	E Protein	A*30:02	10	ILTALRLCAY	0.05849	97.14% (34/35)	Non-Toxin	1.42	1.34	-2.24	2.76	0.52	172.9	
9	E Protein	B*15:01	9	LIVNSVLLF	-0.13119	100.00% (35/35)	Non-Toxin	1.15	1.2	-1.38	2.35	0.97	23.8	
10	E Protein	B*15:01	9	LLFLAFVVF	0.2341	100.00% (35/35)	Non-Toxin	1.53	1.18	-2.08	2.71	0.63	120.3	
11	E Protein	B*15:01	9	LTALRLCAY	0.01886	97.14% (34/35)	Non-Toxin	1.42	1.27	-1.69	2.69	1	49.5	
12	E Protein	B*15:01	9	LTALRLCAY	0.01886	97.14% (34/35)	Non-Toxin	1.42	1.27	-1.69	2.69	1	49.5	
13	E Protein	A*30:02	9	LTALRLCAY	0.01886	97.14% (34/35)	Non-Toxin	1.42	1.27	-2.03	2.69	0.67	106	
14	E Protein	A*01:01	9	LTALRLCAY	0.01886	97.14% (34/35)	Non-Toxin	1.42	1.27	-2.09	2.69	0.6	123.3	
15	E Protein	B*15:01	9	LVKPSFYVY	-0.11106	100.00% (35/35)	Non-Toxin	1.51	1.35	-1.42	2.86	1.44	26.3	
16	E Protein	A*30:02	9	LVKPSFYVY	-0.11106	100.00% (35/35)	Non-Toxin	1.51	1.35	-1.61	2.86	1.25	40.4	
17	E Protein	B*15:01	9	LVKPSFYVY	-0.11106	100.00% (35/35)	Non-Toxin	1.51	1.35	-1.42	2.86	1.44	26.3	
18	E Protein	A*30:02	9	LVKPSFYVY	-0.11106	100.00% (35/35)	Non-Toxin	1.51	1.35	-1.61	2.86	1.25	40.4	
19	E Protein	B*35:01	9	LVKPSFYVY	-0.11106	100.00% (35/35)	Non-Toxin	1.51	1.35	-1.96	2.86	0.9	90.4	
20	E Protein	A*31:01	9	RVKNLNSSR	-0.32968	100.00% (35/35)	Non-Toxin	0.86	0.83	-0.9	1.7	0.8	7.9	
21	E Protein	B*15:01	10	SLVKPSFYVY	-0.2443	100.00% (35/35)	Non-Toxin	1.51	1.36	-1.39	2.86	1.47	24.6	
22	E Protein	B*15:01	10	SLVKPSFYVY	-0.2443	100.00% (35/35)	Non-Toxin	1.51	1.36	-1.39	2.86	1.47	24.6	
23	E Protein	A*30:02	10	SLVKPSFYVY	-0.2443	100.00% (35/35)	Non-Toxin	1.51	1.36	-1.88	2.86	0.98	75.4	
24	E Protein	A*11:01	10	SLVKPSFYVY	-0.2443	100.00% (35/35)	Non-Toxin	1.51	1.36	-2.28	2.86	0.58	192.1	
25	E Protein	A*30:02	9	VSLVKPSFY	-0.25372	100.00% (35/35)	Non-Toxin	1.19	1.38	-1.74	2.58	0.84	54.9	
S.No.	ORF	Allele	Peptide Length	Peptide	Immunogenicity	Conservancy	Toxicity	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]	
26	M Protein	A*30:02	9	ATSRTLSYY	-0.11604	100.00% (41/41)	Non-Toxin	1.26	1.34	-1.12	2.6	1.48	13.3	
27	M Protein	A*11:01	9	ATSRTLSYY	-0.11604	100.00% (41/41)	Non-Toxin	1.26	1.34	-1.52	2.6	1.08	32.9	
28	M Protein	B*08:01	10	FARTRSMWSF	-0.12986	100.00% (41/41)	Non-Toxin	1.41	1.12	-1.34	2.53	1.19	22.1	
29	M Protein	A*02:01	10	FLWLLWPVTL	0.31272	100.00% (41/41)	Non-Toxin	1.85	0.46	-1.16	2.31	1.16	14.3	
30	M Protein	A*68:01	9	LSYFIASFR	0.21181	100.00% (41/41)	Non-Toxin	0.84	0.72	-0.46	1.56	1.1	2.9	
31	M Protein	A*23:01	11	LSYFIASFRLF	0.2706	100.00% (41/41)	Non-Toxin	1.25	1.18	-1.36	2.43	1.07	23	
32	M Protein	A*23:01	10	MWLSYFIASF	0.00197	100.00% (41/41)	Non-Toxin	1.38	1.26	-0.91	2.63	1.73	8.1	
33	M Protein	A*24:02	10	MWLSYFIASF	0.00197	100.00% (41/41)	Non-Toxin	1.38	1.26	-1.27	2.63	1.36	18.7	
34	M Protein	B*15:01	10	MWLSYFIASF	0.00197	100.00% (41/41)	Non-Toxin	1.38	1.26	-1.33	2.63	1.3	21.6	
35	M Protein	A*23:01	10	RFLYIIKLIF	0.11728	100.00% (41/41)	Non-Toxin	1.25	1.35	-1.33	2.6	1.27	21.3	
36	M Protein	A*30:01	8	RTRSMWSF	-0.25178	100.00% (41/41)	Non-Toxin	1.41	1.28	-1.51	2.69	1.18	32.7	
37	M Protein	A*30:02	9	SGFAAYSRY	0.00261	100.00% (41/41)	Non-Toxin	1.53	1.17	-1.4	2.69	1.3	25	
38	M Protein	B*15:01	10	SQRVAGDSGF	0.0305	100.00% (41/41)	Non-Toxin	1.33	1.24	-1.35	2.58	1.23	22.4	
39	M Protein	A*23:01	9	SYFIASFRL	0.18333	100.00% (41/41)	Non-Toxin	1.45	0.62	-0.99	2.08	1.09	9.8	
40	M Protein	A*23:01	10	SYFIASFRLF	0.19632	100.00% (41/41)	Non-Toxin	1.25	1.31	-0.56	2.56	2	3.6	
41	M Protein	A*24:02	10	SYFIASFRLF	0.19632	100.00% (41/41)	Non-Toxin	1.25	1.31	-0.76	2.56	1.8	5.7	
42	M Protein	B*35:01	9	VATSRTLSY	-0.17295	100.00% (41/41)	Non-Toxin	1.34	1.31	-1.38	2.65	1.27	23.9	

43	M Protein	B*35:01	9	YANRNRFLY	0.18472	100.00% (41/41)	Non-Toxin	1.18	1.31	-0.83	2.49	1.66	6.8	
44	M Protein	A*30:02	9	YANRNRFLY	0.18472	100.00% (41/41)	Non-Toxin	1.18	1.31	-1.46	2.49	1.03	28.9	
45	M Protein	A*23:01	9	YFIASFRLF	0.06887	100.00% (41/41)	Non-Toxin	1.25	1.22	-0.73	2.47	1.74	5.4	
46	M Protein	A*24:02	9	YFIASFRLF	0.06887	100.00% (41/41)	Non-Toxin	1.25	1.22	-1	2.47	1.48	9.9	
47	M Protein	A*30:02	9	YSRYRIGNY	0.21358	100.00% (41/41)	Non-Toxin	1.36	1.37	-1.61	2.73	1.12	40.6	
S.No.	ORF	Allele	Peptide Length	Peptide	Immunogenicity	Conservancy	Toxicity	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]	
48	N Protein	B*15:01	10	AQFAPSASAF	-0.17446	100.00% (40/40)	Non-Toxin	1.23	1.25	-0.7	2.48	1.78	5	
49	N Protein	B*15:01	10	AQFAPSASAF	-0.17446	100.00% (40/40)	Non-Toxin	1.23	1.25	-0.7	2.48	1.78	5	
50	N Protein	B*15:01	11	AQFAPSASAFF	-0.11074	100.00% (40/40)	Non-Toxin	1.3	1.25	-1.46	2.55	1.08	29	
51	N Protein	B*15:01	11	AQFAPSASAFF	-0.11074	100.00% (40/40)	Non-Toxin	1.3	1.25	-1.46	2.55	1.08	29	
52	N Protein	B*35:01	9	FAPSASAFF	-0.18628	100.00% (40/40)	Non-Toxin	1.3	1.05	-1.54	2.35	0.81	35	
53	N Protein	A*30:02	9	GTTLPKGFY	-0.11536	100.00% (40/40)	Non-Toxin	1.48	1.15	-1.88	2.62	0.74	76.3	
54	N Protein	B*15:01	11	IAQFAPSASAF	-0.13353	100.00% (40/40)	Non-Toxin	1.23	1.1	-1.84	2.33	0.49	69.1	
55	N Protein	A*31:01	9	IGYYRRATR	0.1499	100.00% (40/40)	Non-Toxin	1.27	0.6	-1.16	1.87	0.71	14.3	
56	N Protein	A*32:01	9	KAYNVTQAF	-0.00587	100.00% (40/40)	Non-Toxin	1.21	1.25	-0.98	2.46	1.48	9.5	
57	N Protein	B*15:01	9	KAYNVTQAF	-0.00587	100.00% (40/40)	Non-Toxin	1.21	1.25	-1.34	2.46	1.12	21.9	
58	N Protein	A*32:01	9	KAYNVTQAF	-0.00587	100.00% (40/40)	Non-Toxin	1.21	1.25	-0.98	2.46	1.48	9.5	
59	N Protein	B*15:01	9	KAYNVTQAF	-0.00587	100.00% (40/40)	Non-Toxin	1.21	1.25	-1.34	2.46	1.12	21.9	
60	N Protein	B*58:01	9	KAYNVTQAF	-0.00587	100.00% (40/40)	Non-Toxin	1.21	1.25	-1.48	2.46	0.98	30.1	
61	N Protein	B*35:01	9	KAYNVTQAF	-0.00587	100.00% (40/40)	Non-Toxin	1.21	1.25	-1.9	2.46	0.56	79.8	
62	N Protein	A*30:02	10	KDLSPRWYFY	0.14332	100.00% (40/40)	Non-Toxin	1.58	1.21	-1.68	2.79	1.1	48.3	
63	N Protein	A*30:02	10	KDLSPRWYFY	0.14332	100.00% (40/40)	Non-Toxin	1.58	1.21	-1.68	2.79	1.1	48.3	
64	N Protein	A*03:01	10	KDLSPRWYFY	0.14332	100.00% (40/40)	Non-Toxin	1.58	1.21	-1.99	2.79	0.8	97.5	
65	N Protein	A*30:02	10	KMKDLSPRWY	-0.05692	100.00% (40/40)	Non-Toxin	1.31	1.35	-1.56	2.66	1.1	36.2	
66	N Protein	A*30:02	10	KMKDLSPRWY	-0.05692	100.00% (40/40)	Non-Toxin	1.31	1.35	-1.56	2.66	1.1	36.2	
67	N Protein	B*15:01	10	KMKDLSPRWY	-0.05692	100.00% (40/40)	Non-Toxin	1.31	1.35	-2.04	2.66	0.62	110.6	
68	N Protein	A*02:03	9	LLLDRLNQL	-0.01446	100.00% (40/40)	Non-Toxin	1.48	0.46	-0.89	1.94	1.05	7.7	
69	N Protein	A*02:03	9	LLLDRLNQL	-0.01446	100.00% (40/40)	Non-Toxin	1.48	0.46	-0.89	1.94	1.05	7.7	
70	N Protein	A*02:01	9	LLLDRLNQL	-0.01446	100.00% (40/40)	Non-Toxin	1.48	0.46	-0.99	1.94	0.95	9.8	
71	N Protein	A*02:06	9	LLLDRLNQL	-0.01446	100.00% (40/40)	Non-Toxin	1.48	0.46	-1.11	1.94	0.83	12.8	
72	N Protein	B*15:01	9	LLNKHIDAY	-0.02074	100.00% (40/40)	Non-Toxin	1.31	1.24	-1.58	2.55	0.98	37.6	
73	N Protein	B*35:01	9	LPAADLDDF	0.09491	100.00% (40/40)	Non-Toxin	0.94	1	-1.43	1.94	0.5	27.2	
74	N Protein	B*35:01	9	LPNNTASWF	0.05582	100.00% (40/40)	Non-Toxin	1.21	0.92	-1.25	2.13	0.88	17.7	
75	N Protein	B*53:01	9	LPNNTASWF	0.05582	100.00% (40/40)	Non-Toxin	1.21	0.92	-1.51	2.13	0.62	32.7	
76	N Protein	A*30:02	9	LSPRWYFYY	0.35734	100.00% (40/40)	Non-Toxin	1.07	1.22	-1.71	2.3	0.59	50.8	
77	N Protein	B*44:02	9	MEVTPSGTW	-0.06279	100.00% (40/40)	Non-Toxin	1.44	0.37	-1.26	1.8	0.54	18.2	
78	N Protein	A*30:02	11	MKDLSPRWYFY	0.14833	100.00% (40/40)	Non-Toxin	1.58	1.28	-2.31	2.86	0.55	202.5	
79	N Protein	B*15:01	10	NQRNAPRITF	0.22131	100.00% (40/40)	Non-Toxin	1.49	1.15	-2.04	2.64	0.6	110.4	
80	N Protein	A*01:01	11	NSSPDDQIGYY	0.01726	100.00% (40/40)	Non-Toxin	1.24	1.31	-2.01	2.54	0.53	102.4	
81	N Protein	A*68:02	9	NTASWFTAL	0.22775	100.00% (40/40)	Non-Toxin	1.42	0.49	-0.79	1.91	1.12	6.2	
82	N Protein	A*68:02	9	NTASWFTAL	0.22775	100.00% (40/40)	Non-Toxin	1.42	0.49	-0.79	1.91	1.12	6.2	
83	N Protein	A*23:01	10	QFAPSASAFF	-0.17577	100.00% (40/40)	Non-Toxin	1.3	1.25	-1.97	2.55	0.58	92.6	
84	N Protein	B*15:01	10	RQKRTATKAY	-0.06462	100.00% (40/40)	Non-Toxin	1.51	1.34	-1.55	2.85	1.3	35.5	
85	N Protein	B*15:01	10	RQKRTATKAY	-0.06462	100.00% (40/40)	Non-Toxin	1.51	1.34	-1.55	2.85	1.3	35.5	
86	N Protein	A*30:02	10	RQKRTATKAY	-0.06462	100.00% (40/40)	Non-Toxin	1.51	1.34	-2.03	2.85	0.82	107.5	
87	N Protein	B*35:01	9	SPDDQIGYY	0.06844	100.00% (40/40)	Non-Toxin	1.24	1.11	-1.8	2.35	0.55	63.2	
88	N Protein	B*07:02	9	SPRWYFYYL	0.34101	100.00% (40/40)	Non-Toxin	1.61	0.35	-1.2	1.96	0.76	15.7	
89	N Protein	B*08:01	9	SPRWYFYYL	0.34101	100.00% (40/40)	Non-Toxin	1.61	0.35	-1.41	1.96	0.55	25.5	
90	N Protein	A*01:01	10	SSPDDQIGYY	0.07924	100.00% (40/40)	Non-Toxin	1.24	1.36	-1.16	2.6	1.45	14.3	
91	N Protein	A*01:01	10	SSPDDQIGYY	0.07924	100.00% (40/40)	Non-Toxin	1.24	1.36	-1.16	2.6	1.45	14.3	
92	N Protein	B*35:01	9	TPSGTWLTY	0.24003	100.00% (40/40)	Non-Toxin	1.52	1.15	-0.84	2.67	1.83	6.9	

93	N Protein	B*35:01	9	TPSGTWLTY	0.24003	100.00% (40/40)	Non-Toxin	1.52	1.15	-0.84	2.67	1.83	6.9	
94	N Protein	B*53:01	9	TPSGTWLTY	0.24003	100.00% (40/40)	Non-Toxin	1.52	1.15	-2.07	2.67	0.6	117.2	
95	N Protein	B*35:01	10	VTPSGTWLTY	0.12256	100.00% (40/40)	Non-Toxin	1.52	1.21	-1.93	2.73	0.8	84.5	
96	N Protein	A*30:02	10	VTPSGTWLTY	0.12256	100.00% (40/40)	Non-Toxin	1.52	1.21	-2.06	2.73	0.67	115.4	

S.No.	ORF	Allele	Peptide Length	Peptide	Immunogenicity	Conservancy	Toxicity	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]	
97	ORF10	A*02:06	10	AQVDVVNFNL	0.20505	100.00% (28/28)	Non-Toxin	1.4	0.55	-1.35	1.95	0.6	22.6	
98	ORF10	B*35:01	8	FAFPFTIY	0.2897	100.00% (28/28)	Non-Toxin	1.47	1.32	-1.93	2.79	0.86	85.1	
99	ORF10	A*68:02	10	FAFPFTIYSL	0.20414	100.00% (28/28)	Non-Toxin	1.38	0.47	-1.39	1.85	0.46	24.5	
100	ORF10	A*68:01	10	FTIYSLLLCR	-0.18372	100.00% (28/28)	Non-Toxin	1.19	0.56	-1.06	1.75	0.69	11.4	
101	ORF10	A*23:01	8	GYINVFAF	0.22011	100.00% (28/28)	Non-Toxin	1.16	1.18	-1.84	2.35	0.51	68.7	
102	ORF10	A*23:01	10	GYINVFAFPF	0.32004	100.00% (28/28)	Non-Toxin	1.05	1.18	-0.82	2.23	1.41	6.6	
103	ORF10	A*24:02	10	GYINVFAFPF	0.32004	100.00% (28/28)	Non-Toxin	1.05	1.18	-1.17	2.23	1.06	14.9	
104	ORF10	A*23:01	10	GYINVFAFPF	0.32004	100.00% (28/28)	Non-Toxin	1.05	1.18	-0.82	2.23	1.41	6.6	
105	ORF10	A*24:02	10	GYINVFAFPF	0.32004	100.00% (28/28)	Non-Toxin	1.05	1.18	-1.17	2.23	1.06	14.9	
106	ORF10	B*15:01	10	LLCRMNSRNY	-0.25855	100.00% (28/28)	Non-Toxin	1.23	1.31	-1.93	2.53	0.6	84.8	
107	ORF10	B*35:01	9	MGYINVFAF	0.28694	100.00% (28/28)	Non-Toxin	1.16	1.14	-1.56	2.3	0.74	36.6	
108	ORF10	A*68:02	9	NVFAFPFTI	0.30241	100.00% (28/28)	Non-Toxin	1.25	0.36	-0.71	1.61	0.9	5.1	
109	ORF10	A*32:01	9	NVFAFPFTI	0.30241	100.00% (28/28)	Non-Toxin	1.25	0.36	-1	1.61	0.61	10.1	
110	ORF10	A*02:06	9	NVFAFPFTI	0.30241	100.00% (28/28)	Non-Toxin	1.25	0.36	-1	1.61	0.61	10.1	
111	ORF10	A*02:01	9	NVFAFPFTI	0.30241	100.00% (28/28)	Non-Toxin	1.25	0.36	-1.11	1.61	0.5	13	
112	ORF10	A*68:01	10	NVFAFPFTIY	0.40129	100.00% (28/28)	Non-Toxin	1.47	1.4	-1.84	2.86	1.02	69.7	
113	ORF10	A*68:01	10	NVFAFPFTIY	0.40129	100.00% (28/28)	Non-Toxin	1.47	1.4	-1.84	2.86	1.02	69.7	
114	ORF10	A*11:01	10	NVFAFPFTIY	0.40129	100.00% (28/28)	Non-Toxin	1.47	1.4	-2.2	2.86	0.67	157.8	
115	ORF10	A*30:02	10	NVFAFPFTIY	0.40129	100.00% (28/28)	Non-Toxin	1.47	1.4	-2.29	2.86	0.57	196.8	
116	ORF10	B*15:01	10	NVFAFPFTIY	0.40129	100.00% (28/28)	Non-Toxin	1.47	1.4	-2.3	2.86	0.56	200.7	
117	ORF10	A*68:01	9	TIYSLLLCR	-0.22977	100.00% (28/28)	Non-Toxin	1.19	0.73	-1.18	1.91	0.74	15.1	
118	ORF10	A*30:02	9	VFAFPFTIY	0.34042	100.00% (28/28)	Non-Toxin	1.47	1.44	-2.21	2.9	0.69	161.8	
119	ORF10	B*15:01	10	YIAQVDVVNF	0.02786	100.00% (28/28)	Non-Toxin	1.52	1.22	-1.76	2.74	0.98	57.9	
120	ORF10	B*35:01	9	YINVFAFPF	0.28259	100.00% (28/28)	Non-Toxin	1.05	1.09	-1.37	2.14	0.77	23.6	

S.No.	ORF	Allele	Peptide Length	Peptide	Immunogenicity	Conservancy	Toxicity	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]	NSP
121	ORF1ab	A*01:01	10	ACTDDNALAY	0.10055	100.00% (36/36)	Non-Toxin	1.49	1.33	-0.82	2.82	2	6.6	nsp9
122	ORF1ab	A*01:01	11	ACTDDNALAYY	0.10874	100.00% (36/36)	Non-Toxin	1.35	1.33	-1.12	2.68	1.56	13.1	nsp9
123	ORF1ab	B*15:01	10	ARLYYDSMSY	-0.38991	97.22% (35/36)	Non-Toxin	1.45	1.47	-1.39	2.92	1.53	24.5	nsp12
124	ORF1ab	B*15:01	10	AVMYMGTLSY	-0.2682	100.00% (36/36)	Non-Toxin	1.3	1.35	-0.95	2.64	1.7	8.9	nsp3
125	ORF1ab	A*23:01	9	AYILFTRFF	0.29466	100.00% (36/36)	Non-Toxin	1.5	1.33	-1.28	2.83	1.55	19	nsp3
126	ORF1ab	A*23:01	10	AYVNTFSSTF	-0.11398	100.00% (36/36)	Non-Toxin	1.4	1.25	-1.13	2.65	1.52	13.5	nsp3
127	ORF1ab	A*01:01	9	CTDDNALAY	0.07355	100.00% (36/36)	Non-Toxin	1.49	1.23	-0.45	2.72	2.27	2.8	nsp9
128	ORF1ab	A*01:01	10	CTDDNALAYY	0.08174	100.00% (36/36)	Non-Toxin	1.35	1.23	-0.57	2.58	2.01	3.7	nsp9
129	ORF1ab	A*01:01	9	DTDFVNEFY	0.31201	97.22% (35/36)	Non-Toxin	1.55	1.07	-0.91	2.62	1.71	8.1	nsp12
130	ORF1ab	A*26:01	9	ETISLAGSY	-0.1653	100.00% (36/36)	Non-Toxin	1.4	1.21	-0.53	2.61	2.08	3.4	nsp3
131	ORF1ab	B*35:01	9	FAIGLALYY	0.09181	97.22% (35/36)	Non-Toxin	1.2	1.27	-0.71	2.47	1.77	5.1	nsp13
132	ORF1ab	B*35:01	9	FAVDAAKAY	-0.04849	100.00% (36/36)	Non-Toxin	1.73	1.35	-0.46	3.08	2.62	2.9	nsp10
133	ORF1ab	A*02:03	9	FLNRFTTTL	0.25596	100.00% (36/36)	Non-Toxin	1.81	0.32	-0.46	2.12	1.66	2.9	nsp5
134	ORF1ab	B*35:01	10	FPLCANGQVF	-0.06779	97.22% (35/36)	Non-Toxin	1.55	0.96	-1	2.51	1.51	10	nsp13
135	ORF1ab	B*35:01	9	FVSLAIDAY	0.1401	97.22% (35/36)	Non-Toxin	1.26	1.24	-0.96	2.5	1.53	9.2	nsp12
136	ORF1ab	A*01:01	9	GTDLEGNFY	0.18838	100.00% (36/36)	Non-Toxin	1.42	1.17	-0.99	2.59	1.61	9.7	nsp5
137	ORF1ab	B*15:01	9	ILMTARTVY	0.12576	100.00% (36/36)	Non-Toxin	1.65	1.34	-1.1	2.99	1.89	12.5	nsp6
138	ORF1ab	B*35:01	10	IPMDSTVKNY	-0.3049	97.22% (35/36)	Non-Toxin	1.53	1.16	-1.18	2.7	1.52	15.1	nsp15
139	ORF1ab	A*01:01	9	ISDYDYYRY	0.04872	97.22% (35/36)	Non-Toxin	1.49	1.29	-1.06	2.77	1.71	11.5	nsp12
140	ORF1ab	B*58:01	9	KAYKIEELF	0.08367	97.22% (35/36)	Non-Toxin	1.24	1.19	-0.9	2.43	1.53	7.9	nsp14
141	ORF1ab	A*32:01	9	KLFDRYFKY	0.08004	97.22% (35/36)	Non-Toxin	1.51	1.39	-1.17	2.9	1.74	14.7	nsp12

142	ORF1ab	A*30:02	9	KLFDRYFKY	0.08004	97.22% (35/36)	Non-Toxin	1.51	1.39	-1.27	2.9	1.64	18.5	nsp12
143	ORF1ab	A*03:01	9	KLFDRYFKY	0.08004	97.22% (35/36)	Non-Toxin	1.51	1.39	-1.31	2.9	1.6	20.2	nsp12
144	ORF1ab	B*15:01	10	LILMTARTVY	0.0012	100.00% (36/36)	Non-Toxin	1.65	1.36	-1.23	3.01	1.78	16.9	nsp6
145	ORF1ab	B*15:01	9	LMNVLTLVY	0.07994	100.00% (36/36)	Non-Toxin	1.51	1.26	-1.16	2.77	1.61	14.5	nsp6
146	ORF1ab	B*15:01	10	LMSNLGMPSY	-0.30933	100.00% (36/36)	Non-Toxin	1.55	1.34	-1	2.9	1.89	10.1	nsp3
147	ORF1ab	B*35:01	9	LPGVYSVIY	0.00581	100.00% (36/36)	Non-Toxin	1.39	1.02	-0.81	2.42	1.6	6.5	nsp4
148	ORF1ab	B*35:01	9	LPSLATVAY	0.06748	100.00% (36/36)	Non-Toxin	1.47	1.15	-0.34	2.62	2.28	2.2	nsp6
149	ORF1ab	B*35:01	9	LVAEWFLAY	0.45285	100.00% (36/36)	Non-Toxin	1.21	1.33	-1.01	2.54	1.52	10.3	nsp3
150	ORF1ab	B*35:01	10	LVPFWITIAY	0.63122	100.00% (36/36)	Non-Toxin	1.42	1.26	-0.91	2.68	1.77	8.1	nsp4
151	ORF1ab	B*15:01	9	MMSAPPAQY	-0.07023	100.00% (36/36)	Non-Toxin	1.27	1.36	-1.11	2.63	1.52	12.9	nsp3
152	ORF1ab	B*35:01	9	MSNLGMPSY	-0.25158	100.00% (36/36)	Non-Toxin	1.55	1.29	-1.28	2.84	1.56	18.9	nsp3
153	ORF1ab	B*15:01	10	MVMFTPLVPF	0.10572	100.00% (36/36)	Non-Toxin	1.2	1.18	-0.74	2.38	1.64	5.5	nsp4
154	ORF1ab	A*23:01	11	MYMGTLSYEQF	-0.14366	100.00% (36/36)	Non-Toxin	1.36	1.28	-0.96	2.65	1.68	9.2	nsp3
155	ORF1ab	B*44:03	10	QEYADVFHLY	0.23099	97.22% (35/36)	Non-Toxin	1.22	1.36	-1.01	2.57	1.57	10.2	nsp12
156	ORF1ab	B*35:01	9	QVVDMSMTY	-0.41653	100.00% (36/36)	Non-Toxin	1.49	1.37	-1.03	2.87	1.84	10.6	nsp3
157	ORF1ab	B*15:01	9	RLYYDSMSY	-0.38391	97.22% (35/36)	Non-Toxin	1.45	1.53	-1	2.98	1.97	10.1	nsp12
158	ORF1ab	A*03:01	9	RLYYDSMSY	-0.38391	97.22% (35/36)	Non-Toxin	1.45	1.53	-1.02	2.98	1.96	10.4	nsp12
159	ORF1ab	A*30:02	9	RLYYDSMSY	-0.38391	97.22% (35/36)	Non-Toxin	1.45	1.53	-1.14	2.98	1.84	13.9	nsp12
160	ORF1ab	A*32:01	9	RLYYDSMSY	-0.38391	97.22% (35/36)	Non-Toxin	1.45	1.53	-1.16	2.98	1.82	14.4	nsp12
161	ORF1ab	A*32:01	9	RMYIFFASF	0.29328	100.00% (36/36)	Non-Toxin	1.32	1.36	-0.82	2.68	1.86	6.6	nsp3
162	ORF1ab	A*30:02	10	RMYIFFASFY	0.32633	100.00% (36/36)	Non-Toxin	1.28	1.53	-0.97	2.81	1.83	9.4	nsp3
163	ORF1ab	A*03:01	10	RMYIFFASFY	0.32633	100.00% (36/36)	Non-Toxin	1.28	1.53	-1	2.81	1.8	10.1	nsp3
164	ORF1ab	B*15:01	10	RTIAFGGCVF	0.24009	100.00% (36/36)	Non-Toxin	1.51	1.21	-1.17	2.73	1.56	14.7	nsp2
165	ORF1ab	A*30:02	10	RYFKYWDQTY	-0.0211	97.22% (35/36)	Non-Toxin	1.49	1.48	-1.42	2.97	1.54	26.6	nsp12
166	ORF1ab	A*30:02	10	RYFRLTLGVY	0.15936	100.00% (36/36)	Non-Toxin	1.41	1.6	-1.34	3.01	1.66	22.1	nsp6
167	ORF1ab	B*44:03	9	SEFSSLPSY	-0.40603	100.00% (36/36)	Non-Toxin	1.49	1.35	-1.03	2.84	1.82	10.6	nsp8
168	ORF1ab	A*23:01	10	SYFVVKRHTF	0.00844	97.22% (35/36)	Non-Toxin	1.5	1.23	-1.02	2.73	1.71	10.4	nsp12
169	ORF1ab	A*01:01	11	TACTDDNALAY	0.10879	100.00% (36/36)	Non-Toxin	1.49	1.27	-1.19	2.75	1.56	15.6	nsp9
170	ORF1ab	A*02:01	9	TMADLVYAL	0.08282	97.22% (35/36)	Non-Toxin	1.73	0.44	-0.56	2.17	1.62	3.6	nsp12
171	ORF1ab	A*02:03	9	TMADLVYAL	0.08282	97.22% (35/36)	Non-Toxin	1.73	0.44	-0.64	2.17	1.53	4.4	nsp12
172	ORF1ab	A*02:06	9	TMADLVYAL	0.08282	97.22% (35/36)	Non-Toxin	1.73	0.44	-0.67	2.17	1.5	4.7	nsp12
173	ORF1ab	B*15:01	10	TQVVDMSMTY	-0.37571	100.00% (36/36)	Non-Toxin	1.49	1.32	-1.25	2.81	1.56	17.6	nsp3
174	ORF1ab	A*01:01	10	TTDPSFLGRY	-0.00266	100.00% (36/36)	Non-Toxin	1.29	1.16	-0.83	2.46	1.63	6.7	nsp3
175	ORF1ab	B*35:01	9	TVAYFNMVY	-0.00719	100.00% (36/36)	Non-Toxin	1.52	1.39	-1.23	2.92	1.69	16.9	nsp6
176	ORF1ab	A*01:01	10	VDTDFVNEFY	0.33593	97.22% (35/36)	Non-Toxin	1.55	1.09	-0.9	2.64	1.74	7.9	nsp12
177	ORF1ab	B*15:01	10	VMFLARGIVF	0.28368	100.00% (36/36)	Non-Toxin	1.57	1.23	-1.09	2.8	1.71	12.4	nsp6
178	ORF1ab	B*15:01	9	VMFTPLVPF	0.08418	100.00% (36/36)	Non-Toxin	1.2	1.24	-0.92	2.44	1.52	8.4	nsp4
179	ORF1ab	B*15:01	9	VMYMGTLSY	-0.21438	100.00% (36/36)	Non-Toxin	1.3	1.5	-0.8	2.79	1.99	6.3	nsp3
180	ORF1ab	A*03:01	9	VMYMGTLSY	-0.21438	100.00% (36/36)	Non-Toxin	1.3	1.5	-0.98	2.79	1.82	9.5	nsp3
181	ORF1ab	A*30:02	9	VMYMGTLSY	-0.21438	100.00% (36/36)	Non-Toxin	1.3	1.5	-1.09	2.79	1.7	12.4	nsp3
182	ORF1ab	B*35:01	9	VPFWITIAY	0.56221	100.00% (36/36)	Non-Toxin	1.42	1.23	-0.51	2.65	2.14	3.2	nsp4
183	ORF1ab	B*35:01	9	VPWDTIANY	0.28654	100.00% (36/36)	Non-Toxin	1.37	1.26	-1.06	2.63	1.57	11.4	nsp3
184	ORF1ab	B*15:01	9	VVYRGTTTY	0.17586	97.22% (35/36)	Non-Toxin	1.54	1.51	-1.41	3.05	1.64	25.5	nsp13
185	ORF1ab	A*30:02	9	VVYRGTTTY	0.17586	97.22% (35/36)	Non-Toxin	1.54	1.51	-1.43	3.05	1.62	27	nsp13
186	ORF1ab	A*23:01	9	WSMATYYLF	0.00709	97.22% (35/36)	Non-Toxin	1.17	1.06	-0.73	2.23	1.5	5.4	nsp3
187	ORF1ab	B*35:01	8	YAFEHIVY	0.33037	97.22% (35/36)	Non-Toxin	1.68	1.32	-1.49	3	1.51	30.9	nsp15
188	ORF1ab	B*08:01	8	YLKRRVVF	0.10618	100.00% (36/36)	Non-Toxin	1.62	1.16	-1.2	2.78	1.58	15.7	nsp4
189	ORF1ab	B*35:01	9	YPNASFDNF	0.00131	100.00% (36/36)	Non-Toxin	1.27	0.86	-0.56	2.12	1.56	3.6	nsp3
190	ORF1ab	A*02:01	10	YTMADLVYAL	0.05177	97.22% (35/36)	Non-Toxin	1.73	0.47	-0.58	2.2	1.62	3.8	nsp12
191	ORF1ab	A*02:06	10	YTMADLVYAL	0.05177	97.22% (35/36)	Non-Toxin	1.73	0.47	-0.63	2.2	1.57	4.3	nsp12
192	ORF1ab	A*02:03	10	YTMADLVYAL	0.05177	97.22% (35/36)	Non-Toxin	1.73	0.47	-0.67	2.2	1.53	4.7	nsp12

193	ORF1ab	B*35:01	9	YVMHANYIF	0.0822	97.22% (35/36)	Non-Toxin	1.37	1.17	-1.03	2.53	1.5	10.8	nsp16
194	ORF1ab	B*35:01	9	YVNTFSSTF	-0.12171	100.00% (36/36)	Non-Toxin	1.4	1.18	-1.01	2.58	1.57	10.2	nsp3
195	ORF1ab	B*15:01	9	YVNTFSSTF	-0.12171	100.00% (36/36)	Non-Toxin	1.4	1.18	-1.07	2.58	1.5	11.8	nsp3
196	ORF1ab	A*23:01	10	YYFMRFRRAF	0.14096	100.00% (36/36)	Non-Toxin	1.34	1.32	-0.95	2.66	1.7	9	nsp4
S.No.	ORF	Allele	Peptide Length	Peptide	Immunogenicity	Conservancy	Toxicity	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]	
197	ORF3a	B*44:03	11	AGLEAPFLYLY	0.21841	100.00% (28/28)	Non-Toxin	1.51	1.29	-1.63	2.8	1.17	42.9	
198	ORF3a	B*44:03	11	AGLEAPFLYLY	0.21841	100.00% (28/28)	Non-Toxin	1.51	1.29	-1.63	2.8	1.17	42.9	
199	ORF3a	B*44:02	11	AGLEAPFLYLY	0.21841	100.00% (28/28)	Non-Toxin	1.51	1.29	-1.94	2.8	0.86	86.3	
200	ORF3a	A*02:03	9	ALSKGVHFV	-0.10314	100.00% (28/28)	Non-Toxin	1.07	0.23	-0.57	1.3	0.73	3.7	
201	ORF3a	A*02:03	9	ALVYFLQSI	-0.08118	100.00% (28/28)	Non-Toxin	1.25	0.31	-0.83	1.56	0.73	6.8	
202	ORF3a	A*26:01	10	DTGVEHVTFF	0.32156	100.00% (28/28)	Non-Toxin	1.24	0.89	-1.64	2.13	0.49	43.5	
203	ORF3a	B*15:01	9	FLYLYALVY	0.03563	100.00% (28/28)	Non-Toxin	1.58	1.26	-2.26	2.83	0.58	181.1	
204	ORF3a	A*23:01	10	FLYLYALVYF	0.04438	100.00% (28/28)	Non-Toxin	1.18	1.09	-1.79	2.27	0.48	61.1	
205	ORF3a	B*44:03	10	GLEAPFLYLY	0.15503	100.00% (28/28)	Non-Toxin	1.51	1.2	-1.26	2.71	1.46	18.1	
206	ORF3a	B*44:02	10	GLEAPFLYLY	0.15503	100.00% (28/28)	Non-Toxin	1.51	1.2	-1.61	2.71	1.1	40.7	
207	ORF3a	B*44:03	10	GLEAPFLYLY	0.15503	100.00% (28/28)	Non-Toxin	1.51	1.2	-1.26	2.71	1.46	18.1	
208	ORF3a	B*44:02	10	GLEAPFLYLY	0.15503	100.00% (28/28)	Non-Toxin	1.51	1.2	-1.61	2.71	1.1	40.7	
209	ORF3a	A*23:01	10	HFVCNLLLLF	-0.08423	100.00% (28/28)	Non-Toxin	1.34	1.19	-1.75	2.52	0.77	56.3	
210	ORF3a	B*35:01	9	IPIQASLPF	-0.20683	100.00% (28/28)	Non-Toxin	0.98	1.01	-0.43	1.99	1.56	2.7	
211	ORF3a	B*35:01	9	IPIQASLPF	-0.20683	100.00% (28/28)	Non-Toxin	0.98	1.01	-0.43	1.99	1.56	2.7	
212	ORF3a	B*53:01	9	IPIQASLPF	-0.20683	100.00% (28/28)	Non-Toxin	0.98	1.01	-1.28	1.99	0.71	19.2	
213	ORF3a	B*07:02	9	IPIQASLPF	-0.20683	100.00% (28/28)	Non-Toxin	0.98	1.01	-1.39	1.99	0.6	24.7	
214	ORF3a	B*15:01	10	IVGVALLAVF	0.12654	100.00% (28/28)	Non-Toxin	1.3	1.12	-1.76	2.42	0.66	57.1	
215	ORF3a	B*44:03	9	LEAPFLYLY	0.0955	100.00% (28/28)	Non-Toxin	1.51	1.21	-1.3	2.72	1.41	20.1	
216	ORF3a	B*44:03	9	LEAPFLYLY	0.0955	100.00% (28/28)	Non-Toxin	1.51	1.21	-1.3	2.72	1.41	20.1	
217	ORF3a	B*44:02	9	LEAPFLYLY	0.0955	100.00% (28/28)	Non-Toxin	1.51	1.21	-1.73	2.72	0.99	53.3	
218	ORF3a	B*15:01	11	LLVAAGLEAPF	0.23386	100.00% (28/28)	Non-Toxin	0.86	1.16	-1.49	2.02	0.54	30.8	
219	ORF3a	B*15:01	10	LVAAGLEAPF	0.19506	100.00% (28/28)	Non-Toxin	0.86	1.19	-1.1	2.05	0.95	12.5	
220	ORF3a	A*23:01	10	LVYFLQSINF	-0.05419	100.00% (28/28)	Non-Toxin	1.3	1.31	-1.39	2.61	1.23	24.3	
221	ORF3a	A*23:01	10	LVYFLQSINF	-0.05419	100.00% (28/28)	Non-Toxin	1.3	1.31	-1.39	2.61	1.23	24.3	
222	ORF3a	A*24:02	10	LVYFLQSINF	-0.05419	100.00% (28/28)	Non-Toxin	1.3	1.31	-1.84	2.61	0.77	69	
223	ORF3a	B*15:01	10	LVYFLQSINF	-0.05419	100.00% (28/28)	Non-Toxin	1.3	1.31	-1.93	2.61	0.68	85.6	
224	ORF3a	A*23:01	9	LYLYALVYF	0.05302	100.00% (28/28)	Non-Toxin	1.18	1.18	-1.29	2.36	1.07	19.6	
225	ORF3a	A*23:01	9	LYLYALVYF	0.05302	100.00% (28/28)	Non-Toxin	1.18	1.18	-1.29	2.36	1.07	19.6	
226	ORF3a	A*24:02	9	LYLYALVYF	0.05302	100.00% (28/28)	Non-Toxin	1.18	1.18	-1.86	2.36	0.5	71.7	
227	ORF3a	A*02:01	10	LYLYALVYFL	0.12412	100.00% (28/28)	Non-Toxin	1.45	0.5	-1	1.94	0.94	10.1	
228	ORF3a	A*32:01	10	RIFTIGTVTL	0.33372	100.00% (28/28)	Non-Toxin	1.77	0.64	-1.59	2.41	0.82	38.6	
229	ORF3a	A*31:01	9	RLWLCWKCR	0.00325	100.00% (28/28)	Non-Toxin	1.27	0.85	-1.25	2.11	0.87	17.7	
230	ORF3a	B*15:01	10	TIPIQASLPF	-0.11595	100.00% (28/28)	Non-Toxin	0.98	1.21	-1.31	2.18	0.87	20.6	
231	ORF3a	B*35:01	10	TIPIQASLPF	-0.11595	100.00% (28/28)	Non-Toxin	0.98	1.21	-1.39	2.18	0.79	24.8	
232	ORF3a	A*02:03	9	TVYSHLLLV	-0.16245	100.00% (28/28)	Non-Toxin	1.17	0.29	-0.79	1.45	0.66	6.2	
233	ORF3a	A*02:06	9	TVYSHLLLV	-0.16245	100.00% (28/28)	Non-Toxin	1.17	0.29	-0.91	1.45	0.54	8.2	
234	ORF3a	B*35:01	9	VAAGLEAPF	0.15679	100.00% (28/28)	Non-Toxin	0.86	1.18	-1.2	2.04	0.84	15.8	
235	ORF3a	B*44:03	9	VEHVTFFIY	0.3766	100.00% (28/28)	Non-Toxin	1.28	1.24	-1.9	2.52	0.62	78.7	
236	ORF3a	A*30:02	10	VVNPVMEPIY	0.01859	100.00% (28/28)	Non-Toxin	1.25	1.3	-1.92	2.55	0.63	82.7	
237	ORF3a	A*23:01	9	VYFLQSINF	-0.13315	100.00% (28/28)	Non-Toxin	1.3	1.31	-0.96	2.61	1.65	9.2	
238	ORF3a	A*24:02	9	VYFLQSINF	-0.13315	100.00% (28/28)	Non-Toxin	1.3	1.31	-1.28	2.61	1.33	19.2	
239	ORF3a	A*23:01	9	VYFLQSINF	-0.13315	100.00% (28/28)	Non-Toxin	1.3	1.31	-0.96	2.61	1.65	9.2	
240	ORF3a	A*24:02	9	VYFLQSINF	-0.13315	100.00% (28/28)	Non-Toxin	1.3	1.31	-1.28	2.61	1.33	19.2	
241	ORF3a	A*33:01	10	YFLQSINFVR	-0.03483	100.00% (28/28)	Non-Toxin	1.09	0.74	-1.27	1.82	0.56	18.5	
242	ORF3a	A*02:01	9	YLYALVYFL	0.13151	100.00% (28/28)	Non-Toxin	1.45	0.52	-0.38	1.96	1.58	2.4	

243	ORF3a	A*02:06	9	YLYALVYFL	0.13151	100.00% (28/28)	Non-Toxin	1.45	0.52	-0.61	1.96	1.35	4.1	
244	ORF3a	A*02:03	9	YLYALVYFL	0.13151	100.00% (28/28)	Non-Toxin	1.45	0.52	-0.76	1.96	1.21	5.7	
245	ORF3a	A*02:01	9	YLYALVYFL	0.13151	100.00% (28/28)	Non-Toxin	1.45	0.52	-0.38	1.96	1.58	2.4	
246	ORF3a	A*02:06	9	YLYALVYFL	0.13151	100.00% (28/28)	Non-Toxin	1.45	0.52	-0.61	1.96	1.35	4.1	
247	ORF3a	A*02:03	9	YLYALVYFL	0.13151	100.00% (28/28)	Non-Toxin	1.45	0.52	-0.76	1.96	1.21	5.7	
248	ORF3a	A*24:02	9	YYQLYSTQL	-0.24301	100.00% (28/28)	Non-Toxin	1.66	0.4	-1.56	2.06	0.5	36.4	
249	ORF3a	A*23:01	9	YYQLYSTQL	-0.24301	100.00% (28/28)	Non-Toxin	1.66	0.4	-1.58	2.06	0.48	38.3	
S.No.	ORF	Allele	Peptide Length	Peptide	Immunogenicity	Conservancy	Toxicity	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]	
250	ORF6	A*02:01	10	FHLVDFQVTI	0.12202	100.00% (34/34)	Non-Toxin	1.57	0.22	-1.16	1.78	0.62	14.5	
251	ORF6	A*02:03	10	FHLVDFQVTI	0.12202	100.00% (34/34)	Non-Toxin	1.57	0.22	-1.17	1.78	0.61	14.9	
252	ORF6	A*02:06	9	FQVTIAEIL	0.38115	100.00% (34/34)	Non-Toxin	1.59	0.38	-1.58	1.97	0.39	38.1	
253	ORF6	A*02:03	9	HLVDFQVTI	0.0982	100.00% (34/34)	Non-Toxin	1.57	0.19	-1.22	1.76	0.53	16.7	
254	ORF6	A*02:01	9	HLVDFQVTI	0.0982	100.00% (34/34)	Non-Toxin	1.57	0.19	-1.25	1.76	0.51	17.7	
255	ORF6	A*30:02	9	KVSIWNLDY	0.29343	100.00% (34/34)		1.21	1.33	-1.46	2.54	1.08	28.8	
256	ORF6	A*30:02	9	KVSIWNLDY	0.29343	100.00% (34/34)	Non-Toxin	1.21	1.33	-1.46	2.54	1.08	28.8	
257	ORF6	A*30:02	10	LSKSLTENKY	-0.24668	100.00% (34/34)	Non-Toxin	1.52	1.35	-2.37	2.87	0.5	234.3	
258	ORF6	B*58:01	8	RTFKVSIW	-0.18221	100.00% (34/34)	Non-Toxin	1.42	0.54	-1.34	1.97	0.63	21.7	
259	ORF6	B*57:01	8	RTFKVSIW	-0.18221	100.00% (34/34)	Non-Toxin	1.42	0.54	-1.38	1.97	0.59	24	
S.No.	ORF	Allele	Peptide Length	Peptide	Immunogenicity	Conservancy	Toxicity	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]	
260	ORF7a	A*02:03	10	ALITLATCEL	0.1591	100.00% (28/28)	Non-Toxin	1.69	0.54	-1.66	2.23	0.57	45.8	
261	ORF7a	B*15:01	9	ALTCFSTQF	-0.1183	100.00% (28/28)	Non-Toxin	1.46	1.11	-1.91	2.57	0.66	82.2	
262	ORF7a	B*35:01	9	CPDGVKHVY	-0.07008	100.00% (28/28)		1.43	1.11	-1.34	2.54	1.2	22	
263	ORF7a	B*35:01	9	CPDGVKHVY	-0.07008	100.00% (28/28)	Non-Toxin	1.43	1.11	-1.34	2.54	1.2	22	
264	ORF7a	B*35:01	11	FACPDGVKHVY	-0.08544	100.00% (28/28)	Non-Toxin	1.43	1.32	-1.97	2.76	0.78	94.4	
265	ORF7a	B*15:01	10	FALTCFSTQF	-0.09369	100.00% (28/28)	Non-Toxin	1.46	1.13	-1.93	2.59	0.67	84.9	
266	ORF7a	B*35:01	10	FALTCFSTQF	-0.09369	100.00% (28/28)	Non-Toxin	1.46	1.13	-2.07	2.59	0.52	118.4	
267	ORF7a	A*68:01	10	FITLCFTLKR	-0.03588	100.00% (28/28)	Non-Toxin	1.16	0.66	-1.25	1.83	0.58	17.8	
268	ORF7a	B*15:01	9	FLIVAAIVF	0.29611	100.00% (28/28)	Non-Toxin	1.56	1.1	-2.17	2.67	0.5	146.3	
269	ORF7a	B*15:01	9	GTYEGNSPF	-0.01964	100.00% (28/28)	Non-Toxin	0.85	1.12	-1.34	1.96	0.63	21.7	
270	ORF7a	A*23:01	10	IFLIVAAIVF	0.38189	100.00% (28/28)	Non-Toxin	1.56	1.13	-1.98	2.69	0.71	96.6	
271	ORF7a	A*02:01	9	ILFLALITL	0.1895	100.00% (28/28)	Non-Toxin	1.92	0.49	-1.83	2.4	0.57	68.1	
272	ORF7a	A*30:02	9	ITLATCELY	0.10084	100.00% (28/28)	Non-Toxin	1.23	1.3	-1.73	2.53	0.8	53.3	
273	ORF7a	B*58:01	9	ITLATCELY	0.10084	100.00% (28/28)	Non-Toxin	1.23	1.3	-1.84	2.53	0.68	69.7	
274	ORF7a	A*23:01	11	KFALTCFSTQF	-0.08981	100.00% (28/28)	Non-Toxin	1.46	1.29	-2.18	2.75	0.57	150.6	
275	ORF7a	B*35:01	9	LATCELYHY	0.06119	100.00% (28/28)	Non-Toxin	1.32	1.28	-1.93	2.6	0.67	84.3	
276	ORF7a	B*15:01	11	LLKEPCSSGTY	-0.2981	100.00% (28/28)	Non-Toxin	1.39	1.3	-1.96	2.69	0.73	91.4	
277	ORF7a	B*58:01	10	LTCFSTQFAF	-0.01038	100.00% (28/28)	Non-Toxin	1.32	1.16	-1.54	2.48	0.94	34.8	
278	ORF7a	B*15:01	10	LTCFSTQFAF	-0.01038	100.00% (28/28)	Non-Toxin	1.32	1.16	-1.62	2.48	0.87	41.3	
279	ORF7a	A*30:01	9	RARSVSPKL	-0.40056	100.00% (28/28)	Non-Toxin	1.57	0.59	-1.23	2.15	0.93	16.9	
280	ORF7a	A*30:01	10	RARSVSPKLF	-0.46949	100.00% (28/28)	Non-Toxin	1.09	1.27	-1.89	2.37	0.48	77.5	
281	ORF7a	A*31:01	10	RSVSPKLFIR	-0.20775	100.00% (28/28)	Non-Toxin	0.98	0.87	-1.3	1.85	0.55	20	
S.No.	ORF	Allele	Peptide Length	Peptide	Immunogenicity	Conservancy	Toxicity	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]	
282	ORF7b	A*23:01	11	FYLCFLAFLLF	0.17781	100.00% (2/2)	Non-Toxin	1.24	1.12	-1.75	2.36	0.61	56.8	
283	ORF7b	B*44:03	9	IELSLIDFY	0.03153	100.00% (2/2)	Non-Toxin	1.13	1.24	-1.83	2.37	0.54	67.4	
284	ORF7b	A*02:01	10	IELSLIDFYL	0.06625	100.00% (2/2)	Non-Toxin	1.42	0.39	-1.28	1.81	0.53	18.9	
285	ORF7b	A*02:01	9	IIFWFSLEL	0.2683	100.00% (2/2)	Non-Toxin	1.65	0.55	-1.2	2.21	1.01	15.7	
286	ORF7b	A*02:01	9	IIFWFSLEL	0.2683	100.00% (2/2)	Non-Toxin	1.65	0.55	-1.2	2.21	1.01	15.7	
287	ORF7b	A*02:06	9	IIFWFSLEL	0.2683	100.00% (2/2)	Non-Toxin	1.65	0.55	-1.55	2.21	0.66	35.5	
288	ORF7b	A*02:01	9	LIDFYLCFL	0.13386	100.00% (2/2)	Non-Toxin	1.7	0.42	-1.64	2.12	0.49	43.4	
289	ORF7b	B*58:01	10	LSLIDFYLCF	0.22158	100.00% (2/2)	Non-Toxin	1.38	1.05	-1.96	2.43	0.48	90.2	
290	ORF7b	B*44:03	10	MIELSLIDFY	0.06184	100.00% (2/2)	Non-Toxin	1.13	1.24	-1.63	2.36	0.74	42.5	

291	ORF7b	B*15:01	9	SLIDFYLCF	0.13518	100.00% (2/2)	Non-Toxin	1.38	1.18	-1.76	2.56	0.8	57.2
292	ORF7b	A*02:01	10	SLIDFYLCFL	0.18838	100.00% (2/2)	Non-Toxin	1.7	0.5	-0.74	2.2	1.46	5.5
293	ORF7b	A*02:03	10	SLIDFYLCFL	0.18838	100.00% (2/2)	Non-Toxin	1.7	0.5	-0.79	2.2	1.41	6.2
294	ORF7b	A*02:06	10	SLIDFYLCFL	0.18838	100.00% (2/2)	Non-Toxin	1.7	0.5	-0.93	2.2	1.27	8.6
295	ORF7b	A*02:01	10	SLIDFYLCFL	0.18838	100.00% (2/2)	Non-Toxin	1.7	0.5	-0.74	2.2	1.46	5.5
296	ORF7b	A*02:03	10	SLIDFYLCFL	0.18838	100.00% (2/2)	Non-Toxin	1.7	0.5	-0.79	2.2	1.41	6.2
297	ORF7b	A*02:06	10	SLIDFYLCFL	0.18838	100.00% (2/2)	Non-Toxin	1.7	0.5	-0.93	2.2	1.27	8.6
298	ORF7b	A*02:01	9	YLCFLAFLL	0.21865	100.00% (2/2)	Non-Toxin	1.36	0.37	-0.9	1.73	0.83	7.9
S.No.	ORF	Allele	Peptide Length	Peptide	Immunogenicity	Conservancy	Toxicity	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
299	ORF8	A*30:02	10	CSFYEDFLEY	0.31272	100.00% (34/34)	Non-Toxin	1.47	1.38	-1.96	2.85	0.89	91.9
300	ORF8	A*01:01	10	CSFYEDFLEY	0.31272	100.00% (34/34)	Non-Toxin	1.47	1.38	-2.03	2.85	0.82	108.2
301	ORF8	B*58:01	10	CSFYEDFLEY	0.31272	100.00% (34/34)	Non-Toxin	1.47	1.38	-2.12	2.85	0.73	132.5
302	ORF8	A*11:01	10	CSFYEDFLEY	0.31272	100.00% (34/34)	Non-Toxin	1.47	1.38	-2.29	2.85	0.56	195
303	ORF8	B*15:01	10	CSFYEDFLEY	0.31272	100.00% (34/34)	Non-Toxin	1.47	1.38	-2.37	2.85	0.48	236.6
304	ORF8	B*15:01	9	GIITTVAAF	0.2148	100.00% (34/34)	Non-Toxin	1.27	1.13	-1.26	2.4	1.14	18.1
305	ORF8	B*15:01	9	GIITTVAAF	0.2148	100.00% (34/34)	Non-Toxin	1.27	1.13	-1.26	2.4	1.14	18.1
306	ORF8	A*30:02	10	GSLVVRCSFY	0.00657	100.00% (34/34)	Non-Toxin	1.38	1.24	-1.82	2.61	0.79	66.4
307	ORF8	A*33:01	9	HFYSKWYIR	-0.09452	100.00% (34/34)	Non-Toxin	1.08	0.76	-0.68	1.84	1.16	4.8
308	ORF8	A*31:01	9	HFYSKWYIR	-0.09452	100.00% (34/34)	Non-Toxin	1.08	0.76	-0.79	1.84	1.05	6.2
309	ORF8	A*33:01	9	HFYSKWYIR	-0.09452	100.00% (34/34)	Non-Toxin	1.08	0.76	-0.68	1.84	1.16	4.8
310	ORF8	A*31:01	9	HFYSKWYIR	-0.09452	100.00% (34/34)	Non-Toxin	1.08	0.76	-0.79	1.84	1.05	6.2
311	ORF8	A*31:01	10	IHFYSKWYIR	-0.05367	100.00% (34/34)	Non-Toxin	1.08	0.64	-1.2	1.72	0.53	15.7
312	ORF8	A*30:02	9	IQYIDIGNY	0.30442	100.00% (34/34)	Non-Toxin	1.2	1.33	-1.66	2.53	0.87	45.4
313	ORF8	B*15:01	9	IQYIDIGNY	0.30442	100.00% (34/34)	Non-Toxin	1.2	1.33	-1.66	2.53	0.87	45.4
314	ORF8	B*40:01	10	LEYHDVRVVL	0.20083	100.00% (34/34)	Non-Toxin	1.75	0.4	-1.64	2.15	0.51	43.5
315	ORF8	B*15:01	10	LGIITTVAAF	0.34746	100.00% (34/34)	Non-Toxin	1.27	0.97	-1.1	2.24	1.14	12.7
316	ORF8	B*15:01	10	LGIITTVAAF	0.34746	100.00% (34/34)	Non-Toxin	1.27	0.97	-1.1	2.24	1.14	12.7
317	ORF8	B*15:01	10	LQSCTQHQPY	-0.25674	100.00% (34/34)	Non-Toxin	1	1.33	-1.57	2.32	0.75	37
318	ORF8	A*30:02	9	SFYEDFLEY	0.28049	100.00% (34/34)	Non-Toxin	1.47	1.44	-2.04	2.92	0.88	110.3
319	ORF8	B*35:01	9	SFYEDFLEY	0.28049	100.00% (34/34)	Non-Toxin	1.47	1.44	-2.28	2.92	0.63	192.4
S.No.	ORF	Allele	Peptide Length	Peptide	Immunogenicity	Conservancy	Toxicity	Proteasome Score	TAP Score	MHC Score	Processing Score	Total Score	MHC IC50[nM]
320	S protein	A*30:02	9	ASFSTFKCY	-0.19397	100.00% (41/41)	Non-Toxin	1.47	1.42	-1.6	2.89	1.29	39.6
321	S protein	B*35:01	9	CVADYSVLY	-0.09595	100.00% (41/41)	Non-Toxin	1.51	1.38	-1.39	2.89	1.5	24.4
322	S protein	A*26:01	9	CVADYSVLY	-0.09595	100.00% (41/41)	Non-Toxin	1.51	1.38	-1.56	2.89	1.34	36
323	S protein	A*01:01	9	CVADYSVLY	-0.09595	100.00% (41/41)	Non-Toxin	1.51	1.38	-1.74	2.89	1.16	54.5
324	S protein	B*35:01	9	FAMQMAYRF	-0.28061	100.00% (41/41)	Non-Toxin	1.45	1.05	-0.8	2.5	1.7	6.3
325	S protein	B*53:01	9	FAMQMAYRF	-0.28061	100.00% (41/41)	Non-Toxin	1.45	1.05	-1.15	2.5	1.35	14.1
326	S protein	B*58:01	9	FAMQMAYRF	-0.28061	100.00% (41/41)	Non-Toxin	1.45	1.05	-1.42	2.5	1.07	26.4
327	S protein	A*23:01	9	FAMQMAYRF	-0.28061	100.00% (41/41)	Non-Toxin	1.45	1.05	-1.43	2.5	1.07	26.7
328	S protein	B*40:01	9	FEYVSQPFL	-0.17076	100.00% (41/41)	Non-Toxin	1.84	0.4	-1.14	2.24	1.09	13.9
329	S protein	B*53:01	10	FLPFFSNVTW	0.11853	100.00% (41/41)	Non-Toxin	1.69	0.37	-0.88	2.06	1.18	7.6
330	S protein	B*35:01	10	FPNITNLCPF	0.1009	100.00% (41/41)	Non-Toxin	1.02	0.94	-0.59	1.97	1.38	3.9
331	S protein	B*35:01	11	FPQSAPHGVVF	-0.05441	100.00% (41/41)	Non-Toxin	1.56	0.94	-1.47	2.5	1.02	29.7
332	S protein	B*35:01	9	FVFKNIDGY	-0.0215	100.00% (41/41)	Non-Toxin	1.1	1.26	-1.18	2.36	1.19	15.1
333	S protein	A*26:01	9	FVFKNIDGY	-0.0215	100.00% (41/41)	Non-Toxin	1.1	1.26	-1.36	2.36	1.01	22.8
334	S protein	B*58:01	9	GTITSGWTF	0.16268	100.00% (41/41)	Non-Toxin	1.58	1.11	-1.65	2.69	1.04	44.6
335	S protein	B*35:01	9	IPFAMQMAY	-0.32801	100.00% (41/41)	Non-Toxin	1.42	1.17	-0.36	2.6	2.24	2.3
336	S protein	B*53:01	9	IPFAMQMAY	-0.32801	100.00% (41/41)	Non-Toxin	1.42	1.17	-1.23	2.6	1.37	16.9
337	S protein	B*58:01	10	KRSFIEDLLF	0.29624	100.00% (41/41)	Non-Toxin	1.23	1.26	-1.11	2.49	1.37	12.9
338	S protein	A*30:02	10	KSFTVEKGIY	0.11812	100.00% (41/41)	Non-Toxin	1.25	1.4	-1.37	2.65	1.28	23.4
339	S protein	B*58:01	10	KSNIIRGWIF	0.60842	100.00% (41/41)	Non-Toxin	1.45	1.05	-1.43	2.5	1.07	27

340	S protein	A*30:02	10	KVGGNYNYLY	0.01951	100.00% (41/41)	Non-Toxin	1.4	1.33	-1.43	2.73	1.29	27.1	
341	S protein	A*23:01	10	KWPWYIWLGF	0.56424	100.00% (41/41)	Non-Toxin	1.26	1.25	-1.04	2.51	1.47	11	
342	S protein	A*24:02	10	KWPWYIWLGF	0.56424	100.00% (41/41)	Non-Toxin	1.26	1.25	-1.14	2.51	1.37	13.9	
343	S protein	A*01:01	10	LLTDEMIAQY	0.05204	100.00% (41/41)	Non-Toxin	1.21	1.2	-1.08	2.42	1.33	12.1	
344	S protein	B*53:01	9	LPFFSNVTW	0.04613	100.00% (41/41)	Non-Toxin	1.69	0.26	-0.77	1.95	1.18	5.9	
345	S protein	B*35:01	9	LPFNDGVYF	0.11767	100.00% (41/41)	Non-Toxin	1.41	1.04	-0.54	2.45	1.9	3.5	
346	S protein	B*53:01	9	LPFNDGVYF	0.11767	100.00% (41/41)	Non-Toxin	1.41	1.04	-0.98	2.45	1.47	9.6	
347	S protein	B*35:01	11	LQIPFAMQMAY	-0.22124	100.00% (41/41)	Non-Toxin	1.42	1.4	-1.25	2.82	1.57	17.8	
348	S protein	B*15:01	11	LQIPFAMQMAY	-0.22124	100.00% (41/41)	Non-Toxin	1.42	1.4	-1.64	2.82	1.19	43.2	
349	S protein	A*01:01	9	LTDEMIAQY	0.02757	100.00% (41/41)	Non-Toxin	1.21	1.21	-0.72	2.42	1.71	5.2	
350	S protein	A*23:01	10	LYNSASFSTF	-0.29831	100.00% (41/41)	Non-Toxin	1.33	1.2	-0.95	2.52	1.57	9	
351	S protein	A*24:02	10	LYNSASFSTF	-0.29831	100.00% (41/41)	Non-Toxin	1.33	1.2	-0.99	2.52	1.53	9.8	
352	S protein	A*68:01	10	NVYADSFVIR	0.12147	100.00% (41/41)	Non-Toxin	1.47	0.81	-1.03	2.28	1.24	10.8	
353	S protein	A*24:02	9	NYNYLYRLF	0.0171	100.00% (41/41)	Non-Toxin	1.2	1.18	-1.37	2.38	1.01	23.4	
354	S protein	A*33:01	10	NYNYLYRLFR	0.08754	100.00% (41/41)	Non-Toxin	1.16	0.72	-0.86	1.88	1.02	7.3	
355	S protein	B*35:01	10	QIPFAMQMAY	-0.25308	100.00% (41/41)	Non-Toxin	1.42	1.35	-1.16	2.77	1.61	14.5	
356	S protein	A*30:02	9	RISNCVADY	-0.02787	100.00% (41/41)	Non-Toxin	1.16	1.47	-1.26	2.63	1.37	18.2	
357	S protein	B*58:01	9	RSFIEDLLF	0.27446	100.00% (41/41)	Non-Toxin	1.23	1.32	-0.72	2.54	1.82	5.3	
358	S protein	B*57:01	9	RSFIEDLLF	0.27446	100.00% (41/41)	Non-Toxin	1.23	1.32	-1.18	2.54	1.36	15.2	
359	S protein	B*15:01	10	RVYSTGSNVF	-0.23394	100.00% (41/41)	Non-Toxin	1.51	1.32	-1.02	2.83	1.81	10.5	
360	S protein	A*32:01	10	RVYSTGSNVF	-0.23394	100.00% (41/41)	Non-Toxin	1.51	1.32	-1.69	2.83	1.14	48.9	
361	S protein	B*35:01	9	SANNCTFEY	0.13273	100.00% (41/41)	Non-Toxin	1.18	1.3	-1.11	2.48	1.37	12.8	
362	S protein	B*15:01	10	SVASQSIIAY	-0.16721	100.00% (41/41)	Non-Toxin	1.32	1.42	-1.74	2.74	1	55.2	
363	S protein	B*35:01	9	VASQSIIAY	-0.0709	100.00% (41/41)	Non-Toxin	1.32	1.34	-0.86	2.66	1.8	7.2	
364	S protein	A*24:02	10	VYSSANNCTF	-0.21728	100.00% (41/41)	Non-Toxin	1.42	1.3	-1.62	2.71	1.09	41.7	
365	S protein	A*23:01	10	VYSSANNCTF	-0.21728	100.00% (41/41)	Non-Toxin	1.42	1.3	-1.71	2.71	1.01	50.8	
366	S protein	A*26:01	9	WTAGAAAYY	0.15259	100.00% (41/41)	Non-Toxin	1.24	1.24	-1.06	2.48	1.41	11.6	
367	S protein	A*68:01	9	WTAGAAAYY	0.15259	100.00% (41/41)	Non-Toxin	1.24	1.24	-1.37	2.48	1.11	23.5	
368	S protein	A*02:01	9	YLQPRTFLL	0.1305	100.00% (41/41)	Non-Toxin	1.46	0.39	-0.66	1.85	1.18	4.6	
369	S protein	B*35:01	9	YSSANNCTF	-0.04954	100.00% (41/41)	Non-Toxin	1.42	1.13	-1.29	2.54	1.26	19.4	
370	S protein	B*58:01	9	YSSANNCTF	-0.04954	100.00% (41/41)	Non-Toxin	1.42	1.13	-1.49	2.54	1.05	31.1	
371	S protein	B*15:01	10	YSVLYNSASF	-0.22703	100.00% (41/41)	Non-Toxin	1.39	1.08	-1.36	2.47	1.11	23	
372	S protein	A*30:02	10	YTNSFTRGVY	0.08467	95.12% (39/41)	Non-Toxin	1.36	1.28	-1.26	2.64	1.38	18.2	
373	S protein	A*01:01	10	YTNSFTRGVY	0.08467	95.12% (39/41)	Non-Toxin	1.36	1.28	-1.45	2.64	1.19	28	
374	S protein	B*15:01	10	YTNSFTRGVY	0.08467	95.12% (39/41)	Non-Toxin	1.36	1.28	-1.6	2.64	1.04	40.2	
375	S protein	A*01:01	11	YTNSFTRGVYY	0.09821	95.12% (39/41)	Non-Toxin	1.45	1.28	-1.51	2.72	1.22	32.1	
376	S protein	A*23:01	11	YYVGYLQPRTF	-0.02378	100.00% (41/41)	Non-Toxin	1.36	1.31	-1.38	2.67	1.29	24	
377	S protein	A*24:02	11	YYVGYLQPRTF	-0.02378	100.00% (41/41)	Non-Toxin	1.36	1.31	-1.67	2.67	1	46.5	

Supplementary Table S2: High Scoring CTL epitopes-HLA allele pairs screened from entire proteome of SARS-CoV-2 by the “MHC-I Binding Predictions” tool of IEDB. These epitopes were further utilized to identify the potentially immunogenic multiple epitope cluster based CTL Ag-Patches from the entire proteome of the SRAS-CoV-2. The epitopes shown in **RED** are the epitope which form Overlapping epitope clusters. The screened epitopes are in consensus with the previous studies [Srivastava et al. 2020a; Srivastava et al., 2020b and Grifoni et al., 2020a].

S.No.	ORF	Allele	Length	Peptide	Immunogenicity	Method used	Percentile Rank	Conservancy	Toxicity	
378	E Protein	A*02:01	9	FLAFVVFLL	0.30188	Consensus (ann/comblib_sidney2008/smm)	0.2	99.59% (480/482)	Non-Toxin	
379	E Protein	A*02:03	9	FLAFVVFLL	0.30188	Consensus (ann/smm)	0.25	99.59% (480/482)	Non-Toxin	
380	E Protein	A*02:06	9	FLAFVVFLL	0.30188	Consensus (ann/smm)	0.53	99.59% (480/482)	Non-Toxin	
381	E Protein	A*02:01	10	FLAFVVFLLV	0.30526	Consensus (ann/smm)	0.15	99.59% (480/482)	Non-Toxin	
382	E Protein	A*02:03	10	FLAFVVFLLV	0.30526	Consensus (ann/smm)	0.23	99.59% (480/482)	Non-Toxin	
383	E Protein	A*02:06	10	FLAFVVFLLV	0.30526	Consensus (ann/smm)	0.47	99.59% (480/482)	Non-Toxin	
384	E Protein	A*02:01	9	FLLVTLAIL	0.17608	Consensus (ann/comblib_sidney2008/smm)	0.43	99.59% (480/482)	Non-Toxin	
385	E Protein	A*02:06	9	FVVFLLVTL	0.16748	Consensus (ann/smm)	0.46	99.59% (480/482)	Non-Toxin	
386	E Protein	B*15:01	10	ILTALRLCAY	0.05849	Consensus (ann/smm)	0.41	99.17% (478/482)	Non-Toxin	
387	E Protein	B*51:01	9	LAFVVFLLV	0.2141	Consensus (ann/comblib_sidney2008/smm)	0.2	99.59% (480/482)	Non-Toxin	
388	E Protein	A*02:01	11	LFLAFVVFLLV	0.32453	Consensus (ann/smm)	0.39	99.59% (480/482)	Non-Toxin	
389	E Protein	B*15:01	9	LLFLAFVVF	0.2341	Consensus (ann/comblib_sidney2008/smm)	0.1	99.59% (480/482)	Non-Toxin	
390	E Protein	A*32:01	9	LLFLAFVVF	0.2341	Consensus (ann/comblib_sidney2008/smm)	0.3	99.59% (480/482)	Non-Toxin	
391	E Protein	A*02:01	10	LLFLAFVVFL	0.32104	Consensus (ann/smm)	0.48	99.59% (480/482)	Non-Toxin	
392	E Protein	A*01:01	9	LTALRLCAY	0.01886	Consensus (ann/smm)	0.12	99.17% (478/482)	Non-Toxin	
393	E Protein	A*26:01	9	LTALRLCAY	0.01886	Consensus (ann/smm)	0.41	99.17% (478/482)	Non-Toxin	
394	E Protein	B*15:01	9	LVKPSFYVY	-0.11106	Consensus (ann/comblib_sidney2008/smm)	0.2	99.59% (480/482)	Non-Toxin	
395	E Protein	A*30:02	9	LVKPSFYVY	-0.11106	Consensus (ann/smm)	0.46	99.59% (480/482)	Non-Toxin	
396	E Protein	A*68:02	10	NSVLLFLAFV	0.19642	Consensus (ann/smm)	0.38	99.59% (480/482)	Non-Toxin	
397	E Protein	A*31:01	9	RVKNLNSSR	-0.32968	Consensus (ann/smm)	0.16	99.59% (480/482)	Non-Toxin	
398	E Protein	B*40:01	9	SEETGTLIV	0.2095	Consensus (ann/smm)	0.45	99.59% (480/482)	Non-Toxin	
399	E Protein	A*02:06	9	SLVKPSFYV	-0.27349	Consensus (ann/smm)	0.4	99.59% (480/482)	Non-Toxin	
400	E Protein	A*02:01	9	SLVKPSFYV	-0.27349	Consensus (ann/comblib_sidney2008/smm)	0.5	99.59% (480/482)	Non-Toxin	
401	E Protein	B*15:01	10	SLVKPSFYVY	-0.2443	Consensus (ann/smm)	0.28	99.59% (480/482)	Non-Toxin	
402	E Protein	A*30:02	10	SLVKPSFYVY	-0.2443	Consensus (ann/smm)	0.58	99.59% (480/482)	Non-Toxin	
403	E Protein	A*02:06	9	SVLLFLAFV	0.19022	Consensus (ann/smm)	0.33	99.59% (480/482)	Non-Toxin	
404	E Protein	A*02:06	10	SVLLFLAFVV	0.24819	Consensus (ann/smm)	0.48	99.59% (480/482)	Non-Toxin	
405	E Protein	A*68:01	9	TLAILTALR	0.1989	Consensus (ann/smm)	0.21	99.17% (478/482)	Non-Toxin	
406	E Protein	A*23:01	9	VFLLVTLAI	0.07548	Consensus (ann/smm)	0.5	99.59% (480/482)	Non-Toxin	
407	E Protein	A*02:01	9	VLLFLAFVV	0.26315	Consensus (ann/comblib_sidney2008/smm)	0.3	99.59% (480/482)	Non-Toxin	
408	E Protein	B*15:01	10	VLLFLAFVVF	0.31066	Consensus (ann/smm)	0.46	99.59% (480/482)	Non-Toxin	
409	E Protein	A*30:02	9	VSLVKPSFY	-0.25372	Consensus (ann/smm)	0.33	99.59% (480/482)	Non-Toxin	
410	E Protein	A*68:01	10	VTLAILTALR	0.21765	Consensus (ann/smm)	0.52	99.17% (478/482)	Non-Toxin	
S.No.	ORF	Allele	Length	Peptide	Immunogenicity	Method used	Percentile Rank	Conservancy	Toxicity	
411	M Protein	B*58:01	10	AMACLVGLMW	-0.09221	Consensus (ann/smm)	0.41	98.53% (470/477)	Non-Toxin	
412	M Protein	B*44:02	10	AMACLVGLMW	-0.09221	Consensus (ann/smm)	0.41	98.53% (470/477)	Non-Toxin	
413	M Protein	A*30:01	9	ANRNRFLYI	0.15937	Consensus (ann/comblib_sidney2008/smm)	0.5	99.16% (473/477)	Non-Toxin	
414	M Protein	A*31:01	8	ASFRLFAR	0.2225	ann	0.27	99.79% (476/477)	Non-Toxin	
415	M Protein	A*31:01	10	ASFRLFARTR	0.29647	Consensus (ann/smm)	0.27	99.79% (476/477)	Non-Toxin	
416	M Protein	A*30:02	9	ATSRTLSYY	-0.11604	Consensus (ann/smm)	0.17	98.95% (472/477)	Non-Toxin	
417	M Protein	A*01:01	9	ATSRTLSYY	-0.11604	Consensus (ann/smm)	0.17	98.95% (472/477)	Non-Toxin	
418	M Protein	A*26:01	9	ATSRTLSYY	-0.11604	Consensus (ann/smm)	0.26	98.95% (472/477)	Non-Toxin	
419	M Protein	A*11:01	10	ATSRTLSYYK	-0.13563	Consensus (ann/smm)	0.06	98.95% (472/477)	Non-Toxin	

420	M Protein	A*03:01	10	ATSRTLSYYK	-0.13563	Consensus (ann/smm)	0.14	98.95% (472/477)	Non-Toxin	
421	M Protein	A*30:01	10	ATSRTLSYYK	-0.13563	Consensus (ann/smm)	0.17	98.95% (472/477)	Non-Toxin	
422	M Protein	A*31:01	9	AVILRGHLR	0.13516	Consensus (ann/smm)	0.43	99.79% (476/477)	Non-Toxin	
423	M Protein	A*30:02	10	AYANRNRFLY	0.19133	Consensus (ann/smm)	0.24	98.95% (472/477)	Non-Toxin	
424	M Protein	A*30:02	10	AYSRYRIGNY	0.19528	Consensus (ann/smm)	0.27	98.32% (469/477)	Non-Toxin	
425	M Protein	B*15:01	10	CLVGLMWLSY	-0.03181	Consensus (ann/smm)	0.49	97.48% (465/477)	Non-Toxin	
426	M Protein	A*30:02	10	DSGFAAYSRY	0.09214	Consensus (ann/smm)	0.38	98.32% (469/477)	Non-Toxin	
427	M Protein	B*44:03	10	EELKKLLEQW	-0.43502	Consensus (ann/smm)	0.2	98.74% (471/477)	Non-Toxin	
428	M Protein	B*44:02	10	EELKKLLEQW	-0.43502	Consensus (ann/smm)	0.24	98.74% (471/477)	Non-Toxin	
429	M Protein	A*23:01	11	EQWNLVIGFLF	0.34861	Consensus (ann/smm)	0.38	99.16% (473/477)	Non-Toxin	
430	M Protein	B*51:01	9	FAAYSRYRI	-0.07628	Consensus (ann/comblib_sidney2008/smm)	0.46	98.32% (469/477)	Non-Toxin	
431	M Protein	A*68:02	9	FAAYSRYRI	-0.07628	Consensus (ann/comblib_sidney2008/smm)	0.5	98.32% (469/477)	Non-Toxin	
432	M Protein	B*35:01	9	FAYANRNRF	0.10537	Consensus (ann/comblib_sidney2008/smm)	0.3	98.95% (472/477)	Non-Toxin	
433	M Protein	A*68:01	10	FIASFRLFAR	0.12185	Consensus (ann/smm)	0.12	99.79% (476/477)	Non-Toxin	
434	M Protein	A*33:01	10	FIASFRLFAR	0.12185	Consensus (ann/smm)	0.14	99.79% (476/477)	Non-Toxin	
435	M Protein	A*31:01	10	FIASFRLFAR	0.12185	Consensus (ann/smm)	0.3	99.79% (476/477)	Non-Toxin	
436	M Protein	A*02:01	9	FLFLTWICL	0.35397	Consensus (ann/comblib_sidney2008/smm)	0.4	98.95% (472/477)	Non-Toxin	
437	M Protein	A*02:01	10	FLFLTWICLL	0.35364	Consensus (ann/smm)	0.15	98.95% (472/477)	Non-Toxin	
438	M Protein	A*02:01	10	FLWLLWPVTL	0.31272	Consensus (ann/smm)	0.28	98.53% (470/477)	Non-Toxin	
439	M Protein	A*02:01	10	FLYIIKLIFL	0.2226	Consensus (ann/smm)	0.29	98.53% (470/477)	Non-Toxin	
440	M Protein	B*08:01	10	FRLFARTRSM	0.18626	Consensus (ann/smm)	0.43	99.79% (476/477)	Non-Toxin	
441	M Protein	A*31:01	9	GFAAYSRYR	-0.06574	Consensus (ann/smm)	0.41	98.32% (469/477)	Non-Toxin	
442	M Protein	A*02:01	9	GLMWLSYFI	0.06464	Consensus (ann/comblib_sidney2008/smm)	0.2	97.48% (465/477)	Non-Toxin	
443	M Protein	A*32:01	9	GLMWLSYFI	0.06464	Consensus (ann/comblib_sidney2008/smm)	0.4	97.48% (465/477)	Non-Toxin	
444	M Protein	A*11:01	9	GTITVEELK	0.29473	Consensus (ann/smm)	0.36	98.74% (471/477)	Non-Toxin	
445	M Protein	A*68:01	9	GTITVEELK	0.29473	Consensus (ann/smm)	0.47	98.74% (471/477)	Non-Toxin	
446	M Protein	A*11:01	10	GTITVEELKK	0.17885	Consensus (ann/smm)	0.27	98.53% (470/477)	Non-Toxin	
447	M Protein	B*51:01	9	IAIAMACLV	-0.10358	Consensus (ann/comblib_sidney2008/smm)	0.5	99.58% (475/477)	Non-Toxin	
448	M Protein	B*58:01	11	IAMACLVGLMW	-0.12079	Consensus (ann/smm)	0.42	98.53% (470/477)	Non-Toxin	
449	M Protein	A*33:01	9	IASFRLFAR	0.22572	Consensus (ann/smm)	0.23	99.79% (476/477)	Non-Toxin	
450	M Protein	A*68:01	9	IASFRLFAR	0.22572	Consensus (ann/smm)	0.26	99.79% (476/477)	Non-Toxin	
451	M Protein	A*31:01	9	IASFRLFAR	0.22572	Consensus (ann/smm)	0.29	99.79% (476/477)	Non-Toxin	
452	M Protein	A*02:06	9	IFLWLLWPV	0.37851	Consensus (ann/smm)	0.28	98.53% (470/477)	Non-Toxin	
453	M Protein	B*40:01	11	KEITVATSRTL	0.10899	ann	0.42	98.74% (471/477)	Non-Toxin	
454	M Protein	A*32:01	11	KKLLEQWNLVI	0.19431	ann	0.39	98.74% (471/477)	Non-Toxin	
455	M Protein	B*58:01	9	KLIFLWLLW	0.34287	Consensus (ann/comblib_sidney2008/smm)	0.2	98.32% (469/477)	Non-Toxin	
456	M Protein	A*32:01	9	KLIFLWLLW	0.34287	Consensus (ann/comblib_sidney2008/smm)	0.3	98.32% (469/477)	Non-Toxin	
457	M Protein	B*57:01	9	KLIFLWLLW	0.34287	Consensus (ann/smm)	0.42	98.32% (469/477)	Non-Toxin	
458	M Protein	A*02:01	11	KLIFLWLLWPV	0.52512	Consensus (ann/smm)	0.14	98.11% (468/477)	Non-Toxin	
459	M Protein	A*32:01	11	KLIFLWLLWPV	0.52512	ann	0.2	98.11% (468/477)	Non-Toxin	
460	M Protein	A*02:06	9	KLLEQWNLV	0.18092	Consensus (ann/smm)	0.17	98.95% (472/477)	Non-Toxin	
461	M Protein	A*02:01	9	KLLEQWNLV	0.18092	Consensus (ann/comblib_sidney2008/smm)	0.4	98.95% (472/477)	Non-Toxin	
462	M Protein	A*32:01	11	KLLEQWNLVIG	0.29591	ann	0.38	98.95% (472/477)	Non-Toxin	
463	M Protein	B*44:02	10	LEQWNLVIGF	0.33917	Consensus (ann/smm)	0.29	99.16% (473/477)	Non-Toxin	
464	M Protein	B*44:03	10	LEQWNLVIGF	0.33917	Consensus (ann/smm)	0.48	99.16% (473/477)	Non-Toxin	
465	M Protein	A*02:06	10	LIFLWLLWPV	0.40176	Consensus (ann/smm)	0.08	98.32% (469/477)	Non-Toxin	
466	M Protein	A*02:01	10	LIFLWLLWPV	0.40176	Consensus (ann/smm)	0.15	98.32% (469/477)	Non-Toxin	
467	M Protein	A*02:03	10	LIFLWLLWPV	0.40176	Consensus (ann/smm)	0.3	98.32% (469/477)	Non-Toxin	
468	M Protein	B*15:01	10	LLWPVTLACF	0.12982	Consensus (ann/smm)	0.13	98.53% (470/477)	Non-Toxin	
469	M Protein	A*02:01	11	LLWPVTLACFV	0.18767	Consensus (ann/smm)	0.35	98.53% (470/477)	Non-Toxin	
470	M Protein	B*15:01	11	LMWLSYFIASF	0.07168	ann	0.42	97.69% (466/477)	Non-Toxin	

471	M Protein	A*23:01	11	LMWLSYFIASF	0.07168	Consensus (ann/smm)	0.47	97.69% (466/477)	Non-Toxin	
472	M Protein	A*68:01	9	LSYFIASFR	0.21181	Consensus (ann/smm)	0.11	97.90% (467/477)	Non-Toxin	
473	M Protein	A*31:01	9	LSYFIASFR	0.21181	Consensus (ann/smm)	0.17	97.90% (467/477)	Non-Toxin	
474	M Protein	A*33:01	9	LSYFIASFR	0.21181	Consensus (ann/smm)	0.41	97.90% (467/477)	Non-Toxin	
475	M Protein	A*03:01	9	LSYFIASFR	0.21181	Consensus (ann/smm)	0.48	97.90% (467/477)	Non-Toxin	
476	M Protein	A*23:01	11	LSYFIASFRLF	0.2706	Consensus (ann/smm)	0.34	97.90% (467/477)	Non-Toxin	
477	M Protein	B*53:01	10	LVIGFLFLTW	0.30402	Consensus (ann/smm)	0.15	98.95% (472/477)	Non-Toxin	
478	M Protein	A*23:01	9	LWLLWPVTL	0.24802	Consensus (ann/smm)	0.43	98.53% (470/477)	Non-Toxin	
479	M Protein	A*24:02	9	LWLLWPVTL	0.24802	Consensus (ann/smm)	0.43	98.53% (470/477)	Non-Toxin	
480	M Protein	A*24:02	9	LWPVTLACF	0.06682	Consensus (ann/smm)	0.2	98.74% (471/477)	Non-Toxin	
481	M Protein	A*23:01	10	LYIIKLIFLW	0.17392	Consensus (ann/smm)	0.17	98.53% (470/477)	Non-Toxin	
482	M Protein	A*24:02	10	LYIIKLIFLW	0.17392	Consensus (ann/smm)	0.23	98.53% (470/477)	Non-Toxin	
483	M Protein	B*57:01	9	MACLVGLMW	-0.06852	Consensus (ann/smm)	0.15	98.53% (470/477)	Non-Toxin	
484	M Protein	B*58:01	9	MACLVGLMW	-0.06852	Consensus (ann/comblib_sidney2008/smm)	0.2	98.53% (470/477)	Non-Toxin	
485	M Protein	B*53:01	9	MACLVGLMW	-0.06852	Consensus (ann/comblib_sidney2008/smm)	0.2	98.53% (470/477)	Non-Toxin	
486	M Protein	A*23:01	10	MWLSYFIASF	0.00197	Consensus (ann/smm)	0.11	97.69% (466/477)	Non-Toxin	
487	M Protein	A*24:02	10	MWLSYFIASF	0.00197	Consensus (ann/smm)	0.13	97.69% (466/477)	Non-Toxin	
488	M Protein	A*32:01	10	MWLSYFIASF	0.00197	Consensus (ann/smm)	0.46	97.69% (466/477)	Non-Toxin	
489	M Protein	A*68:01	11	MWLSYFIASFR	0.03554	ann	0.09	97.69% (466/477)	Non-Toxin	
490	M Protein	A*33:01	11	MWLSYFIASFR	0.03554	ann	0.1	97.69% (466/477)	Non-Toxin	
491	M Protein	A*30:01	10	NRNRFLYIIK	0.33978	Consensus (ann/smm)	0.45	98.95% (472/477)	Non-Toxin	
492	M Protein	A*23:01	10	QWNLVIGFLF	0.28076	Consensus (ann/smm)	0.12	99.16% (473/477)	Non-Toxin	
493	M Protein	A*24:02	10	QWNLVIGFLF	0.28076	Consensus (ann/smm)	0.14	99.16% (473/477)	Non-Toxin	
494	M Protein	A*23:01	9	RFLYIIKLI	0.05908	Consensus (ann/smm)	0.47	98.74% (471/477)	Non-Toxin	
495	M Protein	A*23:01	10	RFLYIIKLIF	0.11728	Consensus (ann/smm)	0.12	98.74% (471/477)	Non-Toxin	
496	M Protein	A*24:02	10	RFLYIIKLIF	0.11728	Consensus (ann/smm)	0.45	98.74% (471/477)	Non-Toxin	
497	M Protein	A*31:01	9	RIAGHHLGR	0.11919	Consensus (ann/smm)	0.46	99.58% (475/477)	Non-Toxin	
498	M Protein	A*32:01	11	RINWITGGIAI	0.58827	ann	0.33	99.37% (474/477)	Non-Toxin	
499	M Protein	A*32:01	11	RINWITGGIAI	0.58827	ann	0.33	99.37% (474/477)	Non-Toxin	
500	M Protein	B*08:01	9	RLFARTRSM	0.11133	Consensus (ann/comblib_sidney2008/smm)	0.3	99.79% (476/477)	Non-Toxin	
501	M Protein	A*32:01	9	RLFARTRSM	0.11133	Consensus (ann/comblib_sidney2008/smm)	0.4	99.79% (476/477)	Non-Toxin	
502	M Protein	B*15:01	9	RLFARTRSM	0.11133	Consensus (ann/comblib_sidney2008/smm)	0.5	99.79% (476/477)	Non-Toxin	
503	M Protein	A*30:01	9	RNRFLYIIK	0.3104	Consensus (ann/comblib_sidney2008/smm)	0.2	98.95% (472/477)	Non-Toxin	
504	M Protein	A*32:01	8	RTRSMWSF	-0.25178	ann	0.1	99.58% (475/477)	Non-Toxin	
505	M Protein	A*30:01	8	RTRSMWSF	-0.25178	ann	0.29	99.58% (475/477)	Non-Toxin	
506	M Protein	B*57:01	8	RTRSMWSF	-0.25178	ann	0.39	99.58% (475/477)	Non-Toxin	
507	M Protein	A*30:01	9	RTRSMWSFN	-0.18338	Consensus (ann/comblib_sidney2008/smm)	0.3	99.37% (474/477)	Non-Toxin	
508	M Protein	A*30:01	8	RYRIGNYK	0.17451	ann	0.19	98.53% (470/477)	Non-Toxin	
509	M Protein	A*23:01	9	RYRIGNYKL	0.04851	Consensus (ann/smm)	0.4	98.53% (470/477)	Non-Toxin	
510	M Protein	A*30:02	9	SGFAAYSRY	0.00261	Consensus (ann/smm)	0.41	98.32% (469/477)	Non-Toxin	
511	M Protein	A*31:01	10	SGFAAYSRYR	-0.00234	Consensus (ann/smm)	0.35	98.32% (469/477)	Non-Toxin	
512	M Protein	A*01:01	9	SSDNIALLV	0.15128	Consensus (ann/smm)	0.2	99.16% (473/477)	Non-Toxin	
513	M Protein	A*33:01	8	SYFIASFR	0.15309	ann	0.42	98.74% (471/477)	Non-Toxin	
514	M Protein	A*24:02	9	SYFIASFRL	0.18333	Consensus (ann/smm)	0.22	98.74% (471/477)	Non-Toxin	
515	M Protein	A*23:01	9	SYFIASFRL	0.18333	Consensus (ann/smm)	0.36	98.74% (471/477)	Non-Toxin	
516	M Protein	A*23:01	10	SYFIASFRLF	0.19632	Consensus (ann/smm)	0.11	98.74% (471/477)	Non-Toxin	
517	M Protein	A*24:02	10	SYFIASFRLF	0.19632	Consensus (ann/smm)	0.11	98.74% (471/477)	Non-Toxin	
518	M Protein	A*33:01	10	SYYKLGASQR	-0.36647	Consensus (ann/smm)	0.27	99.37% (474/477)	Non-Toxin	
519	M Protein	A*02:03	9	TLACFVLAA	0.12481	Consensus (ann/smm)	0.42	99.16% (473/477)	Non-Toxin	
520	M Protein	A*02:03	10	TLACFVLAAV	0.15809	Consensus (ann/smm)	0.12	98.32% (469/477)	Non-Toxin	
521	M Protein	A*02:01	10	TLACFVLAAV	0.15809	Consensus (ann/smm)	0.21	98.32% (469/477)	Non-Toxin	

522	M Protein	A*30:01	9	TSRTLSYYK	-0.11595	Consensus (ann/comblib_sidney2008/smm)	0.3	99.16% (473/477)	Non-Toxin
523	M Protein	A*11:01	9	TSRTLSYYK	-0.11595	Consensus (ann/smm)	0.35	99.16% (473/477)	Non-Toxin
524	M Protein	B*15:01	10	TVATSRTLSY	-0.12842	Consensus (ann/smm)	0.21	98.74% (471/477)	Non-Toxin
525	M Protein	A*26:01	10	TVATSRTLSY	-0.12842	Consensus (ann/smm)	0.22	98.74% (471/477)	Non-Toxin
526	M Protein	A*01:01	10	VATSRTLSYY	-0.21789	Consensus (ann/smm)	0.28	98.95% (472/477)	Non-Toxin
527	M Protein	A*30:02	10	VATSRTLSYY	-0.21789	Consensus (ann/smm)	0.41	98.95% (472/477)	Non-Toxin
528	M Protein	A*11:01	11	VATSRTLSYYK	-0.23748	Consensus (ann/smm)	0.17	98.95% (472/477)	Non-Toxin
529	M Protein	A*01:01	9	WICLLQFAY	-0.02684	Consensus (ann/smm)	0.37	98.95% (472/477)	Non-Toxin
530	M Protein	B*15:01	9	WLSYFIASF	0.11822	Consensus (ann/comblib_sidney2008/smm)	0.3	97.69% (466/477)	Non-Toxin
531	M Protein	A*32:01	9	WLSYFIASF	0.11822	Consensus (ann/comblib_sidney2008/smm)	0.5	97.69% (466/477)	Non-Toxin
532	M Protein	A*68:01	10	WLSYFIASFR	0.15179	Consensus (ann/smm)	0.21	97.69% (466/477)	Non-Toxin
533	M Protein	A*33:01	10	WLSYFIASFR	0.15179	Consensus (ann/smm)	0.23	97.69% (466/477)	Non-Toxin
534	M Protein	A*31:01	10	WLSYFIASFR	0.15179	Consensus (ann/smm)	0.4	97.69% (466/477)	Non-Toxin
535	M Protein	B*51:01	10	WPVTLACFVL	0.15193	Consensus (ann/smm)	0.34	98.95% (472/477)	Non-Toxin
536	M Protein	A*01:01	9	YANRNRFLY	0.18472	Consensus (ann/smm)	0.28	99.16% (473/477)	Non-Toxin
537	M Protein	B*35:01	9	YANRNRFLY	0.18472	Consensus (ann/comblib_sidney2008/smm)	0.4	99.16% (473/477)	Non-Toxin
538	M Protein	A*23:01	9	YFIASFRLF	0.06887	Consensus (ann/smm)	0.11	99.37% (474/477)	Non-Toxin
539	M Protein	A*24:02	9	YFIASFRLF	0.06887	Consensus (ann/smm)	0.18	99.37% (474/477)	Non-Toxin
540	M Protein	A*33:01	11	YFIASFRLFAR	0.19709	ann	0.03	99.37% (474/477)	Non-Toxin
541	M Protein	B*58:01	9	YIIKLIFLW	0.033	Consensus (ann/comblib_sidney2008/smm)	0.3	98.53% (470/477)	Non-Toxin
542	M Protein	B*53:01	9	YIIKLIFLW	0.033	Consensus (ann/comblib_sidney2008/smm)	0.3	98.53% (470/477)	Non-Toxin
543	M Protein	B*57:01	9	YIIKLIFLW	0.033	Consensus (ann/smm)	0.48	98.53% (470/477)	Non-Toxin
544	M Protein	A*26:01	9	YSRYRIGNY	0.21358	Consensus (ann/smm)	0.4	98.53% (470/477)	Non-Toxin
545	M Protein	A*30:02	9	YSRYRIGNY	0.21358	Consensus (ann/smm)	0.49	98.53% (470/477)	Non-Toxin
546	M Protein	A*03:01	10	YSRYRIGNYK	0.21736	Consensus (ann/smm)	0.47	98.53% (470/477)	Non-Toxin
547	M Protein	A*33:01	9	YYKLGASQR	-0.21863	Consensus (ann/smm)	0.27	99.37% (474/477)	Non-Toxin
S.No.	ORF	Allele	Length	Peptide	Immunogenicity	Method used	Percentile Rank	Conservancy	Toxicity
548	N Protein	B*07:02	10	APRITFGGPS	0.35654	Consensus (ann/smm)	0.39	96.79% (482/498)	Non-Toxin
549	N Protein	B*15:01	10	AQFAPSASAF	-0.17446	Consensus (ann/smm)	0.16	97.59% (486/498)	Non-Toxin
550	N Protein	B*15:01	11	AQFAPSASAFF	-0.11074	ann	0.12	97.59% (486/498)	Non-Toxin
551	N Protein	A*11:01	9	ASAFFGMSR	0.03154	Consensus (ann/smm)	0.38	97.59% (486/498)	Non-Toxin
552	N Protein	A*26:01	10	DLSPRWYFYY	0.2944	Consensus (ann/smm)	0.31	99.60% (496/498)	Non-Toxin
553	N Protein	A*01:01	10	DLSPRWYFYY	0.2944	Consensus (ann/smm)	0.35	99.60% (496/498)	Non-Toxin
554	N Protein	A*26:01	9	ELIRQGTDY	0.0601	Consensus (ann/smm)	0.39	97.39% (485/498)	Non-Toxin
555	N Protein	B*35:01	9	FAPSASAFF	-0.18628	Consensus (ann/comblib_sidney2008/smm)	0.4	97.59% (486/498)	Non-Toxin
556	N Protein	A*68:01	9	FTALTQHGK	-0.0226	Consensus (ann/smm)	0.18	99.40% (495/498)	Non-Toxin
557	N Protein	A*02:03	9	GMSRIGMEV	0.07018	Consensus (ann/smm)	0.46	97.59% (486/498)	Non-Toxin
558	N Protein	A*31:01	9	GYYRRATRR	0.20111	Consensus (ann/smm)	0.45	99.40% (495/498)	Non-Toxin
559	N Protein	B*15:01	11	IAQFAPSASAF	-0.13353	ann	0.4	97.39% (485/498)	Non-Toxin
560	N Protein	A*31:01	9	IGYYRRATR	0.1499	Consensus (ann/smm)	0.38	99.40% (495/498)	Non-Toxin
561	N Protein	A*32:01	9	KAYNVTQAF	-0.00587	Consensus (ann/comblib_sidney2008/smm)	0.2	97.59% (486/498)	Non-Toxin
562	N Protein	B*58:01	9	KAYNVTQAF	-0.00587	Consensus (ann/comblib_sidney2008/smm)	0.4	97.59% (486/498)	Non-Toxin
563	N Protein	A*30:02	10	KDLSPRWYFY	0.14332	Consensus (ann/smm)	0.47	99.60% (496/498)	Non-Toxin
564	N Protein	A*31:01	8	KMKDLSPR	-0.22357	ann	0.15	99.60% (496/498)	Non-Toxin
565	N Protein	A*30:02	10	KMKDLSPRWY	-0.05692	Consensus (ann/smm)	0.33	99.60% (496/498)	Non-Toxin
566	N Protein	B*07:02	9	KPRQKRTAT	-0.20542	Consensus (ann/comblib_sidney2008/smm)	0.1	97.79% (487/498)	Non-Toxin
567	N Protein	B*07:02	10	KPRQKRTATK	-0.16712	Consensus (ann/smm)	0.2	97.79% (487/498)	Non-Toxin
568	N Protein	A*03:01	9	KSAAEASKK	-0.07922	Consensus (ann/smm)	0.45	97.79% (487/498)	Non-Toxin
569	N Protein	A*11:01	9	KTFPPTEPK	0.1306	Consensus (ann/smm)	0.11	96.99% (483/498)	Non-Toxin
570	N Protein	A*30:01	9	KTFPPTEPK	0.1306	Consensus (ann/comblib_sidney2008/smm)	0.2	96.99% (483/498)	Non-Toxin
571	N Protein	A*03:01	9	KTFPPTEPK	0.1306	Consensus (ann/smm)	0.23	96.99% (483/498)	Non-Toxin

572	N Protein	A*11:01	10	KTFPPTEPKK	0.01273	Consensus (ann/smm)	0.28	96.99% (483/498)	Non-Toxin	
573	N Protein	B*08:01	9	LLLDRLNQL	-0.01446	Consensus (ann/comblib_sidney2008/smm)	0.4	97.59% (486/498)	Non-Toxin	
574	N Protein	B*15:01	9	LLNKHIDAY	-0.02074	Consensus (ann/comblib_sidney2008/smm)	0.3	97.59% (486/498)	Non-Toxin	
575	N Protein	A*03:01	10	LLNKHIDAYK	-0.00626	Consensus (ann/smm)	0.43	97.59% (486/498)	Non-Toxin	
576	N Protein	B*35:01	9	LPAADLDDF	0.09491	Consensus (ann/comblib_sidney2008/smm)	0.5	97.59% (486/498)	Non-Toxin	
577	N Protein	B*53:01	9	LPNNTASWF	0.05582	Consensus (ann/comblib_sidney2008/smm)	0.3	99.40% (495/498)	Non-Toxin	
578	N Protein	B*51:01	10	LPYGANKDGI	-0.09978	Consensus (ann/smm)	0.23	99.20% (494/498)	Non-Toxin	
579	N Protein	A*01:01	9	LSPRWYFYY	0.35734	Consensus (ann/smm)	0.22	99.60% (496/498)	Non-Toxin	
580	N Protein	B*44:02	9	MEVTPSGTW	-0.06279	Consensus (ann/smm)	0.06	97.39% (485/498)	Non-Toxin	
581	N Protein	B*44:03	9	MEVTPSGTW	-0.06279	Consensus (ann/smm)	0.13	97.39% (485/498)	Non-Toxin	
582	N Protein	B*40:01	10	MEVTPSGTWL	0.07464	Consensus (ann/smm)	0.2	97.39% (485/498)	Non-Toxin	
583	N Protein	A*01:01	11	NSSPDDQIGYY	0.01726	Consensus (ann/smm)	0.49	99.40% (495/498)	Non-Toxin	
584	N Protein	A*68:02	9	NTASWFTAL	0.22775	Consensus (ann/comblib_sidney2008/smm)	0.4	99.60% (496/498)	Non-Toxin	
585	N Protein	A*68:02	10	NTASWFTALT	0.23901	Consensus (ann/smm)	0.48	99.40% (495/498)	Non-Toxin	
586	N Protein	B*44:03	10	QELIRQGTDY	0.14554	Consensus (ann/smm)	0.25	97.19% (484/498)	Non-Toxin	
587	N Protein	B*44:02	10	QELIRQGTDY	0.14554	Consensus (ann/smm)	0.28	97.19% (484/498)	Non-Toxin	
588	N Protein	B*07:02	10	RPQGLPNNTA	-0.01397	Consensus (ann/smm)	0.46	99.40% (495/498)	Non-Toxin	
589	N Protein	B*15:01	10	RQKRTATKAY	-0.06462	Consensus (ann/smm)	0.2	97.79% (487/498)	Non-Toxin	
590	N Protein	A*30:02	10	RQKRTATKAY	-0.06462	Consensus (ann/smm)	0.28	97.79% (487/498)	Non-Toxin	
591	N Protein	A*30:01	9	RSKQRRPQG	-0.16448	Consensus (ann/comblib_sidney2008/smm)	0.4	99.60% (496/498)	Non-Toxin	
592	N Protein	A*30:01	9	RSRNSSRNS	-0.26664	Consensus (ann/comblib_sidney2008/smm)	0.4	93.37% (465/498)	Non-Toxin	
593	N Protein	A*68:01	10	SASAFFGMSR	0.00071	Consensus (ann/smm)	0.31	97.59% (486/498)	Non-Toxin	
594	N Protein	A*11:01	10	SASAFFGMSR	0.00071	Consensus (ann/smm)	0.47	97.59% (486/498)	Non-Toxin	
595	N Protein	B*07:02	9	SPRWYFYYL	0.34101	Consensus (ann/comblib_sidney2008/smm)	0.2	99.60% (496/498)	Non-Toxin	
596	N Protein	B*08:01	9	SPRWYFYYL	0.34101	Consensus (ann/comblib_sidney2008/smm)	0.2	99.60% (496/498)	Non-Toxin	
597	N Protein	A*01:01	10	SSPDDQIGYY	0.07924	Consensus (ann/smm)	0.2	99.40% (495/498)	Non-Toxin	
598	N Protein	A*30:02	10	SSPDDQIGYY	0.07924	Consensus (ann/smm)	0.42	99.40% (495/498)	Non-Toxin	
599	N Protein	B*35:01	9	TPSGTWLTY	0.24003	Consensus (ann/comblib_sidney2008/smm)	0.2	97.39% (485/498)	Non-Toxin	
600	N Protein	B*53:01	9	TPSGTWLTY	0.24003	Consensus (ann/comblib_sidney2008/smm)	0.3	97.39% (485/498)	Non-Toxin	
601	N Protein	B*53:01	10	YGANKDGIIW	0.03977	Consensus (ann/smm)	0.24	99.40% (495/498)	Non-Toxin	
602	N Protein	A*24:02	9	YYRRATRRI	0.21744	Consensus (ann/smm)	0.26	99.40% (495/498)	Non-Toxin	
603	N Protein	A*33:01	10	YYRRATRRIR	0.31494	Consensus (ann/smm)	0.32	99.40% (495/498)	Non-Toxin	
S.No.	ORF	Allele	Length	Peptide	Immunogenicity	Method used	Percentile Rank	Conservancy	Toxicity	
604	ORF10	A*02:06	10	FAFPFTIYSL	0.20414	Consensus (ann/smm)	0.48	99.79% (478/479)	Non-Toxin	
605	ORF10	B*51:01	8	FPFTIYSL	0.06356	Consensus (ann/smm)	0.39	100.00% (479/479)	Non-Toxin	
606	ORF10	B*51:01	9	FPFTIYSLL	0.05708	Consensus (ann/comblib_sidney2008/smm)	0.3	100.00% (479/479)	Non-Toxin	
607	ORF10	B*53:01	9	FPFTIYSLL	0.05708	Consensus (ann/comblib_sidney2008/smm)	0.5	100.00% (479/479)	Non-Toxin	
608	ORF10	B*53:01	10	FPFTIYSLLL	0.03149	Consensus (ann/smm)	0.13	100.00% (479/479)	Non-Toxin	
609	ORF10	B*51:01	10	FPFTIYSLLL	0.03149	Consensus (ann/smm)	0.14	100.00% (479/479)	Non-Toxin	
610	ORF10	A*68:01	10	FTIYSLLLCR	-0.18372	Consensus (ann/smm)	0.12	100.00% (479/479)	Non-Toxin	
611	ORF10	A*33:01	10	FTIYSLLLCR	-0.18372	Consensus (ann/smm)	0.35	100.00% (479/479)	Non-Toxin	
612	ORF10	A*23:01	10	GYINVFAFPF	0.32004	Consensus (ann/smm)	0.11	99.37% (476/479)	Non-Toxin	
613	ORF10	A*24:02	10	GYINVFAFPF	0.32004	Consensus (ann/smm)	0.13	99.37% (476/479)	Non-Toxin	
614	ORF10	B*35:01	9	MGYINVFAF	0.28694	Consensus (ann/comblib_sidney2008/smm)	0.1	99.37% (476/479)	Non-Toxin	
615	ORF10	A*23:01	9	MGYINVFAF	0.28694	Consensus (ann/smm)	0.5	99.37% (476/479)	Non-Toxin	
616	ORF10	A*23:01	11	MGYINVFAFPF	0.40977	Consensus (ann/smm)	0.41	99.37% (476/479)	Non-Toxin	
617	ORF10	A*68:02	9	NVFAFPFTI	0.30241	Consensus (ann/comblib_sidney2008/smm)	0.4	99.58% (477/479)	Non-Toxin	
618	ORF10	A*32:01	9	NVFAFPFTI	0.30241	Consensus (ann/comblib_sidney2008/smm)	0.5	99.58% (477/479)	Non-Toxin	
619	ORF10	A*26:01	10	NVFAFPFTIY	0.40129	Consensus (ann/smm)	0.48	99.58% (477/479)	Non-Toxin	
620	ORF10	A*68:01	9	TIYSLLLCR	-0.22977	Consensus (ann/smm)	0.47	100.00% (479/479)	Non-Toxin	
621	ORF10	B*53:01	9	YINVFAFPF	0.28259	Consensus (ann/comblib_sidney2008/smm)	0.35	99.37% (476/479)	Non-Toxin	

622	ORF10	A*32:01	9	YINVFAFPF	0.28259	Consensus (ann/comblib_sidney2008/smm)	0.4	99.37% (476/479)	Non-Toxin	
S.No.	ORF	Allele	Length	Peptide	Immunogenicity	Method used	Percentile Rank	Conservancy	Toxicity	NSP
623	ORF-1ab	A*30:02	10	ASFYYVWKSY	0.00073	Consensus (ann/smm)	0.07	99.77%(452/453)	Non-Toxin	nsp3
624	ORF-1ab	A*30:02	10	CANGQVFGLY	0.09172	Consensus (ann/smm)	0.1	99.55%(451/453)	Non-Toxin	nsp13
625	ORF-1ab	A*30:02	10	CANGQVFGLY	0.09172	Consensus (ann/smm)	0.1	99.55%(451/453)	Non-Toxin	nsp13
626	ORF-1ab	A*33:01	11	CLAYYFMRFRR	0.12614	ann	0.07	100%(453/453)	Non-Toxin	nsp4
627	ORF-1ab	A*01:01	9	CTDDNALAY	0.07355	Consensus (ann/smm)	0.06	99.77%(452/453)	Non-Toxin	nsp9
628	ORF-1ab	A*01:01	10	CTDDNALAYY	0.08174	Consensus (ann/smm)	0.06	99.77%(452/453)	Non-Toxin	nsp9
629	ORF-1ab	B*44:03	9	DEWSMATYY	-0.19814	Consensus (ann/smm)	0.07	99.55%(451/453)	Non-Toxin	nsp3
630	ORF-1ab	A*26:01	9	ETISLAGSY	-0.1653	Consensus (ann/smm)	0.1	100%(453/453)	Non-Toxin	nsp3
631	ORF-1ab	A*68:01	10	ETISLAGSYK	-0.20585	Consensus (ann/smm)	0.06	100%(453/453)	Non-Toxin	nsp3
632	ORF-1ab	B*35:01	9	FAVDAAKAY	-0.04849	Consensus (ann/comblib_sidney2008/smm)	0.1	98.89%(448/453)	Non-Toxin	nsp10
633	ORF-1ab	A*02:01	10	FLFVAAIFYL	0.37766	Consensus (ann/smm)	0.06	99.77%(452/453)	Non-Toxin	nsp4
634	ORF-1ab	A*02:03	9	FLNGSCGSV	-0.24791	Consensus (ann/smm)	0.06	99.55%(451/453)	Non-Toxin	nsp5
635	ORF-1ab	B*53:01	10	FPLCANGQVF	-0.06779	Consensus (ann/smm)	0.1	99.55%(451/453)	Non-Toxin	nsp13
636	ORF-1ab	B*53:01	10	FPLCANGQVF	-0.06779	Consensus (ann/smm)	0.1	99.55%(451/453)	Non-Toxin	nsp13
637	ORF-1ab	A*33:01	11	FYWFFSNYLKR	-0.00254	ann	0.04	98.67%(447/453)	Non-Toxin	nsp4
638	ORF-1ab	B*53:01	10	IPLMYKGLPW	-0.37784	Consensus (ann/smm)	0.07	100%(453/453)	Non-Toxin	nsp14
639	ORF-1ab	B*53:01	10	IPLMYKGLPW	-0.37784	Consensus (ann/smm)	0.07	100%(453/453)	Non-Toxin	nsp14
640	ORF-1ab	B*07:02	9	IPRRNVATL	0.15714	Consensus (ann/comblib_sidney2008/smm)	0.1	100%(453/453)	Non-Toxin	nsp13
641	ORF-1ab	B*07:02	9	IPRRNVATL	0.15714	Consensus (ann/comblib_sidney2008/smm)	0.1	100%(453/453)	Non-Toxin	nsp13
642	ORF-1ab	B*58:01	8	ISNSWLMW	-0.11151	ann	0.05	100%(453/453)	Non-Toxin	nsp3
643	ORF-1ab	A*30:02	9	KMNYQVNGY	-0.06542	Consensus (ann/smm)	0.07	100%(453/453)	Non-Toxin	nsp14
644	ORF-1ab	A*30:02	9	KMNYQVNGY	-0.06542	Consensus (ann/smm)	0.07	100%(453/453)	Non-Toxin	nsp14
645	ORF-1ab	A*30:01	9	KVKYLYFIK	0.08856	Consensus (ann/comblib_sidney2008/smm)	0.1	100%(453/453)	Non-Toxin	nsp9
646	ORF-1ab	B*15:01	9	LMNVLTLVY	0.07994	Consensus (ann/comblib_sidney2008/smm)	0.1	98.01%(444/453)	Non-Toxin	nsp6
647	ORF-1ab	B*35:01	9	LPSLATVAY	0.06748	Consensus (ann/comblib_sidney2008/smm)	0.1	98.01%(444/453)	Non-Toxin	nsp6
648	ORF-1ab	B*53:01	10	LPVNVAFELW	0.27341	Consensus (ann/smm)	0.06	100%(453/453)	Non-Toxin	nsp15
649	ORF-1ab	A*33:01	11	MYKGLPWNVVR	0.21107	ann	0.06	100%(453/453)	Non-Toxin	nsp14
650	ORF-1ab	A*33:01	11	MYKGLPWNVVR	0.21107	ann	0.06	100%(453/453)	Non-Toxin	nsp14
651	ORF-1ab	B*44:02	9	QEILGTVSW	0.03976	Consensus (ann/smm)	0.06	100%(453/453)	Non-Toxin	nsp3
652	ORF-1ab	A*32:01	9	RMYIFFASF	0.29328	Consensus (ann/comblib_sidney2008/smm)	0.1	99.11%(449/453)	Non-Toxin	nsp3
653	ORF-1ab	B*15:01	9	RMYIFFASF	0.29328	Consensus (ann/comblib_sidney2008/smm)	0.1	99.11%(449/453)	Non-Toxin	nsp3
654	ORF-1ab	A*30:02	10	RMYIFFASFY	0.32633	Consensus (ann/smm)	0.06	99.11%(449/453)	Non-Toxin	nsp3
655	ORF-1ab	A*03:01	10	RMYIFFASFY	0.32633	Consensus (ann/smm)	0.1	99.11%(449/453)	Non-Toxin	nsp3
656	ORF-1ab	A*30:02	10	RYFRLTLGVY	0.15936	Consensus (ann/smm)	0.06	100%(453/453)	Non-Toxin	nsp6
657	ORF-1ab	B*44:02	11	SEMVMCGGSLY	-0.32016	ann	0.03	100%(453/453)	Non-Toxin	nsp12
658	ORF-1ab	A*11:01	10	SIINNTVYTK	0.12661	Consensus (ann/smm)	0.06	100%(453/453)	Non-Toxin	nsp15
659	ORF-1ab	A*11:01	9	STFNVPMEK	-0.02845	Consensus (ann/smm)	0.06	99.77%(452/453)	Non-Toxin	nsp3
660	ORF-1ab	A*30:02	9	STNVTIATY	0.25822	Consensus (ann/smm)	0.09	99.33%(450/453)	Non-Toxin	nsp3
661	ORF-1ab	A*32:01	8	TYNLWNTF	0.22911	ann	0.1	98.67%(447/453)	Non-Toxin	nsp14
662	ORF-1ab	B*35:01	9	VPFWITIAY	0.56221	Consensus (ann/comblib_sidney2008/smm)	0.1	100%(453/453)	Non-Toxin	nsp4
663	ORF-1ab	B*08:01	10	YAYLRKHFSM	-0.13937	Consensus (ann/smm)	0.07	100%(453/453)	Non-Toxin	nsp12
664	ORF-1ab	A*02:06	10	YIFFASFYYV	0.13772	Consensus (ann/smm)	0.07	99.55%(451/453)	Non-Toxin	nsp3
665	ORF-1ab	A*02:06	10	YILFTRFFYV	0.40924	Consensus (ann/smm)	0.07	100%(453/453)	Non-Toxin	nsp3
666	ORF-1ab	B*53:01	10	YVMHANYIFW	0.18459	Consensus (ann/smm)	0.1	98.89%(448/453)	Non-Toxin	nsp16
667	ORF-1ab	A*33:01	8	YYFMRFRR	0.06558	ann	0.1	100%(453/453)	Non-Toxin	nsp4
S.No.	ORF	Allele	Length	Peptide	Immunogenicity	Method used	Percentile Rank	Conservancy	Toxicity	
668	ORF3a	B*44:02	11	AGLEAPFLYLY	0.21841	ann	0.41	96.67%(465/481)	Non-Toxin	
669	ORF3a	A*02:03	9	ALSKGVHFV	-0.10314	Consensus (ann/smm)	0.12	99.67%(477/481)	Non-Toxin	
670	ORF3a	A*02:01	9	ALSKGVHFV	-0.10314	Consensus (ann/comblib_sidney2008/smm)	0.4	99.67%(477/481)	Non-Toxin	

671	ORF3a	B*07:02	9	APFLYLYAL	0.03254	Consensus (ann/comblib_sidney2008/smm)	0.5	96.88%(466/481)	Non-Toxin	
672	ORF3a	A*30:01	9	ASKIITLKK	0.0947	Consensus (ann/comblib_sidney2008/smm)	0.4	99.37%(478/481)	Non-Toxin	
673	ORF3a	A*11:01	9	ASKIITLKK	0.0947	Consensus (ann/smm)	0.46	99.37%(478/481)	Non-Toxin	
674	ORF3a	B*58:01	9	ASLPFGWLI	0.3116	Consensus (ann/comblib_sidney2008/smm)	0.3	98.96%(476/481)	Non-Toxin	
675	ORF3a	A*30:02	9	CWHTNCYDY	0.00235	Consensus (ann/smm)	0.38	97.29%(468/481)	Non-Toxin	
676	ORF3a	A*68:01	9	DATPSDFVR	-0.01586	Consensus (ann/smm)	0.21	99.58%(479/481)	Non-Toxin	
677	ORF3a	A*26:01	10	DTGVEHVTFF	0.32156	Consensus (ann/smm)	0.41	99.58%(479/481)	Non-Toxin	
678	ORF3a	A*26:01	10	EIKDATPSDF	-0.10888	Consensus (ann/smm)	0.28	99.58%(479/481)	Non-Toxin	
679	ORF3a	A*01:01	9	FLCWHTNCY	0.23647	Consensus (ann/smm)	0.42	97.29%(468/481)	Non-Toxin	
680	ORF3a	A*68:01	9	FLQSINFVR	0.04236	Consensus (ann/smm)	0.23	97.08%(467/481)	Non-Toxin	
681	ORF3a	A*33:01	9	FLQSINFVR	0.04236	Consensus (ann/smm)	0.39	97.08%(467/481)	Non-Toxin	
682	ORF3a	B*15:01	9	FLYLYALVY	0.03563	Consensus (ann/comblib_sidney2008/smm)	0.42	96.88%(466/481)	Non-Toxin	
683	ORF3a	A*01:01	9	FLYLYALVY	0.03563	Consensus (ann/smm)	0.45	96.88%(466/481)	Non-Toxin	
684	ORF3a	A*23:01	10	FLYLYALVYF	0.04438	Consensus (ann/smm)	0.27	96.88%(466/481)	Non-Toxin	
685	ORF3a	A*02:03	10	FMRIFTIGTV	0.47908	Consensus (ann/smm)	0.17	99.37%(478/481)	Non-Toxin	
686	ORF3a	A*68:01	9	FTIGTVTLK	0.18024	Consensus (ann/smm)	0.16	99.37%(478/481)	Non-Toxin	
687	ORF3a	A*11:01	9	FTIGTVTLK	0.18024	Consensus (ann/smm)	0.37	99.37%(478/481)	Non-Toxin	
688	ORF3a	A*26:01	9	FVCNLLLLF	-0.06109	Consensus (ann/smm)	0.36	97.92%(471/481)	Non-Toxin	
689	ORF3a	A*02:06	10	FVCNLLLLFV	0.00299	Consensus (ann/smm)	0.21	97.50%(469/481)	Non-Toxin	
690	ORF3a	A*02:01	10	FVCNLLLLFV	0.00299	Consensus (ann/smm)	0.42	97.50%(469/481)	Non-Toxin	
691	ORF3a	B*57:01	9	FVRIIMRLW	0.15222	Consensus (ann/smm)	0.27	96.67%(465/481)	Non-Toxin	
692	ORF3a	A*01:01	10	GLEAPFLYLY	0.15503	Consensus (ann/smm)	0.43	97.08%(467/481)	Non-Toxin	
693	ORF3a	A*23:01	9	HFVCNLLLL	-0.07343	Consensus (ann/smm)	0.48	97.92%(471/481)	Non-Toxin	
694	ORF3a	A*23:01	10	HFVCNLLLLF	-0.08423	Consensus (ann/smm)	0.28	97.92%(471/481)	Non-Toxin	
695	ORF3a	A*26:01	9	HTIDGSSGV	-0.17703	Consensus (ann/smm)	0.23	95.42%(459/481)	Non-Toxin	
696	ORF3a	A*68:02	9	HTIDGSSGV	-0.17703	Consensus (ann/comblib_sidney2008/smm)	0.3	95.42%(459/481)	Non-Toxin	
697	ORF3a	A*68:01	9	HVTFFIYNK	0.36278	Consensus (ann/smm)	0.16	99.79%(480/481)	Non-Toxin	
698	ORF3a	A*11:01	9	HVTFFIYNK	0.36278	Consensus (ann/smm)	0.24	99.79%(480/481)	Non-Toxin	
699	ORF3a	A*30:01	9	HVTFFIYNK	0.36278	Consensus (ann/comblib_sidney2008/smm)	0.34	99.79%(480/481)	Non-Toxin	
700	ORF3a	B*58:01	9	IIMRLWLCW	0.15193	Consensus (ann/comblib_sidney2008/smm)	0.3	96.67%(465/481)	Non-Toxin	
701	ORF3a	B*57:01	9	IIMRLWLCW	0.15193	Consensus (ann/smm)	0.49	96.67%(465/481)	Non-Toxin	
702	ORF3a	A*03:01	10	IIMRLWLCWK	0.27346	Consensus (ann/smm)	0.13	96.67%(465/481)	Non-Toxin	
703	ORF3a	A*11:01	10	IIMRLWLCWK	0.27346	Consensus (ann/smm)	0.36	96.67%(465/481)	Non-Toxin	
704	ORF3a	A*03:01	9	IMRLWLCWK	0.29482	Consensus (ann/smm)	0.34	96.67%(465/481)	Non-Toxin	
705	ORF3a	A*31:01	11	IMRLWLCWKCR	0.15305	Consensus (ann/smm)	0.41	96.67%(465/481)	Non-Toxin	
706	ORF3a	A*33:01	11	IMRLWLCWKCR	0.15305	ann	0.46	96.67%(465/481)	Non-Toxin	
707	ORF3a	A*33:01	9	INFVRIIMR	0.26494	Consensus (ann/smm)	0.41	96.88%(466/481)	Non-Toxin	
708	ORF3a	B*53:01	9	IPIQASLPF	-0.20683	Consensus (ann/comblib_sidney2008/smm)	0.2	99.67%(477/481)	Non-Toxin	
709	ORF3a	B*35:01	9	IPIQASLPF	-0.20683	Consensus (ann/comblib_sidney2008/smm)	0.2	99.67%(477/481)	Non-Toxin	
710	ORF3a	B*07:02	9	IPIQASLPF	-0.20683	Consensus (ann/comblib_sidney2008/smm)	0.3	99.67%(477/481)	Non-Toxin	
711	ORF3a	B*51:01	10	IPYNSVTSSI	-0.32835	Consensus (ann/smm)	0.11	97.92%(471/481)	Non-Toxin	
712	ORF3a	B*07:02	10	IPYNSVTSSI	-0.32835	Consensus (ann/smm)	0.46	97.92%(471/481)	Non-Toxin	
713	ORF3a	B*53:01	9	IQASLPFGW	-0.05641	Consensus (ann/comblib_sidney2008/smm)	0.4	98.96%(476/481)	Non-Toxin	
714	ORF3a	B*58:01	9	IQASLPFGW	-0.05641	Consensus (ann/comblib_sidney2008/smm)	0.5	98.96%(476/481)	Non-Toxin	
715	ORF3a	B*15:01	10	IVGVALLAVF	0.12654	Consensus (ann/smm)	0.32	99.67%(477/481)	Non-Toxin	
716	ORF3a	B*57:01	9	KIITLKKRW	-0.2833	Consensus (ann/smm)	0.23	99.67%(477/481)	Non-Toxin	
717	ORF3a	B*58:01	9	KIITLKKRW	-0.2833	Consensus (ann/comblib_sidney2008/smm)	0.4	99.67%(477/481)	Non-Toxin	
718	ORF3a	B*44:03	9	LEAPFLYLY	0.0955	Consensus (ann/smm)	0.24	97.29%(468/481)	Non-Toxin	
719	ORF3a	B*44:02	9	LEAPFLYLY	0.0955	Consensus (ann/smm)	0.4	97.29%(468/481)	Non-Toxin	
720	ORF3a	B*40:01	11	LEAPFLYLYAL	0.11044	ann	0.49	96.88%(466/481)	Non-Toxin	
721	ORF3a	A*02:06	10	LIVGVALLAV	0.12886	Consensus (ann/smm)	0.2	99.37%(478/481)	Non-Toxin	

722	ORF3a	A*03:01	10	LLAVFQSASK	-0.16393	Consensus (ann/smm)	0.28	77.33%(372/481)	Non-Toxin	
723	ORF3a	B*15:01	11	LLVAAGLEAPF	0.23386	ann	0.28	97.08%(467/481)	Non-Toxin	
724	ORF3a	B*51:01	10	LPFGWLIVGV	0.45692	Consensus (ann/smm)	0.22	98.96%(476/481)	Non-Toxin	
725	ORF3a	B*15:01	10	LVAAGLEAPF	0.19506	Consensus (ann/smm)	0.27	97.08%(467/481)	Non-Toxin	
726	ORF3a	A*23:01	9	LYLYALVYF	0.05302	Consensus (ann/smm)	0.11	96.88%(466/481)	Non-Toxin	
727	ORF3a	A*24:02	9	LYLYALVYF	0.05302	Consensus (ann/smm)	0.14	96.88%(466/481)	Non-Toxin	
728	ORF3a	A*23:01	10	LYLYALVYFL	0.12412	Consensus (ann/smm)	0.18	96.88%(466/481)	Non-Toxin	
729	ORF3a	A*24:02	10	LYLYALVYFL	0.12412	Consensus (ann/smm)	0.35	96.88%(466/481)	Non-Toxin	
730	ORF3a	A*32:01	11	MRIFTIGTVTL	0.45546	ann	0.35	99.37%(478/481)	Non-Toxin	
731	ORF3a	A*02:06	9	NLLLLFVTV	0.14216	Consensus (ann/smm)	0.49	97.50%(469/481)	Non-Toxin	
732	ORF3a	B*58:01	8	QASLPFGW	0.06314	ann	0.35	98.96%(476/481)	Non-Toxin	
733	ORF3a	A*68:01	10	QSASKIITLK	-0.08261	Consensus (ann/smm)	0.4	77.33%(372/481)	Non-Toxin	
734	ORF3a	A*32:01	11	RIFTIGTVTLK	0.3426	ann	0.36	99.37%(478/481)	Non-Toxin	
735	ORF3a	A*31:01	9	RLWLCWKCR	0.00325	Consensus (ann/smm)	0.3	96.88%(466/481)	Non-Toxin	
736	ORF3a	A*11:01	9	SASKIITLK	0.01046	Consensus (ann/smm)	0.3	99.37%(478/481)	Non-Toxin	
737	ORF3a	A*68:01	9	SASKIITLK	0.01046	Consensus (ann/smm)	0.4	99.37%(478/481)	Non-Toxin	
738	ORF3a	A*11:01	10	SASKIITLKK	-0.11032	Consensus (ann/smm)	0.35	99.37%(478/481)	Non-Toxin	
739	ORF3a	B*44:03	10	SEHDYQIGGY	0.0901	Consensus (ann/smm)	0.19	99.58%(479/481)	Non-Toxin	
740	ORF3a	B*44:02	10	SEHDYQIGGY	0.0901	Consensus (ann/smm)	0.38	99.58%(479/481)	Non-Toxin	
741	ORF3a	A*68:01	10	SINFVRIIMR	0.3413	Consensus (ann/smm)	0.39	96.88%(466/481)	Non-Toxin	
742	ORF3a	A*02:06	9	TQLSTDTGV	-0.05883	Consensus (ann/smm)	0.39	99.58%(479/481)	Non-Toxin	
743	ORF3a	A*01:01	10	TTSPISEHDY	0.03815	Consensus (ann/smm)	0.22	97.92%(471/481)	Non-Toxin	
744	ORF3a	A*02:06	9	TVYSHLLLV	-0.16245	Consensus (ann/smm)	0.44	97.92%(471/481)	Non-Toxin	
745	ORF3a	B*44:03	9	VEHVTFFIY	0.3766	Consensus (ann/smm)	0.18	99.58%(479/481)	Non-Toxin	
746	ORF3a	A*32:01	9	VTFFIYNKI	0.15046	Consensus (ann/comblib_sidney2008/smm)	0.4	99.58%(479/481)	Non-Toxin	
747	ORF3a	A*24:02	9	VYFLQSINF	-0.13315	Consensus (ann/smm)	0.23	96.88%(466/481)	Non-Toxin	
748	ORF3a	A*23:01	9	VYFLQSINF	-0.13315	Consensus (ann/smm)	0.24	96.88%(466/481)	Non-Toxin	
749	ORF3a	A*33:01	11	VYFLQSINFVR	-0.00063	ann	0.43	96.88%(466/481)	Non-Toxin	
750	ORF3a	B*40:01	11	WESGVKDCVVL	-0.15959	ann	0.21	96.25%(463/481)	Non-Toxin	
751	ORF3a	A*01:01	10	YFLCWHTNCY	0.18893	Consensus (ann/smm)	0.48	97.08%(467/481)	Non-Toxin	
752	ORF3a	A*33:01	10	YFLQSINFVR	-0.03483	Consensus (ann/smm)	0.2	96.88%(466/481)	Non-Toxin	
753	ORF3a	A*02:01	9	YLYALVYFL	0.13151	Consensus (ann/comblib_sidney2008/smm)	0.1	96.88%(466/481)	Non-Toxin	
754	ORF3a	A*02:03	9	YLYALVYFL	0.13151	Consensus (ann/smm)	0.18	96.88%(466/481)	Non-Toxin	
755	ORF3a	A*02:06	9	YLYALVYFL	0.13151	Consensus (ann/smm)	0.37	96.88%(466/481)	Non-Toxin	
756	ORF3a	A*24:02	9	YYQLYSTQL	-0.24301	Consensus (ann/smm)	0.29	99.58%(479/481)	Non-Toxin	
S.No.	ORF	Allele	Length	Peptide	Immunogenicity	Method used	Percentile Rank	Conservancy	Toxicity	
757	ORF6	B*40:01	8	AEILLIIM	0.25884	Consensus (ann/smm)	0.41	99.58% (479/481)	Non-Toxin	
758	ORF6	B*44:02	11	AEILLIIMRTF	0.1815	ann	0.06	99.58% (479/481)	Non-Toxin	
759	ORF6	A*02:06	9	FQVTIAEIL	0.38115	Consensus (ann/smm)	0.52	99.17% (477/481)	Non-Toxin	
760	ORF6	A*03:01	10	ILLIIMRTFK	0.2388	Consensus (ann/smm)	0.17	99.58% (479/481)	Non-Toxin	
761	ORF6	A*32:01	9	IMRTFKVSI	-0.09496	Consensus (ann/comblib_sidney2008/smm)	0.44	99.79% (480/481)	Non-Toxin	
762	ORF6	A*30:02	9	KVSIWNLDY	0.29343	Consensus (ann/smm)	0.41	99.58% (479/481)	Non-Toxin	
763	ORF6	A*03:01	9	LLIIMRTFK	0.156	Consensus (ann/smm)	0.36	99.58% (479/481)	Non-Toxin	
764	ORF6	A*30:02	10	LSKSLTENKY	-0.24668	Consensus (ann/smm)	0.48	98.75% (475/481)	Non-Toxin	
765	ORF6	B*57:01	8	RTFKVSIW	-0.18221	ann	0.05	99.79% (480/481)	Non-Toxin	
766	ORF6	B*58:01	8	RTFKVSIW	-0.18221	ann	0.07	99.79% (480/481)	Non-Toxin	
767	ORF6	A*32:01	8	RTFKVSIW	-0.18221	ann	0.44	99.79% (480/481)	Non-Toxin	
768	ORF6	A*32:01	9	SIWNLDYII	0.15011	Consensus (ann/comblib_sidney2008/smm)	0.2	99.58% (479/481)	Non-Toxin	
769	ORF6	B*58:01	9	VTIAEILLI	0.28951	Consensus (ann/comblib_sidney2008/smm)	0.34	99.17% (477/481)	Non-Toxin	
S.No.	ORF	Allele	Length	Peptide	Immunogenicity	Method used	Percentile Rank	Conservancy	Toxicity	
770	ORF7a	B*44:02	10	ADNKFALTCF	-0.07618	Consensus (ann/smm)	0.36	98.75% (474/480)	Non-Toxin	

771	ORF7a	A*03:01	10	CVRGTTVLLK	0.14952	Consensus (ann/smm)	0.17	99.58% (478/480)	Non-Toxin	
772	ORF7a	A*26:01	9	EVQELYSPI	-0.09723	Consensus (ann/smm)	0.21	98.12% (471/480)	Non-Toxin	
773	ORF7a	A*68:02	9	EVQELYSPI	-0.09723	Consensus (ann/comblib_sidney2008/smm)	0.5	98.12% (471/480)	Non-Toxin	
774	ORF7a	A*26:01	10	EVQELYSPIF	-0.03858	Consensus (ann/smm)	0.22	98.12% (471/480)	Non-Toxin	
775	ORF7a	B*53:01	10	FALTCFSTQF	-0.09369	Consensus (ann/smm)	0.22	98.75% (474/480)	Non-Toxin	
776	ORF7a	A*33:01	10	FITLCFTLKR	-0.03588	Consensus (ann/smm)	0.32	97.92% (470/480)	Non-Toxin	
777	ORF7a	A*68:01	10	FITLCFTLKR	-0.03588	Consensus (ann/smm)	0.48	97.92% (470/480)	Non-Toxin	
778	ORF7a	B*15:01	9	FLIVAAIVF	0.29611	Consensus (ann/comblib_sidney2008/smm)	0.2	98.96% (475/480)	Non-Toxin	
779	ORF7a	A*02:01	10	FLIVAAIVFI	0.38946	Consensus (ann/smm)	0.21	98.33% (472/480)	Non-Toxin	
780	ORF7a	A*32:01	9	GTYEGNSPF	-0.01964	Consensus (ann/comblib_sidney2008/smm)	0.4	98.96% (475/480)	Non-Toxin	
781	ORF7a	A*23:01	10	IFLIVAAIVF	0.38189	Consensus (ann/smm)	0.34	98.33% (472/480)	Non-Toxin	
782	ORF7a	B*15:01	10	IFLIVAAIVF	0.38189	Consensus (ann/smm)	0.47	98.33% (472/480)	Non-Toxin	
783	ORF7a	A*03:01	10	ITLCFTLKRK	-0.06825	Consensus (ann/smm)	0.17	97.92% (470/480)	Non-Toxin	
784	ORF7a	A*11:01	10	ITLCFTLKRK	-0.06825	Consensus (ann/smm)	0.33	97.92% (470/480)	Non-Toxin	
785	ORF7a	A*32:01	9	KIILFLALI	0.16214	Consensus (ann/comblib_sidney2008/smm)	0.4	99.58% (478/480)	Non-Toxin	
786	ORF7a	B*08:01	9	MKIILFLAL	0.29002	Consensus (ann/comblib_sidney2008/smm)	0.5	99.58% (478/480)	Non-Toxin	
787	ORF7a	B*40:01	9	QELYSPIFL	0.00186	Consensus (ann/smm)	0.19	98.33% (472/480)	Non-Toxin	
788	ORF7a	B*44:02	10	QELYSPIFLI	0.03838	Consensus (ann/smm)	0.22	98.33% (472/480)	Non-Toxin	
789	ORF7a	B*44:03	10	QELYSPIFLI	0.03838	Consensus (ann/smm)	0.25	98.33% (472/480)	Non-Toxin	
790	ORF7a	A*03:01	10	QLRARSVSPK	-0.16177	Consensus (ann/smm)	0.16	98.33% (472/480)	Non-Toxin	
791	ORF7a	A*30:01	8	RARSVSPK	-0.27456	ann	0.11	98.33% (472/480)	Non-Toxin	
792	ORF7a	A*30:01	9	RARSVSPKL	-0.40056	Consensus (ann/comblib_sidney2008/smm)	0.2	98.33% (472/480)	Non-Toxin	
793	ORF7a	B*58:01	9	RSVSPKLFI	-0.30783	Consensus (ann/comblib_sidney2008/smm)	0.2	98.33% (472/480)	Non-Toxin	
794	ORF7a	A*31:01	10	RSVSPKLFIR	-0.20775	Consensus (ann/smm)	0.31	98.33% (472/480)	Non-Toxin	
795	ORF7a	B*07:02	10	SPIFLIVAAI	0.37454	Consensus (ann/smm)	0.47	98.33% (472/480)	Non-Toxin	
796	ORF7a	A*31:01	9	SVSPKLFIR	-0.10874	Consensus (ann/smm)	0.45	98.33% (472/480)	Non-Toxin	
797	ORF7a	A*11:01	9	SVSPKLFIR	-0.10874	Consensus (ann/smm)	0.46	98.33% (472/480)	Non-Toxin	
798	ORF7a	A*01:01	10	TLATCELYHY	0.1021	Consensus (ann/smm)	0.35	99.79% (479/480)	Non-Toxin	
799	ORF7a	B*40:01	11	TYEGNSPFHPL	0.01942	ann	0.46	98.96% (475/480)	Non-Toxin	
800	ORF7a	A*23:01	9	VFITLCFTL	0.14219	Consensus (ann/smm)	0.3	98.33% (472/480)	Non-Toxin	
801	ORF7a	A*24:02	9	VFITLCFTL	0.14219	Consensus (ann/smm)	0.44	98.33% (472/480)	Non-Toxin	
802	ORF7a	B*40:01	10	YEGNSPFHPL	-0.03639	Consensus (ann/smm)	0.28	98.96% (475/480)	Non-Toxin	
S.No.	ORF	Allele	Length	Peptide	Immunogenicity	Method used	Percentile Rank	Conservancy	Toxicity	
803	ORF7b	A*02:01	10	CFLAFLLFLV	0.22085	Consensus (ann/smm)	0.47	98.31% (232/236)	Non-Toxin	
804	ORF7b	A*02:06	10	CFLAFLLFLV	0.22085	Consensus (ann/smm)	0.48	98.31% (232/236)	Non-Toxin	
805	ORF7b	A*23:01	9	DFYLCFLAF	0.05884	Consensus (ann/smm)	0.29	98.31% (232/236)	Non-Toxin	
806	ORF7b	A*33:01	10	DFYLCFLAFL	0.14012	Consensus (ann/smm)	0.4	98.31% (232/236)	Non-Toxin	
807	ORF7b	A*02:03	9	FLAFLLFLV	0.20158	Consensus (ann/smm)	0.07	98.31% (232/236)	Non-Toxin	
808	ORF7b	A*02:06	9	FLAFLLFLV	0.20158	Consensus (ann/smm)	0.08	98.31% (232/236)	Non-Toxin	
809	ORF7b	A*02:01	9	FLAFLLFLV	0.20158	Consensus (ann/comblib_sidney2008/smm)	0.1	98.31% (232/236)	Non-Toxin	
810	ORF7b	A*68:02	9	FLAFLLFLV	0.20158	Consensus (ann/comblib_sidney2008/smm)	0.33	98.31% (232/236)	Non-Toxin	
811	ORF7b	A*02:01	10	FLAFLLFLVL	0.23386	Consensus (ann/smm)	0.26	98.31% (232/236)	Non-Toxin	
812	ORF7b	A*02:01	10	FLLFLVLIML	0.14288	Consensus (ann/smm)	0.3	99.58% (235/236)	Non-Toxin	
813	ORF7b	A*23:01	9	FYLCFLAFL	0.14713	Consensus (ann/smm)	0.36	98.31% (232/236)	Non-Toxin	
814	ORF7b	A*24:02	9	FYLCFLAFL	0.14713	Consensus (ann/smm)	0.54	98.31% (232/236)	Non-Toxin	
815	ORF7b	A*23:01	10	FYLCFLAFLL	0.1745	Consensus (ann/smm)	0.13	98.31% (232/236)	Non-Toxin	
816	ORF7b	A*24:02	10	FYLCFLAFLL	0.1745	Consensus (ann/smm)	0.28	98.31% (232/236)	Non-Toxin	
817	ORF7b	A*23:01	10	IDFYLCFLAF	0.09468	Consensus (ann/smm)	0.36	98.31% (232/236)	Non-Toxin	
818	ORF7b	B*44:03	9	IELSLIDFY	0.03153	Consensus (ann/smm)	0.19	99.58% (235/236)	Non-Toxin	
819	ORF7b	B*44:02	9	IELSLIDFY	0.03153	Consensus (ann/smm)	0.42	99.58% (235/236)	Non-Toxin	
820	ORF7b	A*32:01	10	IMLIIFWFSL	0.58457	Consensus (ann/smm)	0.4	99.58% (235/236)	Non-Toxin	

821	ORF7b	B*08:01	10	IMLIIFWFSL	0.58457	Consensus (ann/smm)	0.41	99.58% (235/236)	Non-Toxin	
822	ORF7b	A*02:01	10	IMLIIFWFSL	0.58457	Consensus (ann/smm)	0.43	99.58% (235/236)	Non-Toxin	
823	ORF7b	A*23:01	9	LFLVLIMLI	-0.00226	Consensus (ann/smm)	0.44	99.58% (235/236)	Non-Toxin	
824	ORF7b	B*53:01	10	LVLIMLIIFW	0.25452	Consensus (ann/smm)	0.32	99.58% (235/236)	Non-Toxin	
825	ORF7b	A*01:01	10	MIELSLIDFY	0.06184	Consensus (ann/smm)	0.35	99.58% (235/236)	Non-Toxin	
826	ORF7b	A*02:01	9	MLIIFWFSL	0.50177	Consensus (ann/comblib_sidney2008/smm)	0.2	99.58% (235/236)	Non-Toxin	
827	ORF7b	A*02:06	9	MLIIFWFSL	0.50177	Consensus (ann/smm)	0.41	99.58% (235/236)	Non-Toxin	
828	ORF7b	A*02:01	10	SLIDFYLCFL	0.18838	Consensus (ann/smm)	0.14	98.31% (232/236)	Non-Toxin	
829	ORF7b	A*02:03	10	SLIDFYLCFL	0.18838	Consensus (ann/smm)	0.49	98.31% (232/236)	Non-Toxin	
830	ORF7b	A*02:01	9	YLCFLAFLL	0.21865	Consensus (ann/comblib_sidney2008/smm)	0.3	98.31% (232/236)	Non-Toxin	
831	ORF7b	A*23:01	10	YLCFLAFLLF	0.22196	Consensus (ann/smm)	0.42	98.31% (232/236)	Non-Toxin	
S.No.	ORF	Allele	Length	Peptide	Immunogenicity	Method used	Percentile Rank	Conservancy	Toxicity	
832	ORF8	B*53:01	9	CPIHFYSKW	-0.07935	Consensus (ann/comblib_sidney2008/smm)	0.2	99.38% (477/480)	Non-Toxin	
833	ORF8	B*51:01	9	CPIHFYSKW	-0.07935	Consensus (ann/comblib_sidney2008/smm)	0.8	99.38% (477/480)	Non-Toxin	
834	ORF8	B*53:01	10	CPIHFYSKWY	-0.02216	Consensus (ann/smm)	0.2	99.38% (477/480)	Non-Toxin	
835	ORF8	A*01:01	10	CSFYEDFLEY	0.31272	Consensus (ann/smm)	0.24	99.79% (479/480)	Non-Toxin	
836	ORF8	A*30:02	10	CSFYEDFLEY	0.31272	Consensus (ann/smm)	0.8	99.79% (479/480)	Non-Toxin	
837	ORF8	A*33:01	9	DFLEYHDVR	0.16684	Consensus (ann/smm)	0.13	99.58% (478/480)	Non-Toxin	
838	ORF8	A*02:03	10	FLEYHDVRVV	0.18854	Consensus (ann/smm)	0.7	99.79% (479/480)	Non-Toxin	
839	ORF8	B*40:01	11	FLEYHDVRVVL	0.22976	ann	0.93	99.79% (479/480)	Non-Toxin	
840	ORF8	A*02:03	8	FLGIITTV	0.34382	Consensus (ann/smm)	0.51	99.17% (476/480)	Non-Toxin	
841	ORF8	A*02:01	8	FLGIITTV	0.34382	Consensus (ann/smm)	0.72	99.17% (476/480)	Non-Toxin	
842	ORF8	A*02:03	9	FLGIITTVA	0.36794	Consensus (ann/smm)	0.72	99.17% (476/480)	Non-Toxin	
843	ORF8	A*02:03	10	FLGIITTVAA	0.40656	Consensus (ann/smm)	0.85	99.17% (476/480)	Non-Toxin	
844	ORF8	B*15:01	11	FLGIITTVAAF	0.44486	ann	0.7	99.17% (476/480)	Non-Toxin	
845	ORF8	A*02:01	11	FLVFLGIITTV	0.46372	Consensus (ann/smm)	0.46	99.17% (476/480)	Non-Toxin	
846	ORF8	A*68:01	9	FTINCQEPK	-0.04683	Consensus (ann/smm)	0.18	100.00% (480/480)	Non-Toxin	
847	ORF8	A*11:01	9	FTINCQEPK	-0.04683	Consensus (ann/smm)	0.54	100.00% (480/480)	Non-Toxin	
848	ORF8	A*31:01	8	FYSKWYIR	0.05384	ann	0.38	99.38% (477/480)	Non-Toxin	
849	ORF8	A*33:01	8	FYSKWYIR	0.05384	ann	0.47	99.38% (477/480)	Non-Toxin	
850	ORF8	A*24:02	9	FYSKWYIRV	0.08408	Consensus (ann/smm)	0.8	99.38% (477/480)	Non-Toxin	
851	ORF8	A*30:01	9	GARKSAPLI	-0.34031	Consensus (ann/comblib_sidney2008/smm)	0.3	99.17% (476/480)	Non-Toxin	
852	ORF8	B*15:01	9	GIITTVAAF	0.2148	Consensus (ann/comblib_sidney2008/smm)	0.3	99.17% (476/480)	Non-Toxin	
853	ORF8	A*26:01	9	GIITTVAAF	0.2148	Consensus (ann/smm)	0.45	99.17% (476/480)	Non-Toxin	
854	ORF8	B*57:01	9	GSLVVRCSF	-0.0153	Consensus (ann/smm)	0.88	100.00% (480/480)	Non-Toxin	
855	ORF8	A*30:02	10	GSLVVRCSFY	0.00657	Consensus (ann/smm)	0.24	100.00% (480/480)	Non-Toxin	
856	ORF8	A*31:01	9	HFYSKWYIR	-0.09452	Consensus (ann/smm)	0.11	99.38% (477/480)	Non-Toxin	
857	ORF8	A*33:01	9	HFYSKWYIR	-0.09452	Consensus (ann/smm)	0.12	99.38% (477/480)	Non-Toxin	
858	ORF8	A*23:01	11	IGNYTVSCLPF	-0.15551	Consensus (ann/smm)	1	51.46% (247/480)	Non-Toxin	
859	ORF8	A*31:01	10	IHFYSKWYIR	-0.05367	Consensus (ann/smm)	0.53	99.38% (477/480)	Non-Toxin	
860	ORF8	A*30:02	9	IQYIDIGNY	0.30442	Consensus (ann/smm)	0.12	99.38% (477/480)	Non-Toxin	
861	ORF8	B*15:01	9	IQYIDIGNY	0.30442	Consensus (ann/comblib_sidney2008/smm)	0.34	99.38% (477/480)	Non-Toxin	
862	ORF8	A*32:01	11	KLGSLVVRCSF	-0.17931	ann	0.83	100.00% (480/480)	Non-Toxin	
863	ORF8	B*58:01	9	KSAPLIELC	0.19404	Consensus (ann/comblib_sidney2008/smm)	0.4	99.17% (476/480)	Non-Toxin	
864	ORF8	A*31:01	9	KWYIRVGAR	0.27344	Consensus (ann/smm)	0.46	99.38% (477/480)	Non-Toxin	
865	ORF8	B*40:01	10	LEYHDVRVVL	0.20083	Consensus (ann/smm)	0.36	99.79% (479/480)	Non-Toxin	
866	ORF8	B*15:01	10	LGIITTVAAF	0.34746	Consensus (ann/smm)	0.31	99.17% (476/480)	Non-Toxin	
867	ORF8	B*15:01	10	LQSCTQHQPY	-0.25674	Consensus (ann/smm)	0.17	96.04% (461/480)	Non-Toxin	
868	ORF8	A*02:03	10	LVFLGIITTV	0.37016	Consensus (ann/smm)	0.48	99.17% (476/480)	Non-Toxin	
869	ORF8	A*02:06	10	LVFLGIITTV	0.37016	Consensus (ann/smm)	0.79	99.17% (476/480)	Non-Toxin	
870	ORF8	B*51:01	9	MKFLVFLGI	0.18768	Consensus (ann/comblib_sidney2008/smm)	0.98	99.17% (476/480)	Non-Toxin	

871	ORF8	A*23:01	9	NYTVSCLPF	-0.17355	Consensus (ann/smm)	0.23	51.46% (247/480)	Non-Toxin	
872	ORF8	A*24:02	9	NYTVSCLPF	-0.17355	Consensus (ann/smm)	0.34	51.46% (247/480)	Non-Toxin	
873	ORF8	A*33:01	11	PIHFYSKWYIR	0.03675	ann	0.94	99.38% (477/480)	Non-Toxin	
874	ORF8	A*01:01	9	QSCTQHQPY	-0.16503	Consensus (ann/smm)	0.28	96.04% (461/480)	Non-Toxin	
875	ORF8	A*23:01	10	QYIDIGNYTV	0.24159	Consensus (ann/smm)	0.58	99.79% (479/480)	Non-Toxin	
876	ORF8	A*01:01	11	RCSFYEDFLEY	0.33894	Consensus (ann/smm)	0.56	99.79% (479/480)	Non-Toxin	
877	ORF8	B*08:01	10	RVGARKSAPL	-0.23842	Consensus (ann/smm)	0.44	99.17% (476/480)	Non-Toxin	
878	ORF8	A*30:02	9	SLVVRCSFY	-0.01663	Consensus (ann/smm)	0.57	100.00% (480/480)	Non-Toxin	
879	ORF8	A*68:02	9	TVSCLPFTI	-0.00771	Consensus (ann/comblib_sidney2008/smm)	0.9	51.46% (247/480)	Non-Toxin	
880	ORF8	A*02:01	9	YIDIGNYTV	0.18759	Consensus (ann/comblib_sidney2008/smm)	0.5	99.79% (479/480)	Non-Toxin	
881	ORF8	A*02:06	9	YIDIGNYTV	0.18759	Consensus (ann/smm)	0.73	99.79% (479/480)	Non-Toxin	
882	ORF8	A*02:06	10	YTVSCLPFTI	-0.10533	Consensus (ann/smm)	0.53	51.46% (247/480)	Non-Toxin	
883	ORF8	A*02:06	9	YVVDDPCPI	-0.0051	Consensus (ann/smm)	0.68	99.17% (476/480)	Non-Toxin	
S.No.	ORF	Allele	Length	Peptide	Immunogenicity	Method used	Percentile Rank	Conservancy	Toxicity	
884	S Protein	B*40:01	9	AEIRASANL	0.00689	Consensus (ann/smm)	0.12	93.23% (468/502)	Non-Toxin	
885	S Protein	B*44:03	9	AEIRASANL	0.00689	Consensus (ann/smm)	0.2	93.23% (468/502)	Non-Toxin	
886	S Protein	B*44:02	9	AEIRASANL	0.00689	Consensus (ann/smm)	0.23	93.23% (468/502)	Non-Toxin	
887	S Protein	B*44:02	9	AENSVAYSN	-0.19132	Consensus (ann/smm)	0.21	93.82% (471/502)	Non-Toxin	
888	S Protein	B*44:03	9	AENSVAYSN	-0.19132	Consensus (ann/smm)	0.27	93.82% (471/502)	Non-Toxin	
889	S Protein	B*44:02	9	AEVQIDRLI	0.08452	Consensus (ann/smm)	0.18	92.63% (465/502)	Non-Toxin	
890	S Protein	B*44:03	9	AEVQIDRLI	0.08452	Consensus (ann/smm)	0.2	92.63% (465/502)	Non-Toxin	
891	S Protein	A*26:01	9	CVADYSVLY	-0.09595	Consensus (ann/smm)	0.17	93.82% (471/502)	Non-Toxin	
892	S Protein	A*26:01	10	EFVFKNIDGY	0.0787	Consensus (ann/smm)	0.22	92.03% (462/502)	Non-Toxin	
893	S Protein	B*51:01	8	EPLVDLPI	0.03974	Consensus (ann/smm)	0.18	93.63% (470/502)	Non-Toxin	
894	S Protein	A*26:01	9	ETKCTLKSF	-0.37555	Consensus (ann/smm)	0.17	93.43% (469/502)	Non-Toxin	
895	S Protein	A*26:01	10	EVFAQVKQIY	-0.21823	Consensus (ann/smm)	0.13	92.43% (464/502)	Non-Toxin	
896	S Protein	B*35:01	9	FAMQMAYRF	-0.28061	Consensus (ann/comblib_sidney2008/smm)	0.2	93.82% (471/502)	Non-Toxin	
897	S Protein	B*40:01	9	FEYVSQPFL	-0.17076	Consensus (ann/smm)	0.28	92.83% (466/502)	Non-Toxin	
898	S Protein	A*02:03	9	FIAGLIAIV	0.27206	Consensus (ann/smm)	0.16	93.82% (471/502)	Non-Toxin	
899	S Protein	B*53:01	10	FLPFFSNVTW	0.11853	Consensus (ann/smm)	0.21	93.43% (469/502)	Non-Toxin	
900	S Protein	B*08:01	9	FNATRFASV	0.14872	Consensus (ann/comblib_sidney2008/smm)	0.2	93.43% (469/502)	Non-Toxin	
901	S Protein	B*53:01	10	FPNITNLCPF	0.1009	Consensus (ann/smm)	0.06	93.82% (471/502)	Non-Toxin	
902	S Protein	B*35:01	10	FPNITNLCPF	0.1009	Consensus (ann/smm)	0.08	93.82% (471/502)	Non-Toxin	
903	S Protein	B*51:01	10	FPNITNLCPF	0.1009	Consensus (ann/smm)	0.17	93.82% (471/502)	Non-Toxin	
904	S Protein	B*51:01	10	FPQSAPHGVV	-0.0936	Consensus (ann/smm)	0.27	93.43% (469/502)	Non-Toxin	
905	S Protein	A*68:02	9	FTISVTTEI	0.04473	Consensus (ann/comblib_sidney2008/smm)	0.2	93.82% (471/502)	Non-Toxin	
906	S Protein	A*26:01	9	FVFKNIDGY	-0.0215	Consensus (ann/smm)	0.11	92.03% (462/502)	Non-Toxin	
907	S Protein	A*02:06	10	FVFLVLLPLV	0.02996	Consensus (ann/smm)	0.1	92.83% (466/502)	Non-Toxin	
908	S Protein	A*02:01	10	FVFLVLLPLV	0.02996	Consensus (ann/smm)	0.28	92.83% (466/502)	Non-Toxin	
909	S Protein	A*68:01	9	FVIRGDEVR	0.25778	Consensus (ann/smm)	0.17	93.63% (470/502)	Non-Toxin	
910	S Protein	A*02:06	10	FVSNGTHWFV	0.29638	Consensus (ann/smm)	0.18	93.43% (469/502)	Non-Toxin	
911	S Protein	A*02:01	10	FVSNGTHWFV	0.29638	Consensus (ann/smm)	0.21	93.43% (469/502)	Non-Toxin	
912	S Protein	A*68:02	10	FVSNGTHWFV	0.29638	Consensus (ann/smm)	0.27	93.43% (469/502)	Non-Toxin	
913	S Protein	B*44:03	9	GEVFNATRF	0.22473	Consensus (ann/smm)	0.2	93.63% (470/502)	Non-Toxin	
914	S Protein	A*33:01	11	GNYNYLYRLFR	0.08205	ann	0.11	92.63% (465/502)	Non-Toxin	
915	S Protein	A*31:01	9	GTHWFVTQR	0.35133	Consensus (ann/smm)	0.24	93.23% (468/502)	Non-Toxin	
916	S Protein	A*03:01	9	GVYFASTEK	0.09023	Consensus (ann/smm)	0.2	93.63% (470/502)	Non-Toxin	
917	S Protein	A*11:01	9	GVYFASTEK	0.09023	Consensus (ann/smm)	0.23	93.63% (470/502)	Non-Toxin	
918	S Protein	A*03:01	9	GVYYHKNNK	-0.18566	Consensus (ann/smm)	0.2	92.03% (462/502)	Non-Toxin	
919	S Protein	A*68:01	10	GVYYPDKVFR	-0.09388	Consensus (ann/smm)	0.27	93.82% (471/502)	Non-Toxin	
920	S Protein	B*51:01	9	IAIPTNFTI	0.18523	Consensus (ann/comblib_sidney2008/smm)	0.2	93.82% (471/502)	Non-Toxin	

921	S Protein	A*30:02	9	IGAGICASY	0.06201	Consensus (ann/smm)	0.21	93.82% (471/502)	Non-Toxin	
922	S Protein	B*35:01	9	IPFAMQMAY	-0.32801	Consensus (ann/comblib_sidney2008/smm)	0.1	93.82% (471/502)	Non-Toxin	
923	S Protein	A*30:01	9	ITRFQTLLA	0.0425	Consensus (ann/comblib_sidney2008/smm)	0.2	93.43% (469/502)	Non-Toxin	
924	S Protein	A*31:01	10	KGIYQTSNFR	-0.12831	Consensus (ann/smm)	0.28	93.43% (469/502)	Non-Toxin	
925	S Protein	A*32:01	9	KIYSKHTPI	-0.32094	Consensus (ann/comblib_sidney2008/smm)	0.2	93.03% (467/502)	Non-Toxin	
926	S Protein	A*31:01	9	KQGNFKNLR	-0.09645	Consensus (ann/smm)	0.19	92.63% (465/502)	Non-Toxin	
927	S Protein	A*30:02	10	KSFTVEKGIY	0.11812	Consensus (ann/smm)	0.11	93.23% (468/502)	Non-Toxin	
928	S Protein	B*58:01	8	KSNIIRGW	0.33874	ann	0.25	93.82% (471/502)	Non-Toxin	
929	S Protein	B*57:01	8	KSNIIRGW	0.33874	ann	0.29	93.82% (471/502)	Non-Toxin	
930	S Protein	A*31:01	9	KSNLKPFER	-0.0764	Consensus (ann/smm)	0.14	92.63% (465/502)	Non-Toxin	
931	S Protein	A*31:01	9	KSWMESEFR	-0.01013	Consensus (ann/smm)	0.26	92.43% (464/502)	Non-Toxin	
932	S Protein	A*30:02	9	KTSVDCTMY	-0.11115	Consensus (ann/smm)	0.12	93.82% (471/502)	Non-Toxin	
933	S Protein	A*30:02	10	KVGGNYNYLY	0.01951	Consensus (ann/smm)	0.21	92.63% (465/502)	Non-Toxin	
934	S Protein	A*24:02	10	KWPWYIWLGF	0.56424	Consensus (ann/smm)	0.11	93.43% (469/502)	Non-Toxin	
935	S Protein	A*23:01	10	KWPWYIWLGF	0.56424	Consensus (ann/smm)	0.12	93.43% (469/502)	Non-Toxin	
936	S Protein	A*32:01	10	KWPWYIWLGF	0.56424	Consensus (ann/smm)	0.18	93.43% (469/502)	Non-Toxin	
937	S Protein	A*02:03	9	LLFNKVTLA	-0.11337	Consensus (ann/smm)	0.23	93.23% (468/502)	Non-Toxin	
938	S Protein	A*01:01	10	LLTDEMIAQY	0.05204	Consensus (ann/smm)	0.28	93.43% (469/502)	Non-Toxin	
939	S Protein	B*51:01	10	LPDDFTGCVI	0.19184	Consensus (ann/smm)	0.14	93.63% (470/502)	Non-Toxin	
940	S Protein	B*53:01	10	LPDDFTGCVI	0.19184	Consensus (ann/smm)	0.28	93.63% (470/502)	Non-Toxin	
941	S Protein	B*53:01	9	LPFFSNVTW	0.04613	Consensus (ann/comblib_sidney2008/smm)	0.2	93.43% (469/502)	Non-Toxin	
942	S Protein	B*53:01	10	LPFFSNVTWF	0.18944	Consensus (ann/smm)	0.13	91.83% (461/502)	Non-Toxin	
943	S Protein	B*51:01	10	LPFFSNVTWF	0.18944	Consensus (ann/smm)	0.2	91.83% (461/502)	Non-Toxin	
944	S Protein	B*53:01	10	LPIGINITRF	0.38888	Consensus (ann/smm)	0.12	93.43% (469/502)	Non-Toxin	
945	S Protein	B*35:01	10	LPIGINITRF	0.38888	Consensus (ann/smm)	0.17	93.43% (469/502)	Non-Toxin	
946	S Protein	B*51:01	9	LPLVSSQCV	-0.40815	Consensus (ann/comblib_sidney2008/smm)	0.2	93.82% (471/502)	Non-Toxin	
947	S Protein	B*51:01	10	LPVSMTKTSV	-0.55317	Consensus (ann/smm)	0.2	93.82% (471/502)	Non-Toxin	
948	S Protein	B*15:01	11	LQIPFAMQMAY	-0.22124	ann	0.28	93.82% (471/502)	Non-Toxin	
949	S Protein	A*01:01	9	LTDEMIAQY	0.02757	Consensus (ann/smm)	0.11	93.43% (469/502)	Non-Toxin	
950	S Protein	A*24:02	10	LYNSASFSTF	-0.29831	Consensus (ann/smm)	0.11	93.82% (471/502)	Non-Toxin	
951	S Protein	A*23:01	10	LYNSASFSTF	-0.29831	Consensus (ann/smm)	0.14	93.82% (471/502)	Non-Toxin	
952	S Protein	A*02:06	10	MQMAYRFNGI	0.15371	Consensus (ann/smm)	0.18	93.82% (471/502)	Non-Toxin	
953	S Protein	A*68:01	9	NSASFSTFK	-0.09434	Consensus (ann/smm)	0.16	93.82% (471/502)	Non-Toxin	
954	S Protein	A*68:02	9	NTQEVFAQV	0.17889	Consensus (ann/comblib_sidney2008/smm)	0.2	92.83% (466/502)	Non-Toxin	
955	S Protein	A*01:01	10	NTSNQVAVLY	-0.06762	Consensus (ann/smm)	0.27	93.82% (471/502)	Non-Toxin	
956	S Protein	A*68:01	10	NVYADSFVIR	0.12147	Consensus (ann/smm)	0.14	93.82% (471/502)	Non-Toxin	
957	S Protein	A*33:01	8	NYLYRLFR	0.13144	ann	0.07	92.63% (465/502)	Non-Toxin	
958	S Protein	A*24:02	9	NYNYLYRLF	0.0171	Consensus (ann/smm)	0.17	92.63% (465/502)	Non-Toxin	
959	S Protein	A*33:01	10	NYNYLYRLFR	0.08754	Consensus (ann/smm)	0.07	92.63% (465/502)	Non-Toxin	
960	S Protein	A*01:01	11	PLLTDEMIAQY	0.07418	Consensus (ann/smm)	0.17	93.43% (469/502)	Non-Toxin	
961	S Protein	A*23:01	9	PYRVVVLSF	0.03138	Consensus (ann/smm)	0.2	92.63% (465/502)	Non-Toxin	
962	S Protein	A*03:01	9	QIYKTPPIK	-0.12244	Consensus (ann/smm)	0.27	92.23% (463/502)	Non-Toxin	
963	S Protein	A*23:01	9	QYIKWPWYI	0.21624	Consensus (ann/smm)	0.11	93.43% (469/502)	Non-Toxin	
964	S Protein	A*24:02	9	QYIKWPWYI	0.21624	Consensus (ann/smm)	0.11	93.43% (469/502)	Non-Toxin	
965	S Protein	A*23:01	10	QYIKWPWYIW	0.31425	Consensus (ann/smm)	0.16	93.43% (469/502)	Non-Toxin	
966	S Protein	A*24:02	10	QYIKWPWYIW	0.31425	Consensus (ann/smm)	0.21	93.43% (469/502)	Non-Toxin	
967	S Protein	A*30:02	9	RISNCVADY	-0.02787	Consensus (ann/smm)	0.12	93.82% (471/502)	Non-Toxin	
968	S Protein	A*03:01	9	RLFRKSNLK	-0.28759	Consensus (ann/smm)	0.1	92.63% (465/502)	Non-Toxin	
969	S Protein	A*32:01	11	RLFRKSNLKPF	-0.48624	ann	0.26	92.63% (465/502)	Non-Toxin	
970	S Protein	B*57:01	9	RSFIEDLLF	0.27446	Consensus (ann/smm)	0.23	93.43% (469/502)	Non-Toxin	
971	S Protein	B*15:01	10	RVYSTGSNVF	-0.23394	Consensus (ann/smm)	0.21	93.82% (471/502)	Non-Toxin	

972	S Protein	A*30:02	9	SANNCTFEY	0.13273	Consensus (ann/smm)	0.26	92.83% (466/502)	Non-Toxin	
973	S Protein	B*44:03	10	SETKCTLKSF	-0.5082	Consensus (ann/smm)	0.19	93.43% (469/502)	Non-Toxin	
974	S Protein	A*30:02	11	SKVGGNYNYLY	0.05491	Consensus (ann/smm)	0.18	92.63% (465/502)	Non-Toxin	
975	S Protein	B*07:02	8	SPRRARSV	0.01608	Consensus (ann/smm)	0.17	93.82% (471/502)	Non-Toxin	
976	S Protein	B*07:02	9	SPRRARSVA	0.0402	Consensus (ann/comblib_sidney2008/smm)	0.1	93.82% (471/502)	Non-Toxin	
977	S Protein	B*07:02	10	SPRRARSVAS	0.05935	Consensus (ann/smm)	0.14	93.82% (471/502)	Non-Toxin	
978	S Protein	A*30:02	10	SSANNCTFEY	0.14123	Consensus (ann/smm)	0.23	92.83% (466/502)	Non-Toxin	
979	S Protein	A*01:01	10	SSANNCTFEY	0.14123	Consensus (ann/smm)	0.25	92.83% (466/502)	Non-Toxin	
980	S Protein	A*32:01	9	STQDLFLPF	0.06828	Consensus (ann/comblib_sidney2008/smm)	0.2	93.03% (467/502)	Non-Toxin	
981	S Protein	A*26:01	10	SVASQSIIAY	-0.16721	Consensus (ann/smm)	0.19	93.82% (471/502)	Non-Toxin	
982	S Protein	B*44:03	10	TECSNLLLQY	-0.28855	Consensus (ann/smm)	0.28	93.82% (471/502)	Non-Toxin	
983	S Protein	A*11:01	10	TEILPVSMTK	-0.21981	Consensus (ann/smm)	0.28	93.82% (471/502)	Non-Toxin	
984	S Protein	B*44:02	10	TEKSNIIRGW	0.07559	Consensus (ann/smm)	0.24	93.63% (470/502)	Non-Toxin	
985	S Protein	B*53:01	9	TPGDSSSGW	-0.40333	Consensus (ann/comblib_sidney2008/smm)	0.2	93.43% (469/502)	Non-Toxin	
986	S Protein	A*01:01	9	TSNQVAVLY	-0.01327	Consensus (ann/smm)	0.28	93.82% (471/502)	Non-Toxin	
987	S Protein	A*30:01	9	TTRTQLPPA	-0.08322	Consensus (ann/comblib_sidney2008/smm)	0.2	93.43% (469/502)	Non-Toxin	
988	S Protein	A*30:02	9	VLPFNDGVY	0.1815	Consensus (ann/smm)	0.28	93.82% (471/502)	Non-Toxin	
989	S Protein	A*24:02	11	VLYNSASFSTF	-0.29855	Consensus (ann/smm)	0.2	93.82% (471/502)	Non-Toxin	
990	S Protein	A*11:01	10	VTLADAGFIK	0.30393	Consensus (ann/smm)	0.22	93.23% (468/502)	Non-Toxin	
991	S Protein	A*03:01	9	VTYVPAQEK	0.02711	Consensus (ann/smm)	0.27	93.63% (470/502)	Non-Toxin	
992	S Protein	A*23:01	10	VYSSANNCTF	-0.21728	Consensus (ann/smm)	0.12	92.63% (465/502)	Non-Toxin	
993	S Protein	A*24:02	10	VYSSANNCTF	-0.21728	Consensus (ann/smm)	0.12	92.63% (465/502)	Non-Toxin	
994	S Protein	A*24:02	9	VYSTGSNVF	-0.11871	Consensus (ann/smm)	0.17	93.82% (471/502)	Non-Toxin	
995	S Protein	A*31:01	9	VYYPDKVFR	-0.09052	Consensus (ann/smm)	0.18	93.82% (471/502)	Non-Toxin	
996	S Protein	B*53:01	9	WPWYIWLGF	0.41673	Consensus (ann/comblib_sidney2008/smm)	0.2	93.43% (469/502)	Non-Toxin	
997	S Protein	B*51:01	10	WPWYIWLGFI	0.50004	Consensus (ann/smm)	0.14	93.43% (469/502)	Non-Toxin	
998	S Protein	A*26:01	9	WTAGAAAYY	0.15259	Consensus (ann/smm)	0.11	93.43% (469/502)	Non-Toxin	
999	S Protein	A*30:02	9	WTAGAAAYY	0.15259	Consensus (ann/smm)	0.12	93.43% (469/502)	Non-Toxin	
1000	S Protein	A*01:01	9	WTAGAAAYY	0.15259	Consensus (ann/smm)	0.17	93.43% (469/502)	Non-Toxin	
1001	S Protein	A*68:02	10	WTAGAAAYYV	0.15455	Consensus (ann/smm)	0.06	93.43% (469/502)	Non-Toxin	
1002	S Protein	B*44:02	9	YEQYIKWPW	0.06574	Consensus (ann/smm)	0.11	93.63% (470/502)	Non-Toxin	
1003	S Protein	B*44:03	9	YEQYIKWPW	0.06574	Consensus (ann/smm)	0.12	93.63% (470/502)	Non-Toxin	
1004	S Protein	B*44:03	10	YEQYIKWPWY	0.20685	Consensus (ann/smm)	0.14	93.43% (469/502)	Non-Toxin	
1005	S Protein	B*44:02	10	YEQYIKWPWY	0.20685	Consensus (ann/smm)	0.24	93.43% (469/502)	Non-Toxin	
1006	S Protein	A*02:01	9	YLQPRTFLL	0.1305	Consensus (ann/comblib_sidney2008/smm)	0.3	93.43% (469/502)	Non-Toxin	
1007	S Protein	A*03:01	10	YLQPRTFLLK	0.1338	Consensus (ann/smm)	0.18	93.43% (469/502)	Non-Toxin	
1008	S Protein	A*33:01	9	YNYLYRLFR	0.0918	Consensus (ann/smm)	0.12	92.63% (465/502)	Non-Toxin	
1009	S Protein	B*07:02	10	YPDKVFRSSV	-0.24316	Consensus (ann/smm)	0.26	93.82% (471/502)	Non-Toxin	
1010	S Protein	A*02:06	9	YQDVNCTEV	0.08295	Consensus (ann/smm)	0.19	67.33% (338/502)	Non-Toxin	
1011	S Protein	A*01:01	10	YTNSFTRGVY	0.08467	Consensus (ann/smm)	0.17	93.43% (469/502)	Non-Toxin	
1012	S Protein	A*30:02	10	YTNSFTRGVY	0.08467	Consensus (ann/smm)	0.18	93.43% (469/502)	Non-Toxin	
1013	S Protein	A*24:02	11	YYVGYLQPRTF	-0.02378	Consensus (ann/smm)	0.15	93.43% (469/502)	Non-Toxin	

Supplementary Table S3: High Percentile Ranking HTL epitopes-HLA allele pairs screened from entire proteome of SARS-CoV-2 by the “MHC-II Binding Predictions” tool of IEDB. These epitopes were further utilized to identify the potentially immunogenic multiple epitope cluster based HTL Ag-Patches from the entire proteome of the SRAS-CoV-2. The epitopes shown in **BLUE** are the epitope which form Overlapping epitope clusters. The screened epitopes are in consensus with the previous studies [Srivastava et al. 2020a; Srivastava et al., 2020b and Grifoni et al., 2020a].

S.No.	ORF	Allele	Length	Method used	Peptide	Percentile Rank	Adjusted rank	Conservancy	Toxicity	
1	E Protein	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	FLAFVVFLLVTLAIL	0.06	0.06	99.59% (480/482)	Non-Toxin	
2	E Protein	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	LAFVVFLLVTLAILT	0.06	0.06	99.59% (480/482)	Non-Toxin	
3	E Protein	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	LFLAFVVFLLVTLAI	0.03	0.03	99.59% (480/482)	Non-Toxin	
4	E Protein	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	LFLAFVVFLLVTLAI	0.04	0.04	99.59% (480/482)	Non-Toxin	
5	E Protein	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	LFLAFVVFLLVTLAI	0.08	0.08	99.59% (480/482)	Non-Toxin	
6	E Protein	DPA1*02:01/DPB1*01:01	15	Consensus (comb.lib./smm/nn)	LFLAFVVFLLVTLAI	0.1	0.1	99.59% (480/482)	Non-Toxin	
7	E Protein	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	LLFLAFVVFLLVTLA	0.02	0.02	99.59% (480/482)	Non-Toxin	
8	E Protein	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	LLFLAFVVFLLVTLA	0.03	0.03	99.59% (480/482)	Non-Toxin	
9	E Protein	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	LLFLAFVVFLLVTLA	0.06	0.06	99.59% (480/482)	Non-Toxin	
10	E Protein	DPA1*02:01/DPB1*01:01	15	Consensus (comb.lib./smm/nn)	LLFLAFVVFLLVTLA	0.1	0.1	99.59% (480/482)	Non-Toxin	
11	E Protein	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	NSVLLFLAFVVFLLV	0.04	0.04	99.59% (480/482)	Non-Toxin	
12	E Protein	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	NSVLLFLAFVVFLLV	0.06	0.06	99.59% (480/482)	Non-Toxin	
13	E Protein	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	NSVLLFLAFVVFLLV	0.07	0.07	99.59% (480/482)	Non-Toxin	
14	E Protein	DPA1*02:01/DPB1*01:01	15	Consensus (comb.lib./smm/nn)	NSVLLFLAFVVFLLV	0.1	0.1	99.59% (480/482)	Non-Toxin	
15	E Protein	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	SVLLFLAFVVFLLVT	0.04	0.04	99.59% (480/482)	Non-Toxin	
16	E Protein	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	SVLLFLAFVVFLLVT	0.06	0.06	99.59% (480/482)	Non-Toxin	
17	E Protein	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	SVLLFLAFVVFLLVT	0.07	0.07	99.59% (480/482)	Non-Toxin	
18	E Protein	DPA1*02:01/DPB1*01:01	15	Consensus (comb.lib./smm/nn)	SVLLFLAFVVFLLVT	0.1	0.1	99.59% (480/482)	Non-Toxin	
19	E Protein	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	VLLFLAFVVFLLVTL	0.02	0.02	99.59% (480/482)	Non-Toxin	
20	E Protein	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	VLLFLAFVVFLLVTL	0.04	0.04	99.59% (480/482)	Non-Toxin	
21	E Protein	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	VLLFLAFVVFLLVTL	0.06	0.06	99.59% (480/482)	Non-Toxin	
22	E Protein	DPA1*02:01/DPB1*01:01	15	Consensus (comb.lib./smm/nn)	VLLFLAFVVFLLVTL	0.1	0.1	99.59% (480/482)	Non-Toxin	
23	E Protein	DPA1*02:01/DPB1*01:01	15	Consensus (comb.lib./smm/nn)	VNSVLLFLAFVVFLL	0.1	0.1	99.59% (480/482)	Non-Toxin	
S.No.	ORF	Allele	Length	Method used	Peptide	Percentile Rank	Adjusted rank	Conservancy	Toxicity	
24	M Protein	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	GLMWLSYFIASFRLF	0.05	0.05	97.48% (465/477)	Non-Toxin	
25	M Protein	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	IKLIFLWLLWPVTLA	0.07	0.07	97.48% (465/477)	Non-Toxin	
26	M Protein	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	KLIFLWLLWPVTLAC	0.11	0.11	97.48% (465/477)	Non-Toxin	
27	M Protein	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	LMWLSYFIASFRLFA	0.05	0.05	97.48% (465/477)	Non-Toxin	
28	M Protein	DRB1*09:01	15	Consensus (comb.lib./smm/nn)	LSYYKLGASQRVAGD	0.06	0.06	97.48% (465/477)	Non-Toxin	
29	M Protein	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	LSYYKLGASQRVAGD	0.67	0.67	97.48% (465/477)	Non-Toxin	
30	M Protein	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	MWLSYFIASFRLFAR	0.08	0.08	97.48% (465/477)	Non-Toxin	
31	M Protein	DRB1*09:01	15	Consensus (comb.lib./smm/nn)	RTLSYYKLGASQRVA	0.06	0.06	97.48% (465/477)	Non-Toxin	
32	M Protein	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	RTLSYYKLGASQRVA	0.67	0.67	97.48% (465/477)	Non-Toxin	
33	M Protein	DRB1*09:01	15	Consensus (comb.lib./smm/nn)	SRTLSYYKLGASQRV	0.07	0.07	97.48% (465/477)	Non-Toxin	
34	M Protein	DRB1*09:01	15	Consensus (comb.lib./smm/nn)	SYYKLGASQRVAGDS	0.48	0.48	97.48% (465/477)	Non-Toxin	
35	M Protein	DRB1*09:01	15	Consensus (comb.lib./smm/nn)	TLSYYKLGASQRVAG	0.07	0.07	97.48% (465/477)	Non-Toxin	
36	M Protein	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	TLSYYKLGASQRVAG	0.67	0.67	97.48% (465/477)	Non-Toxin	
37	M Protein	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	VGLMWLSYFIASFRL	0.07	0.07	97.48% (465/477)	Non-Toxin	
S.No.	ORF	Allele	Length	Method used	Peptide	Percentile Rank	Adjusted rank	Conservancy	Toxicity	
38	N Protein	DQA1*01:02/DQB1*06:02	15	Consensus (comb.lib./smm/nn)	ANNAAIVLQLPQGTT	0.2	0.2	97.59% (486/498)	Non-Toxin	
39	N Protein	DRB1*09:01	15	Consensus (comb.lib./smm/nn)	AQFAPSASAFFGMSR	0.01	0.01	97.59% (486/498)	Non-Toxin	
40	N Protein	DRB1*11:01	15	Consensus (smm/nn/sturniolo)	DDQIGYYRRATRRIR	0.42	0.42	97.59% (486/498)	Non-Toxin	
41	N Protein	DRB1*11:01	15	Consensus (smm/nn/sturniolo)	DQIGYYRRATRRIRG	0.42	0.42	97.59% (486/498)	Non-Toxin	

42	N Protein	DRB5*01:01	15	Consensus (smm/nn/sturniolo)	DQIGYYRRATRRIRG	0.58	0.58	97.59% (486/498)	Non-Toxin	
43	N Protein	DQA1*01:02/DQB1*06:02	15	Consensus (comb.lib./smm/nn)	GTRNPANNAAIVLQL	0.05	0.05	97.59% (486/498)	Non-Toxin	
44	N Protein	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	GTWLTYTGAIKLDDK	0.58	0.58	97.59% (486/498)	Non-Toxin	
45	N Protein	DRB1*11:01	15	Consensus (smm/nn/sturniolo)	GYYRRATRRIRGGDG	0.42	0.42	97.59% (486/498)	Non-Toxin	
46	N Protein	DRB1*09:01	15	Consensus (comb.lib./smm/nn)	IAQFAPSASAFFGMS	0.01	0.01	97.59% (486/498)	Non-Toxin	
47	N Protein	DRB1*11:01	15	Consensus (smm/nn/sturniolo)	IGYYRRATRRIRGGD	0.42	0.42	97.59% (486/498)	Non-Toxin	
48	N Protein	DQA1*01:02/DQB1*06:02	15	Consensus (comb.lib./smm/nn)	NNAAIVLQLPQGTTL	0.42	0.42	97.59% (486/498)	Non-Toxin	
49	N Protein	DQA1*01:02/DQB1*06:02	15	Consensus (comb.lib./smm/nn)	NPANNAAIVLQLPQG	0.03	0.03	97.59% (486/498)	Non-Toxin	
50	N Protein	DQA1*01:02/DQB1*06:02	15	Consensus (comb.lib./smm/nn)	PANNAAIVLQLPQGT	0.04	0.04	97.59% (486/498)	Non-Toxin	
51	N Protein	DRB1*09:01	15	Consensus (comb.lib./smm/nn)	PQIAQFAPSASAFFG	0.01	0.01	97.59% (486/498)	Non-Toxin	
52	N Protein	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	PSGTWLTYTGAIKLD	0.58	0.58	97.59% (486/498)	Non-Toxin	
53	N Protein	DRB1*09:01	15	Consensus (comb.lib./smm/nn)	QIAQFAPSASAFFGM	0.01	0.01	97.59% (486/498)	Non-Toxin	
54	N Protein	DRB1*11:01	15	Consensus (smm/nn/sturniolo)	QIGYYRRATRRIRGG	0.39	0.39	97.59% (486/498)	Non-Toxin	
55	N Protein	DRB5*01:01	15	Consensus (smm/nn/sturniolo)	QIGYYRRATRRIRGG	0.58	0.58	97.59% (486/498)	Non-Toxin	
56	N Protein	DQA1*01:02/DQB1*06:02	15	Consensus (comb.lib./smm/nn)	RNPANNAAIVLQLPQ	0.04	0.04	97.59% (486/498)	Non-Toxin	
57	N Protein	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	SGTWLTYTGAIKLDD	0.58	0.58	97.59% (486/498)	Non-Toxin	
58	N Protein	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	TPSGTWLTYTGAIKL	0.58	0.58	97.59% (486/498)	Non-Toxin	
59	N Protein	DQA1*01:02/DQB1*06:02	15	Consensus (comb.lib./smm/nn)	TRNPANNAAIVLQLP	0.04	0.04	97.59% (486/498)	Non-Toxin	
60	N Protein	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	TWLTYTGAIKLDDKD	0.58	0.58	97.59% (486/498)	Non-Toxin	
61	N Protein	DRB1*09:01	15	Consensus (comb.lib./smm/nn)	WPQIAQFAPSASAFF	0.01	0.01	97.59% (486/498)	Non-Toxin	
S.No.	ORF	Allele	Length	Method used	Peptide	Percentile Rank	Adjusted rank	Conservancy	Toxicity	
62	ORF10	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	FAFPFTIYSLLLCRM	0.56	0.56	99.79% (478/479)	Non-Toxin	
63	ORF10	DPA1*02:01/DPB1*01:01	15	Consensus (comb.lib./smm/nn)	FAFPFTIYSLLLCRM	1.1	1.1	99.79% (478/479)	Non-Toxin	
64	ORF10	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	FAFPFTIYSLLLCRM	1.1	1.1	99.79% (478/479)	Non-Toxin	
65	ORF10	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	INVFAFPFTIYSLLL	0.29	0.29	99.37% (476/479)	Non-Toxin	
66	ORF10	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	INVFAFPFTIYSLLL	0.46	0.46	99.37% (476/479)	Non-Toxin	
67	ORF10	DPA1*02:01/DPB1*01:01	15	Consensus (comb.lib./smm/nn)	INVFAFPFTIYSLLL	0.72	0.72	99.37% (476/479)	Non-Toxin	
68	ORF10	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	NVFAFPFTIYSLLLC	0.4	0.4	99.58% (477/479)	Non-Toxin	
69	ORF10	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	NVFAFPFTIYSLLLC	0.56	0.56	99.58% (477/479)	Non-Toxin	
70	ORF10	DPA1*02:01/DPB1*01:01	15	Consensus (comb.lib./smm/nn)	NVFAFPFTIYSLLLC	0.69	0.69	99.58% (477/479)	Non-Toxin	
71	ORF10	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	VFAFPFTIYSLLLCR	0.56	0.56	99.58% (477/479)	Non-Toxin	
72	ORF10	DPA1*02:01/DPB1*01:01	15	Consensus (comb.lib./smm/nn)	VFAFPFTIYSLLLCR	0.66	0.66	99.58% (477/479)	Non-Toxin	
73	ORF10	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	VFAFPFTIYSLLLCR	0.71	0.71	99.58% (477/479)	Non-Toxin	
74	ORF10	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	VFAFPFTIYSLLLCR	1.1	1.1	99.58% (477/479)	Non-Toxin	
75	ORF10	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	YINVFAFPFTIYSLL	0.29	0.29	99.37% (476/479)	Non-Toxin	
S.No.	ORF	Allele	Length	Method used	Peptide	Percentile Rank	Adjusted rank	Conservancy	Toxicity	NSP
76	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	AAIMQLFFSYFAVHF	0.05	0.05	100%(453/453)	Non-Toxin	nsp3
77	ORF1ab	DQA1*01:02/DQB1*06:02	15	Consensus (comb.lib./smm/nn)	AFASEAARVVRSIFS	0.08	0.08	99.55%(451/453)	Non-Toxin	nsp2
78	ORF1ab	DRB1*04:01	15	Consensus (smm/nn/sturniolo)	AIASEFSSLPSYAAF	0.13	0.13	99.33%(450/453)	Non-Toxin	nsp8
79	ORF1ab	DRB1*09:01	15	Consensus (comb.lib./smm/nn)	AIILASFSASTSAFV	0.01	0.01	100%(453/453)	Non-Toxin	nsp2
80	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	AIMQLFFSYFAVHFI	0.05	0.05	100%(453/453)	Non-Toxin	nsp3
81	ORF1ab	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	AMPNMLRIMASLVLA	0.01	0.01	100%(453/453)	Non-Toxin	nsp12
82	ORF1ab	DRB3*02:02	15	NetMHCIIpan	ANYIFWRNTNPIQLS	0.05	0.05	98.89%(448/453)	Non-Toxin	nsp16
83	ORF1ab	DRB1*04:01	15	Consensus (smm/nn/sturniolo)	ASEFSSLPSYAAFAT	0.12	0.12	99.33%(450/453)	Non-Toxin	nsp8
84	ORF1ab	DQA1*05:01/DQB1*03:01	15	Consensus (comb.lib./smm/nn)	ASIVAGGIVAIVVTC	0.03	0.03	100%(453/453)	Non-Toxin	nsp4
85	ORF1ab	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	AVGNICYTPSKLIEY	0.09	0.09	99.55%(451/453)	Non-Toxin	nsp4
86	ORF1ab	DRB3*02:02	15	NetMHCIIpan	AWWTAFVTNVNASSS	0.01	0.01	98.89%(448/453)	Non-Toxin	nsp16
87	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	AYILFTRFFYVLGLA	0.01	0.01	100%(453/453)	Non-Toxin	nsp3
88	ORF1ab	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	AYILFTRFFYVLGLA	0.08	0.08	100%(453/453)	Non-Toxin	nsp3
89	ORF1ab	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	CTFTRSTNSRIKASM	0.12	0.12	98.67%(447/453)	Non-Toxin	nsp3
90	ORF1ab	DQA1*05:01/DQB1*03:01	15	Consensus (comb.lib./smm/nn)	DISASIVAGGIVAIV	0.03	0.03	100%(453/453)	Non-Toxin	nsp4

91	ORF1ab	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	EETKFLTENLLLYID	0.03	0.03	99.77%(452/453)	Non-Toxin	nsp3
92	ORF1ab	DRB1*11:01	15	Consensus (smm/nn/sturniolo)	EFYAYLRKHFSMMIL	0.05	0.05	100%(453/453)	Non-Toxin	nsp12
93	ORF1ab	DQA1*05:01/DQB1*02:01	15	Consensus (comb.lib./smm/nn)	EIDFLELAMDEFIER	0.04	0.04	99.11%(449/453)	Non-Toxin	nsp15
94	ORF1ab	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	ESPFVMMSAPPAQYE	0.01	0.01	100%(453/453)	Non-Toxin	nsp3
95	ORF1ab	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	ETKFLTENLLLYIDI	0.03	0.03	99.77%(452/453)	Non-Toxin	nsp3
96	ORF1ab	DRB1*13:02	15	Consensus (smm/nn/sturniolo)	EVKILNNLGVDIAAN	0.12	0.12	99.77%(452/453)	Non-Toxin	nsp15
97	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	EWFLAYILFTRFFYV	0.03	0.03	100%(453/453)	Non-Toxin	nsp3
98	ORF1ab	DRB3*02:02	15	NetMHCIIpan	FAWWTAFVTNVNASS	0.01	0.01	98.89%(448/453)	Non-Toxin	nsp16
99	ORF1ab	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	FISNSWLMWLIINLV	0.05	0.05	100%(453/453)	Non-Toxin	nsp3
100	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	FLAYILFTRFFYVLG	0.01	0.01	100%(453/453)	Non-Toxin	nsp3
101	ORF1ab	DPA1*02:01/DPB1*01:01	15	Consensus (comb.lib./smm/nn)	FLAYILFTRFFYVLG	0.07	0.07	100%(453/453)	Non-Toxin	nsp3
102	ORF1ab	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	FLAYILFTRFFYVLG	0.09	0.09	100%(453/453)	Non-Toxin	nsp3
103	ORF1ab	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	FLFVAAIFYLITPVH	0.11	0.11	99.77%(452/453)	Non-Toxin	nsp4
104	ORF1ab	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	FSAVGNICYTPSKLI	0.06	0.06	99.55%(451/453)	Non-Toxin	nsp4
105	ORF1ab	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	FTPLVPFWITIAYII	0.03	0.03	100%(453/453)	Non-Toxin	nsp4
106	ORF1ab	DRB1*11:01	15	Consensus (smm/nn/sturniolo)	FVNEFYAYLRKHFSM	0.11	0.11	100%(453/453)	Non-Toxin	nsp12
107	ORF1ab	DRB3*02:02	15	NetMHCIIpan	HANYIFWRNTNPIQL	0.11	0.11	98.89%(448/453)	Non-Toxin	nsp16
108	ORF1ab	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	HFISNSWLMWLIINL	0.05	0.05	100%(453/453)	Non-Toxin	nsp3
109	ORF1ab	DRB1*04:01	15	Consensus (smm/nn/sturniolo)	IASEFSSLPSYAAFA	0.13	0.13	99.33%(450/453)	Non-Toxin	nsp8
110	ORF1ab	DQA1*05:01/DQB1*02:01	15	Consensus (comb.lib./smm/nn)	IDFLELAMDEFIERY	0.05	0.05	99.33%(450/453)	Non-Toxin	nsp15
111	ORF1ab	DRB1*09:01	15	Consensus (comb.lib./smm/nn)	IILASFSASTSAFVE	0.01	0.01	100%(453/453)	Non-Toxin	nsp2
112	ORF1ab	DRB1*09:01	15	Consensus (comb.lib./smm/nn)	ILASFSASTSAFVET	0.02	0.02	100%(453/453)	Non-Toxin	nsp2
113	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	ILFTRFFYVLGLAAI	0.11	0.11	100%(453/453)	Non-Toxin	nsp3
114	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	IMQLFFSYFAVHFIS	0.05	0.05	100%(453/453)	Non-Toxin	nsp3
115	ORF1ab	DQA1*05:01/DQB1*03:01	15	Consensus (comb.lib./smm/nn)	ISASIVAGGIVAIVV	0.03	0.03	100%(453/453)	Non-Toxin	nsp4
116	ORF1ab	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	ISNSWLMWLIINLVQ	0.07	0.07	100%(453/453)	Non-Toxin	nsp3
117	ORF1ab	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	KLINIIIWFLLLSVC	0.09	0.09	97.79%(443/453)	Non-Toxin	nsp3
118	ORF1ab	DPA1*02:01/DPB1*05:01	15	Consensus (comb.lib./smm/nn)	KQLIKVTLVFLFVAA	0.13	0.13	99.77%(452/453)	Non-Toxin	nsp4
119	ORF1ab	DPA1*02:01/DPB1*05:01	15	Consensus (comb.lib./smm/nn)	KVTLVFLFVAAIFYL	0.04	0.04	99.77%(452/453)	Non-Toxin	nsp4
120	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	LAAIMQLFFSYFAVH	0.07	0.07	100%(453/453)	Non-Toxin	nsp3
121	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	LAYILFTRFFYVLGL	0.01	0.01	100%(453/453)	Non-Toxin	nsp3
122	ORF1ab	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	LAYILFTRFFYVLGL	0.08	0.08	100%(453/453)	Non-Toxin	nsp3
123	ORF1ab	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	LCTFTRSTNSRIKAS	0.12	0.12	99.11%(449/453)	Non-Toxin	nsp3
124	ORF1ab	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	LEETKFLTENLLLYI	0.03	0.03	99.77%(452/453)	Non-Toxin	nsp3
125	ORF1ab	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	LINIIIWFLLLSVCL	0.09	0.09	97.79%(443/453)	Non-Toxin	nsp3
126	ORF1ab	DPA1*02:01/DPB1*05:01	15	Consensus (comb.lib./smm/nn)	LKQLIKVTLVFLFVA	0.13	0.13	99.77%(452/453)	Non-Toxin	nsp4
127	ORF1ab	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	LLQLCTFTRSTNSRI	0.12	0.12	98.89%(448/453)	Non-Toxin	nsp3
128	ORF1ab	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	LQLCTFTRSTNSRIK	0.12	0.12	98.89%(448/453)	Non-Toxin	nsp3
129	ORF1ab	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	LVFLFVAAIFYLITP	0.11	0.11	99.77%(452/453)	Non-Toxin	nsp4
130	ORF1ab	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	LVPFWITIAYIICIS	0.03	0.03	100%(453/453)	Non-Toxin	nsp4
131	ORF1ab	DQA1*05:01/DQB1*02:01	15	Consensus (comb.lib./smm/nn)	MEIDFLELAMDEFIE	0.04	0.04	99.11%(449/453)	Non-Toxin	nsp15
132	ORF1ab	DPA1*02:01/DPB1*14:01	15	NetMHCIIpan	MNLKYAISAKNRART	0.08	0.08	99.77%(452/453)	Non-Toxin	nsp12
133	ORF1ab	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	MPNMLRIMASLVLAR	0.01	0.01	100%(453/453)	Non-Toxin	nsp12
134	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	MQLFFSYFAVHFISN	0.05	0.05	100%(453/453)	Non-Toxin	nsp3
135	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	MYIFFASFYYVWKSY	0.04	0.04	99.11%(449/453)	Non-Toxin	nsp3
136	ORF1ab	DRB1*11:01	15	Consensus (smm/nn/sturniolo)	NEFYAYLRKHFSMMI	0.02	0.02	100%(453/453)	Non-Toxin	nsp12
137	ORF1ab	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	NMLRIMASLVLARKH	0.01	0.01	100%(453/453)	Non-Toxin	nsp12
138	ORF1ab	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	NSWLMWLIINLVQMA	0.1	0.1	100%(453/453)	Non-Toxin	nsp3
139	ORF1ab	DRB3*02:02	15	NetMHCIIpan	NYIFWRNTNPIQLSS	0.04	0.04	98.89%(448/453)	Non-Toxin	nsp16
140	ORF1ab	DRB1*13:02	15	Consensus (smm/nn/sturniolo)	PEVKILNNLGVDIAA	0.12	0.12	99.77%(452/453)	Non-Toxin	nsp15
141	ORF1ab	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	PLVPFWITIAYIICI	0.02	0.02	100%(453/453)	Non-Toxin	nsp4

142	ORF1ab	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	PNMLRIMASLVLARK	0.01	0.01	100%(453/453)	Non-Toxin	nsp12
143	ORF1ab	DRB1*04:01	15	Consensus (smm/nn/sturniolo)	QAIASEFSSLPSYAA	0.13	0.13	99.33%(450/453)	Non-Toxin	nsp8
144	ORF1ab	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	QESPFVMMSAPPAQY	0.01	0.01	100%(453/453)	Non-Toxin	nsp3
145	ORF1ab	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	QLCTFTRSTNSRIKA	0.12	0.12	98.67%(447/453)	Non-Toxin	nsp3
146	ORF1ab	DQA1*05:01/DQB1*02:01	15	Consensus (comb.lib./smm/nn)	QMEIDFLELAMDEFI	0.03	0.03	99.11%(449/453)	Non-Toxin	nsp15
147	ORF1ab	DPA1*02:01/DPB1*14:01	15	NetMHCIIpan	QMNLKYAISAKNRAR	0.07	0.07	99.77%(452/453)	Non-Toxin	nsp12
148	ORF1ab	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	QQESPFVMMSAPPAQ	0.1	0.1	99.77%(452/453)	Non-Toxin	nsp3
149	ORF1ab	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	QSTQWSLFFFLYENA	0.1	0.1	92.27%(418/453)	Non-Toxin	nsp6
150	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	QWSLFFFLYENAFLP	0.04	0.04	92.27%(418/453)	Non-Toxin	nsp6
151	ORF1ab	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	RAMPNMLRIMASLVL	0.01	0.01	100%(453/453)	Non-Toxin	nsp12
152	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	RMYIFFASFYYVWKS	0.04	0.04	99.11%(449/453)	Non-Toxin	nsp3
153	ORF1ab	DQA1*05:01/DQB1*03:01	15	Consensus (comb.lib./smm/nn)	SASIVAGGIVAIVVT	0.03	0.03	100%(453/453)	Non-Toxin	nsp4
154	ORF1ab	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	SAVGNICYTPSKLIE	0.09	0.09	99.55%(451/453)	Non-Toxin	nsp4
155	ORF1ab	DQA1*05:01/DQB1*03:01	15	Consensus (comb.lib./smm/nn)	SIVAGGIVAIVVTCL	0.03	0.03	100%(453/453)	Non-Toxin	nsp4
156	ORF1ab	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	SKLINIIIWFLLLSV	0.09	0.09	97.79%(443/453)	Non-Toxin	nsp3
157	ORF1ab	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	SNSWLMWLIINLVQM	0.07	0.07	100%(453/453)	Non-Toxin	nsp3
158	ORF1ab	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	SPFVMMSAPPAQYEL	0.01	0.01	100%(453/453)	Non-Toxin	nsp3
159	ORF1ab	DQA1*05:01/DQB1*02:01	15	Consensus (comb.lib./smm/nn)	SQMEIDFLELAMDEF	0.05	0.05	99.11%(449/453)	Non-Toxin	nsp15
160	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	STQWSLFFFLYENAF	0.05	0.05	92.27%(418/453)	Non-Toxin	nsp6
161	ORF1ab	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	STQWSLFFFLYENAF	0.1	0.1	92.27%(418/453)	Non-Toxin	nsp6
162	ORF1ab	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	TKFLTENLLLYIDIN	0.05	0.05	99.77%(452/453)	Non-Toxin	nsp3
163	ORF1ab	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	TLEETKFLTENLLLY	0.05	0.05	99.77%(452/453)	Non-Toxin	nsp3
164	ORF1ab	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	TLVFLFVAAIFYLIT	0.11	0.11	99.77%(452/453)	Non-Toxin	nsp4
165	ORF1ab	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	TPLVPFWITIAYIIC	0.03	0.03	100%(453/453)	Non-Toxin	nsp4
166	ORF1ab	DPA1*02:01/DPB1*14:01	15	NetMHCIIpan	TQMNLKYAISAKNRA	0.11	0.11	99.77%(452/453)	Non-Toxin	nsp12
167	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	TQWSLFFFLYENAFL	0.04	0.04	92.27%(418/453)	Non-Toxin	nsp6
168	ORF1ab	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	TQWSLFFFLYENAFL	0.09	0.09	92.27%(418/453)	Non-Toxin	nsp6
169	ORF1ab	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	VFLFVAAIFYLITPV	0.11	0.11	99.77%(452/453)	Non-Toxin	nsp4
170	ORF1ab	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	VGNICYTPSKLIEYT	0.13	0.13	99.77%(452/453)	Non-Toxin	nsp4
171	ORF1ab	DRB1*11:01	15	Consensus (smm/nn/sturniolo)	VNEFYAYLRKHFSMM	0.05	0.05	100%(453/453)	Non-Toxin	nsp12
172	ORF1ab	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	VPFWITIAYIICIST	0.03	0.03	100%(453/453)	Non-Toxin	nsp4
173	ORF1ab	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	VQQESPFVMMSAPPA	0.1	0.1	99.77%(452/453)	Non-Toxin	nsp3
174	ORF1ab	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	VQSTQWSLFFFLYEN	0.11	0.11	92.27%(418/453)	Non-Toxin	nsp6
175	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	VRMYIFFASFYYVWK	0.03	0.03	98.45%(446/453)	Non-Toxin	nsp3
176	ORF1ab	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	VRMYIFFASFYYVWK	0.1	0.1	98.45%(446/453)	Non-Toxin	nsp3
177	ORF1ab	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	VTLVFLFVAAIFYLI	0.11	0.11	99.77%(452/453)	Non-Toxin	nsp4
178	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	WFLAYILFTRFFYVL	0.01	0.01	100%(453/453)	Non-Toxin	nsp3
179	ORF1ab	DPA1*02:01/DPB1*01:01	15	Consensus (comb.lib./smm/nn)	WFLAYILFTRFFYVL	0.06	0.06	100%(453/453)	Non-Toxin	nsp3
180	ORF1ab	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	WFLAYILFTRFFYVL	0.08	0.08	100%(453/453)	Non-Toxin	nsp3
181	ORF1ab	DPA1*02:01/DPB1*05:01	15	Consensus (comb.lib./smm/nn)	WLKQLIKVTLVFLFV	0.13	0.13	99.77%(452/453)	Non-Toxin	nsp4
182	ORF1ab	DQA1*01:02/DQB1*06:02	15	Consensus (comb.lib./smm/nn)	YAFASEAARVVRSIF	0.08	0.08	99.77%(452/453)	Non-Toxin	nsp2
183	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	YIFFASFYYVWKSYV	0.05	0.05	99.55%(451/453)	Non-Toxin	nsp3
184	ORF1ab	DRB3*02:02	15	NetMHCIIpan	YIFWRNTNPIQLSSY	0.05	0.05	98.89%(448/453)	Non-Toxin	nsp16
185	ORF1ab	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	YILFTRFFYVLGLAA	0.08	0.08	100%(453/453)	Non-Toxin	nsp3
S.No.	ORF	Allele	Length	Method used	Peptide	Percentile Rank	Adjusted rank	Conservancy	Toxicity	
186	ORF3a	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	APFLYLYALVYFLQS	0.12	0.12	96.88%(466/481)	Non-Toxin	
187	ORF3a	DPA1*02:01/DPB1*14:01	15	NetMHCIIpan	DFVRATATIPIQASL	0.12	0.12	99.37%(478/481)	Non-Toxin	
188	ORF3a	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	DTGVEHVTFFIYNKI	1.1	1.1	99.37%(478/481)	Non-Toxin	
189	ORF3a	DPA1*02:01/DPB1*05:01	15	Consensus (comb.lib./smm/nn)	DTGVEHVTFFIYNKI	1.6	1.6	99.37%(478/481)	Non-Toxin	
190	ORF3a	DRB1*04:05	15	Consensus (smm/nn/sturniolo)	FFIYNKIVDEPEEHV	0.94	0.94	99.58%(479/481)	Non-Toxin	
191	ORF3a	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	FLYLYALVYFLQSIN	0.12	0.12	96.67%(465/481)	Non-Toxin	

192	ORF3a	DPA1*02:01/DPB1*14:01	15	NetMHCIIpan	FVRATATIPIQASLP	0.12	0.12	99.37%(478/481)	Non-Toxin	
193	ORF3a	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	GVEHVTFFIYNKIVD	1.2	1.2	99.37%(478/481)	Non-Toxin	
194	ORF3a	DRB1*04:05	15	Consensus (smm/nn/sturniolo)	HVTFFIYNKIVDEPE	0.84	0.84	99.58%(479/481)	Non-Toxin	
195	ORF3a	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	LLFVTVYSHLLLVAA	0.1	0.1	97.08%(467/481)	Non-Toxin	
196	ORF3a	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	LYLYALVYFLQSINF	0.12	0.12	96.46%(464/481)	Non-Toxin	
197	ORF3a	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	PFLYLYALVYFLQSI	0.12	0.12	96.67%(465/481)	Non-Toxin	
198	ORF3a	DPA1*02:01/DPB1*14:01	15	NetMHCIIpan	SDFVRATATIPIQAS	0.12	0.12	99.37%(478/481)	Non-Toxin	
199	ORF3a	DRB1*04:05	15	Consensus (smm/nn/sturniolo)	TFFIYNKIVDEPEEH	0.81	0.81	99.58%(479/481)	Non-Toxin	
200	ORF3a	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	TGVEHVTFFIYNKIV	0.93	0.93	99.37%(478/481)	Non-Toxin	
201	ORF3a	DPA1*02:01/DPB1*05:01	15	Consensus (comb.lib./smm/nn)	TGVEHVTFFIYNKIV	1.4	1.4	99.37%(478/481)	Non-Toxin	
202	ORF3a	DRB1*04:05	15	Consensus (smm/nn/sturniolo)	VTFFIYNKIVDEPEE	0.81	0.81	99.58%(479/481)	Non-Toxin	
203	ORF3a	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	YLYALVYFLQSINFV	0.14	0.14	96.46%(464/481)	Non-Toxin	
S.No.	ORF	Allele	Length	Method used	Peptide	Percentile Rank	Adjusted rank	Conservancy	Toxicity	
204	ORF6	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	EILLIIMRTFKVSIW	0.1	0.1	99.58% (479/481)	Non-Toxin	
205	ORF6	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	FKVSIWNLDYIINLI	0.02	0.02	99.38% (478/481)	Non-Toxin	
206	ORF6	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	ILLIIMRTFKVSIWN	0.1	0.1	99.38% (478/481)	Non-Toxin	
207	ORF6	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	KVSIWNLDYIINLII	0.02	0.02	99.38% (478/481)	Non-Toxin	
208	ORF6	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	TFKVSIWNLDYIINL	0.02	0.02	99.38% (478/481)	Non-Toxin	
209	ORF6	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	VSIWNLDYIINLIIK	0.05	0.05	99.38% (478/481)	Non-Toxin	
	ORF	Allele	Length	Method used	Peptide	Percentile Rank	Adjusted rank	Conservancy	Toxicity	
210	ORF7a	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	IILFLALITLATCEL	0.16	0.16	99.79% (479/480)	Non-Toxin	
211	ORF7a	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	ILFLALITLATCELY	0.16	0.16	99.79% (479/480)	Non-Toxin	
212	ORF7a	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	KIILFLALITLATCE	0.16	0.16	99.58% (478/480)	Non-Toxin	
213	ORF7a	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	MKIILFLALITLATC	0.16	0.16	99.58% (478/480)	Non-Toxin	
214	ORF7a	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	MKIILFLALITLATC	0.39	0.39	99.58% (478/480)	Non-Toxin	
S.No.	ORF	Allele	Length	Method used	Peptide	Percentile Rank	Adjusted rank	Conservancy	Toxicity	
215	ORF7b	DRB4*01:01	15	Consensus (comb.lib./smm/nn)	AFLLFLVLIMLIIFW	0.14	0.14	99.58% (235/236)	Non-Toxin	
216	ORF7b	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	CFLAFLLFLVLIMLI	0.03	0.03	97.88% (231/236)	Non-Toxin	
217	ORF7b	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	CFLAFLLFLVLIMLI	0.08	0.08	97.88% (231/236)	Non-Toxin	
218	ORF7b	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	CFLAFLLFLVLIMLI	0.11	0.11	97.88% (231/236)	Non-Toxin	
219	ORF7b	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	DFYLCFLAFLLFLVL	0.03	0.03	98.31% (232/236)	Non-Toxin	
220	ORF7b	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	DFYLCFLAFLLFLVL	0.08	0.08	98.31% (232/236)	Non-Toxin	
221	ORF7b	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	DFYLCFLAFLLFLVL	0.09	0.09	98.31% (232/236)	Non-Toxin	
222	ORF7b	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	FLAFLLFLVLIMLII	0.06	0.06	97.88% (231/236)	Non-Toxin	
223	ORF7b	DRB4*01:01	15	Consensus (comb.lib./smm/nn)	FLAFLLFLVLIMLII	0.14	0.14	97.88% (231/236)	Non-Toxin	
224	ORF7b	DRB4*01:01	15	Consensus (comb.lib./smm/nn)	FLLFLVLIMLIIFWF	0.19	0.19	99.58% (235/236)	Non-Toxin	
225	ORF7b	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	FYLCFLAFLLFLVLI	0.03	0.03	97.88% (231/236)	Non-Toxin	
226	ORF7b	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	FYLCFLAFLLFLVLI	0.06	0.06	97.88% (231/236)	Non-Toxin	
227	ORF7b	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	FYLCFLAFLLFLVLI	0.09	0.09	97.88% (231/236)	Non-Toxin	
228	ORF7b	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	IDFYLCFLAFLLFLV	0.06	0.06	98.31% (232/236)	Non-Toxin	
229	ORF7b	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	IDFYLCFLAFLLFLV	0.16	0.16	98.31% (232/236)	Non-Toxin	
230	ORF7b	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	LAFLLFLVLIMLIIF	0.08	0.08	99.58% (235/236)	Non-Toxin	
231	ORF7b	DRB4*01:01	15	Consensus (comb.lib./smm/nn)	LAFLLFLVLIMLIIF	0.12	0.12	99.58% (235/236)	Non-Toxin	
232	ORF7b	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	LCFLAFLLFLVLIML	0.02	0.02	97.88% (231/236)	Non-Toxin	
233	ORF7b	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	LCFLAFLLFLVLIML	0.06	0.06	97.88% (231/236)	Non-Toxin	
234	ORF7b	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	LCFLAFLLFLVLIML	0.09	0.09	97.88% (231/236)	Non-Toxin	
235	ORF7b	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	LIDFYLCFLAFLLFL	0.05	0.05	98.31% (232/236)	Non-Toxin	
236	ORF7b	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	LSLIDFYLCFLAFLL	0.15	0.15	98.31% (232/236)	Non-Toxin	
237	ORF7b	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	LVLIMLIIFWFSLEL	0.14	0.14	99.58% (235/236)	Non-Toxin	
238	ORF7b	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	SLIDFYLCFLAFLLF	0.07	0.07	98.31% (232/236)	Non-Toxin	
239	ORF7b	DPA1*03:01/DPB1*04:02	15	Consensus (comb.lib./smm/nn)	YLCFLAFLLFLVLIM	0.02	0.02	97.88% (231/236)	Non-Toxin	

240	ORF7b	DPA1*01:03/DPB1*02:01	15	Consensus (comb.lib./smm/nn)	YLCFLAFLLFLVLIM	0.06	0.06	97.88% (231/236)	Non-Toxin	
241	ORF7b	DPA1*01/DPB1*04:01	15	Consensus (comb.lib./smm)	YLCFLAFLLFLVLIM	0.09	0.09	97.88% (231/236)	Non-Toxin	
S.No.	ORF	Allele	Length	Method used	Peptide	Percentile Rank	Adjusted rank	Conservancy	Toxicity	
242	ORF8	DRB3*01:01	15	Consensus (comb.lib./smm/nn)	CTQHQPYVVDDPCPI	0.08	0.08	99.17% (476/480)	Non-Toxin	
243	ORF8	DRB3*01:01	15	Consensus (comb.lib./smm/nn)	HQPYVVDDPCPIHFY	0.08	0.08	99.17% (476/480)	Non-Toxin	
244	ORF8	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	LVVRCSFYEDFLEYH	0.45	0.45	99.58% (478/480)	Non-Toxin	
245	ORF8	DRB3*01:01	15	Consensus (comb.lib./smm/nn)	QHQPYVVDDPCPIHF	0.08	0.08	99.17% (476/480)	Non-Toxin	
246	ORF8	DRB3*01:01	15	Consensus (comb.lib./smm/nn)	QPYVVDDPCPIHFYS	0.07	0.07	99.17% (476/480)	Non-Toxin	
247	ORF8	DRB3*01:01	15	Consensus (comb.lib./smm/nn)	TQHQPYVVDDPCPIH	0.08	0.08	99.17% (476/480)	Non-Toxin	
S.No.	ORF	Allele	Length	Method used	Peptide	Percentile Rank	Adjusted rank	Conservancy	Toxicity	
248	S protein	DRB3*01:01	15	Consensus (comb.lib./smm/nn)	ADSFVIRGDEVRQIA	0.49	0.49	93.63% (470/502)	Non-Toxin	
249	S protein	DRB3*02:02	15	NetMHCIIpan	ADYSVLYNSASFSTF	0.85	0.85	93.82% (471/502)	Non-Toxin	
250	S protein	DQA1*01:02/DQB1*06:02	15	Consensus (comb.lib./smm/nn)	AGLIAIVMVTIMLCC	1.7	1.7	93.82% (471/502)	Non-Toxin	
251	S protein	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	AIPTNFTISVTTEIL	0.4	0.4	93.82% (471/502)	Non-Toxin	
252	S protein	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	CSNLLLQYGSFCTQL	0.58	0.58	93.82% (471/502)	Non-Toxin	
253	S protein	DRB3*01:01	15	Consensus (comb.lib./smm/nn)	DSFVIRGDEVRQIAP	0.51	0.51	93.63% (470/502)	Non-Toxin	
254	S protein	DRB3*02:02	15	NetMHCIIpan	DYSVLYNSASFSTFK	0.68	0.68	93.82% (471/502)	Non-Toxin	
255	S protein	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	ECSNLLLQYGSFCTQ	0.72	0.72	93.82% (471/502)	Non-Toxin	
256	S protein	DRB5*01:01	15	Consensus (smm/nn/sturniolo)	EFVFKNIDGYFKIYS	0.17	0.17	92.03% (462/502)	Non-Toxin	
257	S protein	DRB3*02:02	15	NetMHCIIpan	EGVFVSNGTHWFVTQ	0.21	0.21	93.23% (468/502)	Non-Toxin	
258	S protein	DRB1*04:05	15	Consensus (smm/nn/sturniolo)	ESIVRFPNITNLCPF	0.77	0.77	93.43% (469/502)	Non-Toxin	
259	S protein	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	FQTLLALHRSYLTPG	1.1	1.1	93.23% (468/502)	Non-Toxin	
260	S protein	DRB5*01:01	15	Consensus (smm/nn/sturniolo)	FVFKNIDGYFKIYSK	0.17	0.17	92.03% (462/502)	Non-Toxin	
261	S protein	DRB3*01:01	15	Consensus (comb.lib./smm/nn)	FVIRGDEVRQIAPGQ	0.54	0.54	93.63% (470/502)	Non-Toxin	
262	S protein	DQA1*05:01/DQB1*03:01	15	Consensus (comb.lib./smm/nn)	GFIAGLIAIVMVTIM	1.6	1.6	93.82% (471/502)	Non-Toxin	
263	S protein	DRB5*01:01	15	Consensus (smm/nn/sturniolo)	GINITRFQTLLALHR	0.52	0.52	93.43% (469/502)	Non-Toxin	
264	S protein	DRB1*11:01	15	Consensus (smm/nn/sturniolo)	GNYNYLYRLFRKSNL	0.22	0.22	92.63% (465/502)	Non-Toxin	
265	S protein	DQA1*01:02/DQB1*06:02	15	Consensus (comb.lib./smm/nn)	IAGLIAIVMVTIMLC	1.6	1.6	93.82% (471/502)	Non-Toxin	
266	S protein	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	IAIPTNFTISVTTEI	0.47	0.47	93.82% (471/502)	Non-Toxin	
267	S protein	DRB5*01:01	15	Consensus (smm/nn/sturniolo)	INITRFQTLLALHRS	0.32	0.32	93.23% (468/502)	Non-Toxin	
268	S protein	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	IPTNFTISVTTEILP	0.52	0.52	93.82% (471/502)	Non-Toxin	
269	S protein	DRB5*01:01	15	Consensus (smm/nn/sturniolo)	ITRFQTLLALHRSYL	0.26	0.26	93.23% (468/502)	Non-Toxin	
270	S protein	DPA1*02:01/DPB1*14:01	15	NetMHCIIpan	ITRFQTLLALHRSYL	0.43	0.43	93.23% (468/502)	Non-Toxin	
271	S protein	DQA1*05:01/DQB1*03:01	15	Consensus (comb.lib./smm/nn)	IWLGFIAGLIAIVMV	0.51	0.51	93.43% (469/502)	Non-Toxin	
272	S protein	DRB3*02:02	15	NetMHCIIpan	KTQSLLIVNNATNVV	0.17	0.17	93.82% (471/502)	Non-Toxin	
273		DRB1*13:02	15	Consensus (smm/nn/sturniolo)	KTQSLLIVNNATNVV	0.01	0.01	93.82% (471/502)	Non-Toxin	
274	S protein	DQA1*05:01/DQB1*03:01	15	Consensus (comb.lib./smm/nn)	LGFIAGLIAIVMVTI	1.6	1.6	93.82% (471/502)	Non-Toxin	
275	S protein	DRB1*13:02	15	Consensus (smm/nn/sturniolo)	LIVNNATNVVIKVCE	0.03	0.03	93.23% (468/502)	Non-Toxin	
276	S protein	DRB1*13:02	15	Consensus (smm/nn/sturniolo)	LLIVNNATNVVIKVC	0.01	0.01	93.23% (468/502)	Non-Toxin	
277	S protein	DRB3*02:02	15	NetMHCIIpan	LLIVNNATNVVIKVC	0.09	0.09	93.23% (468/502)	Non-Toxin	
278	S protein	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	LSFELLHAPATVCGP	0.03	0.03	92.23% (463/502)	Non-Toxin	
279	S protein	DRB5*01:01	15	Consensus (smm/nn/sturniolo)	NITRFQTLLALHRSY	0.32	0.32	93.23% (468/502)	Non-Toxin	
280	S protein	DPA1*02:01/DPB1*14:01	15	NetMHCIIpan	NITRFQTLLALHRSY	0.45	0.45	93.23% (468/502)	Non-Toxin	
281	S protein	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	NLLLQYGSFCTQLNR	0.75	0.75	93.82% (471/502)	Non-Toxin	
282	S protein	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	PTESIVRFPNITNLC	0.64	0.64	93.43% (469/502)	Non-Toxin	
283	S protein	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	PTNFTISVTTEILPV	0.51	0.51	93.82% (471/502)	Non-Toxin	
284	S protein	DQA1*01:01/DQB1*05:01	15	Consensus (comb.lib./smm/nn)	PWYIWLGFIAGLIAI	1.9	1.9	93.43% (469/502)	Non-Toxin	
285	S protein	DPA1*02:01/DPB1*14:01	15	NetMHCIIpan	QLIRAAEIRASANLA	0.31	0.31	93.23% (468/502)	Non-Toxin	
286	S protein	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	QPTESIVRFPNITNL	0.69	0.69	93.43% (469/502)	Non-Toxin	
287	S protein	DPA1*02:01/DPB1*14:01	15	NetMHCIIpan	QQLIRAAEIRASANL	0.2	0.2	93.23% (468/502)	Non-Toxin	
288	S protein	DRB1*13:02	15	Consensus (smm/nn/sturniolo)	QSLLIVNNATNVVIK	0.01	0.01	93.63% (470/502)	Non-Toxin	

289	S protein	DRB3*02:02	15	NetMHCIIpan	QSLLIVNNATNVVIK	0.02	0.02	93.63% (470/502)	Non-Toxin	
290	S protein	DRB5*01:01	15	Consensus (smm/nn/sturniolo)	REFVFKNIDGYFKIY	0.17	0.17	91.83% (461/502)	Non-Toxin	
291	S protein	DRB3*02:02	15	NetMHCIIpan	REGVFVSNGTHWFVT	0.2	0.2	93.43% (469/502)	Non-Toxin	
292	S protein	DRB5*01:01	15	Consensus (smm/nn/sturniolo)	RFQTLLALHRSYLTP	0.58	0.58	93.23% (468/502)	Non-Toxin	
293	S protein	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	SFELLHAPATVCGPK	0.09	0.09	92.23% (463/502)	Non-Toxin	
294	S protein	DRB3*01:01	15	Consensus (comb.lib./smm/nn)	SFVIRGDEVRQIAPG	0.51	0.51	93.63% (470/502)	Non-Toxin	
295	S protein	DRB1*04:05	15	Consensus (smm/nn/sturniolo)	SIVRFPNITNLCPFG	0.98	0.98	93.43% (469/502)	Non-Toxin	
296	S protein	DRB1*13:02	15	Consensus (smm/nn/sturniolo)	SKTQSLLIVNNATNV	0.03	0.03	93.82% (471/502)	Non-Toxin	
297	S protein	DRB1*13:02	15	Consensus (smm/nn/sturniolo)	SLLIVNNATNVVIKV	0.01	0.01	93.63% (470/502)	Non-Toxin	
298	S protein	DRB3*02:02	15	NetMHCIIpan	SLLIVNNATNVVIKV	0.03	0.03	93.63% (470/502)	Non-Toxin	
299	S protein	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	SNLLLQYGSFCTQLN	0.6	0.6	93.82% (471/502)	Non-Toxin	
300	S protein	DQA1*05:01/DQB1*03:01	15	Consensus (comb.lib./smm/nn)	SSGWTAGAAAYYVGY	0.94	0.94	93.43% (469/502)	Non-Toxin	
301	S protein	DQA1*05:01/DQB1*03:01	15	Consensus (comb.lib./smm/nn)	SSSGWTAGAAAYYVG	1.1	1.1		Non-Toxin	
302	S protein	DRB1*15:01	15	Consensus (smm/nn/sturniolo)	TESIVRFPNITNLCP	0.69	0.69	93.43% (469/502)	Non-Toxin	
303	S protein	DRB1*07:01	15	Consensus (comb.lib./smm/nn)	TNFTISVTTEILPVS	0.52	0.52	93.82% (471/502)	Non-Toxin	
304	S protein	DRB1*13:02	15	Consensus (smm/nn/sturniolo)	TQSLLIVNNATNVVI	0.01	0.01	93.63% (470/502)	Non-Toxin	
305	S protein	DRB3*02:02	15	NetMHCIIpan	TQSLLIVNNATNVVI	0.06	0.06	93.63% (470/502)	Non-Toxin	
306	S protein	DRB5*01:01	15	Consensus (smm/nn/sturniolo)	TRFQTLLALHRSYLT	0.35	0.35	93.23% (468/502)	Non-Toxin	
307	S protein	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	VLSFELLHAPATVCG	0.03	0.03	92.23% (463/502)	Non-Toxin	
308	S protein	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	VVLSFELLHAPATVC	0.03	0.03	92.23% (463/502)	Non-Toxin	
309	S protein	DRB1*01:01	15	Consensus (comb.lib./smm/nn)	VVVLSFELLHAPATV	0.09	0.09	92.23% (463/502)	Non-Toxin	
310	S protein	DQA1*05:01/DQB1*03:01	15	Consensus (comb.lib./smm/nn)	WLGFIAGLIAIVMVT	1.6	1.6	93.63% (470/502)	Non-Toxin	
311	S protein	DQA1*05:01/DQB1*03:01	15	Consensus (comb.lib./smm/nn)	WYIWLGFIAGLIAIV	0.58	0.58	93.43% (469/502)	Non-Toxin	
312	S protein	DRB3*01:01	15	Consensus (comb.lib./smm/nn)	YADSFVIRGDEVRQI	0.49	0.49	93.63% (470/502)	Non-Toxin	
313	S protein	DQA1*05:01/DQB1*03:01	15	Consensus (comb.lib./smm/nn)	YIWLGFIAGLIAIVM	0.51	0.51	93.43% (469/502)	Non-Toxin	
314	S protein	DRB3*02:02	15	NetMHCIIpan	YSVLYNSASFSTFKC	0.66	0.66	93.82% (471/502)	Non-Toxin	

Supplementary Table S4: HLA alleles covered by the overlapping CTL and HTL epitopes.

S.No.	HLA alleles	Class of HLA alleles
1	HLA-A*01:01	HLA Class I alleles
2	HLA-A*02:01	
3	HLA-A*02:03	
4	HLA-A*02:06	
5	HLA-A*03:01	
6	HLA-A*11:01	
7	HLA-A*23:01	
8	HLA-A*24:02	
9	HLA-A*26:01	
10	HLA-A*30:01	
11	HLA-A*30:02	
12	HLA-A*31:01	
13	HLA-A*32:01	
14	HLA-A*33:01	
15	HLA-A*68:01	
16	HLA-A*68:02	
17	HLA-B*07:02	
18	HLA-B*08:01	
19	HLA-B*15:01	
20	HLA-B*35:01	
21	HLA-B*40:01	
22	HLA-B*44:02	
23	HLA-B*44:03	
24	HLA-B*51:01	
25	HLA-B*53:01	
26	HLA-B*57:01	
27	HLA-B*58:01	
28	HLA-DPA1*01	HLA Class I alleles
29	HLA-DPA1*01:03	
30	HLA-DPA1*02:01	
31	HLA-DPA1*03:01	
32	HLA-DPB1*01:01	
33	HLA-DPB1*02:01	
34	HLA-DPB1*04:01	
35	HLA-DPB1*04:02	

36	HLA-DPB1*05:01	
37	HLA-DPB1*14:01	
38	HLA-DQA1*01:01	
39	HLA-DQA1*01:02	
40	HLA-DQA1*05:01	
41	HLA-DQB1*02:01	
42	HLA-DQB1*05:01	
43	HLA-DQB1*06:02	
44	HLA-DRB1*01:01	
45	HLA-DRB1*04:01	
46	HLA-DRB1*04:05	
47	HLA-DRB1*07:01	
48	HLA-DRB1*09:01	
49	HLA-DRB1*11:01	
50	HLA-DRB1*13:02	
51	HLA-DRB1*15:01	
52	HLA-DRB3*01:01	
53	HLA-DRB3*02:02	
54	HLA-DRB4*01:01	
55	HLA-DRB5*01:01	

Supplementary Table S5: Population coverage by all the overlapping CTL and HTL epitopes forming epitope clusters.

population/area	Class combined		
	coverage[a]	average_hit[b]	pc90[c]
Algeria	79.67%	20.09	1.97
American Samoa	98.75%	65.28	38.26
Argentina	99.74%	95.44	52.01
Australia	98.16%	78.28	31.37
Austria	99.99%	113.11	66.15
Belarus	43.81%	3.23	0.71
Belgium	99.76%	87.08	49.51
Bolivia	38.38%	5.02	0.97
Borneo	38.38%	6.32	0.97
Brazil	99.99%	140.15	88.36
Bulgaria	99.68%	95.65	53.93

Burkina Faso	67.18%	32.67	3.96
Cameroon	99.98%	136.25	72.31
Canada	89.48%	20.21	3.8
Cape Verde	99.76%	117.59	58.01
Central Africa	99.96%	129.22	68.79
Central African Republic	66.32%	20.16	1.78
Central America	80.55%	20.65	3.09
Chile	99.48%	89.01	43.08
China	99.83%	121.35	63.51
Colombia	78.87%	21.53	1.89
Congo	93.93%	22.36	9.86
Cook Islands	100.00%	76.33	46.33
Costa Rica	76.74%	16.09	2.58
Croatia	99.99%	126.99	77.32
Cuba	99.77%	111.02	58.37
Czech Republic	99.95%	117.22	65.85
Denmark	95.41%	25.93	10.65
East Africa	99.98%	135.39	74.29
East Asia	99.81%	115.86	57.72
Ecuador	99.71%	95.91	46.78
England	100.00%	131.07	82.91
Equatorial Guinea	72.14%	14.25	3.23
Ethiopia	96.17%	29.61	11.44
Europe	100.00%	170.31	117.87
Fiji	96.74%	25.75	11.2
Finland	100.00%	120.96	68.64
France	100.00%	176.9	125.21
Gabon	99.95%	73.91	44.53
Gambia	99.90%	65.49	41.85
Georgia	99.85%	109.46	57.53
Germany	100.00%	137.81	86.57
Greece	87.50%	22.14	3.2
Guatemala	20.40%	4.99	0.75
Guinea-Bissau	98.74%	96.3	36.3
Hong Kong	96.05%	58.93	25.23
India	99.94%	123.02	71.53
Indonesia	96.59%	63.06	23.28
Iran	99.72%	100.42	51.81
Ireland Northern	99.99%	117.02	72.08
Ireland South	99.99%	115.21	70.53
Israel	98.99%	82.96	34.51

Italy	99.82%	110.18	59.32
Ivory Coast	67.75%	25.43	3.41
Jamaica	82.25%	18.28	2.25
Japan	99.95%	140.06	78.99
Jordan	98.07%	67.52	25.05
Kenya	99.96%	125.27	66.5
Kiribati	56.35%	9.61	2.06
Korea; South	99.74%	106.67	52.49
Lebanon	61.98%	8.81	1.05
Liberia	91.53%	35.2	26.27
Macedonia	97.86%	37.84	12.81
Malaysia	90.59%	50.93	6.9
Mali	96.02%	83.84	22.38
Martinique	71.03%	25.57	1.38
Mexico	100.00%	149.99	98.41
Mongolia	99.46%	88.15	46.32
Morocco	99.86%	109.88	59.86
Nauru	82.88%	15.4	2.34
Netherlands	87.50%	21.51	3.2
New Caledonia	99.97%	88.65	59.66
New Zealand	90.84%	43.25	5.16
Nigeria	90.03%	39.47	26.01
Niue	91.02%	38.7	10.12
North Africa	99.56%	100.23	45.59
North America	100.00%	166.28	113.61
Northeast Asia	99.84%	121.14	63.63
Norway	97.19%	31.38	12.9
Oceania	99.86%	113.14	62.67
Oman	99.69%	89.6	48.6
Pakistan	97.13%	56.16	26.19
Papua New Guinea	100.00%	122.52	89.36
Paraguay	25.70%	4.63	2.42
Peru	100.00%	106.29	54.99
Philippines	96.26%	64.15	37.87
Poland	99.99%	127.2	78.58
Portugal	99.86%	112.89	61.91
Romania	99.67%	93.68	50.23
Russia	100.00%	157.35	107.43
Rwanda	64.44%	20.73	1.12
Samoa	97.31%	52.21	17.85
Sao Tome and Principe	98.33%	85.65	31.47

Saudi Arabia	99.51%	90.79	46.85
Scotland	98.48%	48.85	18.32
Senegal	96.67%	90.69	29.48
Serbia	73.37%	24.84	4.13
Singapore	96.73%	65.18	25.2
Slovenia	99.99%	80.78	59.26
South Africa	93.56%	63.39	16.23
South America	99.87%	119.99	66.69
South Asia	99.97%	131.94	80.9
Southeast Asia	99.26%	79.48	36.82
Southwest Asia	98.54%	80.38	33.12
Spain	100.00%	130.17	77.24
Sri Lanka	52.39%	22.7	5.25
Sudan	96.25%	72.21	24.29
Sweden	100.00%	184.71	128.28
Taiwan	99.78%	90.33	47.35
Thailand	99.04%	71.41	30.17
Tokelau	94.65%	43.18	44.11
Tonga	87.20%	36.78	4.69
Tunisia	99.63%	101.6	52.14
Turkey	97.28%	52.55	17.49
Uganda	99.98%	136.66	76.57
Ukraine	50.64%	3.87	0.81
United Kingdom	31.77%	8.9	4.1
United States	100.00%	167.87	115.74
Venezuela	95.65%	71.89	16.7
Vietnam	95.32%	60.75	24.19
West Africa	99.99%	154.32	89.11
West Indies	99.90%	118.21	64.3
Zambia	98.10%	89.47	33.81
Zimbabwe	99.78%	97.75	38.46
World	**99.98%**	**150.46**	**92.94**
Average	**91.11**	**79.27**	**41.42**
Standard deviation	**16.97**	**46.69**	**32.37**

Note: Following allele(s) were not available at IEDB “Population coverage” tool database, and therefore not included in the calculation, please note that allele names are case sensitive: DPA1*01, DRB5*01:01, DRB3*02:02, DRB3*01:01, DRB4*01:01.

a: projected population coverage;

b: average number of epitope hits / HLA combinations recognized by the population;
c: minimum number of epitope hits / HLA combinations recognized by 90% of the population

Supplementary Table S6: Construct of CTL-MPV-1, CTL-MPV-2, CTL-MPV-3, HTL-MPV-1, and HTL-MPV-2. Physicochemical property analysis based on the amino acid sequences of all the designed three CTL and two HTL Multi-Patch Vaccines.

S.No.	**Vaccine**	**Vaccine constructs**
1	CTL-MPV-1 construct (Comprising of identified CTL Ag-PATCHES from Membrane and Spike protein of SARS-CoV-2):	GIGDPVTCLKSGAICHPVFCPRRYKQIGTCGLPGTKCCKKPEAAAKGTITVEELKKLLEQWNLVIGFLFLTWICLLQFAYANRNRFLYIIKLIFLWLLWPVTLACFVLAAVGGGGSRINWITGGIAIAMACLVGLMWLSYFIASFRLFARTRSMWSFNGGGGSKEITVATSRTLSYYKLGASQRVAGDSGFAAYSRYRIGNYKLGGGGSTTRTQLPPAYTNSFTRGVYYPDKVFRSSVGGGGSSTQDLFLPFFSNVTWFGGGGSVLPFNDGVYFASTEKSNIIRGWIFGGGGSGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLGGGGSKQGNFKNLREFVFKNIDGYFKIYSKHTPIGGGGSEPLVDLPIGINITRFQTLLAGGGGSTPGDSSSGWTAGAAAYYVGYLQPRTFLLKGGGGSSETKCTLKSFTVEKGIYQTSNFRGGGGSFPNITNLCPFGEVFNATRFASVGGGGSRISNCVADYSVLYNSASFSTFKCYGGGGSNVYADSFVIRGDEVRGGGGSSKVGGNYNYLYRLFRKSNLKPFERGGGGSNTSNQVAVLYQDVNCTEVGGGGSRVYSTGSNVFGGGGSSPRRARSVASQSIIAYGGGGSFTISVTTEILPVSMTKTSVDCTMYGGGGSNTQEVFAQVKQIYKTPPIKGGGGSKRSFIEDLLFNKVTLAGGGGSPLLTDEMIAQYGGGGSLQIPFAMQMAYRFNGIGGGGSFPQSAPHGVVFGGGGSFVSNGTHWFVTQRGGGGSYEQYIKWPWYIWLGFIAGLIAIVEAAAKGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKHHHHHH
2	CTL-MPV-2 construct (Comprising of identified CTL Ag-PATCHES from Nucleocapsid protein and ORF1ab proteins of SARS-CoV-2):	GIGDPVTCLKSGAICHPVFCPRRYKQIGTCGLPGTKCCKKPEAAAKNQRNAPRITFGGPSGGGGSRSKQRRPQGLPNNTASWFTALTQHGKGGGGSNSSPDDQIGYYRRATRRIRGGDGKMKDLSPRWYFYYLGGGGSLPYGANKDGIIWGGGGSKSAAEASKKPRQKRTATKAYNVTQAFGGGGSQELIRQGTDYGGGGSIAQFAPSASAFFGMSRIGMEVTPSGTWLTYGGGGSLLNKHIDAYKTFPPTEPKKGGGGSDEWSMATYYLFGGGGSETISLAGSYKGGGGSTQVVDMSMTYGGGGSAVMYMGTLSYEQFGGGGSLVAEWFLAYILFTRFFYVGGGGSRMYIFFASFYYVWKSYGGGGSAYVNTFSSTFNVPMEKGGGGSCLAYYFMRFRRAFGGGGSMVMFTPLVPFWITIAYGGGGSFYWFFSNYLKRRVVFGGGGSLPSLATVAYFNMVYGGGGSLILMTARTVYGGGGSTACTDDNALAYYGGGGSYTMADLVYALGGGGSKLFDRYFKYWDQTYGGGGSARLYYDSMSYGGGGSVDTDFVNEFYAYLRKHFSMGGGGSFPLCANGQVFGLYGGGGSIPLMYKGLPWNVVRGGGGSYVMHANYIFWEAAAKGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKHHHHHH

3	**CTL-MPV-3 construct** (Comprising of identified CTL Ag-PATCHES from Envelope protein, ORF3a protein, ORF6 protein, ORF7a protein, ORF7b protein, ORF8 protein, and ORF10 protein of SARS-CoV-2):	GIGDPVTCLKSGAICHPVFCPRRYKQIGTCGLPGTKCCKKPEAAAKSEETGTLIVNSVLLFLAFVVFLLVTLAILTALRLCAYGGGGSVSLVKPSFYVYSRVKNLNSSRGGGGSFMRIFTIGTVTLKGGGGSTIPIQASLPFGWLIVGVALLAVFQSASKIITLKKRWGGGGSHFVCNLLLLFVTVGGGGSLLVAAGLEAPFLYLYALVYFLQSINFVRIIMRLWLCWKCRGGGGSYFLCWHTNCYDYGGGGSTTSPISEHDYQIGGYGGGGSYYQLYSTQLSTDTGVEHVTFFIYNKIGGGGSFHLVDFQVTIAEILLIIMRTFKVSIWNLDYIIGGGGSMKIILFLALITLATCELYHYGGGGSLLKEPCSSGTYEGNSPFHPLADNKFALTCFSTQFAFACPDGVKHVYQLRARSVSPKLFIRGGGGSEVQELYSPIFLIVAAIVFITLCFTLKRKGGGGSMIELSLIDFYLCFLAFLLFLVLIMLIIFWFSLELGGGGSMKFLVFLGIITTVAAFGGGGSYVVDDPCPIHFYSKWYIRVGARKSAPLIELCGGGGSIQYIDIGNYTVSCLPFTINCQEPKLGSLVVRCSFYEDFLEYHDVRVVLGGGGSMGYINVFAFPFTIYSLLLCREAAAKGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKHHHHHH
4	**HTL-MPV-1 construct** (Comprising of identified CTL Ag-PATCHES from Envelope protein, Membrane protein, Spike protein, Nucleocapsid protein, ORF3a protein of SARS-CoV-2):	GIGDPVTCLKSGAICHPVFCPRRYKQIGTCGLPGTKCCKKPEAAAKVNSVLLFLAFVVFLLVTLAILTGGGGSIKLIFLWLLWPVTLACGGGGSVGLMWLSYFIASFRLFARGGGGSSRTLSYYKLGASQRVAGDSGGGGSSKTQSLLIVNNATNVVIKVCEGGGGSREFVFKNIDGYFKIYSKGGGGSGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYGGGGSQPTESIVRFPNITNLCPFGGGGGSADYSVLYNSASFSTFKCGGGGSYADSFVIRGDEVRQIAPGQGGGGSVVVLSFELLHAPATVCGPKGGGGSIAIPTNFTISVTTEILPVSGGGGSQQLIRAAEIRASANLAGGGGSREGVFVSNGTHWFVTQGGGGSPWYIWLGFIAGLIAIVMVTIMLCCGGGGSDDQIGYYRRATRRIRGGDGGGGGSGTRNPANNAAIVLQLPQGTTLGGGGSWPQIAQFAPSASAFFGMSRGGGGSTPSGTWLTYTGAIKLDDKDGGGGSSDFVRATATIPIQASLPGGGGSAPFLYLYALVYFLQSINFVGGGGSDTGVEHVTFFIYNKIVDEPEEHVEAAAKGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKHHHHHH
5	**HTL-MPV-2 construct** (Comprising of identified CTL Ag-PATCHES from ORF1ab protein, ORF6 protein, ORF7a protein, ORF7b protein, ORF8 protein, ORF10 protein) of SARS-CoV-2):	GIGDPVTCLKSGAICHPVFCPRRYKQIGTCGLPGTKCCKKPEAAAKAIILASFSASTSAFVETGGGGSYAFASEAARVVRSIFSGGGGSTLEETKFLTENLLLYIDINGGGGSVQQESPFVMMSAPPAQYELGGGGSLLQLCTFTRSTNSRIKASMGGGGSSKLINIIIWFLLLSVCLGGGGSEWFLAYILFTRFFYVLGLAAIMQLFFSYFAVHFISNSWLMWLIINLVQMAGGGGSVRMYIFFASFYYVWKSYVGGGGSWLKQLIKVTLVFLFVAAIFYLITPVHGGGGSFSAVGNICYTPSKLIEYTGGGGSDISASIVAGGIVAIVVTCLGGGGSFTPLVPFWITIAYIICISTGGGGSVQSTQWSLFFFLYENAFLPGGGGSQAIASEFSSLPSYAAFATGGGGSTQMNLKYAISAKNRARTGGGGSRAMPNMLRIMASLVLARKHGGGGSFVNEFYAYLRKHFSMMILGGGGSPEVKILNNLGVDIAANGGGGSSQMEIDFLELAMDEFIERYGGGGSFAWWTAFVTNVNASSSGGGGSHANYIFWRNTNPIQLSSYGGGGSEILLIIMRTFKVSIWNLDYIINLIIKGGGGSMKIILFLALITLATCELYGGGGSLSLIDFYLCFLAFLLFLVLIMLIIFWFSLELGGGGSCTQHQPYVVDDPCPIHFYSGGGGSYINVFAFPFTIYSLLLCRMEAAAKGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKHHHHHH

Supplementary Table S7: INF-γ inducing POSITIVE epitopes with a score of 1 or more than 1, screened from the CTL MPVs.

S.No.	CTL MPV	Start-END	Sequence	Method	Result	Score
1	CTL-MPV-1	21-36	RRYKQIGTCGLPGTK	MERCI	POSITIVE	1
2	CTL-MPV-1	22-37	RYKQIGTCGLPGTKC	MERCI	POSITIVE	1
3	CTL-MPV-1	23-38	YKQIGTCGLPGTKCC	MERCI	POSITIVE	1
4	CTL-MPV-1	24-39	KQIGTCGLPGTKCCK	MERCI	POSITIVE	1
5	CTL-MPV-1	25-40	QIGTCGLPGTKCCKK	MERCI	POSITIVE	1
6	CTL-MPV-1	41-56	EAAAKGTITVEELKK	MERCI	POSITIVE	1
7	CTL-MPV-1	42-57	AAAKGTITVEELKKL	MERCI	POSITIVE	1
8	CTL-MPV-1	43-58	AAKGTITVEELKKLL	MERCI	POSITIVE	1
9	CTL-MPV-1	44-59	AKGTITVEELKKLLE	MERCI	POSITIVE	1
10	CTL-MPV-1	150-165	TRSMWSFNGGGGSKE	MERCI	POSITIVE	1
11	CTL-MPV-1	151-166	RSMWSFNGGGGSKEI	MERCI	POSITIVE	1
12	CTL-MPV-1	152-167	SMWSFNGGGGSKEIT	MERCI	POSITIVE	1
13	CTL-MPV-1	153-168	MWSFNGGGGSKEITV	MERCI	POSITIVE	1
14	CTL-MPV-1	154-169	WSFNGGGGSKEITVA	MERCI	POSITIVE	1
15	CTL-MPV-1	155-170	SFNGGGGSKEITVAT	MERCI	POSITIVE	1
16	CTL-MPV-1	156-171	FNGGGGSKEITVATS	MERCI	POSITIVE	1
17	CTL-MPV-1	157-172	NGGGGSKEITVATSR	MERCI	POSITIVE	1
18	CTL-MPV-1	158-173	GGGGSKEITVATSRT	MERCI	POSITIVE	1
19	CTL-MPV-1	159-174	GGGSKEITVATSRTL	MERCI	POSITIVE	1
20	CTL-MPV-1	163-178	KEITVATSRTLSYYK	MERCI	POSITIVE	1
21	CTL-MPV-1	164-179	EITVATSRTLSYYKL	MERCI	POSITIVE	1
22	CTL-MPV-1	165-180	ITVATSRTLSYYKLG	MERCI	POSITIVE	1
23	CTL-MPV-1	166-181	TVATSRTLSYYKLGA	MERCI	POSITIVE	1
24	CTL-MPV-1	167-182	VATSRTLSYYKLGAS	MERCI	POSITIVE	1
25	CTL-MPV-1	168-183	ATSRTLSYYKLGASQ	MERCI	POSITIVE	1
26	CTL-MPV-1	169-184	TSRTLSYYKLGASQR	MERCI	POSITIVE	1
27	CTL-MPV-1	170-185	SRTLSYYKLGASQRV	MERCI	POSITIVE	1
28	CTL-MPV-1	219-234	TNSFTRGVYYPDKVF	MERCI	POSITIVE	1
29	CTL-MPV-1	220-235	NSFTRGVYYPDKVFR	MERCI	POSITIVE	1
30	CTL-MPV-1	221-236	SFTRGVYYPDKVFRS	MERCI	POSITIVE	1
31	CTL-MPV-1	222-237	FTRGVYYPDKVFRSS	MERCI	POSITIVE	1
32	CTL-MPV-1	262-277	GSVLPFNDGVYFAST	MERCI	POSITIVE	1
33	CTL-MPV-1	263-278	SVLPFNDGVYFASTE	MERCI	POSITIVE	1
34	CTL-MPV-1	264-279	VLPFNDGVYFASTEK	MERCI	POSITIVE	1
35	CTL-MPV-1	265-280	LPFNDGVYFASTEKS	MERCI	POSITIVE	1
36	CTL-MPV-1	266-281	PFNDGVYFASTEKSN	MERCI	POSITIVE	1
37	CTL-MPV-1	267-282	FNDGVYFASTEKSNI	MERCI	POSITIVE	1
38	CTL-MPV-1	268-283	NDGVYFASTEKSNII	MERCI	POSITIVE	1

39	CTL-MPV-1	269-284	DGVYFASTEKSNIIR	MERCI	POSITIVE	1
40	CTL-MPV-1	270-285	GVYFASTEKSNIIRG	MERCI	POSITIVE	1
41	CTL-MPV-1	271-286	VYFASTEKSNIIRGW	MERCI	POSITIVE	1
42	CTL-MPV-1	285-300	WIFGGGGSGVYYHKN	MERCI	POSITIVE	3
43	CTL-MPV-1	286-301	IFGGGGSGVYYHKNN	MERCI	POSITIVE	3
44	CTL-MPV-1	287-302	FGGGGSGVYYHKNNK	MERCI	POSITIVE	3
45	CTL-MPV-1	288-303	GGGGSGVYYHKNNKS	MERCI	POSITIVE	4
46	CTL-MPV-1	289-304	GGGSGVYYHKNNKSW	MERCI	POSITIVE	4
47	CTL-MPV-1	290-305	GGSGVYYHKNNKSWM	MERCI	POSITIVE	4
48	CTL-MPV-1	291-306	GSGVYYHKNNKSWME	MERCI	POSITIVE	4
49	CTL-MPV-1	292-307	SGVYYHKNNKSWMES	MERCI	POSITIVE	4
50	CTL-MPV-1	293-308	GVYYHKNNKSWMESE	MERCI	POSITIVE	4
51	CTL-MPV-1	294-309	VYYHKNNKSWMESEF	MERCI	POSITIVE	2
52	CTL-MPV-1	343-358	FVFKNIDGYFKIYSK	MERCI	POSITIVE	1
53	CTL-MPV-1	344-359	VFKNIDGYFKIYSKH	MERCI	POSITIVE	1
54	CTL-MPV-1	345-360	FKNIDGYFKIYSKHT	MERCI	POSITIVE	1
55	CTL-MPV-1	346-361	KNIDGYFKIYSKHTP	MERCI	POSITIVE	1
56	CTL-MPV-1	347-362	NIDGYFKIYSKHTPI	MERCI	POSITIVE	1
57	CTL-MPV-1	348-363	IDGYFKIYSKHTPIG	MERCI	POSITIVE	1
58	CTL-MPV-1	349-364	DGYFKIYSKHTPIGG	MERCI	POSITIVE	1
59	CTL-MPV-1	350-365	GYFKIYSKHTPIGGG	MERCI	POSITIVE	1
60	CTL-MPV-1	351-366	YFKIYSKHTPIGGGG	MERCI	POSITIVE	1
61	CTL-MPV-1	409-424	YVGYLQPRTFLLKGG	MERCI	POSITIVE	1
62	CTL-MPV-1	410-425	VGYLQPRTFLLKGGG	MERCI	POSITIVE	1
63	CTL-MPV-1	411-426	GYLQPRTFLLKGGGG	MERCI	POSITIVE	1
64	CTL-MPV-1	412-427	YLQPRTFLLKGGGGS	MERCI	POSITIVE	1
65	CTL-MPV-1	413-428	LQPRTFLLKGGGGSS	MERCI	POSITIVE	1
66	CTL-MPV-1	414-429	QPRTFLLKGGGGSSE	MERCI	POSITIVE	2
67	CTL-MPV-1	415-430	PRTFLLKGGGGSSET	MERCI	POSITIVE	2
68	CTL-MPV-1	416-431	RTFLLKGGGGSSETK	MERCI	POSITIVE	2
69	CTL-MPV-1	417-432	TFLLKGGGGSSETKC	MERCI	POSITIVE	2
70	CTL-MPV-1	418-433	FLLKGGGGSSETKCT	MERCI	POSITIVE	2
71	CTL-MPV-1	419-434	LLKGGGGSSETKCTL	MERCI	POSITIVE	1
72	CTL-MPV-1	420-435	LKGGGGSSETKCTLK	MERCI	POSITIVE	1
73	CTL-MPV-1	421-436	KGGGGSSETKCTLKS	MERCI	POSITIVE	1
74	CTL-MPV-1	422-437	GGGGSSETKCTLKSF	MERCI	POSITIVE	1
75	CTL-MPV-1	423-438	GGGSSETKCTLKSFT	MERCI	POSITIVE	1
76	CTL-MPV-1	508-523	GGSNVYADSFVIRGD	MERCI	POSITIVE	2
77	CTL-MPV-1	509-524	GSNVYADSFVIRGDE	MERCI	POSITIVE	2
78	CTL-MPV-1	510-525	SNVYADSFVIRGDEV	MERCI	POSITIVE	2
79	CTL-MPV-1	511-526	NVYADSFVIRGDEVR	MERCI	POSITIVE	2

80	CTL-MPV-1	512-527	VYADSFVIRGDEVRG	MERCI	POSITIVE	2
81	CTL-MPV-1	513-528	YADSFVIRGDEVRGG	MERCI	POSITIVE	2
82	CTL-MPV-1	514-529	ADSFVIRGDEVRGGG	MERCI	POSITIVE	2
83	CTL-MPV-1	515-530	DSFVIRGDEVRGGGG	MERCI	POSITIVE	2
84	CTL-MPV-1	516-531	SFVIRGDEVRGGGGS	MERCI	POSITIVE	2
85	CTL-MPV-1	591-606	VFGGGGSSPRRARSV	MERCI	POSITIVE	1
86	CTL-MPV-1	592-607	FGGGGSSPRRARSVA	MERCI	POSITIVE	1
87	CTL-MPV-1	593-608	GGGGSSPRRARSVAS	MERCI	POSITIVE	1
88	CTL-MPV-1	594-609	GGGSSPRRARSVASQ	MERCI	POSITIVE	1
89	CTL-MPV-1	751-766	THWFVTQRGGGGSYE	MERCI	POSITIVE	1
90	CTL-MPV-1	752-767	HWFVTQRGGGGSYEQ	MERCI	POSITIVE	1
91	CTL-MPV-1	753768	WFVTQRGGGGSYEQY	MERCI	POSITIVE	1
92	CTL-MPV-1	754-769	FVTQRGGGGSYEQYI	MERCI	POSITIVE	1
93	CTL-MPV-1	755-770	VTQRGGGGSYEQYIK	MERCI	POSITIVE	1
94	CTL-MPV-1	756-771	TQRGGGGSYEQYIKW	MERCI	POSITIVE	1
95	CTL-MPV-1	757-772	QRGGGGSYEQYIKWP	MERCI	POSITIVE	1
96	CTL-MPV-1	758-773	RGGGGSYEQYIKWPW	MERCI	POSITIVE	1
97	CTL-MPV-1	759-774	GGGGSYEQYIKWPWY	MERCI	POSITIVE	1
98	CTL-MPV-1	760-775	GGGSYEQYIKWPWYI	MERCI	POSITIVE	1
99	CTL-MPV-1	825-840	STRGRKCCRRKKHHH	MERCI	POSITIVE	1
100	CTL-MPV-1	826-841	TRGRKCCRRKKHHHH	MERCI	POSITIVE	1
101	CTL-MPV-1	827-842	RGRKCCRRKKHHHHH	MERCI	POSITIVE	1
102	CTL-MPV-1	828-843	GRKCCRRKKHHHHHH	MERCI	POSITIVE	2
103	CTL-MPV-1	829-844	RKCCRRKKHHHHHH	MERCI	POSITIVE	2
104	CTL-MPV-1	830-845	KCCRRKKHHHHHH	MERCI	POSITIVE	1
105	CTL-MPV-1	831-846	CCRRKKHHHHHH	MERCI	POSITIVE	1
106	CTL-MPV-1	832-847	CRRKKHHHHHH	MERCI	POSITIVE	1
107	CTL-MPV-1	833-848	RRKKHHHHHH	MERCI	POSITIVE	1
108	CTL-MPV-1	834849	RKKHHHHHH	MERCI	POSITIVE	1
S.No.	**CTL MPV**	**Start-END**	**Sequence**	**Method**	**Result**	**Score**
109	CTL-MPV-2	21-36	RRYKQIGTCGLPGTK	MERCI	POSITIVE	1
110	CTL-MPV-2	22-37	RYKQIGTCGLPGTKC	MERCI	POSITIVE	1
111	CTL-MPV-2	23-38	YKQIGTCGLPGTKCC	MERCI	POSITIVE	1
112	CTL-MPV-2	24-39	KQIGTCGLPGTKCCK	MERCI	POSITIVE	1
113	CTL-MPV-2	25-40	QIGTCGLPGTKCCKK	MERCI	POSITIVE	1
114	CTL-MPV-2	37-52	CKKPEAAAKNQRNAP	MERCI	POSITIVE	1
115	CTL-MPV-2	66-81	SKQRRPQGLPNNTAS	MERCI	POSITIVE	2
116	CTL-MPV-2	67-82	KQRRPQGLPNNTASW	MERCI	POSITIVE	2
117	CTL-MPV-2	68-83	QRRPQGLPNNTASWF	MERCI	POSITIVE	2
118	CTL-MPV-2	69-84	RRPQGLPNNTASWFT	MERCI	POSITIVE	2
119	CTL-MPV-2	70-85	RPQGLPNNTASWFTA	MERCI	POSITIVE	2

120	CTL-MPV-2	71-86	PQGLPNNTASWFTAL	MERCI	POSITIVE	3
121	CTL-MPV-2	72-87	QGLPNNTASWFTALT	MERCI	POSITIVE	1
122	CTL-MPV-2	73-88	GLPNNTASWFTALTQ	MERCI	POSITIVE	1
123	CTL-MPV-2	74-89	LPNNTASWFTALTQH	MERCI	POSITIVE	1
124	CTL-MPV-2	75-90	PNNTASWFTALTQHG	MERCI	POSITIVE	1
125	CTL-MPV-2	76-91	NNTASWFTALTQHGK	MERCI	POSITIVE	1
126	CTL-MPV-2	77-92	NTASWFTALTQHGKG	MERCI	POSITIVE	1
127	CTL-MPV-2	78-93	TASWFTALTQHGKGG	MERCI	POSITIVE	1
128	CTL-MPV-2	173-188	AYNVTQAFGGGGSQE	MERCI	POSITIVE	1
129	CTL-MPV-2	174-189	YNVTQAFGGGGSQEL	MERCI	POSITIVE	1
130	CTL-MPV-2	175-190	NVTQAFGGGGSQELI	MERCI	POSITIVE	1
131	CTL-MPV-2	176-191	VTQAFGGGGSQELIR	MERCI	POSITIVE	1
132	CTL-MPV-2	177-192	TQAFGGGGSQELIRQ	MERCI	POSITIVE	1
133	CTL-MPV-2	178-193	QAFGGGGSQELIRQG	MERCI	POSITIVE	1
134	CTL-MPV-2	179-194	AFGGGGSQELIRQGT	MERCI	POSITIVE	1
135	CTL-MPV-2	180-195	FGGGGSQELIRQGTD	MERCI	POSITIVE	1
136	CTL-MPV-2	181-196	GGGGSQELIRQGTDY	MERCI	POSITIVE	1
137	CTL-MPV-2	182-197	GGGSQELIRQGTDYG	MERCI	POSITIVE	1
138	CTL-MPV-2	252-267	PKKGGGGSDEWSMAT	MERCI	POSITIVE	19
139	CTL-MPV-2	253-268	KKGGGGSDEWSMATY	MERCI	POSITIVE	19
140	CTL-MPV-2	254-269	KGGGGSDEWSMATYY	MERCI	POSITIVE	19
141	CTL-MPV-2	255-270	GGGGSDEWSMATYYL	MERCI	POSITIVE	19
142	CTL-MPV-2	256-271	GGGSDEWSMATYYLF	MERCI	POSITIVE	19
143	CTL-MPV-2	257-272	GGSDEWSMATYYLFG	MERCI	POSITIVE	14
144	CTL-MPV-2	314-329	SYEQFGGGGSLVAEW	MERCI	POSITIVE	2
145	CTL-MPV-2	315-330	YEQFGGGGSLVAEWF	MERCI	POSITIVE	2
146	CTL-MPV-2	316-331	EQFGGGGSLVAEWFL	MERCI	POSITIVE	2
147	CTL-MPV-2	317-332	QFGGGGSLVAEWFLA	MERCI	POSITIVE	2
148	CTL-MPV-2	318-333	FGGGGSLVAEWFLAY	MERCI	POSITIVE	2
149	CTL-MPV-2	319-334	GGGGSLVAEWFLAYI	MERCI	POSITIVE	2
150	CTL-MPV-2	320-335	GGGSLVAEWFLAYIL	MERCI	POSITIVE	2
151	CTL-MPV-2	321-336	GGSLVAEWFLAYILF	MERCI	POSITIVE	2
152	CTL-MPV-2	322-337	GSLVAEWFLAYILFT	MERCI	POSITIVE	2
153	CTL-MPV-2	323-338	SLVAEWFLAYILFTR	MERCI	POSITIVE	1
154	CTL-MPV-2	481-496	GSTACTDDNALAYYG	MERCI	POSITIVE	5
155	CTL-MPV-2	482-497	STACTDDNALAYYGG	MERCI	POSITIVE	5
156	CTL-MPV-2	483-498	TACTDDNALAYYGGG	MERCI	POSITIVE	4
157	CTL-MPV-2	484-499	ACTDDNALAYYGGGG	MERCI	POSITIVE	1
158	CTL-MPV-2	485-500	CTDDNALAYYGGGGS	MERCI	POSITIVE	1
159	CTL-MPV-2	486-501	TDDNALAYYGGGGSY	MERCI	POSITIVE	1
160	CTL-MPV-2	487-502	DDNALAYYGGGGSYT	MERCI	POSITIVE	1

161	CTL-MPV-2	544-559	GGGGSVDTDFVNEFY	MERCI	POSITIVE	1
162	CTL-MPV-2	545-560	GGGSVDTDFVNEFYA	MERCI	POSITIVE	1
163	CTL-MPV-2	546-561	GGSVDTDFVNEFYAY	MERCI	POSITIVE	1
164	CTL-MPV-2	547-562	GSVDTDFVNEFYAYL	MERCI	POSITIVE	1
165	CTL-MPV-2	658-673	STRGRKCCRRKKHHH	MERCI	POSITIVE	1
166	CTL-MPV-2	659-674	TRGRKCCRRKKHHHH	MERCI	POSITIVE	1
167	CTL-MPV-2	660-675	RGRKCCRRKKHHHHH	MERCI	POSITIVE	1
168	CTL-MPV-2	661-676	GRKCCRRKKHHHHHH	MERCI	POSITIVE	2
169	CTL-MPV-2	662-677	RKCCRRKKHHHHHH	MERCI	POSITIVE	2
170	CTL-MPV-2	663-678	KCCRRKKHHHHHH	MERCI	POSITIVE	1
171	CTL-MPV-2	664-679	CCRRKKHHHHHH	MERCI	POSITIVE	1
172	CTL-MPV-2	665-680	CRRKKHHHHHH	MERCI	POSITIVE	1
173	CTL-MPV-2	666-681	RRKKHHHHHH	MERCI	POSITIVE	1
174	CTL-MPV-2	667-682	RKKHHHHHH	MERCI	POSITIVE	1
S.No.	**CTL MPV**	**Start-END**	**Sequence**	**Method**	**Result**	**Score**
175	CTL-MPV-3	21-36	RRYKQIGTCGLPGTK	MERCI	POSITIVE	1
176	CTL-MPV-3	22-37	RYKQIGTCGLPGTKC	MERCI	POSITIVE	1
177	CTL-MPV-3	23-38	YKQIGTCGLPGTKCC	MERCI	POSITIVE	1
178	CTL-MPV-3	24-39	KQIGTCGLPGTKCCK	MERCI	POSITIVE	1
179	CTL-MPV-3	25-40	QIGTCGLPGTKCCKK	MERCI	POSITIVE	1
180	CTL-MPV-3	37-52	CKKPEAAAKSEETGT	MERCI	POSITIVE	2
181	CTL-MPV-3	38-53	KKPEAAAKSEETGTL	MERCI	POSITIVE	1
182	CTL-MPV-3	39-54	KPEAAAKSEETGTLI	MERCI	POSITIVE	1
183	CTL-MPV-3	40-55	PEAAAKSEETGTLIV	MERCI	POSITIVE	1
184	CTL-MPV-3	41-56	EAAAKSEETGTLIVN	MERCI	POSITIVE	1
185	CTL-MPV-3	42-57	AAAKSEETGTLIVNS	MERCI	POSITIVE	1
186	CTL-MPV-3	43-58	AAKSEETGTLIVNSV	MERCI	POSITIVE	1
187	CTL-MPV-3	118-133	FTIGTVTLKGGGGST	MERCI	POSITIVE	2
188	CTL-MPV-3	119-134	TIGTVTLKGGGGSTI	MERCI	POSITIVE	2
189	CTL-MPV-3	120-135	IGTVTLKGGGGSTIP	MERCI	POSITIVE	1
190	CTL-MPV-3	121-136	GTVTLKGGGGSTIPI	MERCI	POSITIVE	1
191	CTL-MPV-3	122-137	TVTLKGGGGSTIPIQ	MERCI	POSITIVE	1
192	CTL-MPV-3	158-173	SKIITLKKRWGGGGS	MERCI	POSITIVE	1
193	CTL-MPV-3	159-174	KIITLKKRWGGGGSH	MERCI	POSITIVE	1
194	CTL-MPV-3	160-175	IITLKKRWGGGGSHF	MERCI	POSITIVE	1
195	CTL-MPV-3	161-176	ITLKKRWGGGGSHFV	MERCI	POSITIVE	1
196	CTL-MPV-3	162-177	TLKKRWGGGGSHFVC	MERCI	POSITIVE	1
197	CTL-MPV-3	199-214	APFLYLYALVYFLQS	MERCI	POSITIVE	1
198	CTL-MPV-3	200-215	PFLYLYALVYFLQSI	MERCI	POSITIVE	2
199	CTL-MPV-3	201-216	FLYLYALVYFLQSIN	MERCI	POSITIVE	2
200	CTL-MPV-3	202-217	LYLYALVYFLQSINF	MERCI	POSITIVE	2

201	CTL-MPV-3	203-218	YLYALVYFLQSINFV	MERCI	POSITIVE	2
202	CTL-MPV-3	204-219	LYALVYFLQSINFVR	MERCI	POSITIVE	2
203	CTL-MPV-3	205-220	YALVYFLQSINFVRI	MERCI	POSITIVE	2
204	CTL-MPV-3	206-221	ALVYFLQSINFVRII	MERCI	POSITIVE	2
205	CTL-MPV-3	220-235	IMRLWLCWKCRGGGG	MERCI	POSITIVE	1
206	CTL-MPV-3	221-236	MRLWLCWKCRGGGGS	MERCI	POSITIVE	1
207	CTL-MPV-3	222-237	RLWLCWKCRGGGGSY	MERCI	POSITIVE	1
208	CTL-MPV-3	223-238	LWLCWKCRGGGGSYF	MERCI	POSITIVE	1
209	CTL-MPV-3	224-239	WLCWKCRGGGGSYFL	MERCI	POSITIVE	1
210	CTL-MPV-3	233-248	GGSYFLCWHTNCYDY	MERCI	POSITIVE	1
211	CTL-MPV-3	270-285	GGSYYQLYSTQLSTD	MERCI	POSITIVE	2
212	CTL-MPV-3	271-286	GSYYQLYSTQLSTDT	MERCI	POSITIVE	2
213	CTL-MPV-3	272-287	SYYQLYSTQLSTDTG	MERCI	POSITIVE	2
214	CTL-MPV-3	273-288	YYQLYSTQLSTDTGV	MERCI	POSITIVE	3
215	CTL-MPV-3	274-289	YQLYSTQLSTDTGVE	MERCI	POSITIVE	2
216	CTL-MPV-3	275-290	QLYSTQLSTDTGVEH	MERCI	POSITIVE	3
217	CTL-MPV-3	276-291	LYSTQLSTDTGVEHV	MERCI	POSITIVE	2
218	CTL-MPV-3	277-292	YSTQLSTDTGVEHVT	MERCI	POSITIVE	2
219	CTL-MPV-3	278-293	STQLSTDTGVEHVTF	MERCI	POSITIVE	2
220	CTL-MPV-3	279-294	TQLSTDTGVEHVTFF	MERCI	POSITIVE	2
221	CTL-MPV-3	280-295	QLSTDTGVEHVTFFI	MERCI	POSITIVE	2
222	CTL-MPV-3	281-296	LSTDTGVEHVTFFIY	MERCI	POSITIVE	1
223	CTL-MPV-3	362-377	GGGGSLLKEPCSSGT	MERCI	POSITIVE	1
224	CTL-MPV-3	363-378	GGGSLLKEPCSSGTY	MERCI	POSITIVE	1
225	CTL-MPV-3	364-379	GGSLLKEPCSSGTYE	MERCI	POSITIVE	1
226	CTL-MPV-3	365-380	GSLLKEPCSSGTYEG	MERCI	POSITIVE	1
227	CTL-MPV-3	366-381	SLLKEPCSSGTYEGN	MERCI	POSITIVE	1
228	CTL-MPV-3	515-530	TVAAFGGGGSYVVDD	MERCI	POSITIVE	1
229	CTL-MPV-3	516-531	VAAFGGGGSYVVDDP	MERCI	POSITIVE	1
230	CTL-MPV-3	517-532	AAFGGGGSYVVDDPC	MERCI	POSITIVE	1
231	CTL-MPV-3	518-533	AFGGGGSYVVDDPCP	MERCI	POSITIVE	1
232	CTL-MPV-3	519-534	FGGGGSYVVDDPCPI	MERCI	POSITIVE	1
233	CTL-MPV-3	520-535	GGGGSYVVDDPCPIH	MERCI	POSITIVE	1
234	CTL-MPV-3	521-536	GGGSYVVDDPCPIHF	MERCI	POSITIVE	1
235	CTL-MPV-3	522-537	GGSYVVDDPCPIHFY	MERCI	POSITIVE	1
236	CTL-MPV-3	523-538	GSYVVDDPCPIHFYS	MERCI	POSITIVE	1
237	CTL-MPV-3	524-539	SYVVDDPCPIHFYSK	MERCI	POSITIVE	1
238	CTL-MPV-3	525-540	YVVDDPCPIHFYSKW	MERCI	POSITIVE	1
239	CTL-MPV-3	526-541	VVDDPCPIHFYSKWY	MERCI	POSITIVE	1
240	CTL-MPV-3	527-542	VDDPCPIHFYSKWYI	MERCI	POSITIVE	1
241	CTL-MPV-3	528-543	DDPCPIHFYSKWYIR	MERCI	POSITIVE	1

242	CTL-MPV-3	529-544	DPCPIHFYSKWYIRV	MERCI	POSITIVE	1
243	CTL-MPV-3	530-545	PCPIHFYSKWYIRVG	MERCI	POSITIVE	1
244	CTL-MPV-3	531-546	CPIHFYSKWYIRVGA	MERCI	POSITIVE	1
245	CTL-MPV-3	532-547	PIHFYSKWYIRVGAR	MERCI	POSITIVE	1
246	CTL-MPV-3	533-548	IHFYSKWYIRVGARK	MERCI	POSITIVE	1
247	CTL-MPV-3	534-549	HFYSKWYIRVGARKS	MERCI	POSITIVE	1
248	CTL-MPV-3	672-687	STRGRKCCRRKKHHH	MERCI	POSITIVE	1
249	CTL-MPV-3	673-688	TRGRKCCRRKKHHHH	MERCI	POSITIVE	1
250	CTL-MPV-3	674-689	RGRKCCRRKKHHHHH	MERCI	POSITIVE	1
251	CTL-MPV-3	675-690	GRKCCRRKKHHHHHH	MERCI	POSITIVE	2
252	CTL-MPV-3	676-691	RKCCRRKKHHHHHH	MERCI	POSITIVE	2
253	CTL-MPV-3	677-692	KCCRRKKHHHHHH	MERCI	POSITIVE	1
254	CTL-MPV-3	678-693	CCRRKKHHHHHH	MERCI	POSITIVE	1
255	CTL-MPV-3	679-694	CRRKKHHHHHH	MERCI	POSITIVE	1
256	CTL-MPV-3	680-695	RRKKHHHHHH	MERCI	POSITIVE	1
257	CTL-MPV-3	681-696	RKKHHHHHH	MERCI	POSITIVE	1

Supplementary Table S8: INF-γ inducing POSITIVE epitopes with a score of 1 or more than 1, screened from the HTL MPVs.

S.No.	HTL MPV	Start-END	Sequence	Method	Result	Score
1	HTL-MPV-1	21-36	RRYKQIGTCGLPGTK	MERCI	POSITIVE	1
2	HTL-MPV-1	22-37	RYKQIGTCGLPGTKC	MERCI	POSITIVE	1
3	HTL-MPV-1	23-38	YKQIGTCGLPGTKCC	MERCI	POSITIVE	1
4	HTL-MPV-1	24-39	KQIGTCGLPGTKCCK	MERCI	POSITIVE	1
5	HTL-MPV-1	25-40	QIGTCGLPGTKCCKK	MERCI	POSITIVE	1
6	HTL-MPV-1	37-52	CKKPEAAAKVNSVLL	MERCI	POSITIVE	1
7	HTL-MPV-1	110-125	ARGGGGSSRTLSYYK	MERCI	POSITIVE	1
8	HTL-MPV-1	111-126	RGGGGSSRTLSYYKL	MERCI	POSITIVE	1
9	HTL-MPV-1	112-127	GGGGSSRTLSYYKLG	MERCI	POSITIVE	1
10	HTL-MPV-1	113-128	GGGSSRTLSYYKLGA	MERCI	POSITIVE	1
11	HTL-MPV-1	114-129	GGSSRTLSYYKLGAS	MERCI	POSITIVE	1
12	HTL-MPV-1	115-130	GSSRTLSYYKLGASQ	MERCI	POSITIVE	1
13	HTL-MPV-1	116-131	SSRTLSYYKLGASQR	MERCI	POSITIVE	1
14	HTL-MPV-1	117-132	SRTLSYYKLGASQRV	MERCI	POSITIVE	1
15	HTL-MPV-1	155-170	VVIKVCEGGGGSREF	MERCI	POSITIVE	2
16	HTL-MPV-1	156-171	VIKVCEGGGGSREFV	MERCI	POSITIVE	1
17	HTL-MPV-1	157-172	IKVCEGGGGSREFVF	MERCI	POSITIVE	1
18	HTL-MPV-1	158-173	KVCEGGGGSREFVFK	MERCI	POSITIVE	1
19	HTL-MPV-1	159-174	VCEGGGGSREFVFKN	MERCI	POSITIVE	1

20	HTL-MPV-1	160-175	CEGGGGSREFVFKNI	MERCI	POSITIVE	1
21	HTL-MPV-1	161-176	EGGGGSREFVFKNID	MERCI	POSITIVE	1
22	HTL-MPV-1	162-177	GGGGSREFVFKNIDG	MERCI	POSITIVE	1
23	HTL-MPV-1	163-178	GGGSREFVFKNIDGY	MERCI	POSITIVE	1
24	HTL-MPV-1	169-184	FVFKNIDGYFKIYSK	MERCI	POSITIVE	1
25	HTL-MPV-1	170-185	VFKNIDGYFKIYSKG	MERCI	POSITIVE	1
26	HTL-MPV-1	171-186	FKNIDGYFKIYSKGG	MERCI	POSITIVE	1
27	HTL-MPV-1	172-187	KNIDGYFKIYSKGGG	MERCI	POSITIVE	1
28	HTL-MPV-1	173-188	NIDGYFKIYSKGGGG	MERCI	POSITIVE	1
29	HTL-MPV-1	174-189	IDGYFKIYSKGGGGS	MERCI	POSITIVE	1
30	HTL-MPV-1	227-242	GGGGSQPTESIVRFP	MERCI	POSITIVE	1
31	HTL-MPV-1	228-243	GGGSQPTESIVRFPN	MERCI	POSITIVE	5
32	HTL-MPV-1	229-244	GGSQPTESIVRFPNI	MERCI	POSITIVE	5
33	HTL-MPV-1	230-245	GSQPTESIVRFPNIT	MERCI	POSITIVE	8
34	HTL-MPV-1	231-246	SQPTESIVRFPNITN	MERCI	POSITIVE	8
35	HTL-MPV-1	232-247	QPTESIVRFPNITNL	MERCI	POSITIVE	7
36	HTL-MPV-1	279-294	YADSFVIRGDEVRQI	MERCI	POSITIVE	2
37	HTL-MPV-1	280-295	ADSFVIRGDEVRQIA	MERCI	POSITIVE	2
38	HTL-MPV-1	281-296	DSFVIRGDEVRQIAP	MERCI	POSITIVE	2
39	HTL-MPV-1	282-297	SFVIRGDEVRQIAPG	MERCI	POSITIVE	2
40	HTL-MPV-1	283-298	FVIRGDEVRQIAPGQ	MERCI	POSITIVE	2
41	HTL-MPV-1	363-378	ANLAGGGGSREGVFV	MERCI	POSITIVE	1
42	HTL-MPV-1	364-379	NLAGGGGSREGVFVS	MERCI	POSITIVE	1
43	HTL-MPV-1	365-380	LAGGGGSREGVFVSN	MERCI	POSITIVE	1
44	HTL-MPV-1	366-381	AGGGGSREGVFVSNG	MERCI	POSITIVE	1
45	HTL-MPV-1	367-382	GGGGSREGVFVSNGT	MERCI	POSITIVE	1
46	HTL-MPV-1	368-383	GGGSREGVFVSNGTH	MERCI	POSITIVE	1
47	HTL-MPV-1	469-484	GGSWPQIAQFAPSAS	MERCI	POSITIVE	1
48	HTL-MPV-1	470-485	GSWPQIAQFAPSASA	MERCI	POSITIVE	1
49	HTL-MPV-1	471-486	SWPQIAQFAPSASAF	MERCI	POSITIVE	1
50	HTL-MPV-1	472-487	WPQIAQFAPSASAFF	MERCI	POSITIVE	1
51	HTL-MPV-1	473-488	PQIAQFAPSASAFFG	MERCI	POSITIVE	1
52	HTL-MPV-1	474-489	QIAQFAPSASAFFGM	MERCI	POSITIVE	1
53	HTL-MPV-1	542-557	APFLYLYALVYFLQS	MERCI	POSITIVE	1
54	HTL-MPV-1	543-558	PFLYLYALVYFLQSI	MERCI	POSITIVE	2
55	HTL-MPV-1	544-559	FLYLYALVYFLQSIN	MERCI	POSITIVE	2
56	HTL-MPV-1	545-560	LYLYALVYFLQSINF	MERCI	POSITIVE	2
57	HTL-MPV-1	546-561	YLYALVYFLQSINFV	MERCI	POSITIVE	2
58	HTL-MPV-1	547-562	LYALVYFLQSINFVG	MERCI	POSITIVE	2
59	HTL-MPV-1	548-563	YALVYFLQSINFVGG	MERCI	POSITIVE	2
60	HTL-MPV-1	549-564	ALVYFLQSINFVGGG	MERCI	POSITIVE	2

61	HTL-MPV-1	550-565	LVYFLQSINFVGGGG	MERCI	POSITIVE	2
62	HTL-MPV-1	551-566	VYFLQSINFVGGGGS	MERCI	POSITIVE	2
63	HTL-MPV-1	568-583	GVEHVTFFIYNKIVD	MERCI	POSITIVE	2
64	HTL-MPV-1	569-584	VEHVTFFIYNKIVDE	MERCI	POSITIVE	4
65	HTL-MPV-1	570-585	EHVTFFIYNKIVDEP	MERCI	POSITIVE	4
66	HTL-MPV-1	571-586	HVTFFIYNKIVDEPE	MERCI	POSITIVE	4
67	HTL-MPV-1	572-587	VTFFIYNKIVDEPEE	MERCI	POSITIVE	4
68	HTL-MPV-1	573-588	TFFIYNKIVDEPEEH	MERCI	POSITIVE	4
69	HTL-MPV-1	574-589	FFIYNKIVDEPEEHV	MERCI	POSITIVE	2
70	HTL-MPV-1	575-590	FIYNKIVDEPEEHVE	MERCI	POSITIVE	1
71	HTL-MPV-1	579-594	KIVDEPEEHVEAAAK	MERCI	POSITIVE	1
72	HTL-MPV-1	580-595	IVDEPEEHVEAAAKG	MERCI	POSITIVE	1
73	HTL-MPV-1	581-596	VDEPEEHVEAAAKGI	MERCI	POSITIVE	1
74	HTL-MPV-1	582-597	STRGRKCCRRKKHHH	MERCI	POSITIVE	1
75	HTL-MPV-1	583-598	TRGRKCCRRKKHHHH	MERCI	POSITIVE	1
76	HTL-MPV-1	584-599	RGRKCCRRKKHHHHH	MERCI	POSITIVE	1
77	HTL-MPV-1	585-600	GRKCCRRKKHHHHHH	MERCI	POSITIVE	2
78	HTL-MPV-1	5860-601	RKCCRRKKHHHHHH	MERCI	POSITIVE	2
79	HTL-MPV-1	587-602	KCCRRKKHHHHHH	MERCI	POSITIVE	1
80	HTL-MPV-1	588-603	CCRRKKHHHHHH	MERCI	POSITIVE	1
81	HTL-MPV-1	589-604	CRRKKHHHHHH	MERCI	POSITIVE	1
82	HTL-MPV-1	590-605	RRKKHHHHHH	MERCI	POSITIVE	1
83	HTL-MPV-1	591-606	RKKHHHHHH	MERCI	POSITIVE	1
S.No.	**CTL MPV**	**Start-END**	**Sequence**	**Method**	**Result**	**Score**
84	HTL-MPV-2	21-36	RRYKQIGTCGLPGTK	MERCI	POSITIVE	1
85	HTL-MPV-2	22-37	RYKQIGTCGLPGTKC	MERCI	POSITIVE	1
86	HTL-MPV-2	23-38	YKQIGTCGLPGTKCC	MERCI	POSITIVE	1
87	HTL-MPV-2	24-39	KQIGTCGLPGTKCCK	MERCI	POSITIVE	1
88	HTL-MPV-2	25-40	QIGTCGLPGTKCCKK	MERCI	POSITIVE	1
89	HTL-MPV-2	114-129	QQESPFVMMSAPPAQ	MERCI	POSITIVE	2
90	HTL-MPV-2	137-152	LLQLCTFTRSTNSRI	MERCI	POSITIVE	1
91	HTL-MPV-2	138-153	LQLCTFTRSTNSRIK	MERCI	POSITIVE	1
92	HTL-MPV-2	139-154	QLCTFTRSTNSRIKA	MERCI	POSITIVE	1
93	HTL-MPV-2	140-155	LCTFTRSTNSRIKAS	MERCI	POSITIVE	1
94	HTL-MPV-2	170-185	FLLLSVCLGGGGSEW	MERCI	POSITIVE	1
95	HTL-MPV-2	171-186	LLLSVCLGGGGSEWF	MERCI	POSITIVE	1
96	HTL-MPV-2	172-187	LLSVCLGGGGSEWFL	MERCI	POSITIVE	1
97	HTL-MPV-2	173-188	LSVCLGGGGSEWFLA	MERCI	POSITIVE	1
98	HTL-MPV-2	174-189	SVCLGGGGSEWFLAY	MERCI	POSITIVE	1
99	HTL-MPV-2	175-190	VCLGGGGSEWFLAYI	MERCI	POSITIVE	1
100	HTL-MPV-2	176-191	CLGGGGSEWFLAYIL	MERCI	POSITIVE	1

101	HTL-MPV-2	177-192	LGGGGSEWFLAYILF	MERCI	POSITIVE	1
102	HTL-MPV-2	178-193	GGGGSEWFLAYILFT	MERCI	POSITIVE	1
103	HTL-MPV-2	179-194	GGGSEWFLAYILFTR	MERCI	POSITIVE	1
104	HTL-MPV-2	185-200	FLAYILFTRFFYVLG	MERCI	POSITIVE	1
105	HTL-MPV-2	186-201	LAYILFTRFFYVLGL	MERCI	POSITIVE	1
106	HTL-MPV-2	187-202	AYILFTRFFYVLGLA	MERCI	POSITIVE	1
107	HTL-MPV-2	188-203	YILFTRFFYVLGLAA	MERCI	POSITIVE	1
108	HTL-MPV-2	198-213	LGLAAIMQLFFSYFA	MERCI	POSITIVE	1
109	HTL-MPV-2	199-214	GLAAIMQLFFSYFAV	MERCI	POSITIVE	1
110	HTL-MPV-2	200-215	LAAIMQLFFSYFAVH	MERCI	POSITIVE	1
111	HTL-MPV-2	201-216	AAIMQLFFSYFAVHF	MERCI	POSITIVE	1
112	HTL-MPV-2	202-217	AIMQLFFSYFAVHFI	MERCI	POSITIVE	1
113	HTL-MPV-2	203-218	IMQLFFSYFAVHFIS	MERCI	POSITIVE	1
114	HTL-MPV-2	204-219	MQLFFSYFAVHFISN	MERCI	POSITIVE	2
115	HTL-MPV-2	205-220	QLFFSYFAVHFISNS	MERCI	POSITIVE	2
116	HTL-MPV-2	206-221	LFFSYFAVHFISNSW	MERCI	POSITIVE	2
117	HTL-MPV-2	207-222	FFSYFAVHFISNSWL	MERCI	POSITIVE	1
118	HTL-MPV-2	364-379	VQSTQWSLFFFLYEN	MERCI	POSITIVE	1
119	HTL-MPV-2	365-380	QSTQWSLFFFLYENA	MERCI	POSITIVE	1
120	HTL-MPV-2	366-381	STQWSLFFFLYENAF	MERCI	POSITIVE	1
121	HTL-MPV-2	367-382	TQWSLFFFLYENAFL	MERCI	POSITIVE	1
122	HTL-MPV-2	368-383	QWSLFFFLYENAFLP	MERCI	POSITIVE	1
123	HTL-MPV-2	369-384	WSLFFFLYENAFLPG	MERCI	POSITIVE	1
124	HTL-MPV-2	370-385	SLFFFLYENAFLPGG	MERCI	POSITIVE	1
125	HTL-MPV-2	371-386	LFFFLYENAFLPGGG	MERCI	POSITIVE	1
126	HTL-MPV-2	372-387	FFFLYENAFLPGGGG	MERCI	POSITIVE	1
127	HTL-MPV-2	381-396	LPGGGGSQAIASEFS	MERCI	POSITIVE	2
128	HTL-MPV-2	382-397	PGGGGSQAIASEFSS	MERCI	POSITIVE	2
129	HTL-MPV-2	383-398	GGGGSQAIASEFSSL	MERCI	POSITIVE	2
130	HTL-MPV-2	384-399	GGGSQAIASEFSSLP	MERCI	POSITIVE	2
131	HTL-MPV-2	385-400	GGSQAIASEFSSLPS	MERCI	POSITIVE	2
132	HTL-MPV-2	386-401	GSQAIASEFSSLPSY	MERCI	POSITIVE	2
133	HTL-MPV-2	387-402	SQAIASEFSSLPSYA	MERCI	POSITIVE	2
134	HTL-MPV-2	388-403	QAIASEFSSLPSYAA	MERCI	POSITIVE	2
135	HTL-MPV-2	389-404	AIASEFSSLPSYAAF	MERCI	POSITIVE	2
136	HTL-MPV-2	409-424	GSTQMNLKYAISAKN	MERCI	POSITIVE	1
137	HTL-MPV-2	410-425	STQMNLKYAISAKNR	MERCI	POSITIVE	1
138	HTL-MPV-2	411-426	TQMNLKYAISAKNRA	MERCI	POSITIVE	1
139	HTL-MPV-2	412-427	QMNLKYAISAKNRAR	MERCI	POSITIVE	1
140	HTL-MPV-2	413-428	MNLKYAISAKNRART	MERCI	POSITIVE	1
141	HTL-MPV-2	414-429	NLKYAISAKNRARTG	MERCI	POSITIVE	1

142	HTL-MPV-2	415-430	LKYAISAKNRARTGG	MERCI	POSITIVE	1
143	HTL-MPV-2	448-463	ARKHGGGGSFVNEFY	MERCI	POSITIVE	2
144	HTL-MPV-2	449-464	RKHGGGGSFVNEFYA	MERCI	POSITIVE	2
145	HTL-MPV-2	450-465	KHGGGGSFVNEFYAY	MERCI	POSITIVE	2
146	HTL-MPV-2	451-466	HGGGGSFVNEFYAYL	MERCI	POSITIVE	2
147	HTL-MPV-2	452-467	GGGGSFVNEFYAYLR	MERCI	POSITIVE	2
148	HTL-MPV-2	453-468	GGGSFVNEFYAYLRK	MERCI	POSITIVE	2
149	HTL-MPV-2	454-469	GGSFVNEFYAYLRKH	MERCI	POSITIVE	2
150	HTL-MPV-2	455-470	GSFVNEFYAYLRKHF	MERCI	POSITIVE	2
151	HTL-MPV-2	456-471	SFVNEFYAYLRKHFS	MERCI	POSITIVE	2
152	HTL-MPV-2	518-533	RYGGGGSFAWWTAFV	MERCI	POSITIVE	1
153	HTL-MPV-2	519-534	YGGGGSFAWWTAFVT	MERCI	POSITIVE	1
154	HTL-MPV-2	520-535	GGGGSFAWWTAFVTN	MERCI	POSITIVE	1
155	HTL-MPV-2	521-536	GGGSFAWWTAFVTNV	MERCI	POSITIVE	1
156	HTL-MPV-2	522-537	GGSFAWWTAFVTNVN	MERCI	POSITIVE	1
157	HTL-MPV-2	523-538	GSFAWWTAFVTNVNA	MERCI	POSITIVE	1
158	HTL-MPV-2	524-539	SFAWWTAFVTNVNAS	MERCI	POSITIVE	1
159	HTL-MPV-2	525-540	FAWWTAFVTNVNASS	MERCI	POSITIVE	1
160	HTL-MPV-2	526-541	AWWTAFVTNVNASSS	MERCI	POSITIVE	1
161	HTL-MPV-2	655-670	GGGSCTQHQPYVVDD	MERCI	POSITIVE	1
162	HTL-MPV-2	656-671	GGSCTQHQPYVVDDP	MERCI	POSITIVE	1
163	HTL-MPV-2	657-672	GSCTQHQPYVVDDPC	MERCI	POSITIVE	1
164	HTL-MPV-2	658-673	SCTQHQPYVVDDPCP	MERCI	POSITIVE	1
165	HTL-MPV-2	659-674	CTQHQPYVVDDPCPI	MERCI	POSITIVE	1
166	HTL-MPV-2	660-675	TQHQPYVVDDPCPIH	MERCI	POSITIVE	1
167	HTL-MPV-2	661-676	QHQPYVVDDPCPIHF	MERCI	POSITIVE	1
168	HTL-MPV-2	662-677	HQPYVVDDPCPIHFY	MERCI	POSITIVE	1
169	HTL-MPV-2	663-678	QPYVVDDPCPIHFYS	MERCI	POSITIVE	1
170	HTL-MPV-2	664-679	PYVVDDPCPIHFYSG	MERCI	POSITIVE	1
171	HTL-MPV-2	665-680	YVVDDPCPIHFYSGG	MERCI	POSITIVE	1
172	HTL-MPV-2	740-755	STRGRKCCRRKKHHH	MERCI	POSITIVE	1
173	HTL-MPV-2	741-756	TRGRKCCRRKKHHHH	MERCI	POSITIVE	1
174	HTL-MPV-2	742-757	RGRKCCRRKKHHHHH	MERCI	POSITIVE	1
175	HTL-MPV-2	743-758	GRKCCRRKKHHHHHH	MERCI	POSITIVE	2
176	HTL-MPV-2	744-759	RKCCRRKKHHHHHH	MERCI	POSITIVE	2
177	HTL-MPV-2	745-760	KCCRRKKHHHHHH	MERCI	POSITIVE	1
178	HTL-MPV-2	746-761	CCRRKKHHHHHH	MERCI	POSITIVE	1
179	HTL-MPV-2	747-762	CRRKKHHHHHH	MERCI	POSITIVE	1
180	HTL-MPV-2	748-763	RRKKHHHHHH	MERCI	POSITIVE	1
181	HTL-MPV-2	749-764	RKKHHHHHH	MERCI	POSITIVE	1

Supplementary Table S9: Parameters for the tertiary structure homology modeling of all the CTL and HTL MPVs by the I-TASSER tool.

S.No.	MPVs	PDB hit	C-Score	TM-Score	RMSD (Å)
1	CTL-MPV-1	6cv0A	-2.39	0.43 ± 0.14	14.5 ± 3.7
2	CTL-MPV-2	5n8pA	-0.64	0.63 ± 0.13	9.5 ± 4.6
3	CTL-MPV-3	6s7tA	-1.23	0.56 ± 0.15	11.0 ± 4.6
4	HTL-MPV-1	6p2mA	-1.67	0.51 ± 0.15	11.9 ±4.4
5	HTL-MPV-2	5kdvA	-0.82	0.61 ± 0.14	10.2 ± 4.6

Supplementary Table S10: Refinement parameter values for CTL and HTL MPV models after refinement by GalaxyRefine tool.

S.No.	MPV Models	GDT-HA	RMSD	MolProbity	Clash score	Poor rotamers	Rama favored
1	CTL-MPV-1	0.8652	0.632	2.594	18.6	1.7	85.2
2	CTL-MPV-2	0.9452	0.427	2.55	22.3	1.4	88.3
3	CTL-MPV-3	0.9311	0.474	2.398	20.4	0.7	88.2
4	HTL-MPV-1	0.9239	0.477	2.577	26.6	1.1	85.7
5	HTL-MPV-2	0.9488	0.425	2.494	22.1	1.4	89.8

MolProbity score indicates the log-weighted combination score of the clash score, the percentage of Ramachandran not favored residues and the percentage of bad side-chain rotamers
Clash score: number of atomic clashes per 1000 atoms.
Poor rotamers: the percentages of rotamer outliers
RMSD value in Å indicated deviation from initial model.
GDT-HA (global distance test-High Accuracy): backbone structure accuracy measured by GDT-HA
Rama favored is the percentage of residues which come in the favored region of the Ramachandran plot

Supplementary Table S11: B cell linear epitopes screened from CTL MPVs.

CTL MPV	No.	Start	End	B Cell Linear Epitopes	Number of residues	Score
CTL-MPV-1	1	309	372	FRVYSSANNCTFEYVSQPFLGGGGSKQGNFKNLREFVFKNIDGYFKIYSKHTPIGGGGSEPLVD	64	0.773
CTL-MPV-1	2	380	440	TRFQTLLAGGGGSTPGDSSSGWTAGAAAYYVGYLQPRTFLLKGGGGSSETKCTLKSFTVEK	61	0.725
CTL-MPV-1	3	38	94	CKKPEAAAKGTITVEELKKLLEQWNLVIGFLFLTWICLLQFAYANRNRFLYIIKLIF	57	0.787
CTL-MPV-1	4	116	165	SRINWITGGIAIAMACLVGLMWLSYFIASFRLFARTRSMWSFNGGGGSKE	50	0.675
CTL-MPV-1	5	701	743	AQYGGGGSLQIPFAMQMAYRFNGIGGGGSFPQSAPHGVVFGGG	43	0.785
CTL-MPV-1	6	800	842	YYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKHHHHHH	43	0.776
CTL-MPV-1	7	587	624	TGSNVFGGGGSSPRRARSVASQSIIAYGGGGSFTISVT	38	0.805
CTL-MPV-1	8	455	482	FPNITNLCPFGEVFNATRFASVGGGGSR	28	0.653
CTL-MPV-1	9	654	676	AQVKQIYKTPPIKGGGGSKRSFI	23	0.557
CTL-MPV-1	10	501	513	TFKCYGGGGSNVY	13	0.71

CTL-MPV-1	11	182	190	SQRVAGDSG	9	0.528
CTL-MPV-1	12	644	651	GGGSNTQE	8	0.584
CTL MPV	**No.**	**Start**	**End**	**B Cell Linear Epitopes**	**Number of residues**	**Score**
CTL-MPV-2	1	577	675	ANGQVFGLYGGGGSIPLMYKGLPWNVVRGGGGSYVMHANYIFWEAAAKGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKHHHHHH	99	0.801
CTL-MPV-2	2	1	105	GIGDPVTCLKSGAICHPVFCPRRYKQIGTCGLPGTKCCKKPEAAAKNQRNAPRITFGGPSGGGGSRSKQRRPQGLPNNTASWFTALTQHGKGGGGSNSSPDDQIG	105	0.789
CTL-MPV-2	3	351	367	IFFASFYYVWKSYGGGG	17	0.732
CTL-MPV-2	4	332	343	AYILFTRFFYVG	12	0.707
CTL-MPV-2	5	374	389	FSSTFNVPMEKGGGGS	16	0.677
CTL-MPV-2	6	248	259	FPPTEPKKGGGG	12	0.65
CTL-MPV-2	7	188	198	ELIRQGTDYGG	11	0.634
CTL-MPV-2	8	310	321	YMGTLSYEQFGG	12	0.613
CTL-MPV-2	9	442	451	VFGGGGSLPS	10	0.6
CTL-MPV-2	10	548	566	SVDTDFVNEFYAYLRKHFS	19	0.597
CTL-MPV-2	11	272	278	GGGGSET	7	0.588
CTL-MPV-2	12	396	406	MRFRRAFGGGG	11	0.566
CTL-MPV-2	13	292	301	TQVVDMSMTY	10	0.535
CTL-MPV-2	14	527	534	TYGGGGSA	8	0.533
CTL MPV	**No.**	**Start**	**End**	**B Cell Linear Epitopes**	**Number of residues**	**Score**
CTL-MPV-3	1	627	689	YSLLLCREAAAKGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKHHHHHH	63	0.843
CTL-MPV-3	2	316	365	EILLIIMRTFKVSIWNLDYIIGGGGSMKIILFLALITLATCELYHYGGGG	50	0.814
CTL-MPV-3	3	18	61	VFCPRRYKQIGTCGLPGTKCCKKPEAAAKSEETGTLIVNSVLLF	44	0.742
CTL-MPV-3	4	481	515	LLFLVLIMLIIFWFSLELGGGGSMKFLVFLGIITT	35	0.78
CTL-MPV-3	5	590	608	VRCSFYEDFLEYHDVRVVL	19	0.726
CTL-MPV-3	6	106	122	NSSRGGGGSFMRIFTIG	17	0.649
CTL-MPV-3	7	537	551	SKWYIRVGARKSAPL	15	0.645
CTL-MPV-3	8	152	163	LAVFQSASKIIT	12	0.734
CTL-MPV-3	9	367	378	LLKEPCSSGTYE	12	0.703
CTL-MPV-3	10	75	86	LTALRLCAYGGG	12	0.627
CTL-MPV-3	11	277	288	LYSTQLSTDTGV	12	0.605
CTL-MPV-3	12	126	134	LKGGGGSTI	9	0.642
CTL-MPV-3	13	231	239	RGGGGSYFL	9	0.522
CTL-MPV-3	14	431	438	SEVQELYS	8	0.59
CTL-MPV-3	15	522	529	GGSYVVDD	8	0.532

Supplementary Table S12: B cell Discontinuous epitopes screened from CTL MPVs.

CTL MPV	**No.**	**B Cell Discontinuous Epitopes residues**	**Number of residues**	**Score**
CTL-MPV-1	1	H838, H839, H840, H841	4	0.901
CTL-MPV-1	2	T587, G588, S589, N590, V591, F592, G593, G594, G595, G596, S597, S598, P599, R600, R601, A602, R603, S604, V605, A606, S607, Q608, S609, I610, I611, A612, Y613, G614, G615, G616, G617, S618, F619, T620, I621, S622, V623, T624, E626, A714, M715, Q716, M717, A718, Y719, R720, F721, N722, G723, I724, G725, G726, G727, G728, S729, F730, P731, Q732, S733, A734, P735, H736, G737, V738, V739, F740, G741, G742, G743, L797, Y800, Y801, C802, R803, V804, R805, G806, G807, R808, C809, A810, V811, L812, S813, C814, L815, P816, K817, E818, E819, Q820, I821, G822, K823, C824, S825, T826, R827, G828, R829, K830, C831, C832, R833, K835, K836, H837	107	0.789
CTL-MPV-1	3	F309, R310, V311, Y312, S313, S314, A315, N316, N317, C318, T319, F320, E321, Y322, V323, S324, Q325, P326, F327, L328, G329, G330, G331, G332, S333, K334, Q335, G336, N337, F338, K339, N340, L341, R342, E343, V345, F346, K347, N348, I349, D350, G351, Y352, F353, K354, I355, Y356, S357, K358, H359, T360, P361, I362, G363, G364, G365, G366, S367, E368, P369, L370, V371, D372, L373, T380, R381, F382, Q383, T384, L385, L386, A387, G388, G389, G390, G391, S392, T393, P394, G395, D396,	169	0.723

		S397, S398, S399, G400, W401, T402, A403, G404, A405, A406, A407, Y408, Y409, V410, G411, Y412, L413, Q414, P415, R416, T417, F418, L419, L420, K421, G422, G423, G424, G425, S426, S427, E428, T429, K430, C431, T432, L433, K434, S435, F436, T437, V438, E439, K440, N447, F448, F455, P456, N457, I458, T459, N460, L461, C462, P463, F464, G465, E466, V467, F468, N469, A470, T471, R472, F473, A474, S475, V476, G477, G478, G479, G480, S481, R482, I483, T501, F502, K503, C504, Y505, G506, G507, G508, G509, S510, N511, V512, Y513		
CTL-MPV-1	4	K39, K40, P41, E42, A43, A44, A45, K46, G47, T48, I49, T50, V51, E52, E53, L54, K55, K56, L57, L58, E59, Q60, W61, N62, L63, V64, I65, G66, F67, L68, F69, L70, T71, W72, I73, C74, L75, L76, Q77, F78, A79, Y80, A81, N82, R83, N84, R85, F86, L87, Y88, I89, I90, K91, L92, I93, F94, L95, G113, G114, G115, R117, I118, N119, W120, I121, T122, G123, G124, I125, A126, I127, A128, M129, A130, C131, L132, V133, G134, L135, M136, W137, L138, S139, Y140, F141, I142, A143, S144, F145, R146, V185, A186, G187, D188, S189, G190, F191, Y194, D231, V233, R235, T245, Q246, D247, L248	105	0.721
CTL-MPV-1	5	K666, G667, G668, G669, G670, S671, K672, R673, S674, F675, A701, Q702, G704, G705, G706, G707, S708, L709, Q710, I711, P712, F713	22	0.636
CTL-MPV-1	6	R152, S153, M154, W155, S156, F157, N158, G159, G160, G161, G162, S163, K164, E165, S209, T210, T211, R212	18	0.57
CTL-MPV-1	7	S636, V637, D638, T640, G643, G644, G645, G646, S647, N648, Q650, E651, A654, Q655, K657, Q658, I659, Y660	18	0.554
CTL MPV	**No.**	**B Cell Discontinuous Epitopes residues**	**Number of residues**	**Score**
CTL-MPV-2	1	R667,K669,H670	3	0.875
CTL-MPV-2	2	G1,I2,G3,D4,P5,V6,T7,C8,L9,K10,S11,G12,A13,I14,C15,H16,P17,V18,F19,C20,P21,R22,R23,Y24,K25,Q26,I27,G28,T29,C30,G31,L32,P33,G34,T35,K36,C37,C38,K39,K40,P41,E42,A43,A44,A45,K46,N47,Q48,R49,N50,A51,P52,R53,I54,T55,F56,G57,G58,P59,S60,G61,G62,G63,G64,S65,R66,S67,K68,Q69,R70,R71,P72,Q73,G74,L75,P76,N77,N78,T79,A80,S81,W82,F83,T84,A85,L86,T87,H89,K91,G92,G93,G94,G95,S96,N97,S98,S99,P100,D101,D102,Q103,I104,G105,Y106,Y107,I114,D118,G119	108	0.777
CTL-MPV-2	3	Q526,T527,Y528,G529,G530,G531,G532,S533,A534,G547,S548,V549,D550,T551,D552,F553,V554,N555,E556,F557,Y558,A559,Y560,L561,H564,F565,S566,M567,G569,A577,N578,G579,Q580,V581,F582,G583,L584,Y585,G586,G587,G588,G589,S590,I591,P592,L593,M594,Y595,K596,G597,L598,P599,W600,N601,V602,V603,R604,G605,G606,G607,G608,S609,Y610,V611,M612,H613,A614,N615,Y616,I617,F618,W619,E620,A621,A622,A623,K624,G625,I626,I627,N628,T629,L630,Q631,K632,Y633,Y634,C635,R636,V637,R638,G639,G640,R641,C642,A643,V644,L645,S646,C647,L648,P649,K650,E651,E652,Q653,I654,G655,K656,C657,S658,T659,R660,G661,R662,K663,C664,C665,R666,H671,H672,H673,H674,H675	124	0.737
CTL-MPV-2	4	E188,L189,I190,R191,Q192,G193,T194,D195	8	0.665
CTL-MPV-2	5	T247,F248,P249,P250,T251,E252,P253,K254,K255,G256,G257,G258,G259,G272,G273,G274,G275,S276,E277,T278,T292,Q293,V294,V295,D296,M297,M299,Y301,M311,G312,T313,L314,S315,Y316,E317,Q318,F319,G320,G321,L325,F330,L331,A332,Y333,I334,L335,F336,T337,R338,F339,F340,Y341,G343,I351,F352,F353,A354,S355,F356,Y357,Y358,W360,K361,S362,Y363,G364,G365,G366,G367,S375,S376,T377,F378,N379,V380,P381,M382,E383,G385,G386,G387,G388,S389,C390,R397,F398,R399,R400,A401,F402,G403,G404,G405,G406,L414,V415,P416,I419,I421,A422,Y436,V442,G444,G445,G446,G447,S448,L449,P450,S451,G465	111	0.626
CTL MPV	**No.**	**B Cell Discontinuous Epitopes residues**	**Number of residues**	**Score**
CTL-MPV-3	1	L9, K10, S11, I14, V18, F19, C20, P21, R22, R23, Y24, K25, Q26, I27, G28, T29, C30, G31, L32, P33, G34, T35, K36, C37, C38, K39, K40, P41, E42, A43, A44, A45, K46, S47, E48, E49, T50, G51, T52, L53, I54, V55, N56, S57, V58, L60, F61, F64, R231, G232, G233, G234, G235, S236, Y237, F238, C240, W241, Y274, L277, Y278, S279, T280, Q281, L282, S283, T284, D285, G287, V288, V291, E316, I317, L319, I320, I321, M322, R323, T324, F325, K326, V327, S328, I329, W330, N331, L332, D333, Y334, I335, I336, G337, G338, G339, G340, S341, M342, K343, I344, I345, L346, F347, L348, A349, L350, I351, T352, L353, A354, T355, C356, E357, L358, Y359, H360	115	0.743
CTL-MPV-3	2	I118, F119, T120, I121, G122, L126, K127, G128, G129, G130, G131, S132, T133, I134, P135, I136, R542, V543, G544, A545, R546, K547, S548, A549, P550, L551, I552, I564, D565, I566, G567, N568, Y569, T570, V571, N579, Q581, E582, P583, G586, S587, V590, R591, C592, S593, F594, Y595, E596, D597, F598, L599, E600, Y601, D603, V604, R605, V606, V607, L608, G612, S613, I617, F620, F624, Y627, S628, L629, L630, L631, C632, R633, E634, A635, A636, A637, K638, G639, I640, I641, N642, T643, L644, Q645, K646, Y647, Y648, C649, R650, V651, R652, G653, G654, R655, C656, A657, V658, L659, S660, C661, L662, P663, K664, E665, E666, I668, G669, K670, C671, S672, T673, G675, R676, K677, C678, C679, R680, K682, K683, H684, H685, H686, H687, H688, H689	124	0.724
CTL-MPV-3	3	G188, G189, G190, S420, P421, F424, I425, R426, G427, G428, S431, E432, Q434, E435, L436, Y437, S438, P439, L481, L482, F483, L484, V485, L486, I487, M488, L489, I490, I491, F492, W493, F494, S495, L496, E497, L498, G499, G500, G501, G502, S503, M504, K505, F506, L507, V508, L510, G511, I512, T514, T515	51	0.716
CTL-MPV-3	4	L152, A153, V154, F155, Q156, S157, A158, S159, K160, I161, I162, T163, R167	13	0.713
CTL-MPV-3	5	N106, S107, S108, R109, G110, G111, G112, G113, S114, M116, R117, Q137	12	0.689
CTL-MPV-3	6	S304, L307, V308, D309, G362, G363, G364, G365, S366, L368, K369, E370, P371, C372, S373, S374, G375, T376, Y377, E378, G379, A387, D388, N389, K390, F391, A392	27	0.596

CTL-MPV-3	7	T71, L75, T76, L78, R79, L80, C81, A82, Y83, G84, G85, G86, G522, G523, S524, Y525, V526, V527, D528, S537, K538	21	0.586

Supplementary Table S13: B cell linear epitopes screened from HTL MPVs.

HTL MPV	No.	Chain	Start	End	B Cell Linear Epitopes	Number of residues	Score
HTL-MPV-1	1	_	273	312	CGGGGSYADSFVIRGDEVRQIAPGQGGGGSVVVLSFELLH	40	0.736
HTL-MPV-1	2	_	504	532	YTGAIKLDDKDGGGGSSDFVRATATIPIQ	29	0.783
HTL-MPV-1	3	_	184	211	KGGGGSGINITRFQTLLALHRSYLTPGD	28	0.749
HTL-MPV-1	4	_	129	155	SQRVAGDSGGGGSSKTQSLLIVNNATN	27	0.71
HTL-MPV-1	5	_	549	571	ALVYFLQSINFVGGGGSDTGVEH	23	0.783
HTL-MPV-1	6	_	234	256	PTESIVRFPNITNLCPFGGGGGS	23	0.672
HTL-MPV-1	7	_	461	482	PQGTTLGGGGSWPQIAQFAPSA	22	0.775
HTL-MPV-1	8	_	419	440	GGSDDQIGYYRRATRRIRGGDG	22	0.697
HTL-MPV-1	9	_	162	179	EGGGGSREFVFKNIDGYF	18	0.813
HTL-MPV-1	10	_	109	124	LFARGGGGSSRTLSYY	16	0.635
HTL-MPV-1	11	_	488	500	MSRGGGGSTPSGT	13	0.632
HTL-MPV-1	12	_	634	644	CRRKKHHHHHH	11	0.764
HTL-MPV-1	13	_	618	628	PKEEQIGKCST	11	0.614
HTL-MPV-1	14	_	579	587	KIVDEPEEH	9	0.809
HTL-MPV-1	15	_	449	457	NPANNAAIV	9	0.653
HTL-MPV-1	16	_	54	60	LAFVVFL	7	0.594
HTL MPV	**No.**	**Chain**	**Start**	**End**	**B Cell Linear Epitopes**	**Number of residues**	**Score**
HTL-MPV-2	1	_	567	591	GSEILLIIMRTFKVSIWNLDYIINL	25	0.793
HTL-MPV-2	2	_	646	663	IFWFSLELGGGGSCTQHQ	18	0.786
HTL-MPV-2	3	_	184	198	EWFLAYILFTRFFYV	15	0.782
HTL-MPV-2	4	_	690	757	PFTIYSLLLCRMEAAAKGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKHHHHHH	68	0.761
HTL-MPV-2	5	_	22	44	RRYKQIGTCGLPGTKCCKKPEAA	23	0.752
HTL-MPV-2	6	_	1	15	GIGDPVTCLKSGAIC	15	0.749
HTL-MPV-2	7	_	210	219	SYFAVHFISN	10	0.728
HTL-MPV-2	8	_	248	265	FYYVWKSYVGGGGSWLKQ	18	0.712
HTL-MPV-2	9	_	385	402	GGSQAIASEFSSLPSYAA	18	0.698
HTL-MPV-2	10	_	456	475	SFVNEFYAYLRKHFSMMILG	20	0.674
HTL-MPV-2	11	_	421	434	AKNRARTGGGGSRA	14	0.667
HTL-MPV-2	12	_	294	306	SAVGNICYTPSKL	13	0.633
HTL-MPV-2	13	_	615	628	ELYGGGGSLSLIDF	14	0.579
HTL-MPV-2	14	_	556	562	NPIQLSS	7	0.555

Supplementary Table S14: B cell Discontinuous epitopes screened from HTL MPVs.

HTL MPV	No.	B Cell Discontinuous Epitope residues	Number of residues	Score
HTL-MPV-1	1	M413, G419, G420, S421, D422, D423, Q424, I425, G426, Y427, Y428, R430, A431, T432, R433, R434, I435, R436, G437, G438, D439, G440, N449, P450, A451, N452, N453, A454, A455, I456, V457, L460, P461, Q462, G463, T464, T465, L466, G467, G468, G469, G470, S471, W472, P473, Q474, I475, A476, Q477, F478, A479, P480, S481, A482, S483, M488, S489, R490, G491, G492, G493, G494, S495, T496, P497, S498,	121	0.727

		G499, T500, Y504, T505, G506, A507, I508, K509, L510, D511, D512, K513, D514, G515, G516, G517, G518, S519, S520, D521, F522, V523, R524, A525, T526, A527, T528, I529, P530, I531, Q532, L547, A549, L550, V551, Y552, F553, L554, Q555, S556, I557, N558, F559, V560, G561, G562, G563, G564, S565, D566, T567, G568, V569, E570, V572		
HTL-MPV-1	2	V261, L262, Y263, N264, S265, A266, S267, F268, C273, G274, G275, G276, G277, S278, Y279, A280, D281, S282, F283, V284, I285, R286, G287, D288, E289, V290, R291, Q292, I293, A294, P295, G296, Q297, G298, G299, G300, G301, S302, V303, V304, V305, L306, S307, F308, T331, N332	46	0.716
HTL-MPV-1	3	I596, N597, T598, L599	4	0.703
HTL-MPV-1	4	L54, A55, F56, V57, V58, F59, L60, K75, F78, L79, L82, W83, V85, T86, L87, L109, F110, A111, R112, G113, G114, G115, G116, S117, S118, R119, T120, L121, S122, Y124, A128, S129, Q130, R131, V132, A133, G134, D135, S136, G137, G138, G139, G140, S141, S142, K143, T144, Q145, S146, L147, L148, I149, V150, N151, N152, A153, T154, N155, E162, G163, G164, G165, G166, S167, R168, E169, F170, V171, F172, N174, I175, D176, G177, Y178, F179, K184, G185, G186, G187, G188, S189, G190, I191, N192, I193, T194, R195, F196, Q197, T198, L199, L200, A201, L202, H203, R204, S205, Y206, L207, T208, P209, G210, D211, A218, G219, A220, A221, Y227, G228, P234, T235, E236, I238, V239, R240, F241, P242, N243, I244, T245, N246, L247, C248, P249, F250, G251, G252, G253, G254, G255, S256	131	0.682
HTL-MPV-1	5	Y603, C604, V606, C634, R635, R636, H639, H640, H643, H644	10	0.675
HTL-MPV-1	6	G1, I2, G368, G369, G370, S371, R372, K579, I580, V581, D582, E583, P584, E585, E586, H587, P618, K619, E620, E621, Q622, G624, K625, C626, S627, T628, R629, G630, R631, C633, K637, K638, H641	33	0.652
HTL-MPV-1	7	F19, C20, P21, R22	4	0.52
HTL-MPV-1	8	E309, L310, L311, H312, P343, V344, S345, G346, G347, G348, G349, S350, Q351	13	0.517
HTL MPV	**No.**	**B Cell Discontinuous Epitope residues**	**Number of residues**	**Score**
HTL-MPV-2	1	F19,R23,K25,Q26,I27,G28,T29,C30,G31,L32,P33,G34,T35,K36,C37,C38,K39,K40,P41,E42,A43,A44,K46,V61,E62,T63,G64,G65,G66,G67,S68,E74,A76,V78,V79,R80,F83,S84,G85,G86,G87,G88,S89,T90,L91,E92,E93,T94,K95,F96,L97,T98,E99,N100,L101,L102,L103,Y104,I105,D106,I107,N108,G109,G110,G111,G112,S113,V114,Q115,Q116,E117,S118,P119,F120,V121,M122,M123,S124,A125,P126,P127,A128,Q129,Y130,E131,L132,G133,G134,G135,G136,S137,L138,L139,Q140,L141,C142,T143,F144,T145,S147,T148,N149,S150,R151,A154,S155,G157,G158,G159,G160,S161,S162,K163,L164,S183,E184,W185,F186,L187,A188,Y189,I190,L191,F192,T193,R194,F195,F196,Y197,V198	130	0.755
HTL-MPV-2	2	G453,S456,F457,V458,N459,E460,Y462,A463,Y464,L465,R466,K467,H468,F469,S470,M471,M472,I473,L474,G475,G476,G564,G565,G566,G567,S568,E569,I570,L571,L572,I573,I574,M575,R576,T577,F578,K579,V580,S581,I582,W583,N584,L585,D586,Y587,I588,I589,N590,L591,K594,Y617,G618,G619,G620,G621,S622,L623,S624,L625,I626,D627,F628,I646,F647,W648,F649,S650,L651,E652,L653,G654,G655,G656,G657,S658,C659,T660,Q661,H662,Q663,P664,Y683,V686,F687,P690,F691,T692,I693,Y694,S695,L696,L697,L698,C699,R700,E702,A703,A704,A705,K706,G707,I708,I709,N710,T711,L712,Q713,K714,Y715,C717,R718,V719,R720,G721,G722,R723,C724,A725,V726,L727,S728,C729,L730,P731,K732,E733,E734,Q735,I736,G737,K738,C739,S740,T741,R742,G743,R744,K745,C746,C747,R748,K750,K751,H752,H753,H755,H756,H757	148	0.724

HTL-MPV-2	3	S294,A295,V296,G297,I299,C300,Y301,G384,G385,G386,S387,Q388,A389,I390,A391,S392,E393,F394,S395,S396,L397,P398,S399,Y400,A401,A402,K416,Y417,A418,A421,K422,R424,A425,R426,T427,G428,G429,G430,G431,S432,R433,A434	42	0.666
HTL-MPV-2	4	G1,I2,G3,D4,P5,V6,T7,C8,L9,K10,S11,G12,A13,I14,C15,V18,R22,M205,L207,S210,Y211,F212,A213,V214,H215,F216,I217,S218,N219,F248,Y249,V251,W252,K253,S254,Y255,V256,G257,G258,G259,G260,S261,W262,L263,K264,Q265,K268,L282,I283,T284,P285,V286,H287,G288,G289,G290,G291,S292,T302,P303,S304,K305,L306,T332,L334,G335,G336,G337,G338,S339,F340,T341,Q365,T367	74	0.638
HTL-MPV-2	5	N556,P557,I558,Q559,L560,S561,S562	7	0.555

Supplementary Table S15: Analysis of codon-optimized cDNA of all the MPVs.

S.No.	MPVs	GC content	CAI (Codon Adaptation Index) score	Tandem rare codons
1	CTL-MPV-1	67.84%	1	0%
2	CTL-MPV-2	69.72%	1	0%
3	CTL-MPV-3	66.22%	1	0%
4	HTL-MPV-1	71.10%	1	0%
5	HTL-MPV-2	66.58%	1	0%
	Ideal values	30-70%	0.8-1.0	<30%