

Table 1. Codon and amino acid alterations in S proteins.

Codon/Amino acid (Wild/Mutant)	Position	Isolate	Country
TAC/AAC; Y/N	82 nt; 28 aa	MT049951	China-Yunnan
CAT/TAT; H/Y	145 nt; 49 aa	MT020781	Finland
TCG/TGG; S/W	662 nt; 221 aa	EPI_ISL_417186	South Africa
GAT/GGT; D/ G	1841 nt; 614 aa	EPI_ISL_420140 and 420144	Georgia
		EPI_ISL_420910	England
		EPI_ISL_418263 and 418264	Greece
		EPI_ISL_420625	France
		MT198653	Spain
		EPI_ISL_420798 and 420793	USA-Texas and New York
		EPI_ISL_418859	Canada-British_Columbia
		EPI_ISL_420600	Argentina
		EPI_ISL_418262	Colombia
		EPI_ISL_420876	Australia-Victoria
		EPI_ISL_420079	Senegal
EPI_ISL_418241	Algeria		
EPI_ISL_420854	Congo		
EPI_ISL_413550	Nigeria		
GCT/GTT; A/V	1868 nt; 623 aa	EPI_ISL_420879	Australia-Queensland
GTT/ATT; V/I	2314 nt; 772 aa	EPI_SPL_424366	Turkey
TTT/TGT; F/C	2390 nt; 797 aa	MT093571	Sweden
AAC/AAT; N/N	2472 nt; 824 aa	EPI_ISL_416538	New Zealand
GCT/GTT; A/V	2789 nt; 930 aa	MT050493	India
GAC/GAT; D/D	3504 nt; 1168 aa	EPI_ISL_418384	Canada-Ontario
GAG/GTG; E/V	3620 nt; 1207 aa	EPI_ISL_417482	Ecuador

Bold bases indicate the single nucleotide polymorphism occurred.

Table 2. Codon and amino acid alterations in N protein.

Codon/Amino acid (Wild/Mutant)	Position	Isolate	Country
GAC/GAT; D/D	384 nt;128 aa	LC528233	Japan
		EPI_ISL_415661	Chile
CTG/TTG; L/L	415 nt;139 aa	LC528233	Japan
		MT019530	China-Wuhan
		MT049951	China-Yunnan
		MT039890	South Korea
		MT050493	India
		EPI_ISL_420140 and 420144	Georgia
		MT240479	Pakistan
		EPI_ISL_414379	Singapore
		EPI_ISL_420910	England
		EPI_ISL_419552	Germany
		EPI_ISL_418263 and 418264	Greece
		EPI_ISL_420625	France
		MT066156	Italy
		MT198653	Spain
		MT093571	Sweden
		MT020781	Finland
		EPI_ISL_420798	USA-Texas
		EPI_ISL_420793	USA-New York
		EPI_ISL_419555	USA-Washington
		EPI_ISL_418859	Canada-British Colombia
		MT126808	Brazil
		EPI_ISL_420600	Argentina
		EPI_ISL_418262	Colombia
		EPI_ISL_415661	Chile
		EPI_ISL_417482	Ecuador
		EPI_ISL_420879	Australia-Queensland
		EPI_ISL_419833	Australia-Northern Territory
		EPI_ISL_420876	Australia-Victoria
		EPI_ISL_416538	New Zealand
		EPI_ISL_420079	Senegal
		EPI_ISL_418241	Algeria
		EPI_ISL_417186	South Africa
		EPI_ISL_420854	Congo
EPI_ISL_413550	Nigeria		

TCA/TTA; S/L	590 nt; 197 aa	LC528233 EPI_ISL_415661	Japan Chile
CCA/TCA; P/S	595 nt; 199 aa	EPI_ISL_414379	Singapore
AGG/AAA; R/K	608-609 nt; 203 aa	EPI_ISL_420144 EPI_ISL_418263 and 418264	Georgia Greece
GGA/CGA; G/R	610 nt; 204 aa	EPI_ISL_420600 EPI_ISL_418262 EPI_ISL_413550	Argentina Colombia Nigeria
TAC/TAT; Y/Y	1080 nt; 360 aa	EPI_ISL_418241	Algeria
GAG/AAG; E/K	1099 nt; 367 aa		
CCT/GCC; P/A	1102-1104 nt; 368 aa		
AAG/CAG; K/Q	1108 nt; 370 aa	EPI_ISL_420079	Senegal
GAC/TAC; D/Y	1111 nt; 371 aa		
AAA/AGT; K/S	1115-1116 nt; 372 aa		

Bold bases indicate the single nucleotide polymorphism occurred.

Table 3. Codon and amino acid alterations in E and M proteins.

	Codon/Amino acid (Wild/Mutant)	Position	Isolate	Country
E protein	CTT/CAT; L/H	110 nt; 37 aa	MT039890	South Korea
			EPI_ISL_417186	South Africa
	CTT/TTT; L/F	217 nt; 73 aa	EPI_ISL_418241	Algeria
M protein	GCT/GCC; A/A	207 nt; 69 aa	EPI_ISL_416538	New Zealand

Bold bases indicate the single nucleotide polymorphism occurred.

Table 4. Physico-chemical parameter results predicted by ExPASyProtParam

	Protein Name	Number of Amino acids	Molecular Weight	Theoretical PI	Total Number of Negatively Charged Residues (Asp + Glu)	Total Number of Positively Charged Residues (Arg + Lys)	The estimated half-life (hour)	The instability index (II)	Aliphatic Index	GRAVY ^a
Structural Proteins	S protein	1273	141178.47	6.24	110	103	30	33.01/stable	84.67	-0.079
	E protein	75	8365.04	8.57	3	5	30	38.68/stable	144.00	1.128
	M protein	222	25146.62	9.51	13	21	30	39.14/stable	120.86	0.446
	N protein	419	45625.70	10.07	36	60	30	55.09/unstable	52.53	-0.971
Non-structural proteins	orf3a	275	31122.94	5.55	24	17	30	32.96/stable	103.42	0.275
	orf6	61	7272.54	4.60	9	5	30	31.16/stable	130.98	0.233
	orf7a	121	13744.17	8.23	10	12	30	48.66/unstable	100.74	0.318
	orf7b	43	5180.27	4.17	5	0	30	50.96/unstable	156.51	1.449
	orf8	121	13831.01	5.42	13	9	30	45.79/unstable	97.36	0.219
	orf10	38	4449.23	7.93	1	2	30	16.06/stable	107.63	0.637
Pp1ab	nsp-1	180	19775.31	5.36	27	19	30	28.83/stable	89.72	-0.378
	nsp-2	638	70511.38	6.25	74	70	4.4	36.06/stable	88.93	-0.062
	nsp-3	1945	217252.61	5.56	222	185	4.4	36.56/stable	86.22	-0.175
	nsp-4	500	56183.98	7.16	37	37	1.3	34.09/stable	95.50	0.343
	nsp-5	306	33796.64	5.95	26	22	1.9	27.65/stable	82.12	-0.019
	nsp-6	290	33033.69	9.11	11	21	1.9	22.94/stable	111.55	0.790
	nsp-7	83	9239.82	5.18	10	8	1.9	51.97/unstable	117.35	0.199
	nsp-8	198	21881.08	6.58	22	22	4.4	37.78/stable	88.33	-0.192
	nsp-9	113	12378.20	9.10	9	13	1.4	34.17/stable	82.92	-0.227
	nsp-10	139	14789.92	6.29	11	10	4.4	34.56/stable	61.80	-0.068
	nsp-12	932	106660.24	6.14	106	94	1.9	28.32/stable	78.43	-0.224
	nsp-13	601	66854.75	8.66	52	64	4.4	33.31/stable	84.49	-0.096
	nsp-14	527	59815.67	7.80	50	52	4.4	28.85/stable	78.96	-0.134
	nsp-15	346	38813.40	5.06	46	34	1.9	36.28/stable	95.09	-0.076
	nsp-16	298	33323.32	7.59	26	27	1.9	26.11/stable	90.64	-0.086

^aGRAVY means the Grand average of hydropathicity

Table 5. Secondary structures results predicted by GOR IV.

	Protein Name	Alpha helix (%)	Extended strand (%)	Random coil (%)
Structural Proteins	S protein	21.52	22.07	56.40
	E protein	33.33	13.33	53.33
	M protein	46.85	13.51	39.64
	N protein	30.55	9.79	59.67
Non-structural proteins	orf3a	18.91	32.73	48.36
	orf6	50.82	3.28	45.90
	orf7a	23.97	26.45	49.59
	orf7b	55.81	6.98	37.21
	orf8	0.00	46.28	53.72
	orf10	0.00	44.74	55.26
Pplab	nsp-1	26.11	15.56	58.33
	nsp-2	26.33	18.97	54.70
	nsp-3	26.12	24.27	49.61
	nsp-4	19.00	28.40	52.60
	nsp-5	14.05	37.58	48.37
	nsp-6	28.28	34.48	37.24
	nsp-7	68.67	3.61	27.71
	nsp-8	64.14	7.07	28.79
	nsp-9	30.97	19.47	49.56
	nsp-10	11.51	34.53	53.96
	nsp-12	27.15	23.50	49.36
	nsp-13	17.64	26.29	56.07
	nsp-14	13.85	29.79	56.36
	nsp-15	18.79	26.59	54.62
	nsp-16	14.43	33.22	52.35

Table 6. Solubility, transmembrane helices, localization and antigenicity results predicted by SolPro, TMHMM, Virus-mPLoc and Vaxijen, respectively.

	Proteins	SolPro	TMHMM	Virus-mPLoc	Vaxijen v2.0 Value
Structural Proteins	S protein	Soluble	1	Host Endoplasmic Reticulum	0.4661 (Probable antigen)
	E protein	Soluble	1	Host Endoplasmic Reticulum	0.6025 (Probable antigen)
	M protein	Insoluble	3	Host Cell Membrane, Endoplasmic Reticulum	0.5102 (Probable antigen)
	N protein	Soluble	0	Host Cell Membrane	0.5059 (Probable antigen)
Non-structural proteins	orf3a	Insoluble	3	Host Cell Membrane	0.4945 (Probable antigen)
	orf6	Soluble	0	Host Endoplasmic Reticulum	0.6131 (Probable antigen)
	orf7a	Soluble	1	Host Endoplasmic Reticulum	0.6441 (Probable antigen)
	orf7b	Soluble	1	*	0.8462 (Probable antigen)
	orf8	Soluble	0	Host cell membrane, endoplasmic reticulum, cytoplasm	0.6502 (Probable antigen)
	orf10	Soluble	0	*	0.7185 (Probable antigen)
Pp1ab	nsp-1	Soluble	0	Host cytoplasm	0.4064 (Probable antigen)
	nsp-2	Insoluble	0	Host cytoplasm	0.4034 (Probable antigen)
	nsp-3	*	4	Host cytoplasm	0.5142 (Probable antigen)
	nsp-4	Insoluble	4	Host cell membrane, endoplasmic reticulum	0.4691 (Probable antigen)
	nsp-5	Insoluble	0	Host cell membrane	0.4159 (Probable antigen)
	nsp-6	Soluble	8	Host cell membrane	0.5813 (Probable antigen)
	nsp-7	Insoluble	0	Host cytoplasm	0.4167 (Probable antigen)
	nsp-8	Soluble	0	Host cytoplasm	0.4008 (Probable antigen)
	nsp-9	Soluble	0	Host cell membrane, cytoplasm	0.6476 (Probable antigen)
	nsp-10	Insoluble	0	Host cell membrane, endoplasmic reticulum	0.4039 (Probable antigen)
	nsp-12	Insoluble	0	Host cytoplasm	0.4064 (Probable antigen)
	nsp-13	Insoluble	0	Host nucleus	0.4480 (Probable antigen)
	nsp-14	Insoluble	0	Host cytoplasm, nucleus	0.4138 (Probable antigen)
	nsp-15	Insoluble	0	Host cytoplasm	0.5554 (Probable antigen)
	nsp-16	Insoluble	0	Host cytoplasm	0.3800 (Probable non-antigen)

* could not be retrieved.

Table 7. The signal peptide results predicted by Signal-BLAST.

	Protein Name	Sensitivity	Specificity	Balanced prediction	Cleavage site
Structural Proteins	S protein	Yes	Yes	Yes	Yes
	Variant D614G	Yes	Yes	Yes	Yes
	E protein	No	No	No	Yes
	Variant L37H	No	No	No	No
	M protein	No	No	No	No
	N protein	No	No	No	Yes
	Variant S197L	No	No	No	Yes
	Variant R203K/G204R	No	No	No	Yes
Non-structural proteins	orf3a	No	No	No	No
	orf6	No	No	No	Yes
	orf7a	Yes	Yes	Yes	Yes
	ORF7b	No	No	No	Yes
	orf8	Yes	Yes	Yes	Yes
	Variant L84S	Yes	Yes	Yes	Yes
	orf10	No	No	No	Yes
Pplab	nsp-1	No	No	No	Yes
	nsp-2	No	No	No	Yes
	nsp-3	No	No	No	No
	nsp-4	No	No	No	Yes
	nsp-5	Yes	No	Yes	Yes
	nsp-6	Yes	No	Yes	Yes
	nsp-7	No	No	No	Yes
	nsp-8	No	No	No	No
	nsp-9	Yes	No	Yes	Yes
	nsp-10	Yes	Yes	Yes	Yes
	nsp-12	No	No	No	Yes
	nsp-13	No	No	No	No
	nsp-14	No	No	No	No
	nsp-15	No	No	No	No
	nsp-16	No	No	No	No

Bold indicates proteins that have a signal peptide.

Table 8. Allergenicity, BetaWrap motifs and host proteome similarity results predicted by AlgPred, BetaWrap and BlastP, respectively.

	Proteins	AlgPred		BetaWrap Motifs	BlastP
		IgE epitopes	MEME/MAST motif		
Structural Proteins	S protein	-	Non allergen	P-value: 0.014	No significant similarity found
	Variant S (D614G)	-	Non allergen	P-value: 0.014	No significant similarity found
	E protein	-	Non allergen	No proteins with BetaWrap P-value less than 0.1	No significant similarity found
		Variant E (L37H)	-	Non allergen	No proteins with BetaWrap P-value less than 0.1
	M protein	-	Non allergen	No proteins with BetaWrap P-value less than 0.1	No significant similarity found
	N protein	-	Non allergen	No proteins with BetaWrap P-value less than 0.1	No significant similarity found (a few insignificant matches)
		Variant N (S197L)	-	Non allergen	No proteins with BetaWrap P-value less than 0.1
	Variant N (R203K 204R)	-	Non allergen	No proteins with BetaWrap P-value less than 0.1	No significant similarity found (a few insignificant matches)
Non-structural proteins	orf7a	-	Non allergen	No proteins with BetaWrap P-value less than 0.1	No significant similarity found
	orf8	-	Non allergen	No proteins with BetaWrap P-value less than 0.1	No significant similarity found
	Variant orf8 (L84S)	-	Non allergen	No proteins with BetaWrap P-value less than 0.1	No significant similarity found
Pp1ab	nsp-10	-	Non allergen	No proteins with BetaWrap P-value less than 0.1	No significant similarity found

Table 9. B cell epitopes predicted by both Bcepred and IEDB and antigenicity value predicted by Vaxijen v2.0.

	Proteins	Antigenicity value	B cell epitopes	Antigenicity value for epitopes
*Vaccine candidate epitopes	S protein Variant (D614G)	0.4661 (Probable antigen)	VYYHKNNKSW	0.4497 (Probable antigen)
		0.4638 (Probable antigen)	YAWNRRKRISN	0.5855 (Probable antigen)
			GDEVVRQ	0.6701 (Probable antigen)
			NLDSKV	0.7443 (Probable antigen)
	E protein Variant E (L37H)	0.6025 (Probable antigen) 0.6298 (Probable antigen)	SRVKNLNSSRVP	0.5572 (Probable antigen)
*Vaccine candidate epitopes	orf8	0.6502 (Probable antigen)	DEAGSKS	0.5885 (Probable antigen)
	Variant orf8 (L84S)	0.6063 (Probable antigen)		
	nsp-10	0.4039 (Probable antigen)	THTGTGQ	1.0789 (Probable antigen)
Diagnostic epitopes	N protein Variant N (S197L) Variant N (R203K/G204R)		NGPQNQRNAP	0.5058 (Probable antigen)
			NTNSSPDDQI	0.4913 (Probable antigen)
			GGDGKMKD	1.4530 (Probable antigen)
			AEGSRGGSQASSRSSSRNSSRNS	0.8682 (Probable antigen)
			AGNGGD	0.8201 (Probable antigen)
			ESKMSGKGGQQQGQT	0.8163 (Probable antigen)
			PQRQKKQQT	0.5997 (Probable antigen)
			QSMSSADS	0.4864 (Probable antigen)

*Vaccine candidate epitopes can also be used to develop serodiagnostic assays.

Table 10. Epitopes specific to selected MHC-I alleles

Proteins	Allele	Start	End	Peptide	IC50	Percentile Rank	Antigenicity	
S protein Variant S (D614G)	HLA-A*24:02	1211	1220	KWPWYIWLGF	9.04	0.02	1.3904 antigen)	(Probable
	HLA-B*15:01	754	763	LQYGSFCTQL	13.44	0.06	1.4443 antigen)	(Probable
	HLA-A*02:01	386	395	KLNDLCFTNV	15.27	0.14	2.6927 antigen)	(Probable
	HLA-B*07:02	680	689	SPRRARSVAS	18.4	0.07	0.5591 antigen)	(Probable
	HLA-A*02:01	1209	1218	YIKWPWYIWL	18.81	0.2	0.8847 antigen)	(Probable
	HLA-A*02:01	515	524	FELLHAPATV	20.98	0.23	0.5982 antigen)	(Probable
	HLA-A*24:02	488	497	CYFPLQSYGF	27.59	0.04	0.7776 antigen)	(Probable
	HLA-B*15:01	49	58	HSTQDLFLPF	27.79	0.17	0.5162 antigen)	(Probable
	HLA-A*02:01	2	11	FVFLVLLPLV	32.64	0.37	0.8044 antigen)	(Probable
	HLA-A*02:01	268	277	GYLQPRTFLL	36.12	0.4	0.7535 antigen)	(Probable
	HLA-B*15:01	698	707	SLGAENSVAY	37.99	0.22	0.6175 antigen)	(Probable
	HLA-A*03:01	408	417	RQIAPGQTGK	38.0	0.15	1.7893 antigen)	(Probable
	HLA-A*03:01	1064	1073	HVTYVPAQEK	38.88	0.15	1.0786 antigen)	(Probable
	HLA-A*24:02	897	906	PFAMQMAYRF	38.93	0.05	1.1051 antigen)	(Probable
	HLA-A*03:01	724	733	TEILPVSMTK	42.81	0.17	1.4160 antigen)	(Probable
HLA-A*24:02	1207	1216	EQYIKWPWYI	45.33	0.06	1.1122 antigen)	(Probable	
E protein	HLA-A*02:01	20	29	FLAFVVFLLV	9.95	0.1	0.5651 antigen)	(Probable
Variant E (L37H)	HLA-A*02:01	18	27	LLFLAFVVFL	32.72	0.37	0.6159 antigen)	(Probable
orf7a	HLA-A*02:01	101	110	FLIVAAIVFI	13.43	0.13	0.6283 antigen)	(Probable
	HLA-B*40:01	40	49	YEGNSPFHPL	18.20	0.06	0.6193 antigen)	(Probable
	HLA-A*03:01	76	85	QLRARSVSPK	28.96	0.12	1.4738 antigen)	(Probable
	HLA-B*15:01	56	65	LTCFSTQFAF	29.06	0.18	1.1543 antigen)	(Probable
	HLA-A*03:01	23	32	CVRGTTVLLK	36.79	0.15	0.7426 antigen)	(Probable
	HLA-B*07:02	47	56	HPLADNKFAL	39.32	0.16	0.6385 antigen)	(Probable
	HLA-A*03:01	110	119	ITLCFTLKRK	39.65	0.15	2.5150 antigen)	(Probable
orf8	HLA-B*15:01	7	16	LGIITTVAAF	6.51	0.02	0.7595 antigen)	(Probable
Variant ORF8 (L84S)	HLA-B*40:01	109	118	LEYHDVRVVL	41.00	0.12	0.9885 antigen)	(Probable
M protein	HLA-B*08:01	103	112	FARTRSMWSF	7.87	0.02	0.9202	(Probable

*Vaccine candidate epitopes

		HLA-B*27:05	42	51	RNRFLYIIKL	8.00	0.02	0.7016 antigen)	(Probable
		HLA-A*02:01	26	35	FLFLTWICLL	10.42	0.1	1.1459 antigen)	(Probable
		HLA-B*15:01	56	65	LLWPVTLACF	11.12	0.05	0.9864 antigen)	(Probable
		HLA-B*27:05	71	80	YRINWITGGI	11.15	0.02	1.3250 antigen)	(Probable
		HLA-B*15:01	17	26	LEQWNLVIGF	14.47	0.07	1.0564 antigen)	(Probable
		HLA-A*02:01	53	62	FLWLLWPVTL	16.02	0.15	0.9162 antigen)	(Probable
		HLA-A*02:01	88	97	VGLMWLSYFI	17.08	0.18	0.6741 antigen)	(Probable
		HLA-B*40:01	136	145	SELVIGAVIL	17.83	0.06	0.6521 antigen)	(Probable
		HLA-A*02:01	61	70	TLACFVLA AV	20.28	0.22	1.2318 antigen)	(Probable
		HLA-A*03:01	171	180	ATSRTL SYYK	21.49	0.08	0.4317 antigen)	(Probable
		HLA-B*27:05	100	109	FRLFARTRSM	31.60	0.1	0.4609 antigen)	(Probable
		HLA-B*15:01	169	178	TVATSRTL SY	40.92	0.23	0.8259 antigen)	(Probable
		HLA-B*58:01	22	31	LVIGFLFLT W	46.78	0.22	1.3639 antigen)	(Probable
Diagnostic epitopes	N protein	HLA-B*15:01	305	314	AQFAPSASAF	3.58	0.02	0.5986 antigen)	(Probable
	Variant N (S197L)	HLA-A*03:01	361	370	KTFPPTEPKK	11.43	0.02	0.7657 antigen)	(Probable
	R203K/G204R	HLA-B*40:01	322	331	MEVTPSGTWL	28.62	0.09	0.6342 antigen)	(Probable
		HLA-A*01:01	78	87	SSPDDQIGYY	33.46	0.1	0.4533 antigen)	(Probable
		HLA-B*07:02	66	75	FPRGQGV PIN	33.85	0.14	0.7135 antigen)	(Probable
		HLA-A*02:01	315	324	FGMSRIGMEV	36.81	0.4	0.8800 antigen)	(Probable
		HLA-B*08:01	104	113	LSPRWYFYYL	37.51	0.11	1.3486 antigen)	(Probable

*Vaccine candidate epitopes can also be used to develop serodiagnostic assays.

Table 11. Epitopes specific to selected MHC-II alleles

	Proteins	Allele	Start	End	Core Sequence	Peptide	IC50	Percentile Rank	Antigenicity
*Vaccine candidate epitopes	S protein	HLA-DRB3*02:02	115	129	LIVNNATNV	QSLIVNNATNVVIK	13.08	0.02	0.4343 (Probable antigen)
	D614G	HLA-DRB5*01:01	894	908	FAMQMAYRF	LQIPFAMQMAYRFNG	20.96	0.59	0.7205 (Probable antigen)
		HLA-DRB1*07:01	715	729	FTISVTTEI	PTNFTISVTTEILPV	25.32	0.63	1.1349 (Probable antigen)
		HLA-DRB3*02:02	1091	1105	FVSNGTHWF	REGVFVSNGTHWVFT	25.75	0.2	0.4461 (Probable antigen)
		HLA-DRB1*07:01	691	705	YTMSLGAEN	SIHAYTMSLGAENSV	35.71	1.4	0.5691 (Probable antigen)
		HLA-DRB1*07:01	199	213	YSKHTPINL	GYFKIYSKHTPINLV	40.49	1.9	0.9278 (Probable antigen)
		HLA-DRB1*15:01	52	66	FLPFSNVT	QDLFLPFSNVTWFH	44.58	0.77	0.4159 (Probable antigen)
	Variant E (L37H)	HLA-DRB5*01:01	29	43	LAILTAHRL	VTLAILTAHRLCAYC	33.95	1.90	1.0545 (Probable antigen)
	M protein	HLA-DRB5*01:01	98	112	FRLFARTRS	ASFRLFARTRSMWSF	16.26	0.29	0.7304 (Probable antigen)
		HLA-DRB5*01:01	175	189	YYKLGASQR	TLSYYKLGASQRVAG	16.67	0.30	0.4376 (Probable antigen)
		HLA-DRB5*01:01	34	48	FAYANRNRF	LLQFAYANRNRFYI	26.30	1.10	0.7387 (Probable antigen)
		HLA-DRB1*07:01	98	112	FARTRSMWS	ASFRLFARTRSMWSF	30.95	1	0.7304 (Probable antigen)
		HLA-DRB1*07:01	174	188	YKLGASQRV	RTLSYYKLGASQRVA	31.50	1.10	0.5644 (Probable antigen)
		HLA-DRB1*07:01	165	179	ITVATSRTL	PKEITVATSRTLSTYY	37.66	1.60	0.7003 (Probable antigen)
		HLA-DRB5*01:01	31	45	FAYANRNRF	WICLLQFAYANRNRF	44.95	3.10	0.6994 (Probable antigen)
		HLA-DRB3*02:02	34	48	AYANRNRF	LLQFAYANRNRFYI	46.63	0.75	0.7387 (Probable antigen)
		HLA-DRB1*15:01	32	46	LQFAYANRN	ICLLQFAYANRNRF	47.01	0.82	0.6221 (Probable antigen)
		HLA-DRB5*01:01	139	153	AVILRGHLR	VIGAVILRGHLRIAG	48.64	3.40	0.4903 (Probable antigen)
		HLA-DRB5*01:01	98	112	FRLFARTRS	ASFRLFARTRSMWSF	16.26	0.29	0.7304 (Probable antigen)
		HLA-DRB5*01:01	34	48	FAYANRNRF	LLQFAYANRNRFYI	26.30	1.10	0.7387 (Probable antigen)
		HLA-DRB1*07:01	98	112	FARTRSMWS	ASFRLFARTRSMWSF	30.95	1	0.7304 (Probable antigen)
		HLA-DRB1*07:01	174	188	YKLGASQRV	RTLSYYKLGASQRVA	31.50	1.10	0.5644 (Probable antigen)
		orf7a	HLA-DRB5*01:01	71	85	VYQLRARSV	VKHVYQLRARSVSPK	40.51	2.6
		HLA-DRB5*01:01	107	121	ITLCFTLKR	IVFITLCFTLKRKTE	49.35	3.4	1.8597 (Probable antigen)
	orf8	HLA-DRB5*01:01	43	57	YIRVGARKS	SKWYIRVGARKSAPL	8.77	0.05	0.8829 (Probable antigen)
	Variant orf8 (L84S)	HLA-DRB3*01:01	28	42	YVDDPCPI	HQPYVDDPCPIHFY	19.07	0.06	0.5587 (Probable antigen)
Diagnostic epitopes	N protein	HLA-DRB5*01:01	264	278	YNVTQAFGR	ATKAYNVTQAFGRRG	29.21	1.40	0.7146 (Probable antigen)
	Variant N (S197L)	HLA-DRB1*07:01	303	317	FAPSASAFF	QIAQFAPSASAFFGM	32.18	1.10	0.4032 (Probable antigen)
	Variant N (R203K/G204R)								

*Vaccine candidate epitopes can also be used to develop serodiagnostic assays.