Design of a Peptide-Based Subunit Vaccine against Novel Coronavirus SARS-CoV-2

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Supplementary Table 1. ToxinPred results for the selected HTL, CTL and B-cell epitopes considered for Vaccine construction.

Toxicity prediction for HTL epitopes			
S. No.	**Epitope**	**SVM score**	**Prediction**
1	GTWLTYTGAIKLDDK	-0.85	Non-Toxin
2	AALALLLLDRLNQLE	-1.67	Non-Toxin
3	NRFLYIIKLIFLWLL	-0.72	Non-Toxin
4	EFVFKNIDGYFKIYS	-1.25	Non-Toxin
5	ITRFQTLLALHRSYL	-1.06	Non-Toxin
6	ATRFASVYAWNRKRI	-1.08	Non-Toxin
Toxicity prediction for B-cell epitopes			
S. No.	**Epitope**	**SVM score**	**Prediction**
1	TRRIRGGDGKMKDLSP	-0.56	Non-Toxin
2	KSAAEASKKPRQKRTA	-1.41	Non-Toxin
3	EGALNTPKDHIGTRNP	-0.38	Non-Toxin
4	RSMWSFNPETNILLNV	-1.2	Non-Toxin
5	SFRLFARTRSMWSFNP	-0.84	Non-Toxin
6	AGTITSGWTFGAGAAL	-0.72	Non-Toxin
7	GWTAGAAAYYVGYLQP	-1.29	Non-Toxin
8	PQIITTDNTFVSGNCD	-0.7	Non-Toxin
9	GVSVITPGTNTSNQVA	-1.58	Non-Toxin
Toxicity prediction for CTL epitopes			
S. No.	**Epitope**	**SVM score**	**Prediction**
1	LLLDRLNQL	-1.52	Non-Toxin
2	GMSRIGMEV	-1.02	Non-Toxin
3	KSAAEASKK	-1.22	Non-Toxin
4	KTFPPTEPK	-0.85	Non-Toxin
5	FPRGQGVPI	-1.46	Non-Toxin
6	KPRQKRTAT	-0.88	Non-Toxin
7	GLMWLSYFI	-1.06	Non-Toxin
8	FVLAAVYRI	-1.77	Non-Toxin
9	LSYFIASFR	-1.09	Non-Toxin
10	RIAGHHLGR	-1.08	Non-Toxin
11	LPKEITVAT	-1.32	Non-Toxin

12	RLFARTRSM	-0.58	Non-Toxin
13	YLQPRTFLL	-1.43	Non-Toxin
14	KIADYNYKL	-0.59	Non-Toxin
15	RLFRKSNLK	-1.10	Non-Toxin
16	GVYFASTEK	-1.45	Non-Toxin
17	SPRRARSVA	-1.20	Non-Toxin
18	IPTNFTISV	-1.09	Non-Toxin

Supplementary Figure 1. Sequence of the vaccine construct. The adjuvant is highlighted in red whereas linkers (EAAAK, GPGPG, AAY and KK) joining Adjuvant, CTL, HTL and BC are highlighted as yellow, green cyan and purple respectively.

*MRTSYLLLFTLCLLLSEMASGGNFLTGLGHRSDHYNCVSSGGQCLYSACPIFTKIQGTCYRGK AKCCK*EAAAKGTWLTYTGAIKLDDKGPGPGAALALLLLDRLNQLEGPGPGNRFLYIIKL IFLWLLGPGPGEFVFKNIDGYFKIYSGPGPGITRFQTLLALHRSYLGPGPGATRFASVYA WNRKRIAAYLLLDRLNQLAAYGMSRIGMEVAAYKSAAEASKKAAYKTFPPTEPKAAYF PRGQGVPIAAYKPRQKRTATAAYGLMWLSYFIAAYFVLAAVYRIAAYLSYFIASFRAAY RIAGHHLGRAAYLPKEITVATAAYRLFARTRSMAAYYLQPRTFLLAAYKIADYNYKLAA YRLFRKSNLKAAYGVYFASTEKAAYSPRRARSVAAAYIPTNFTISVKKTRRIRGGDGKM KDLSPKKKSAAEASKKPRQKRTAKKEGALNTPKDHIGTRNPKKRSMWSFNPETNILLN VKKSFRLFARTRSMWSFNPKKAGTITSGWTFGAGAALKKGVSVITPGTNTSNQVAKKG WTAGAAAYYVGYLQPKKPQIITTDNTFVSGNCD

Supplementary Figure 2. Secondary structure prediction of the vaccine construct using PESIPRED 4.0 server.