# Description of supplementary materials

**Supplementary Tables:**

**Supplementary Table 1.** The epitope target and method of prediction in the collected studies.

**Supplementary Table 2.** B-cell epitopes curated from literature published or preprinted until June 1,2020.

**Supplementary Table 3.** T-cell epitopes curated from literature published or preprinted until June 1,2020.

Supplementary Table 1: The epitope target and method of prediction in the collected studies. "Others" include the unique methods they used to make predictions.

| Epitope target | Predicted method | B cell | T cell | MHC-I | MHC-II | Validation method | Allergy analysis method | Toxicity analysis method | Others | reference |
|---|---|---|---|---|---|---|---|---|---|---|
| Spike glycoprotein, nucleocapsid phosphoprotein, Orf1ab | RapidPeptidesGenerator version 1.1.0[1]f | √ | √ | | | Blastp(1) | | | | [2] |
| nucleocapsid phosphoprotein | | | | NetMHC 4.0[3] ; NetMHCpan 4.0 | NetMHC 4.0 ; NetMHCpan 4.0 | | | | Base on EBOV vaccine preparation experience | [4] |
| Spike protein | Bepipred Linear Epitope Prediction[5] | √ | √ | | | VaxiJen v2.0 | AllerTOP v2 | ToxinPred server | | [6] |
| Spike glycoprotein, membrane protein, envelope protein, nucleocapsid protein | Bepipred Linear Epitope Prediction 2.0, Emini surface accessibility prediction[7], Kolaskar and Tongaonkar | √ | √ | | | VaxiJen v2.0 | Algpred[9] | | For construction of novel corona vaccine, the chosen adjuvants i.e. L7/L12 ribosomal protein, beta defensin (a 45 mer peptide) and HABA protein (M. tuberculosis, accession number: | [10] |

| Epitope target | Predicted method | B cell | T cell | MHC-I | MHC-II | Validation method | Allergy analysis method | Toxicity analysis method | Others | reference |
|---|---|---|---|---|---|---|---|---|---|---|
|  | antigenicity scale[8], ElliPro server |  |  |  |  |  |  |  | AGV15514.1) were used |  |
| Spike protein, membrane protein, envelope protein, nucleocapsid protein | RECON[11] |  | √ | RECON | RECON | Compare with VIPR |  |  |  | [12] |
| Spike protein, Envelop protein, Membrane protein, Nucleocapsid protein | ElliPro server, BCpred 2.0[13] | √ | √ |  | Net MHC II pan 3.2[14] | VaxiJen v2.0 | AllerTOP v2 |  | To ensure high expression of the recombinant vaccine in E. coli, codon optimization and in-silico cloning were also carried out | [15] |
| ORF1ab, Surface protein, ORF3, Envelope Protein, | IEDB tool "B Cell Epitope Prediction Tools", Bepipred Linear | √ | √ | IEDBtools "MHC-I Binding Predictio | IEDB tool "MHC-II Binding Predictions " | RAMPAGE analysis tool[16] | AlgPred | ToxinPred server |  | [17] |

| Epitope target | Predicted method | B cell | T cell | MHC-I | MHC-II | Validation method | Allergy analysis method | Toxicity analysis method | Others | reference |
|---|---|---|---|---|---|---|---|---|---|---|
| Membrane Protein, ORF6, ORF7a, ORF7b, ORF8, Nucleocapsid Protein, ORF10 | Epitope Prediction | | | ns" and "MHC-I Processing Predictions" | | | | | | |
| Spike protein | ElliPro server, ABCpred server[18] | √ | √ | IEDB server | IEDB server | | | | | [19] |
| Spike protein, Envelop protein, Membrane protein, Nucleocapsid protein | IEDB server Bepipred 2.0 | √ | √ | Net-MHC 4.0, IEDB server | IEDB server, RANKPEP[20] | RAMPAGE analysis tool, VaxiJen v2.0 | AllergenFP v.1.0[21] | | Docking of vaccine with Toll-Like Receptors 3, 5 and 8 proved an appropriate interaction between the vaccine and receptor proteins. In silico cloning demonstrated that the vaccine can be efficiently expressed in Escherichia coli. | [22] |
| Spike protein, nucleocapsid protein | IEDB server | | √ | | | | | | To identify the set of epitopes associated with MHC alleles that would | [23] |

| Epitope target | Predicted method | B cell | T cell | MHC-I | MHC-II | Validation method | Allergy analysis method | Toxicity analysis method | Others | reference |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | maximize the population coverage: (i) first identified the MHC allele with the highest individual population coverage and initialized the set with their associated epitopes, then (ii) progressively added epitopes associated with other MHC alleles that resulted in the largest increase of the accumulated population coverage. | |
| Spike glycoprotein | ElliPro server, IEDB server | √ | √ | ProPred-1[24] | ProPred[25] | VaxiJen v2.0 | | | | [26] |
| Spike glycoprotein | Bepipred 2.0 | √ | √ | ProPred-1 | ProPred | VaxiJen v2.0(3) | | | | [27] |
| ORF1AB, ORF3A, ORF6, ORF7A, | Discotope2[28] | √ | √ | netMHCpan4, MARIA[ | netMHCpan4, MARIA | Validated computational | | | | [30] |

| Epitope target | Predicted method | B cell | T cell | MHC-I | MHC-II | Validation method | Allergy analysis method | Toxicity analysis method | Others | reference |
|---|---|---|---|---|---|---|---|---|---|---|
| ORF7B, ORF8, ORF10, Spike protein, Envelop protein, Membrane protein, Nucleocapsid protein | | | | 29] | | pipeline with SARS-Co V experiment al data | | | | |
| Spike protein, Envelop protein, Membrane protein, Nucleocapsid protein | Bepipred, Emini surface accessibility prediction, Kolaskar and Tongaonkar antigenicity scale | √ | √ | netMHC pan, iNeo-Pre d | netMHCpa n, iNeo-Pred | | | | The vaccine peptides were designed by their in-house tool iNeo-Design | [31] |
| Spike protein, Envelop protein, Membrane protein, | Bepipred 2.0, Discotope2 | √ | √ | NetMH Cpan EL 4.0 | NetMHCp an EL 4.0 | IEDB server | | | Use BLAST algorithm to compare Coronavirus Sequences with SARS-CoV-2 | [32] |

| Epitope target | Predicted method | B cell | T cell | MHC-I | MHC-II | Validation method | Allergy analysis method | Toxicity analysis method | Others | reference |
|---|---|---|---|---|---|---|---|---|---|---|
| Nucleocapsid protein | | | | | | | | | | |
| Spike protein, Envelop protein, Membrane protein | ElliPro(4), BepiPred, Kolaskar method | √ | √ | IEDB server, Proteaso mal cleavage /TAP transport /MHC class I combine d predictor | IEDB tool "MHC-II Binding Predictions " | VaxiJen v2.0(5) | AllerTOP v.2 | | Molecular docking of the chimeric vaccine peptide with the 4immune receptors (TLR3 and TLR4) predicted efficient binding | [33] |
| Spike protein, Envelop protein, Membrane protein, Nucleocapsid protein | IEDB server | | √ | | | | | | Calculated the average binding affinity score for each predicted 15mer peptides against all the predominant HLA-DR types from each country/region using a sliding window approach | [34] |

| Epitope target | Predicted method | B cell | T cell | MHC-I | MHC-II | Validation method | Allergy analysis method | Toxicity analysis method | Others | reference |
|---|---|---|---|---|---|---|---|---|---|---|
| Spike protein | Ellipro | √ | √ | | NetMHCII 2.2 | MolProbity server[35] | AllergenFP 1.0 server, AllerTOP 2.0 server | | Human β-defensin 2 (hβD-2) (PDB ID: 1FD3), and sequence of GIGDPVTCLKSGAICHP VFCPRRYKQIGTCGLPG TKCCKKP, and hBD-3 (PDB ID:1KJ6) and sequence of GIINTLQKYYCRVR GGRCAVLSCLPKEEQIG KCSTRGRKCCRRKK were selected as adjuvants at N and Cterminals sequence of the vaccine construct, respectively with linker EAAK | [36] |
| Spike protein | ABCpred server (6), DiscoTope 2.0 | √ | √ | ProPred-1 | ProPred | VaxiJen v.2.0(7) | AllergenFP 1.0 server, AllerTOP 2.0 server | | Predicted MHC I and MHC II epitopes with a VaxiJen score of >1.0 were further assessed for their binding affinity against HLA A*1101 and | [38] |

| Epitope target | Predicted method | B cell | T cell | MHC-I | MHC-II | Validation method | Allergy analysis method | Toxicity analysis method | Others | reference |
|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | DRB1*0101, respectively using MHCPred version 2.0[37] | |
| Spike protein, Envelop protein, Membrane protein, Nucleocapsid protein, etc. | CTLpred[39], ABCpred | √ | √ | | | VaxiJen v.2.0 | | | Use miRanda[40, 41] (3.3 a version) software to identify potential host microRNA target sites in the virus genome sequence. Use psRNATarget[42] server to compare the predicted targets by the two methods. | [43] |
| Spike protein, Envelop protein, Membrane protein | BepiPred 2.0, DiscoTope 2.0 | √ | √ | netMHC -4.0 | netMHCII 2.3 | | | | Proposed two scores for evaluating and prioritizing the safety and immunogenicity regions of the viral genome for vaccination to obtain safe T cell epitopes with immunogenicity. | [44] |

| Epitope target | Predicted method | B cell | T cell | MHC-I | MHC-II | Validation method | Allergy analysis method | Toxicity analysis method | Others | reference |
|---|---|---|---|---|---|---|---|---|---|---|
| Spike protein | Bepipred and Bepipred2.0, Kolaskar and Tongaonkar antigenicity, Parker hydrophilicity, Chou and Fasman beta turn, Karplus and Schulz flexibility, Emini surface accessibility prediction, BcePred[45] | | | IEDB server | IEDB server | VaxiJen v.2.0 | Allergen FP 1.0 | ToxinPred | | [46] |

1. Blastp：Parameters -word_size 1, -gapopen 9, -gapextend 1 and -evalue 200000 were selected. Successful alignments were defined by a 100% identity and a coverage greater than 80%.

2. Using an interatomic clash-cutoff of 1.25 Å, 173 antigen poses were sampled, and each of which yielded a successful (not necessarily unique) antibody design targeted at the seven most solvent accessible ACE2-binding residues of SARS-CoV-2 Spike RBD.

3. The selected epitopes were submitted to the VaxiJen v.2.0 server applying a virus as a target field with the given threshold value of 0.4 for analyzing the antigenic propensity

4. The minimum score value set at 0.4 while the maximum distance selected as 6 Å.

5. The antigenicity of the final chimeric protein sequence was predicted by the VaxiJen 2.0 285 server to be 0.450 with a virus model at a threshold of 0.4 and 0.875 with ANTIGENpro.

6. The default threshold value of 0.51 and window length 20 was fixed for prediction.

7. The server was run with virus as a target field at a default threshold value of 0.4.

8. Energy threshold : -20 kcal/mol

9. The filtering criteria 0.5 was used.

**Supplementary Table 2. B-cell epitopes curated from literature published or preprinted until June 1,2020**

| Author | Sequence |
|---|---|
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | DVVNQNAQALNTLVKQL |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | EAEVQIDRLITGRLQSL |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | EIDRLNEVAKNLNESLIDLQELGKYEQY |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | EVAKNLNESLIDLQELG |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | GAALQIPFAMQMAYRFN |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | GAGICASY |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | AISSVLNDILSRLDKVE |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | GSFCTQLN |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | ILSRLDKVEAEVQIDRL |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | KGIYQTSN |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | AMQMAYRF |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | KNHTSPDVDLGDISGIN |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | MAYRFNGIGVTQNVLYE |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | AATKMSECVLGQSKRVD |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | PFAMQMAYRFNGIGVTQ |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | QALNTLVKQLSSNFGAI |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | QLIRAAEIRASANLAAT |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | QQFGRD |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | RASANLAATKMSECVLG |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | RLITGRLQSLQTYVTQQ |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | EIDRLNEVAKNLNESLIDLQELGKYEQY |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | SLQTYVTQQLIRAAEIR |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | DLGDISGINASVVNIQK |
| Blanco-Míguez, A., Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular traps. bioRxiv. | LTESNKKFLPFQQFGRDIA |
| Blanco-Míguez, A., Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular traps. bioRxiv. | KQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKV |
| Blanco-Míguez, A., Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular traps. bioRxiv. | KQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLA |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | KLNDLCFTN |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | KLNDLCFTNV |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | KLNDLCFTNVY |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | PTKLNDLCFTN |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | SPTKLNDLCFTN |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | VSPTKLNDLCFTN |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | KLNDLCFTNVYA |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | KLNDLCFTNVYAD |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | LNDLCFTNV |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | GVSPTKLNDLCFTN |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | YGVSPTKLNDLCFTN |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | CYGVSPTKLNDLCFTN |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | CVNLTTRTQ |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | QCVNLTTRTQ |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | LDITPCSFGGVSV |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | LDITPCSFGGVSVI |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | VKNKCVNFN |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | SQCVNLTTRTQLPPAYTNSFTRGVY |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | FSNVTWFHAIHVSGTNGTKRFDN |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | DPFLGVYYHKNNKSWME |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | MDLEGKQGNFKNL |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | KHTPINLVRDLPQGFS |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | TPGDSSSGWTA |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | LDPL |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | KSFTVEKGIYQTSNFRVQP |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | FPNITNLCPFGEVFNATRFASVYAWNRKRISNCVA |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | YNSASFSTFKCYGVSPTKLNDLCFT |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | GDEVRQIAPGQTGKIADYNYKLP |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | NLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPC NGVEGFNCYFPLQSYGFQPTN |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | ELLHAPATVCGPKKSTNLVKN |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | SNKKFLPF |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | QTLE |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | TNTSN |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | NCTEVPVAIHADQLTPT |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | RVYSTGSNVFQ |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | VNNSYECDIPI |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | ASYQTQTNSPRRARSVASQ |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | YTMSLGAENSVAYSNN |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | EQDKNTQ |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | KQIYKTPPIKDFGGF |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | PDPSKPSK |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | LADAGFIKQYGDCLG |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | EAEVQ |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | GQSKRVDFC |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | RNFYEPQIITTD |
| Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. | VNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGI |

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LGKY

SCCKFDEDDSEPVLKG

SYGFQPTNGVGYQPY

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IPTNFTISVTTEILP

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APHGVVFLHVTYVPA

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GTKRFDNPVLPFNDGVYFASTEKSNK

LIVNNATNVVIKVCEFQFCNDPFLGVKK

GVYYHKNNKSWMESEFRVYSSANNCTFEY

FKNLREFVFKNIDGYFKIYSKHTP

WTAGAAAYYVGYLQPRTFLLKYKKKKK

KGIYQTSNFRVQPTESIVRFPNITNLCP

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AKNL

LGKYEQY

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KNLNSSRV

SRTL

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SGTNGTKRFDN

LTPGDSSSGWTAG

VRQIAPGQTGKIA

QIAPGQTGKIAD

YGFQPTNGVGYQ

RDIADTTDAVRDPQ

ILPDPSKPSKRS

FPNITNLCPFGEVFNATRFASVYAWNRKRISNCVA

GDEVRQIAPGQTGKIADYNYKLP

ASYQTQTNSPRRARSVASQ

VNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGI

VRQIAPGQTGKIAD

VLGQSKRVDFCGKG

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| Poh, C.M., et al., *Two linear epitopes on the SARS-CoV-2 spike protein that elicit neutralising antibodies in COVID-19 patients.* Nature Communications, 2020. **11**(1). | PSKPSKRSFIEDLLFNKV |
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| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | IRGDEVRQIAPGQTGKIADYNYKLPD |
| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | NLDSKVGGNYNYLYRLFRKSNLKPFER DISTEIYQAGSTPCNGVEG |
| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | QSYGFQPTNGVGYQ |
| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | VYADSFVIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPF ERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLS |
| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | FFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIK VCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVF |
| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | YVPAQEKNFTTAPAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNT VYDPLQPELD |
| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | FKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYL |
| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | NITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYG |
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| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | GVYFASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRV YSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFVF |
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| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | ERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYR |
| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | WNSNNLDSKVGGNYNYLYRLFRK |
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| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | SYQTQTNSPRRARSVASQSII |
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| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | AEHVNNSYE |
| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | ESNKKFLPFQ |
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| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | KQYGDCLGDIA |
| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | AEHVNNS |
| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | PKKSTNLVKN |
| Rahman, M.S., et al., Epitope-based chimeric peptide vaccine design against S, M and E proteins of SARS-CoV-2 etiologic agent of global pandemic COVID-19: an in silico approach. bioRxiv, 2020. | VYSTGSNV |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | FLVLLPLVSSQCVNL |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | RGVYYPDK |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | RSSVLHST |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | DLFLPFFS |

| Reference | Sequence |
|---|---|
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | FHAIHV |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | NPVLPFN |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | QSLLIVN |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | NVVIKVCEFQ |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | CNDPFLGVYYH |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | FEYVSQP |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | QTLLALHRSY |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | AAYYVGYL |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | PRTFLLK |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | AVDCALDP |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | TNLCPFG |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | SNCVADYSVLYNS |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | TFKCYGVSPT |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | TGCVIA |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | CYFPLQSY |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | YQPYRVVVLSFELLHAPATVCGP |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | FGGVSVIT |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | QVAVLYQDV |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | CTEVPVAIHAD |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | AGCLIGA |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | GAGICASY |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | VASQSII |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | TTEILPVS |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | SVDCTMY |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | SNLLLQYGSFCTQL |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | VFAQVKQI |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | SQILPD |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | YGDCLGD |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | RDLICAQ |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | LTVLPPL |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | YTSALLAG |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | LNTLVKQL |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | ISSVLND |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | SLQTYVTQQ |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | SECVLGQS |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | PHGVVFLHVTYVPA |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | PAICHDG |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | SGNCDVVIGI |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | ASVVNI |
| Rehman, H.M., et al., *A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach.* Preprints, 2020. | IAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKF |
| Sardar, R., et al., *Comparative analyses of SAR-CoV2 genomes from different geographical locations and other coronavirus family genomes reveals unique features potentially consequential to host-virus interaction and pathogenesis.* bioRxiv, 2020. | AGTITSGWTFGAGAAL |
| Srivastava, S., et al., *Structural basis to design multi-epitope vaccines against Novel Coronavirus 19 (COVID19) infection, the ongoing pandemic emergency: an in silico approach.* bioRxiv, 2020. | TPGDSSSGWTA |
| Srivastava, S., et al., *Structural basis to design multi-epitope vaccines against Novel Coronavirus 19 (COVID19) infection, the ongoing pandemic emergency: an in silico approach.* bioRxiv, 2020. | FPNITNLCPFGEVFNATRFASVYAWNRKRISNCVA |
| Srivastava, S., et al., *Structural basis to design multi-epitope vaccines against Novel Coronavirus 19 (COVID19) infection, the ongoing pandemic emergency: an in silico approach.* bioRxiv, 2020. | NLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTN |
| Yarmarkovich, M., et al., *A SARS-CoV-2 Vaccination Strategy Focused on Population-Scale Immunity.* Cell Reports Medicine, 2020. | KVCEFQFCNDPFLGVYYHKNNKSWMESEFRVY |
| Yarmarkovich, M., et al., *A SARS-CoV-2 Vaccination Strategy Focused on Population-Scale Immunity.* Cell Reports Medicine, 2020. | GDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGT |
| Yarmarkovich, M., et al., *A SARS-CoV-2 Vaccination Strategy Focused on Population-Scale Immunity.* Cell Reports Medicine, 2020. | KPFERDISTEIYQAGSTPCNGVEGFNCYFPLQS |
| Yarmarkovich, M., et al., *A SARS-CoV-2 Vaccination Strategy Focused on Population-Scale Immunity.* Cell Reports Medicine, 2020. | VGGNYNYLYRLFRKSNLKPFERDISTEIYQAGS |
| Yazdani, Z., et al., *Design an efficient multi-epitope peptide vaccine candidate against SARS-CoV-2: An in silico analysis.* bioRxiv, 2020. | QCVNLTTRTQLPPAYTNSFTRGVYYPDKVF |
| Yazdani, Z., et al., *Design an efficient multi-epitope peptide vaccine candidate against SARS-CoV-2: An in silico analysis.* bioRxiv, 2020. | KIADYNYKLPDDFTGCVIAWNSNNLDSKVG |
| Yazdani, Z., et al., *Design an efficient multi-epitope peptide vaccine candidate against SARS-CoV-2: An in silico analysis.* bioRxiv, 2020. | YQPYRVVVLSFELLHAPATVCGPKKSTNLV |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | RTQLPPAYTNSFTRGVYY |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | HVSGTNGTKRFDN |

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|---|---|
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | DLEGKQGNFKNLRE |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | KYNENGTITD |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | QTSNFRVQPTES |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | VRQIAPGQTGKIADYNYKLPDD |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | NSNNLDSKVGGNYN |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | LKPFERDISTEIYQAGSTPCNGVEG |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | QSYGFQPTNGVGYQ |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | PATVCGPKKSTNL |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | RDIADTTDAVRDPQT |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | VITPGTNTSNQ |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | HADQLTPTWRVYSTGSNVFQTRAG |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | EHVNNSYE |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | SYQTQTNSPRRARSVASQS |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | GAENSVAYSNNSIA |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | IYKTPPIKDFGG |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | ILPDPSKPSKRS |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | NNTVYDPLQPELDSFKE |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | PPAYTNSFTRGVYY |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | IHVSGTNGTKRFDNPVLPFN |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | VYYHKNNKSWMESEFRVYSS |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | DLEGKQGNFKNLREFVFKNI |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | YLTPGDSSSGWT |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | LLKYNENGTITDAVDCALDP |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | RQIAPGQTGKIADYNYKLPD |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | SNLKPFERDISTEIYQAGST |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | LQSYGFQPTNGVGYQP |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | HAPATVCGPKKSTN |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | QQFGRDIADTTDAVRDPQTL |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | VITPGTNTSNQVAV |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | IGAEHVNNSYECDIPIGAGI |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | YQTQTNSPRRARSVASQS |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | AVEQDKNTQEVFAQ |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | IYKTPPIKDFGGFN |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | VIGIVNNTVYDPLQPE |
| Vashi, Y., V. Jagrit, and S. Kumar, *Understanding the B and T cells epitopes of spike protein of severe respiratory syndrome coronavirus-2: A computational way to predict the immunogens.* bioRxiv, 2020. | DKYFKNHTSPDVDLGD |

**Supplementary Table 3. T-cell epitopes curated from literature published or preprinted until June 1,2020**

| Author | Sequence |
|---|---|
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | GAALQIPFAMQMAYRF |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | MAYRFNGIGVTQNVLY |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | QLIRAAEIRASANLAATK |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | FIAGLIAIV |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | ALNTLVKQL |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | LITGRLQSL |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | NLNESLIDL |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | QALNTLVKQLSSNFGAI |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | RLNEVAKNL |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | VLNDILSRL |
| Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Preliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological studies. Viruses, 2020. | VVFLHVTYV |
| Blanco-Míguez, A., *Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular traps.* bioRxiv. | YFASTEKSNIIRGWIFGTTLDSKTQSLLIV |
| Blanco-Míguez, A., *Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular traps.* bioRxiv. | STEKSNIIRGWIFGTTLDSKTQSLLIV |
| Blanco-Míguez, A., *Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular traps. bioRxiv.* | STEKSNIIRGWIFGTTLDSKTQSLLIVNNA |
| Blanco-Míguez, A., *Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular traps. bioRxiv.* | SQPFLMDLEGKQGNFKNLREFVFKN\IDGYFKIYSKHTPINLV |
| Blanco-Míguez, A., *Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular traps. bioRxiv.* | DLPIGINITRFQTLLALHRSYLTPGDSSSGWTA |
| Blanco-Míguez, A., *Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular traps. bioRxiv.* | LDPLSETKCTLKSFTVEKGIYQTSNFRV |
| Blanco-Míguez, A., *Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular traps. bioRxiv.* | WNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQA |
| Blanco-Míguez, A., *Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular traps. bioRxiv.* | GGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGV |
| Blanco-Míguez, A., *Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular traps. bioRxiv.* | DCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIA |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | KLNDLCFTN |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | KLNDLCFTNV |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | KLNDLCFTNVY |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | PTKLNDLCFTN |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | SPTKLNDLCFTN |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | VSPTKLNDLCFTN |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | KLNDLCFTNVYA |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | KLNDLCFTNVYAD |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | LNDLCFTNV |

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|---|---|
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | GVSPTKLNDLCFTN |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | YGVSPTKLNDLCFTN |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | CYGVSPTKLNDLCFTN |
| Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. | CVNLTTRTQ |
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QYIKWPWYIWLGFIA

PTNFTISVTTEILPV

GVVFLHVTYVPAQEK

GYQPYRVVVLSFELL

VFLHVTYVPAQEKNF

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ADYNYKLPD

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DSFVIRGDEVRQIAP

FGADPIHSL

SFYEDFLEY

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TLNGLWLDDVVYCPRHVICTSEDML

GINITRFQTLLALHR

INITRFQTLLALHRS

TSNQVAVLY

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