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.

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	RapidPeptidesG enerator version 1.1.0[1]f	\checkmark	N			Blastp(1)				[2]
nucleocapsid phosphoprotein				NetMH C 4.0[3] ; NetMH Cpan 4.0	NetMHC 4.0 ; NetMHCp an 4.0				Base on EBOV vaccine preparation experience	[4]
Spike protein	Bepipred Linear Epitope Prediction[5]	\checkmark	\checkmark			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	V				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]

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

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

Epitope target	Predicted	В	Т	MHC-I	MHC-II	Validation	Allergy	Toxicity	Others	reference
	method	cell	cell			method	analysis	analysis		
							method	method		
									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	ElliPro server,	\checkmark		ProPred-	ProPred[2	VaxiJen				[26]
glycoprotein	IEDB server			1[24]	5]	v2.0				
Spike	Bepipred 2.0	\checkmark		ProPred-	ProPred	VaxiJen				[27]
glycoprotein				1		v2.0(3)				
ORF1AB.	Discotope2[28]			netMHC	netMHCpa	Validated				[30]
ORF3A ORF6	2.0000000000000000000000000000000000000			nan4	n4	computatio				[00]
ORF7A.				MARIA	MARIA	nal				

Epitope target	Predicted	В	Т	MHC-I	MHC-II	Validation	Allergy	Toxicity	Others	reference
	method	cell	cell			method	analysis	analysis		
							method	method		
ORF7B ORF8				291		pipeline				
ORF10 Spike						with				
protein						SARS-Co				
Envelop						V				
protein						evperiment				
Mombrana						al data				
						aluata				
protein,										
Nucleocapsid										
protein		,	,							
Spike protein,	Bepipred, Emini	$^{\vee}$		netMHC	netMHCpa				The vaccine peptides were	[31]
Envelop	surface			pan,	n,				designed by their in-house	
protein,	accessibility			iNeo-Pre	iNeo-Pred				tool iNeo-Design	
Membrane	prediction,			d						
protein,	Kolaskar and									
Nucleocapsid	Tongaonkar									
protein	antigenicity									
	scale									
Spike protein,	Bepipred 2.0,	\checkmark	\checkmark	NetMH	NetMHCp	IEDB			Use BLAST algorithm to	[32]
Envelop	Discotope2			Cpan EL	an EL 4.0	server			compare Coronavirus	
protein,	1			4.0					Sequences with	
Membrane									SARS-CoV-2	
protein,										

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	~	V	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		V						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	V	V		NetMHCII 2.2	MolProbit y server[35]	AllergenFP 1.0 server, AllerTOP 2.0 server		Humanβ-defensin2(hβD-2)(PDB ID: 1FD3),andsequenceofGIGDPVTCLKSGAICHPVFCPRRYKQIGTCGLPGTKCCKKP, and hBD-3(PDBID:1KJ6)andsequenceofGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKwere selected as adjuvantsatNandCterminalssequenceofthandconstruct,respectivelywith linker EAAK	[36]
Spike protein	ABCpred server (6), DiscoTope 2.0	\checkmark	\checkmark	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	В	Т	MHC-I	MHC-II	Validation	Allergy	Toxicity	Others	reference
	method	cell	cell			method	analysis	analysis		
							method	method		
									DRB1*0101, respectively	
									using MHCPred version	
									2.0[37]	
Spike protein,	CTLpred[39],	\checkmark	\checkmark			VaxiJen			Use miRanda[40, 41] (3.3	[43]
Envelop	ABCpred					v.2.0			a version) software to	
protein,									identify potential host	
Membrane									microRNA target sites in	
protein,									the virus genome	
Nucleocapsid									sequence. Use	
protein, etc.									psRNATarget[42] server to	
									compare the predicted	
									targets by the two	
									methods.	
Spike protein,	BepiPred 2.0,	\checkmark	\checkmark	netMHC	netMHCII				Proposed two scores for	[44]
Envelop	DiscoTope 2.0			-4.0	2.3				evaluating and prioritizing	
protein,									the safety and	
Membrane									immunogenicity regions of	
protein									the viral genome for	
									vaccination to obtain safe	
									T cell epitopes with	
									immunogenicity.	

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

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.

nentary Table 2. B-cell epitopes curated from literature published or preprinted until June 1,2020 Author 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 statilies. Viruses, 2020. 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 stadies. Viruse, 2020. Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Pelliminary identification of potential vaccine targets for the Mund, S.F., A.A. Quadeer, and M.R. McKay, Pelliminary identification of potential vaccine targets for the Mund, S.F., A.A. Quadeer, and M.R. McKay, Pelliminary identification of potential vaccine targets for the Mund, S.F., A.A. Quadeer, and M.R. McKay, Pelliminary in the Markov and M.R. McKawa and M. McKawa and M. McKawa and M. McKawa and M.R. McKawa and M. McKawa and McKawa and M. McK Almed, S.F., A.A. Quadeer, and M.R. McKay, Penliminary identification of potential vaccine targets for the COVID-19 corcumstren (SABS CoV-1) based on SABSCOV immunolocid statuskies. Viruses, 2020. Almed, S.F., A.A. Quadeer, and M.R. McKay, Penliminary identification of potential vaccine targets for the COVID-19 corcumstren (SABS CoV-1) based on SABSCOV immunolocid statuskies. Viruses, 2020. Almed, S.F., A.A. Quadeer, and M.R. McKay, Penliminary identification of potential vaccine targets for the COVID-19 corcumstren (SABS CoV-1) based on SABSCOV immunolocid statuskies. Viruses, 2020. Almed, S.F., A.A. Quadeer, and M.R. McKay, Penliminary identification of potential vaccine targets for the COVID-19 corcumstren (SABS CoV-1) based on SABSCOV immunolocid statuskies. Viruses, 2020. Almed, S.F., A.A. Quadeer, and M.R. McKay, Penliminary identification of potential vaccine targets for the COVID-19 corcumstren (SABS CoV-1) based on SABSCOV immunolocid statuskies. Viruses, 2020. Almed, S.F., A.A. Quadeer, and M.R. McKay, Penliminary identification of potential vaccine targets for the COVID-19 corcumstren (SABS CoV-1) based on SABSCOV immunolocid statuskies. Viruses, 2020. Almed, S.F., A.A. Quadeer, and M.R. McKay, Penliminary identification of potential vaccine targets for the Ahmed, S.F., A.A. Quadeer, and M.R. McKay. Penliminary identification of potential vaccine targets for the Ahmed, S.F., A.A. Quadeer, and M.R. McKay. Penliminary identification of potential vaccine targets for the Ahmed, S.F., A.A. Quadeer, and M.R. McKay. Penliminary identification of potential vaccine targets for the Ahmed SaVE and SaVE Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Peliminary identification of potential vaccine targets for the COVID-19 cormavines (SARS-CoV-2) based on SARSCOV immundooical studies. Viruses, 2020. Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Peliminary identification of potential vaccine targets for the COVID-19 cormavines (SARS-CoV-2) based on SARSCOV immundooical studies. Viruses, 2020. Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Peliminary identification of potential vaccine targets for the COVID-19 cormavines (SARS-CoV-2) based on SARSCOV immundooical studies. Viruses, 2020. Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Peliminary identification of potential vaccine targets for the COVID-19 cormavines (SARSCOV-2) based on SARSCOV immundooical studies. Viruses, 2020. Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Peliminary identification of potential vaccine targets for the COVID-19 cormavines (SARSCOV-2) based on SARSCOV immundooical studies. Viruses, 2020. Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Peliminary identification of potential vaccine targets for the COVID-19 cormavines (SARSCOV-2) based on SARSCOV immundooical studies. Viruses, 2020. Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Peliminary identification of potential vaccine targets for the COVID-19 cormavines (SARSCOV-2) based on SARSCOV immundooical studies. Viruses, 2020. Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Peliminary identification of potential vaccine targets for the COVID-19 cormavines (SARSCOV-2) based on SARSCOV immundooical studies. Viruses, 2020. Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Peliminary identification of potential vaccine targets for the COVID-19 cormavines (SARSCOV-2) based on SARSCOV immundooical studies. Viruses, 2020. Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Peliminary identification of potential vaccine targets for the COVID-19 cormavines (SARSCOV-2) based on SARSCOV immundooical studies. Viruses, 2020. Ahmed, S.F., A.A. Quadeer, and M.R. McKay, Peliminary identification of potential vaccine targets for the COVID-19 corma Anned, S.F., A.A. Quadeer, and M.R. McKay. Perliminary identification of potential vaccine tragets for the COVID-19 coronavirus (SARS-CoV-2) based on SARS-COV immunolocical atudies. Viruses, 2020. Muncl, S.F., A.A. Quadeer, and M.R. McKay, Perliminary identification of potential vaccine targets for the Anned, S.F., A.A. Quadeer, and M.R. McKay, Perliminary identification of potential vaccine targets for the Anned, S.F., A.A. Quadeer, and M.R. McKay, Perliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARS-CoV immunolocical atudies. Viruses, 2020. Anned, S.F., A.A. Quadeer, and M.R. McKay, Perliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARS-CoV immunolocical atudies. Viruses, 2020. Anned, S.F., A.A. Quadeer, and M.R. McKay, Perliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARS-CoV immunolocical atudies. Viruses, 2020. Anned, S.F., A.A. Quadeer, and M.R. McKay, Perliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARS-CoV immunolocical atudies. Viruses, 2020. Anned, S.F., A.A. Quadeer, and M.R. McKay, Perliminary identification of potential vaccine targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARS-CoV immunolocical atudies. Viruses, 2020. Anned, S.F., A.A. Quadeer, and M.R. McKay, Perliminary identification of potential vaccine targets for the neurophile-stratechlar targets, bioRxiv. COVID-19 ccenarus (SARS-CoV-2) based on SARS-CoV immunological studies. Vruess, 2020. Bianco-Miguez, A. Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular rangs. bioRxiv. Bianco-Miguez, A. Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular rangs. bioRxiv. Bianco-Miguez, A. Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular rangs. bioRxiv. Bebhanian, M., Bailco Design of avoil Multi-peitope recombinant Vaccine based on Coronavirus surface glycoprotein bioRxiv, 2020. nni, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface stein. bioRxiv, 2020. glycoprotein, hiofksiv, 2020. Behbahani, M., H. Bilico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein, hiofksiv, 2020. gy-orytorem (motKiv, 2020) Behhahani, M., Baiko Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein, bioRxiv, 2020, Behhahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein, bioRxiv, 2020, plycopotenin, bioRxiv, 2020. Behbhanin, M., In sikio Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycopotenin, bioRxiv, 2020. Behbhanin, M., In sikio Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycopotein, bioRxiv, 2020. glycoprotein, hiokxuv, 2020. Behbahani, M., H. Bilico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein, hiokxiv, 2020. Sproprotein. bioRxiv, 2020. Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. rotem. noncxw, 2020. hani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface roteni. bioRxiv, 2020. hani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprote glycoprotein. bioRxiv, 2020. Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein. bioRxiv, 2020. Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface Detonation, A., in Strice Design in more immergence recommand vacuum states of co-constraints winner glocoprotein, biology, 2020.
Beibaham, M., in silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glocoprotein, biology, 2020.
Beibaham, M., in silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glocoprotein, biology, 2020. glycoproteni bioRxiv, 2020. Behhahani, M., In shiko Design of howel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoproteni bioRxiv, 2020. Blattachary, M., et al., Development of epitope-based pepitde vaccine against novel coronavirus 2019 (SARS-COV-2): hummoninformatics approach. J Med Virul, 2020. Blattachary, M., et al., Development of epitope-based pepitde vaccine against novel coronavirus 2019 (SARS-COV-2): hummoninformatics approach. J Med Virul, 2020. Blattachary, M., et al., Development of epitope-based pepitde vaccine against novel coronavirus 2019 (SARS-COV-2): hummoninformatics approach. J Med Virul, 2020. Blattachary, M., et al., Development of epitope-based pepitde vaccine against novel coronavirus 2019 (SARS-COV-2): hummoninformatics approach. J Med Virul, 2020. COV-2): Immunoinformatics approach. J Med Virol, 2020. Bhattacharya, M., et al., Development of epitope-based pepide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. Bhattacharya, M., et al., Development of epitope-based pepide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. Bhattacharya, M., et al., Development of epitope-based pepide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. Bhattacharya, M., et al., Development of epitope-based pepide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020. LU+2: Lomunonformatic approach. J Med Wird, 2020.
 Bhattacharya, M. et al., Development of printpe-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatic approach. J Med Wird, 2020.
 Bhattacharya, M. et al., Development of printpe-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatic approach. J Med Wird, 2020.
 Bhattacharya, M. et al., Development of printpe-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatic approach. J Med Wird, 2020.
 Bhattacharya, M. et al., Development of printpe-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatic approach. J Med Wird, 2020.
 Bhattacharya, M. et al., Development of printpe-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatic approach. J Med Wird, 2020.
 Bhattacharya, M. et al., Development of printpe-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatic approach. J Med Wird, 2020.
 Bhattacharya, M. et al., Development of gainop-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatic approach. J Med Wird, 2020.
 Bhattacharya, M. et al., Development of gainop-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatic approach. J Med Wird, 2020.
 Bhattacharya, M. et al., Development of gainop-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Development of gainop-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Development of gainop-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Development of gainop-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Development of gainop-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Development of gainop-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Development of gainop-based p COV-2): Immunoinformatics approach. J Med Virol, 2020.
COV-2): Immunoinformatics approach. J Med Virol, 2020.
Battacharya, N., et al., Deredopmot of epitope-based peptide vaccine against novel coronavirus 2019 (SARS: COV-2): Immunoinformatics approach. J Med Virol, 2020.
Battacharya, N., et al., Deredopmot epitope-based peptide vaccine against novel coronavirus 2019 (SARS: COV-2): Immunoinformatics approach. J Med Virol, 2020.
Battacharya, N., et al., Deredopmot epitope-based peptide vaccine against novel coronavirus 2019 (SARS: COV-2): Immunoinformatics approach. J Med Virol, 2020.
Battacharya, N., et al., Deredopmot epitope-based peptide vaccine against novel coronavirus 2019 (SARS: COV-2): Immunoinformatics approach. J Med Virol, 2020.
Battacharya, N., et al., Deredopmot epitope-based peptide vaccine against novel coronavirus 2019 (SARS: COV-2): Immunoinformatics approach. J Med Virol, 2020.
Battacharya, N., et al., Deredopmot epitope-based peptide vaccine against novel coronavirus 2019 (SARS: COV-2): Immunoinformatics approach. J Med Virol, 2020.

DVVNQNAQALNTLVKQL EAEVOIDRLITGRLOSL EIDRLNEVAKNLNESLIDLQELGKYEQY EVAKNLNESLIDLOELG GAALQIPFAMQMAYRFN GAGICASY AISSVLNDILSRLDKVE GSFCTOLN ILSRLDKVEAEVQIDRL KGIYQTSN AMQMAYRF KNHTSPDVDLGDISGIN MAYRENGIGVTONVLYE AATKMSECVLGOSKRVD PFAMOMAYRFNGIGVTO QALNTLVKQLSSNFGAI QLIRAAEIRASANLAAT QQFGRD RASANLAATKMSECVLG RLITGRLQSLQTYVTQQ EIDRLNEVAKNLNESLIDLQELGKYEQY SLOTVVTOOLIRAAFIR DLGDISGINASVVNIQK LTESNKKFLPFQQFGRDIA KQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKV KQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLA KLNDLCFTN KLNDLCFTNV KLNDLCFTNVY PTKLNDLCFTN SPTKLNDLCFTN VSPTKLNDLCFTN KLNDLCFTNVYA KLNDLCFTNVYAD I NDI CETNV GVSPTKLNDLCFTN YGVSPTKLNDLCFTN CYGVSPTKLNDLCFTN CVNLTTRTO QCVNLTTRTQ LDITPCSFGGVSV LDITPCSEGGVSVI VKNKCVNFN SOCVNLTTRTOL PPAYTNSFTRGVY FSNVTWFHAIHVSGTNGTKRFDN DPFLGVYYHKNNKSWME MDLEGKQGNFKNL KHTPINLVRDLPQGFS TPGDSSSGWTA LDPL KSFTVEKGIYQTSNFRVQP FPNITNLCPFGEVFNATRFASVYAWNRKRISNCVA YNSASFSTFKCYGVSPTKLNDLCFT GDEVRQIAPGQTGKIADYNYKLP NLDSKVGGNYNYLYRLFRKSNLKPEERDISTEIYOAGSTPC NGVEGENCYFPLOSYGEOPTN ELLHAPATVCGPKKSTNLVKN SNKKELPE OTLE TNTSN NCTEVPVAIHADQLTPT RVYSTGSNVFQ VNNSYECDIPI ASYQTQTNSPRRARSVASQ YTMSLGAENSVAYSNN EQDKNTQ KOIYKTPPIKDFGGF PDPSKPSK LADAGFIKOYGDCLG EAEVQ GQSKR VDFC RNFYEPQIITTD VNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISG

Bhatacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): humanoinformatics approach. J Med Virol, 2020.
Bhatacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV2): humanoinformatics approach. J Med Virol, 2020. COV-2): humanoinformatics approach. J Med Virol, 2020.
COV-2): humanoinformatics approach. J Med Virol, 2020.
Fast, E., R. A. Human, and B. Chen, Potential T-cell and B-cell Epitopes of 2019-nCoV. bioRxiv, 2020.
Fast, E., R. A. Human, and B. Chen, Potential T-cell and B-cell Epitopes of 2019-nCoV. bioRxiv, 2020.
Fast, E., R. A. Human, and B. Chen, Potential T-cell and B-cell Epitopes of 2019-nCoV. bioRxiv, 2020.
Fast, E., R. A. Human, and B. Chen, Potential T-cell and B-cell Epitopes of 2019-nCoV. bioRxiv, 2020.
Fast, E., R. A. Human, and B. Chen, Potential T-cell and B-cell Epitopes of 2019-nCoV. bioRxiv, 2020.
Fast, E., R. A. Human, and B. Chen, Potential T-cell and B-cell Epitopes of 2019-nCoV. bioRxiv, 2020.
Fast, E., R. A. Human, and B. Chen, Potential T-cell and B-cell Epitopes of 2019-nCoV. bioRxiv, 2020.
Fast, E., R. A. Human, and B. Chen, Potential T-cell and B-cell Epitopes of 2019-nCoV. bioRxiv, 2020.
Fast, E., R. A. Human, and B. Chen, Potential T-cell and B-cell Epitopes of 2019-nCoV.
bioRxiv, 2020.
Fast, E., B. A. Human, and B. Chen, Potential T-cell and B-cell Epitopes of 2019-nCoV.
bioRxiv, 2020.
Fast, E., B. A. Human, and B. Chen, Potential T-cell and B-cell Epitopes of 2019-nCoV.
bioRxiv, 2020.
Fast, E., B. A. Human, Endergin submaticipation and the set of 2019 nord.
bioRxiv, 2020.
Fast, E., B. A. Human, Endergin submaticipation and the set of 2019 nord.
Fast, E., B. A. Human, Endergin submaticipation and the set of 2019 nord.
Fast, E., B. A. Human, B. Chen, Potential T-cell and B-cell Epitopes of 2019-nCoV.
Fast, E., B. A. Human, Endergin submaticipation and the set of 2019 nord.
Fast, E., B. A. Human, Endergin submaticipation and the set of 2019 nord.
Fast, E., B. A. Human, Human, Endergin submaticipation and the set of 2019 nord.
Fast, E., B. A. Human, H cormavirus in Chan (SARS-CoV-2), bookxiv, 2020. Feng, Y, et al., Multi-epilope vaccine design using an immunoinformatics approach for 2019 novel cormavirus in Chan (SARS-CoV-2), bioRxiv, 2020. Feng, Y., et al., Multi-epilope vaccine design using an immunoinformatics approach for 2019 novel cormavirus in Chan (SARS-CoV-2), bioRxiv, 2020. cormavirus in China (SARS-CoV-2). bioRXiV, 2020.
Forg. Y., et al., Multi-epilope vaccine design using an immunoinformatics approach for 2019 novel cormavirus in China (SARS-CoV-2). bioRXiV, 2020.
Forg. Y., et al., Multi-epilope vaccine design using an immunoinformatics approach for 2019 novel cormavirus in China (SARS-CoV-2). bioRXiV, 2020. cormavirus in Chana (SARS-CoV-2), bioRxiv, 2020.
Feng, Y., et al., Multi-epilope vaccine design using an immunoinformatics approach for 2019 novel cormavirus in China (SARS-CoV-2), bioRxiv, 2020.
Feng, Y., et al., Multi-epilope vaccine design using an immunoinformatics approach for 2019 novel cormavirus in China (SARS-CoV-2), bioRxiv, 2020. cormanyas in chini (2007), core-10, backay, 2020. Feng, Y., et al., Multi-phopor-vaccine design naing an immunoinformatics approach for 2019 novel cormanyas in China (SMS-CoV-2), backay, 2020, Feng, Y., et al., Multi-phopor-vaccine design naing an immunoinformatics approach for 2019 novel cormanyas in China (SMS-CoV-2), backay, 2020, Feng, Y., et al., Multi-phopor-vaccine design naing an immunoinformatics approach for 2019 novel feng, Y., et al., Multi-phopor-vaccine design naing an immunoinformatics approach for 2019 novel Figg. Y. et al., Multi-pipor vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SMES CoV-2), bioRxiv, 2020.
Figg. Y. et al., Multi-pipor vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SMES CoV-2), bioRxiv, 2020.
Figg. Y. et al., Multi-pipory vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SMES CoV-2), bioRxiv, 2020.
Figg. Y., et al., Multi-pipory vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SMES CoV-2), bioRxiv, 2020.
Figg. Y., et al., Multi-pipory vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SMES CoV-2), bioRxiv, 2020.
Figg. Y., et al., Multi-pipory vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SMES CoV-2), bioRxiv, 2020.
Figg. Y., et al., Multi-pipory vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SMES CoV-2), bioRxiv, 2020. Yeng, Y., et al., Multi-epitope vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SM85 CoV-2). Bookiv, 2020.
Feng, Y., et al., Multi-epitope vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SM85 CoV-2). Bookiv, 2020.
Feng, Y., et al., Multi-epitope vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SM85 CoV-2). Bookiv, 2020. Feng, Y., et al., Multi-phope surveiled scient statution immunoinformatics approach for 2019 novel community in China (SARS-CoV-2), ISORSiy, 2020.
Feng, Y., et al., Multi-phope succine design unity an immunoinformatics approach for 2019 novel community in China (SARS-CoV-2), ISORSiy, 2020. Feng, Y., et al., Multi-epitope vaccine design using a coronavirus in China (SARS-CoV-2). bioRxiv, 2020. coronavrus in Chan (SARS-CoV-2), bioRxiv, 2020.
Feng, Y., et al., Multi-epilope vaccine design using an immunoinformatics approach for 2019 novel coronavrus in China (SARS-CoV-2), bioRxiv, 2020.
Feng, Y., et al., Multi-epilope vaccine design using an immunoinformatics approach for 2019 novel coronavrus in China (SARS-CoV-2), bioRxiv, 2020. coronavirus in China (SABS-CoV-2), bioRxiv, 2020. Feng, Y., et al., Multi-pipoly veccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SABS-CoV-2), bioRxiv, 2020. Feng, Y., et al., Multi-pipoly veccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SABS-CoV-2), bioRxiv, 2020. Feng, Y., et al., Multi-pipoly veccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SABS-CoV-2), bioRxiv, 2020. Feng, Y., et al., Multi-pipoly veccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SABS-CoV-2), bioRxiv, 2020. Feng, Y., et al., Multi-pipoly veccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SABS-CoV-2), bioRxiv, 2020. coronavirus in China (SABS-CoV-2), bolksvi, 2020). Forg, Y., et al., Multi-infore-vaccine deign nuitga ani immunoinformatics approach for 2019 novel coronavirus in China (SABS-CoV-2), bioRxiv, 2020). Forg, Y., et al., Multi-infore-vaccine deign nuitga ani immunoinformatics approach for 2019 novel coronavirus in China (SABS-CoV-2), bioRxiv, 2020). Forg, Y., et al., Multi-infore-vaccine deign nuitga ani immunoinformatics approach for 2019 novel forge, Y., et al., Multi-infore-vaccine deign nuitga ani immunoinformatics approach for 2019 novel us at., Multi-epitope vaccine design using an immunoinformatics approach for 2019 novel us in China (SARS-CoV-2). bioRxiv, 2020. x al., Multi-epitone vaccine design at the second Feng, Y., et al., Multi communities in China (SMRS-CoV-2), bolksiv, 2020.
Feng, Y., et al., Multi-pipplev sector design using an immunoinformatics approach for 2019 novel communities in China (SMRS-CoV-2), bolksiv, 2020.
Feng, Y., et al., Multi-pipplev sector design using an immunoinformatics approach for 2019 novel communities in China (SMRS-CoV-2), bolksiv, 2020.
Feng, Y., et al., Multi-pipplev sector design using an immunoinformatics approach for 2019 novel feng, Y., et al., Multi-pipplev socies design using an immunoinformatics approach for 2019 novel feng, Y., et al., Multi-pipplev socies design using an immunoinformatics approach for 2019 novel feng, Y., et al., Multi-pipplev socies design aim an immunoinformatics approach for 2019 novel Feng, Y., et al., Multi-epioper succine design using an immunoinformatics approach for 2019 novel coronavirus in China (SARS-CoV-2), bioRxiv, 2020.
Feng, Y., et al., Multi-epioper vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SARS-CoV-2), bioRxiv, 2020.
Feng, Y., et al., Multi-epioper vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SARS-CoV-2), bioRxiv, 2020.
Feng, Y., et al., Multi-epioper vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SARS-CoV-2), bioRxiv, 2020. coronavirus in China (SM8-CoV-2), boltxv, 2000 Fong, V, et al., Multi-phiper veccice design naing an immunoinformatics approach for 2019 novel coronavirus in China (SM8-CoV-2), boltxv), 2000 Fong, V, et al., Multi-phiper veccice design naing an immunoinformatics approach for 2019 novel coronavirus in China (SM8-CoV-2), boltxv), 2000 Fong, V, et al., Multi-phiper veccice design naing an immunoinformatics approach for 2019 novel coronavirus in China (XMS-CoV-2), bolkxy, 2020 Fong, Y., et al., Multi-pipoly-vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (XMS-CoV-2), bolkxiy, 2020 Fong, Y., et al., Multi-pipoly-vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (XMS-CoV-2), bolkxiy, 2020 Eng. Y., et al., Multi-phiope vaccine design using an immunoinformatics approach for 2019 novel consurvirus in China (SMSS-CoV-2). NoRXiv, 2020.
Feng. Y., et al., Multi-phiope vaccine design using an immunoinformatics approach for 2019 novel consurvirus in China (SMSS-CoV-2). NoRXiv, 2020.
Feng. Y., et al., Multi-phiope vaccine design using an immunoinformatics approach for 2019 novel feng. Y., et al., Multi-phiope vaccine design using an immunoinformatics. china (SARS-CoV-2). bioRxiv, 2020. coronarius in China (SABS-CoV-2), bioRxiv, 2020. Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 e.2. Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Response to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 61-680 e.2. Immune Responses to 3x63-C-6V-2. Cell Host Microbe, 2020. 21(4): p. 01-080 €2. Größia, A.; et al., Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to 5ABS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 €2. Größia, A.; et al., Sequence: Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to 5ABS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 €2. Immune neyronesi to 3xx4-X0+2. Uell 1003 MICODE, 2020. 21(4): p. 611-800 e2. Grifoni A, et al. A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 e2. Grapta, E. R. K. Minhan, and R. K. Ming, Identification of potential vaccine candidates against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse Vaccinology Approach. 2020. Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse Vaccinology Approach. 2020.

Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse Vaccinology Approach. 2020.

Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse Vaccinology Approach. 2020.

Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse Vaccinology Approach. 2020.

Gupta, E., R.K. Mishra, and R.R.K. Niraj. Identification of potential vaccine candidates against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse Vaccinology Approach. 2020.

Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse Vaccinology Approach. 2020.

Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse Vaccinology Approach. 2020.

A step foround to fight novel community 2019–46.V: A Reverse Vaccinalogy Approach. 2020. Imail, S. S. Ahmad, and S. S. Azam, Immuno-informatic: Characterization SARS-CoV-2 Spike Glycoprotein for Prioritization of Epitope based Multivalent Peptide Vaccine. biodixiv, 2020. Imail, S. S. Ahmad, and S. S. Azam, Immuno-informatic: Characterization SARS-CoV-2 Spike Glycoprotein for Prioritization of Epitope based Multivalent Peptide Vaccine. biodixiv, 2020. Imail, S. S. Ahmad, and S. S. Azam, Immuno-informatics: Characterization SARS-CoV-2 Spike Glycoprotein for Prioritization of Epitope based Multivalent Peptide Vaccine. biodixiv, 2020. Imail, S. S. Ahmad, and S. S. Azam, Immuno-informatics: Characterization SARS-CoV-2 Spike Glycoprotein for Prioritization of Epitope based Multivalent Peptide Vaccine. biodixiv, 2020. I. J., et al., Epitope-based Peptide vaccine design and arget site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.

LGKY SCCKEDEDDSEPVI KG SYGEOPTNGVGYOP SOSIIAYTMSLGAEN IPTNFTISVTTEILF APHGVVFLHVTYVPA TTRTQLPPAYTNSFTRGVYYPDKVFRSS GTKRFDNPVLPFNDGVYFASTEKSNK LIVNNATNVVIKVCEFOFCNDPFI GVKK GVYYHKNNKSWMESEFRVYSSANNCTFEY FKNLREFVFKNIDGYFKIYSKHTP WTAGAAAYYVGYLQPRTFLLKYKKKKK KGIYQTSNFRVQPTESIVRFPNITNLCP RISNCVADYSVLYNSASFSTFKCYGVSPTK DEVRQIAPGQTGKIADYNYKLPDDFTGKKK NYNYLYRLFRKSNLKPFERDISTEI TPCNGVEGFNCYFPLQSYGFQPTNGVGYKK SYGFOPTNGVGYOPYRVVVLSFELLHAPAT HADQLTPTWRVYSTGSNVFQTRAGCLIG CASYOTOTNSPRRARSVASOSIJAYTMSL AVEQDKNTQEVFAQVKQIYKTPPIKDFGGK II PDPSKPSKRSFIEDI I ENKVTI ADAGEK IPFAMQMAYRFNGIGVTQNVLYENQKLI QLSSNFGAISSVLNDILSRLDKVEAEVKKK FPQSAPHGVVFLHVTYVPAQEK VPAQEKNFTTAPAICHDGKAHFPREGVFV FVSNGTHWFVTQRNFYEPQIITTDNTFVSK NTVYDPLQPELDSFKEELDKYKKKKK DKYFKNHTSPDVDLGDISGINASVVNIOKK AKNLNESLIDLQELGKYEQYIKWPWYIWKK IWLGFIAGLIAIVMVTIMLCKKKKKKKKK KKKKCCSCLKGCCSCGSCCKFDEDDSEPVL TTRTOLPPAYTNSFTRGVYYPDKVF VYFASTEKSN KHTP DEVRQIAPGQTGKIADYNYKLPDDFT SYGFQPTNGVGYQF CASYQTQTNSPRRARSVA AVEQDKNTQEVE QIYKTPPIKDFGG ILPDPSKPSKRS FPQSAPH VPAQEKNFTTAPAICHDGKAHFPR NFYEPQIITTDNTFVS NTVYDPLQPELDSFKEE DKYFKNHTSPDVDLGDISGI AKNL LGKYEQY **KFDEDDSEPVL** KNLNSSRV SRTL DAVDCALDPLSETKCTLKS FTVEKGIYQTSN VCGPKKSTNI, VKNKCVNENENGI, TGTGVI, TESNKKELPEOOEGRDIADTTDA VRDPOTLEJI, DITPCSEGGVSVI GTNTSNQVAVLYQDVNCTEVPVA IHADQLTPTWRVYSTGS FSQILPDPSKPSKRSFIE FGAGAALQIPFAMQMAYRFNG RTQLPPAYTNS SGTNGTKREDN LTPGDSSSGWTAG VRQIAPGQTGKIA QIAPGQTGKIAD YGFQPTNGVGYQ RDIADTTDAVRDPO ILPDPSKPSKRS

FPNITNLCPFGEVFNATRFASVYAWNRKRISNCVA

GDEVRQIAPGQTGKIADYNYKLP

ASYQTQTNSPRRARSVASQ

VNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGI

VRQIAPGQTGKIAD

VLGQSKRVDFCGKG

Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020. Lit, et al., "paper particle parts in the second of the Number of the second vaccine canatata e against SARS - COV - 2 by comprehensive immunoinformatic and molecul approach. Programs, 2020.
Rehman, H.M., et al., A putative prophylactic solution for COVID-19: Development of novel vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecul approach. Preprints, 2020. vaccine candidate agains 3MAS - COV - 2 y comprehensive immunoinformatic and molecular modelling Rehman, H.M., et al., A patative prophilactic solution for COVID-19: Development of novel multicipitope vaccine candidate agains 3ABS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprints, 2020. Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope COV - DV - ovorrehensive immunoinformatic and molecular modelling

GLTGTGVLTESNKK

KIADVNVKI PDDFT

IRGDEVRQIAPGQTGKIADYNYK

GDEVRO

VRQIAPG

TESNKKFLPFQQFGRDIA

RGVYYPDK

RSSVLHST

DLFLPFFS

Rehman, H.M., et al., A putative prophylactic solution for COVID-19: Development of novel multiepitopy vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modellin, approach. Preprints, 2020 Rehman, H.M., et al., A pa FHAIHV outative prophylactic solution for COVID-19: Development of novel multiepitope st SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling vaccine candidate agains 3M80 - UV - 4 vy some -----grenaux - Preprint 2020. Rehman, H.M., et al., A pusative prophylactic solution for COVID-19: Development of novel multicpliope Rehman, H.M., et al., A pusative prophylactic solution for COVID-19: Development of novel multicpliope reference candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling NPVLPFN vaccine candidate agams works - cov. approach. Proprints, 2020. Rehman, H.M., et al., A putative prophylactic solution for COVID-19: Development of novel multiepitope www.ins. candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling OSLLIVN approach. Preprints, 2020. Rehman, H.M., et al., A pataritive prophylactic solution for COVID-19. Development of novel multicplicope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprints, 2020. Rehman, H.M., et al., A pataritive prophylactic solution for COVID-19. Development of novel multicplicope development of the solution NVVIKVCEFQ CNDPFLGVYYH putative prophylactic solution for COVID-19: Development of novel multiepitope as SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling FEYVSQP vaccine candidate against SARS - COV - 2 by comprehensive immunoupformatic and molecular modelling approach. Preprints, 2020. Rehman, HM, et al., A putative prophylactic solution for COVID-19: Development of novel multicpliope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprints, 2020. OTLLALHRSY Vatc.mt (innumar, -______) approach. Preprints, 2020.
Rehman, H.M., et al., A putative prophylactic solution for COVID-19: Development of novel multieptinper vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling AAYYVGYL vaccine candidate against NARS - LOF - 2 03 5000-000 approach. Preprints 2020. Rehman, H.M., et al., A patative prophetacile solution for COVID-19: Development of novel multispitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling PRTFLLK AVDCALDP TNLCPEG SNCVADYSVLYNS approach. Preprints, 2020. Rehman, H.M., et al., A put approach. Preprint, 2020. Rehuma, H.A., et al., A putative prophylactic solution for COVID-19: Development of novel multicpitope vaccine condidate against SMS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprint, 2020. Rehuma, H.M., et al., A putative prophylactic solution for COVID-19: Development of novel multicpitope Vaccine condidate against SMS - COV - 2 by comprehensive immunoinformatic and molecular modelling TFKCYGVSPT vaccine candidate ageins SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprint S2020. Rehman, H.M., et al., A patative prophylactic solution for COVID-19. Development of novel multicipitope vaccine candidate agains SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprint S2020. Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope vaccine candidate agains SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprint S2020. Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicipitope Rehman, H. TGCVIA CYFPLQSY YQPYRVVVLSFELLHAPATVCGF vaccine candidate agains 3485 - LOV - 2 03 comprom------approach. Preprints 2020. Rehman, H.M., et al., A pusative prophylactic solution for COVID-19: Development of novel multicplope www.ine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling FGGVSVII OVAVL YODV vaccine candidate against MAR - UVF - e up sump------approach. Preprint, 2020. Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicpitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling CTEVPVAIHAD vaccine candidate against NARS - LOF - 2 03 5000-000 approach. Preprints 2020. Rehman, H.M., et al., A patative prophetacile solution for COVID-19: Development of novel multispitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling AGCLIGA vaccine candidate agoint SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprints, 2020. Rehman, H.M., et al., A patative prophylactic solution for COVID-19. Development of novel multicplicate vaccine candidate agoints SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprints, 2020. Rehman, H.M., et al., A patative prophylactic solution for COVID-19. Development of novel multicplicape vaccine candidate agoints SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprints, 2020. GAGICASY VASOSI TTEILPVS approach. Preprints, 2020. Rehman, H.M., et al., A patarity repolyhalctic solution for COVID-19: Development of novel multicpitope vaccine candidate agoins XARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprints, 2020. Rehman, H.M., et al., A patarity prophylactic solution for COVID-19: Development of novel multicpitope vaccine candidate agoins XARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprints, 2020. Rehman, H.M., et al., A patarity prophylactic solution for COVID-19: Development of novel multicpitope vaccine candidate agoins XARS - COV - 2 by comprehensive immunoinformatic and molecular modelling moreach. Previous 2001. approach. Preprints, 2020. Rehman, H.M., et al., A pu SVDCTMY SNLLLOYGSFCTOL vaccine candidate agains 30.83 - v.o.7 - e.y. emperative approach. Preprints, S200. Rehman, HM, et al., A patative prophylactic solution for COVID-19: Development of novel multilepitope vaccine candidate agains SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprints, 2020. Rehman, HM, et al., A patative prophylactic solution for COVID-19: Development of novel multipitope vaccine candidate agains SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling succine candidate agains SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling VFAQVKQI SQILPD vaccine candidate agams a start and a s YGDCLGD vaccine candidate agains XARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Perprints, 2020.
Rehman, H.M., et al., A putative prophalactic solution for COVID-19. Development of novel multiciptope vaccine candidate agains XARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Perprints, 2020.
Rehman, H.M., et al., A putative prophetactic solution for COVID-19: Development of novel multiciptope vaccine candidate agains XARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Perprints, 2020.
Rehman, H.M., et al., A putative prophetactic solution for COVID-19: Development of novel multiciptope (Rehman, H.M., et al., A putative prophylactic solution for COVID-19: Development of novel multiciptope RDLICAO LTVLPPL YTSALLAG phylactic solution for COVID-19: Development of novel multiepitope OV - 2 by comprehensive immunoinformatic and molecular modelling st SARS - COV - 2 by comprehensive in te candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling ach. Preprints, 20200. ng, H.M., et al., A putative prophylactic solution for COVID-19: Development of novel multicptiope ex candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling ach. Preprints, 2020. *approe* Rehma LNTLVKQL 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 (Muthation and September 2019) Rehman, H.M., et al., A putative prophylactic solution for COVID-19: Development of novel multicptiope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling SLQTYVTQQ SECVLGQS PHGVVFLHVTYVPA vaccine candidate agains XM85 - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprints 2020. Rehman, H.M., et al., A patative prophylactic solution for COVID-19. Development of novel multicplote vaccine candidate agains XM85 - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprints 2020. Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicplotepe vaccine candidate agains XM85 - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprints 2020. Rehman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicplotepe vaccine candidate agains XM85 - COV - 2 by comprehensive immunoinformatic and molecular modelling PAICHDG SGNCDVVIG ASVVNI Semman, H.M., et al., A patative prophylactic solution for COVID-19: Development of novel multicpitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach. Preprints, 2020.
Sandar, R., et al., Comparative analyses of SAR-COV2 genomestry for different georaphical locations and other coronavirus fluoling personaes reveals unique features potentially consequential to host-virus interaction and pathogenesis. bioRxiv, 2020.
Strustavas, 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.
Strustavas, 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.
Strustavas, 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.
Strustavas, 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.
Strustavas, 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.
Strustavas, S., et al., ASASC-COV-2 Vaccination Strusteve Freuencet – epitation Science Immunity. Cell Reports Machine, et al., ASASC-COV-2 Vaccination Strusteve Freuencet – Provident – Science Immunity. Cell Reports Machine, et al., ASASC-COV-2 Vaccination Strusteve Freuencet – Provident – Science Immunity. IAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKF AGTITSGWTEGAGAAL TPGDSSSGWTA FPNITNLCPFGEVFNATRFASVYAWNRKRISNCVA NLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTN KVCEFQFCNDPFLGVYYHKNNKSWMESEFRVY 2020. et al., A SARS-CoV-2 Vaccination Strategy Focused on Population-Scale Immunity. Cell Supers Mean Her, 2020. Yamarkovich, M., et al., A SARS-CoV-2 Vaccination Strategy Focused on Population-Scale Immunity. Cell Reports Medicine, 2020. GDSSSGWTAGAAAYYVGYLOPRTFLLKYNENGT KPFERDISTEIYQAGSTPCNGVEGFNCYFPLQS dicine, 2020. ich, M., et al., A SARS-CoV-2 Vaccination Strategy Focused on Population-Scale Immunity. Cell divino 2020. marko norte M VGGNYNYLYRI FRKSNI KPEERDISTEIYOAGS ncepton sobiletine, 2020. Yatahi, Z., et al. Design an efficient multi-epitope peptide vaccine candidate against SARS-CoV-2: An in silico analysis. bioRxiv, 2020. Yatahai, Z., et al., Design an efficient multi-epitope peptide vaccine candidate against SARS-CoV-2: An in silico analysis. bioRxiv, 2020. QCVNLTTRTQLPPAYTNSFTRGVYYPDKVF KIADYNYKI PDDFTGCVIAWNSNNI DSKVG Suico analysis: bioKXV, 2020.
Yazdani, Z., et al., Design an efficient multi-epitope peptide vaccine candidate against SARS-CoV-2: An in silico analysis. bioRxiv, 2020. Vashi, Y., V. Jagni, and S. Kumar, Understanding the B and T cells epitopes of pilke protein of severo reprinters y submotic community. 2: A computational way to predict the immangeme. bioRxiv, 2020. Vashi, Y., V. Jagni, and S. Kumar, Understanding the B and T cells epitopes of palke protein of severo reprinters y submotic convariants. 2: A computational way to predict the immangeme. bioRxiv, 2020. YQPYRVVVLSFELLHAPATVCGPKKSTNLV RTQLPPAYTNSFTRGVYY HVSGTNGTKRFDN

Vashi, Y., V. Jagni, and S. Kumar. Understanding the B and T cells optiopes of guike protein of severe repriratory syndrome coronawirus 2: A computational ways to predict the immungens. bioRxiv, 2020.
 Vashi, Y., V. Jagni, and S. Kumar. Understanding the B and T cells optiopes of guike protein of severe repriratory syndrome coronawirus 2: A computational ways to predict the immungens. bioRxiv, 2020.
 Vashi, Y., V. Jagni, and S. Kumar. Understanding the B and T cells optiopes of guike protein of severe repriratory syndrome coronawirus 2: A computational ways to predict the immungens. bioRxiv, 2020.
 Vashi, Y. V. Jagni, and S. Kumar. Understanding the B and T cells optiopes of guike protein of severe repriratory syndrome coronawirus 2: A computational ways to predict the immungens. bioRxiv, 2020.
 Vashi, Y. V. Jagni, and S. Kumar. Understanding the B and T cells optiopes of guike protein of severe repriratory syndrome coronawirus 2: A computational way to prodict the immungens. bioRxiv, 2020.
 Vashi, Y. V. Jagni, and S. Kumar. Understanding the B and T cells optiopes of guike protein of severe repriratory syndrome coronawirus 2: A computational way to prodict the immungens. bioRxiv, 2020.
 Vashi, Y. V. Jagni, and S. Kumar. Understanding the B and T cells optiopes of guike protein of severe repriratory syndrome coronawirus 2: A computational way to prodict the immungens. bioRxiv, 2020.
 Vashi, Y. V. Jagni, and S. Kumar. Understanding the B and T cells optiopes of guike protein of severe repriratory syndrome coronawirus 2: A computational way to prodict the immungens. bioRxiv, 2020.
 Vashi, Y. V. Jagni, and S. Kumar. Understanding the B and T cells optiopes of guike protein of severe repriratory syndrome coronawirus 2: A computational way to predict the immungens. bioRxiv, 2020.
 Vashi, Y. V. Jagni, and S. Kumar. Understanding the B and T cells optiopes of guike protein of severe repriratory synd

DLEGKQGNFKNLRE KYNENGTITD QTSNFRVQPTES VRQIAPGQTGKIADYNYKLPDD NSNNLDSKVGGNYN LKPFERDISTEIYQAGSTPCNGVEG QSYGFQPTNGVGYQ PATVCGPKKSTNL RDIADTTDAVRDPOT VITPGTNTSNQ HADQLTPTWRVYSTGSNVFQTRAG EHVNNSYE SYQTQTNSPRRARSVASQS GAENSVAYSNNSIA IYKTPPIKDFGG ILPDPSKPSKRS NNTVYDPLQPELDSFKE PPAYTNSFTRGVYY IHVSGTNGTKRFDNPVLPFN VYYHKNNKSWMESEFRVYSS DLEGKQGNFKNLREFVFKNI VI TPGDSSSGWT LLKYNENGTITDAVDCALDP RQIAPGQTGKIADYNYKLPD SNLKPFERDISTEIYQAGST LQSYGFQPTNGVGYQP HAPATVCGPKKSTN QQFGRDIADTTDAVRDPQTL VITPGTNTSNOVAV IGAEHVNNSYECDIPIGAGI YOTOTNSPRRARSVASOS AVEQDKNTQEVFAQ IYKTPPIKDFGGFN VIGIVNNTVYDPLQPE 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	GAALQIPFAMQMAYRF
studies. Viruses, 2020.	
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	MAYRFNGIGVTONVLY
studies Viruses 2020	
Abread S.E. A.A. Quadaan and M.D. MaKau Dralinging and destification of natural languing	
Anmed, S.F., A.A. Quadeer, and M.K. McKay, Preliminary identification of potential vaccine	
targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological	QLIRAAEIRASANLAATK
studies. Viruses, 2020.	
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	FIAGLIAIV
studies Viruses 2020	
Alexal SE A A O alexa IMD M K D Finite il d'étaite état aire	
Anmed, S.F., A.A. Quadeer, and M.K. McKay, Preliminary identification of potential vaccine	
targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological	ALNTLVKQL
studies. Viruses, 2020.	
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	LITGRLOSL
studios Virmos 2020	2.1012202
Aluel SE AA O lue IMP MK. D living it differing for the	
Anmed, S.F., A.A. Quadeer, and M.K. McKay, Preliminary identification of potential vaccine	
targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological	NLNESLIDL
studies. Viruses, 2020.	
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	OALNTLVKOLSSNEGAL
agets for the COVID-19 coronavirus (SAK5-COV-2) based on SAK5COV inimunological	QALIVILVKQLSSNI'OAI
studies. Viruses, 2020.	
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	RLNEVAKNL
studies, Viruses, 2020.	
Abmod SE A A Quadoar and M.P. McKay Praliminary identification of potential vaccine	
Anned, S.F., A.A. Quadeer, and W.K. WcKay, Flemminary identification of potential vacchie	
targets for the COVID-19 coronavirus (SARS-CoV-2) based on SARSCoV immunological	VLNDILSRL
studies. Viruses, 2020.	
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	VVFLHVTYV
studies Viruses 2020	
Bianco-Miguez, A., Release of potential pro-inflammatory peptiaes from SARS-Cov-2 spike	YFASTEKSNIIRGWIFGTTLDSKTQSLLIV
glycoproteins in neutrophil-extracellular traps. bioRxiv.	
Blanco-Míguez, A., Release of potential pro-inflammatory peptides from SARS-CoV-2 spike	STEVENIID CWIECTTI DEVTOSI I IV
glycoproteins in neutrophil-extracellular traps, bioRxiv.	STEKSNIKGWIFGTTLDSKTQSLLIV
Blanco-Míguez A Release of notential pro-inflammatory pentides from SARS-CoV-2 spike	
Shaomataina in naturabil autanaallulat tama kioRxii.	STEKSNIIRGWIFGTTLDSKTQSLLIVNNA
grycoproteins in neutrophil-extracellular traps. blokxiv.	
Blanco-Míguez, A., Release of potential pro-inflammatory peptides from SARS-CoV-2 spike	SOPFLMDLEGKOGNFKNLREFVFKN\IDGYFKIYSKHTPINLV
glycoproteins in neutrophil-extracellular traps. bioRxiv.	
Blanco-Míguez, A., Release of potential pro-inflammatory peptides from SARS-CoV-2 spike	
elycoproteins in neutrophil-extracellular trans bioRxiv	DEPIGINITREQTELALHRSYLTPGDSSSGWTA
Plance Miguez A Pologes of potential are inflammatory pontides from SAPS CoV 2 spike	
Blanco-Miguez, A., Release of potential pro-inflummatory peptides from SARS-Cov-2 spike	LDPLSETKCTLKSFTVEKGIYQTSNFRV
glycoproteins in neutrophil-extracellular traps. bioRxiv.	
Blanco-Míguez, A., <i>Release of potential pro-inflammatory peptides from SARS-CoV-2 spike</i>	WNENNI DEVVCCNVNVI VDI EDVENI VDEEDDISTEIVOA
glycoproteins in neutrophil-extracellular traps. bioRxiv.	WINSINGEDSKY OON TITTET KEI KKSNEKI TEKDISTEIT (K
Blanco-Míguez, A., Release of potential pro-inflammatory peptides from SARS-CoV-2 spike	
abconrotains in neutronhil avtracellular trans hioRxiv	GGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGV
grycoproteins in neurophil-extracellular haps, blockiv.	
Blanco-Miguez, A., Release of potential pro-inflammatory peptides from SARS-Cov-2 spike	DCTMYICGDSTECSNLLLOYGSFCTOLNRALTGIA
glycoproteins in neutrophil-extracellular traps. bioRxiv.	
Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on	1/1 NIDI CETNI
Coronavirus surface glycoprotein, bioRxiv, 2020.	KLNDLCFIN
Behahani M. In silico Design of novel Multi-enitone recombinant Vaccine based on	
Conserving surface descention his Print 2020	KLNDLCFTNV
Coronavirus surface glycoprotein. bioKxiv, 2020.	
Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on	KI NDI CETNVY
Coronavirus surface glycoprotein. bioRxiv, 2020.	RENDEET HVV I
Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on	
Coronavirus surface alycoprotein bioRxiv 2020	PTKLNDLCFTN
Dilla in Surface grycoprotein for the last in the last	
Bendanani, M., in silico Design of novel Multi-epitope recombinant vaccine based on	SPTKLNDLCFTN
Coronavirus surface glycoprotein. bioRxiv, 2020.	
Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on	
Coronavirus surface glycoprotein. bioRxiv, 2020.	V5P1KLNDLCF1N
Rehhahani M. In silico Design of novel Multi-enitone recombinant Vaccine based on	
Coronauirus surfaça glucoprotain bioPxiy 2020	KLNDLCFTNVYA
Coronavirus surface grycoprotein. 010KX1V, 2020.	
Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on	KLNDI CETNVY AD
Coronavirus surface glycoprotein. bioRxiv, 2020.	
Behbahani, M., In silico Design of novel Multi-epitope recombinant Vaccine based on	
Coronavirus surface glycoprotein. bioRxiv. 2020.	LNDLCFINV

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	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.	SQCVNLTTR
Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020.	GVYYHKNNK
Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020.	GKQGNFKNL
Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020.	GIYQTSNFR
Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020.	VSPTKLNDL
Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020.	KIADYNYKL
Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020.	KVGGNYNYL
Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020.	EGFNCYFPL
Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020.	GPKKSTNLV
Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020.	SPRRARSVA
Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020.	LGAENSVAY
Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020.	FKNHTSPDV
Bhattacharya, M., et al., Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach. J Med Virol, 2020.	DEDDSEPVL
Feng, Y., et al., Multi-epitope vaccine design using an immunoinformatics approach for 2019 novel coronavirus in China (SARS-CoV-2) bioRxiv 2020	FIAGLIAIV
Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27 (4): p. 671-680	IRGWIFGTTLDSKTQSLL
Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680	CTFEYVSQPFLMD
Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27 (4): p. 671-680	QPFLMDLEGKQGN
Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27 (4): p. 671-680	TRFQTLLALHRSYLTPGD SSSGW
Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate	

Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 e2.

KSFTVEKGIYQTSNFRVQ

Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate SASFSTFKCYGVSPTKL Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 e2. Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 KLPDDFTGCV e2. Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate NLDSKVGGNYNYLYRLFR Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 e2. Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 YLYRLFRKSNLKPFERDI e2. Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 **KPFERDISTEIYQ** e2 Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate QSIIAYTMSLGAENSVAY Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 e2. Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 SIIAYTMSL e2. Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 TECSNLLLQYGSFCTQL e2 Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate VKQIYKTPPIKDFGGFNF Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 e2 Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 DSLSSTASALGKLODVV e2. Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 ALNTLVKQL e2. Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate VLNDILSRL Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 e2 Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate LITGRLQSL Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 e2. Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 QLIRAAEIRASANLAATK e2. Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 HWFVTQRNFYEPQII e2 Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate RLNEVAKNL Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 e2. Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 FIAGLIAIV e2. Grifoni, A., et al., A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2. Cell Host Microbe, 2020. 27(4): p. 671-680 NUNESLIDL. e2. Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse **GVYFASTEK** Vaccinology Approach. 2020. Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse VTYVPAQEK Vaccinology Approach. 2020. Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse ASANLAATK Vaccinology Approach. 2020. Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse TLADAGFIK Vaccinology Approach. 2020. Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse TEILPVSMTK Vaccinology Approach. 2020. Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse SSTASALGK

Vaccinology Approach. 2020.

Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates	
against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse	EILPVSMTK
Vaccinology Approach. 2020.	
Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates	
against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse	SNFRVQPTESI
Vaccinology Approach. 2020.	
Gupta, E., R.K. Mishra, and R.R.K. Niraj, <i>Identification of potential vaccine candidates</i>	
against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse	NFRVOPTESIV
Vaccinology Approach. 2020.	
Gunta E R K Mishra and R R K Nirai Identification of potential vaccine candidates	
against SARS-CoV-2. A step forward to fight novel coronavirus 2019-nCoV· A Reverse	LGVYYHKNNKS
Vaccinology Approach 2020	
Gunta E B K Mishra and B P K Nirai Identification of notantial vaccine candidates	
aggingt SAPS CoV 2. A stap forward to fight noval coronavirus 2010 nCoV: A Bayarsa	CVVVHKNNKSW
Variale and America and 2020	OV I IIIKINKSW
Vaccinology Approach. 2020.	
Gupta, E., R.K. Misnira, and R.K.K. Iviraj, <i>Identification of potential vaccine canalaates</i>	
against SAKS-Cov-2, A step forward to fight novel coronavirus 2019-nCov: A Reverse	LLIVINIATINVV
Vaccinology Approach. 2020.	
Gupta, E., R.K. Mishra, and R.R.K. Niraj, <i>Identification of potential vaccine candidates</i>	
against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse	GVYFASTEK
Vaccinology Approach. 2020.	
Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates	
against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse	VTYVPAQEK
Vaccinology Approach. 2020.	
Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates	
against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse	ASANLAATK
Vaccinology Approach. 2020.	
Gupta, E., R.K. Mishra, and R.R.K. Niraj, <i>Identification of potential vaccine candidates</i>	
against SARS-CoV-2. A step forward to fight novel coronavirus 2019-nCoV: A Reverse	TLADAGEIK
Vaccinology Approach 2020	
Gunta E R K Mishra and R R K Nirai Identification of potential vaccine candidates	
against SARS-CoV-2 A step forward to fight novel coronavirus 2019-nCoV- A Reverse	TEII PVSMTK
Vaccinology Approach 2020	
Gunta E. B.K. Mishra and B.P.K. Nirai Identification of notantial vaccine candidates	
aggingt SAPS CoV 2. A stap forward to fight noval coronavirus 2010 nCoV: A Bayarsa	SSTASALCK
Vaccinclosy Approach 2020	SSTASALOK
Vaccinology Approach. 2020.	
Gupta, E., K.K. Misnra, and K.K.K. Niraj, <i>Identification of potential vaccine candidates</i>	
against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse	EILPVSM1K
Vaccinology Approach. 2020.	
Gupta, E., R.K. Mishra, and R.R.K. Niraj, <i>Identification of potential vaccine candidates</i>	
against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse	NFRVQPTESIV
Vaccinology Approach. 2020.	
Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates	
against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse	LLIVNNATNVV
Vaccinology Approach. 2020.	
Gupta, E., R.K. Mishra, and R.R.K. Niraj, Identification of potential vaccine candidates	
against SARS-CoV-2, A step forward to fight novel coronavirus 2019-nCoV: A Reverse	IRASANLAATK
Vaccinology Approach. 2020.	
Gupta, E., R.K. Mishra, and R.R.K. Nirai, <i>Identification of potential vaccine candidates</i>	
against SARS-CoV-2. A step forward to fight novel coronavirus 2019-nCoV: A Reverse	EIRASANLAAT
Vaccinology Approach 2020	
Herst C V et al An Effective CTL Pentide Vaccine for Fhola Zaire Based on Survivors'	
CD8+ Targating of a Particular Nucleocansid Protain Enitone with Potential Implications for	I SPRWVEVV
COVID 10 Vaccine Design bioPrint 2020	LSI KW II I I
COVID-19 Vaccine Design. DIORAIV, 2020.	
CD8. There exists a first Provided CTL February and Destering Friday and Destering Desterior Desterior Desterior Survivors	VTEDDTEDV
CD8+ Targeting of a Particular Nucleocapsia Protein Epitope with Potential Implications for	KIFFFIEFK
COVID-19 vaccine Design. blockxiv, 2020.	
Herst, C.V., et al., An Effective CTL Peptide Vaccine for Ebola Zaire Based on Survivors'	
CD8+ Targeting of a Particular Nucleocapsid Protein Epitope with Potential Implications for	KTFPPTEPK
COVID-19 Vaccine Design. bioRxiv, 2020.	
Herst, C.V., et al., An Effective CTL Peptide Vaccine for Ebola Zaire Based on Survivors'	
CD8+ Targeting of a Particular Nucleocapsid Protein Epitope with Potential Implications for	IGYYRRATR
COVID-19 Vaccine Design. bioRxiv, 2020.	
Herst, C.V., et al., An Effective CTL Peptide Vaccine for Ebola Zaire Based on Survivors'	
CD8+ Targeting of a Particular Nucleocapsid Protein Epitope with Potential Implications for	FPRGQGVPI
COVID-19 Vaccine Design. bioRxiv, 2020.	
Herst, C.V., et al., An Effective CTL Peptide Vaccine for Ebola Zaire Based on Survivors'	
CD8+ Targeting of a Particular Nucleocapsid Protein Epitope with Potential Implications for	SPRWYFYYL
COVID-19 Vaccine Design. bioRxiv, 2020.	
Herst, C.V., et al., An Effective CTL Peptide Vaccine for Ebola Zaire Based on Survivors'	
CD8+ Targeting of a Particular Nucleocapsid Protein Epitope with Potential Implications for	KAYNVTOAF
COVID-19 Vaccine Design. bioRxiv, 2020.	
-	

Herst, C.V., et al., An Effective CTL Peptide Vaccine for Ebola Zaire Based on Survivors' CD8+ Targeting of a Particular Nucleocapsid Protein Epitope with Potential Implications for COVID-19 Vaccine Design, bioRxiv, 2020	MEVTPSGTW
Herst, C.V., et al., An Effective CTL Peptide Vaccine for Ebola Zaire Based on Survivors' CD8+ Targeting of a Particular Nucleocapsid Protein Epitope with Potential Implications for COVID-19 Vaccine Design. bioRxiv. 2020.	KAYNVTQAF
Herst, C.V., et al., An Effective CTL Peptide Vaccine for Ebola Zaire Based on Survivors' CD8+ Targeting of a Particular Nucleocapsid Protein Epitope with Potential Implications for COVID-19 Vaccine Design. bioRxiv, 2020.	QRNAPRITF
Ismail, S., S. Ahmad, and S.S. Azam, Immuno-informatics Characterization SARS-CoV-2 Spike Glycoprotein for Prioritization of Epitope based Multivalent Peptide Vaccine. bioRxiv, 2020.	YAWNRKRIS
Ismail, S., S. Ahmad, and S.S. Azam, <i>Immuno-informatics Characterization SARS-CoV-2</i> Spike Glycoprotein for Prioritization of Epitope based Multivalent Peptide Vaccine. bioRxiv, 2020.	IAPGQTGKI
Ismail, S., S. Ahmad, and S.S. Azam, <i>Immuno-informatics Characterization SARS-CoV-2</i> Spike Glycoprotein for Prioritization of Epitope based Multivalent Peptide Vaccine. bioRxiv, 2020.	PRRARSVAS
Ismail, S., S. Ahmad, and S.S. Azam, <i>Immuno-informatics Characterization SARS-CoV-2</i> Spike Glycoprotein for Prioritization of Epitope based Multivalent Peptide Vaccine. bioRxiv, 2020.	TVYDPLQPE
Ismail, S., S. Ahmad, and S.S. Azam, <i>Immuno-informatics Characterization SARS-CoV-2</i> Spike Glycoprotein for Prioritization of Epitope based Multivalent Peptide Vaccine. bioRxiv, 2020.	VYDPLQPEL
Ismail, S., S. Ahmad, and S.S. Azam, <i>Immuno-informatics Characterization SARS-CoV-2</i> Spike Glycoprotein for Prioritization of Epitope based Multivalent Peptide Vaccine. bioRxiv, 2020.	FKNHTSPDV
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	IPFAMQMAYR
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	VVFLHVTYV
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	FPNITNLCPF
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	KWPWYIWLGF
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	LPIGINITRF
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	IAIVMVTIM
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	ESNKKFLPF
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	LPFFSNVTW
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	FAMQMAYRF
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	VGYQPYRVVVLSFEL
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	FAMQMAYRFNGIGVT
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	IPFAMQMAYRFNGIG
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	NFTISVTTEILPVSM
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	LVLLPLVSSQCVNLT
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	VVFLHVTYVPAQEKN

Li, L., et al., <i>Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2.</i> bioRxiv, 2020.	TNFTISVTTEILPVS
Li, L., et al., <i>Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2.</i> bioRxiv, 2020.	QYIKWPWYIWLGFIA
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	PTNFTISVTTEILPV
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	GVVFLHVTYVPAQEK
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	GYQPYRVVVLSFELL
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	VFLHVTYVPAQEKNF
Li, L., et al., Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2. bioRxiv, 2020.	ALQIPFAMQMAYRFN
Nazneen Akhand, M.R., et al., Genome based Evolutionary study of SARS-CoV-2 towards the Prediction of Enitone Based Chimeric Vaccing, bioPriv, 2020	ADYNYKLPD
Nazneen Akhand, M.R., et al., Genome based Evolutionary study of SARS-CoV-2 towards the Prediction of Epitone Based Chinaric Vaccine, bioPxiv, 2020.	SFVIRGDEVRQIAPG
Nazneen Akhand, M.R., et al., Genome based Evolutionary study of SARS-CoV-2 towards the	DSFVIRGDEVRQIAP
Prediction of Epitope Based Chimeric Vaccine. blockiv, 2020. Poran, A., et al., Sequence-based prediction of vaccine targets for inducing T cell responses to SARS-CoV-2 utilizing the bioinformatics predictor RECON. bioRxiv, 2020.	FGADPIHSL
Poran, A., et al., Sequence-based prediction of vaccine targets for inducing T cell responses to SARS-CoV-2 utilizing the bioinformatics predictor RECON. bioRxiv, 2020.	SFYEDFLEY
Poran, A., et al., Sequence-based prediction of vaccine targets for inducing T cell responses to SARS-CoV-2 utilizing the bioinformatics predictor RECON. bioRxiv, 2020.	QWLPTGTLL
Poran, A., et al., Sequence-based prediction of vaccine targets for inducing T cell responses to SARS-CoV-2 utilizing the bioinformatics predictor RECON. bioRxiv, 2020.	LLTKGTLEPEYFNSVCRLMKTIGPD
Poran, A., et al., Sequence-based prediction of vaccine targets for inducing T cell responses to SARS-CoV-2 utilizing the bioinformatics predictor RECON. bioRxiv, 2020.	GVYDYLVSTQEFRYMNSQGLLPPKN
Poran, A., et al., Sequence-based prediction of vaccine targets for inducing T cell responses to SARS-CoV-2 utilizing the bioinformatics predictor RECON. bioRxiv, 2020.	EIDRLNEVAKNLNESLIDLQELGKY
Poran, A., et al., Sequence-based prediction of vaccine targets for inducing T cell responses to SARS-CoV-2 utilizing the bioinformatics predictor RECON. bioRxiv, 2020.	TLNGLWLDDVVYCPRHVICTSEDML
Ramaiah, A. and V. Arumugaswami, Insights into Cross-species Evolution of Novel Human Coronavirus 2019-nCoV and Defining Immune Determinants for Vaccine Development.	GINITRFQTLLALHR
Ramaiah, A. and V. Arumugaswami, Insights into Cross-species Evolution of Novel Human Coronavirus 2019-nCoV and Defining Immune Determinants for Vaccine Development.	INITRFQTLLALHRS
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.	TSNQVAVLY
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.	CVADYSVLY
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.	KTSVDCTMY
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.	VASQSIIAY

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.	CNDPFLGVY
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.	GAAAYYVGY
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.	RISNCVADY
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.	ITDAVDCAL
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.	MTSCCSCLK
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.	STQDLFLPF
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.	ECSNLLLQY
Saha, R. and B.V.L.S. Prasad, In silico approach for designing of a multi-epitope based	TLDSKTQSL
Saha, R. and B.V.L.S. Prasad, In silico approach for designing of a multi-epitope based	GKQGNFKNL
Saha, R. and B.V.L.S. Prasad, In silico approach for designing of a multi-epitope based	CYGVSPTKL
vaccine against novel Coronavirus(SARS-COV-2). bioRxiv, 2020. Saha, R. and B.V.L.S. Prasad, In silico approach for designing of a multi-epitope based	KIADYNYKL
vaccine against novel Coronavirus(SARS-COV-2). bioRxiv, 2020. Saha, R. and B.V.L.S. Prasad, In silico approach for designing of a multi-epitope based	VVVI SFELL
vaccine against novel Coronavirus(SARS-COV-2). bioRxiv, 2020. Saha, R. and B.V.L.S. Prasad, In silico approach for designing of a multi-epitope based	IGINITEO
vaccine against novel Coronavirus(SARS-COV-2). bioRxiv, 2020. Saha, R. and B.V.L.S. Prasad, In silico approach for designing of a multi-epitope based	NGEODENCU
vaccine against novel Coronavirus(SARS-COV-2). bioRxiv, 2020.	YGFQPINGV
vaccine against novel Coronavirus(SARS-COV-2). bioRxiv, 2020.	VLSFELLHA
Sana, K. and B. V.L.S. Prasad, in suico approach for designing of a multi-epitope based vaccine against novel Coronavirus(SARS-COV-2). bioRxiv, 2020.	LQIPFAMQM
Saha, R. and B.V.L.S. Prasad, In silico approach for designing of a multi-epitope based vaccine against novel Coronavirus(SARS-COV-2). bioRxiv, 2020.	IAIVMVTIM
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.	LTTRTQLPP
Singh, A., et al., <i>Designing a multi-epitope peptide-based vaccine against SARS-CoV-2</i> .	IPFAMQMA YRFNGIG
Singh, A., et al., <i>Designing a multi-epitope peptide-based vaccine against SARS-CoV-2</i> .	FVFLVLLPLVSSQCV
Singh, A., et al., Designing a multi-epitope peptide-based vaccine against SARS-CoV-2.	FAMOMAYRF
bioRxiv, 2020. Singh, A., et al., Designing a multi-epitope peptide-based vaccine against SARS-CoV-2.	EVELVI I PI
bioRxiv, 2020. 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.	KTQSLLIVNNATNVV
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.	TQSLLIVNNATNVVI
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.	QSLLIVNNATNVVIK
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.	SLLIVNNATNVVIKV

Srivastava, S., et al., Structural basis to design multi-epitope vaccines against Novel Coronavirus 19 (COVID19) infection, the ongoing pandemic emergency: an in silico	LLIVNNATNVVIKVC
<i>approach.</i> bioRxiv, 2020. Srivastava, S., et al., <i>Structural basis to design multi-epitope vaccines against Novel</i> <i>Coronavirus 19 (COVID19) infection, the ongoing pandemic emergency: an in silico</i> <i>approach.</i> bioRxiv, 2020.	FPNITNLCPF
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.	NYLYRLFR
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.	NYNYLYRLFR
Sivastava, 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.	WTAGAAAYYV
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.	KPFERDISTEIYQAGSTPCNGVEGFNCYFPLQS
Yarmarkovich, M., et al., A SARS-CoV-2 Vaccination Strategy Focused on Population-Scale Immunity. Cell Reports Medicine, 2020.	GEVFNATRFASVYAWNRKRISNCVADYSVLYNS
Yarmarkovich, M., et al., A SARS-CoV-2 Vaccination Strategy Focused on Population-Scale Immunity. Cell Reports Medicine, 2020.	GDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGT
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

Reference

[1]N. Maillet. Rapid Peptides Generator: fast and efficient in silico protein digestion[J]. NAR Genomics and Bioinformatics, 2020, 1,

[2]A. Blanco-Míguez. Release of potential pro-inflammatory peptides from SARS-CoV-2 spike glycoproteins in neutrophil-extracellular traps[J]. bioRxiv,

[3]N. M. Andreatta M. Gapped sequence alignment using artificial neural networks: application to the MHC class I system.):[J]. Bioinformatics, 2016, 511-7.

[4]C. V. Herst, S. Burkholz, J. Sidney, A. Sette, P. E. Harris, S. Massey, T. Brasel, E. Cunha-Neto, D. S. Rosa, W. C. H. Chao, R. Carback, T. Hodge, L. Wang, S. Ciotlos, P. Lloyd and R. Rubsamen. An Effective CTL Peptide Vaccine for Ebola Zaire Based on Survivors' CD8+ Targeting of a Particular Nucleocapsid Protein Epitope with Potential Implications for COVID-19 Vaccine Design[J]. bioRxiv, 2020,

[5]M. C. Jespersen, B. Peters, M. Nielsen and P. Marcatili. BepiPred-2.0: improving sequence-based B-cell epitope prediction using conformational epitopes[J]. Nucleic Acids Res, 2017, W1, W24-W29.

[6]S. Ismail, S. Ahmad and S. S. Azam. Immuno-informatics Characterization SARS-CoV-2 Spike Glycoprotein for Prioritization of Epitope based Multivalent Peptide Vaccine[J]. bioRxiv, 2020,

[7]J. V. H. EMILIO A. EMINI, DEBRA S. PERLOW, AND JOSHUA BOGER. Induction of Hepatitis A Virus-Neutralizing Antibody by a VirusSpecific Synthetic Peptide[J]. JOURNAL OF VIROLOGY, 1985,

[8]P. C. T. A.S.Kolaskar. A semi-empirical method for prediction of antigenic dete~inants on protein antigens[J]. 1990,

[9]K. F. Azim, M. Hasan, M. N. Hossain, S. R. Somana, S. F. Hoque, M. N. I. Bappy, A. T. Chowdhury and T. Lasker. Immunoinformatics approaches for designing a novel multi epitope peptide vaccine against human norovirus (Norwalk virus)[J]. Infect Genet Evol, 2019, 103936.

[10] M. R. Nazneen Akhand, K. F. Azim, S. F. Hoque, M. A. Moli, B. D. Joy, H. Akter, I. K. Afif, N. Ahmed and M. Hasan. Genome based Evolutionary study of SARS-CoV-2 towards the Prediction of Epitope Based Chimeric Vaccine[J]. bioRxiv, 2020,

[11]J. G. Abelin, D. B. Keskin, S. Sarkizova, C. R. Hartigan, W. Zhang, J. Sidney, J. Stevens, W. Lane, G. L. Zhang, T. M. Eisenhaure, K. R. Clauser, N. Hacohen, M. S. Rooney, S. A. Carr and C. J. Wu. Mass Spectrometry Profiling of HLA-Associated Peptidomes in Mono-allelic Cells Enables More Accurate Epitope Prediction[J]. Immunity, 2017, 2, 315-326.

[12]A. Poran, D. Harjanto, M. Malloy, M. S. Rooney, L. Srinivasan and R. B. Gaynor. Sequence-based prediction of vaccine targets for inducing T cell responses to SARS-CoV-2 utilizing the bioinformatics predictor RECON[J]. bioRxiv, 2020,

[13]Y. El-Manzalawy, D. Dobbs and V. Honavar. Predicting linear B-cell epitopes using string kernels[J]. J Mol Recognit, 2008, 4, 243-55.

[14]K. K. e. a. Jensen. Improved methods for predicting peptide binding affinity to MHC class II molecules. . , [J]. Immunology, 2018, 394-406.

[15]A. Singh, M. Thakur, L. K. Sharma and K. Chandra. Designing a multi-epitope peptide-based vaccine against SARS-CoV-2[J]. bioRxiv, 2020,

[16]I. W. D. Simon C. Lovell, W. Bryan Arendall III, Paul I. W. de Bakker, J. Michael Word, Michael G. Prisant, Jane S. Richardson, David C. Richardson. Structure validation by Calpha geometry: phi, psi and Cbeta deviation.[J]. PROTEINS: Structure, Function, and Genetics, 2003,

[17]S. Srivastava, S. Verma, M. Kamthania, R. Kaur, R. K. Badyal, A. K. Saxena, H.-J. Shin, M. Kolbe and K. C. Pandey. Structural basis to design multi-epitope vaccines against Novel Coronavirus 19 (COVID19) infection, the ongoing pandemic emergency: an in silico approach[J]. bioRxiv, 2020,

[18]S. Saha and G. P. Raghava. Prediction of continuous B-cell epitopes in an antigen using recurrent neural network[J]. Proteins, 2006, 1, 40-8.

[19]Y. Vashi, 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[J]. bioRxiv, 2020,

[20]P. A. Reche, J. P. Glutting, H. Zhang and E. L. Reinherz. Enhancement to the RANKPEP resource for the prediction of peptide binding to MHC molecules using profiles[J]. Immunogenetics, 2004, 6, 405-19.

[21]J. Sidney, E. Assarsson, C. Moore, S. Ngo, C. Pinilla, A. Sette and B. Peters. Quantitative peptide binding motifs for 19 human and mouse MHC class I molecules derived using positional scanning combinatorial peptide libraries[J]. Immunome Res, 2008, 2.

[22]Z. Yazdani, A. Rafiei, M. Yazdani and R. Valadan. Design an efficient multi-epitope peptide vaccine candidate against SARS-CoV-2: An in silico analysis[J]. bioRxiv, 2020,

[23]S. F. Ahmed, 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[J]. Viruses, 2020,

[24]H. Singh and G. P. Raghava. ProPred1: prediction of promiscuous MHC Class-I binding sites[J]. Bioinformatics, 2003, 8, 1009-14.

[25]H. S. a. G. P. S. Raghava. ProPred: prediction of HLA-DR binding sites[J]. Bioinformatics, 2001,

[26]M. Behbahani. In silico Design of novel Multi-epitope recombinant Vaccine based on Coronavirus surface glycoprotein[J]. bioRxiv, 2020,

[27]M. Bhattacharya, A. R. Sharma, P. Patra, P. Ghosh, G. Sharma, B. C. Patra, S. S. Lee and C. Chakraborty. Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach[J]. J Med Virol, 2020,

[28]J. V. Kringelum, C. Lundegaard, O. Lund and M. Nielsen. Reliable B cell epitope predictions: impacts of method development and improved benchmarking[J]. PLoS Comput Biol, 2012, 12, e1002829.

[29]B. Chen, M. S. Khodadoust, N. Olsson, L. E. Wagar, E. Fast, C. L. Liu, Y. Muftuoglu, B. J. Sworder, M. Diehn, R. Levy, M. M. Davis, J. E. Elias, R. B. Altman and A. A. Alizadeh. Predicting HLA class II antigen presentation through integrated deep learning[J]. Nat Biotechnol, 2019, 11, 1332-1343.

[30]E. Fast, R. B. Altman and B. Chen. Potential T-cell and B-cell Epitopes of 2019-nCoV[J]. bioRxiv, 2020,

[31]Y. Feng, M. Qiu, S. Zou, Y. Li, K. Luo, R. Chen, Y. Sun, K. Wang, X. Zhuang, S. Zhang, S. Chen and F. Mo. Multi-epitope vaccine design using an immunoinformatics

approach for 2019 novel coronavirus in China (SARS-CoV-2)[J]. bioRxiv, 2020,

[32]A. Grifoni, J. Sidney, Y. Zhang, R. H. Scheuermann, B. Peters and A. Sette. A Sequence Homology and Bioinformatic Approach Can Predict Candidate Targets for Immune Responses to SARS-CoV-2[J]. Cell Host Microbe, 2020, 4, 671-680 e2.

[33] M. S. Rahman, M. N. Hoque, M. R. Islam, S. Akter, A. S. M. Rubayet-Ul-Alam, M. A. Siddique, O. Saha, M. M. Rahaman, M. Sultana and M. A. Hossain. 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[J]. biorxiv, 2020,

[34]A. Ramaiah and V. Arumugaswami. Insights into Cross-species Evolution of Novel Human Coronavirus 2019-nCoV and Defining Immune Determinants for Vaccine Development.[J]. bioRxiv, 2020,

[35]I. W. Davis, A. Leaver-Fay, V. B. Chen, J. N. Block, G. J. Kapral, X. Wang, L. W. Murray, W. B. Arendall, 3rd, J. Snoeyink, J. S. Richardson and D. C. Richardson. MolProbity: all-atom contacts and structure validation for proteins and nucleic acids[J]. Nucleic Acids Res, 2007, Web Server issue, W375-83.

[36]H. M. Rehman, M. U. Mirza, M. Saleem, M. Froeyen, S. Ahmad, R. Gul, M. S. Aslam, M. Sajjad and M. A. Bhinder. A putative prophylactic solution for COVID-19: Development of novel multiepitope vaccine candidate against SARS - COV - 2 by comprehensive immunoinformatic and molecular modelling approach[J]. Preprints, 2020,

[37]C. K. H. Pingping Guan, Irini A. Doytchinova and Darren R. Flower. MHCPred 2.0 An Updated Quantitative T-Cell Epitope Prediction Server[J]. Appl. Bioinformatics, 2006,

[38]R. Saha and B. V. L. S. Prasad. In silico approach for designing of a multi-epitope based vaccine against novel Coronavirus(SARS-COV-2)[J]. bioRxiv, 2020,

[39]R. G. Bhasin M. Prediction of CTL epitopes using QM, SVM and ANN techniques.[J]. Vaccines (Basel), 2004, 3195-204.

[40]D. Satish, S. K. Mukherjee and D. Gupta. PAmiRDB: A web resource for plant miRNAs targeting viruses[J]. Sci Rep, 2019, 1, 4627.

[41]D. Betel, M. Wilson, A. Gabow, D. S. Marks and C. Sander. The microRNA.org resource: targets and expression[J]. Nucleic Acids Res, 2008, Database issue, D149-53.

[42]X. Dai and P. X. Zhao. psRNATarget: a plant small RNA target analysis server[J]. Nucleic Acids Res, 2011, Web Server issue, W155-9.

[43]R. Sardar, D. Satish, S. Birla and D. Gupta. 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[J]. bioRxiv, 2020,

[44]M. Yarmarkovich, J. M. Warrington, A. Farrel and J. M. Maris. A SARS-CoV-2 Vaccination Strategy Focused on Population-Scale Immunity[J]. Cell Reports Medicine, 2020, [45]S. a. G. P. S. R. Saha. BcePred: Prediction of Continuous B-Cell Epitopes in Antigenic Sequences Using Physico-chemical Properties. Berlin, Heidelberg: Springer Berlin Heidelberg[J]. Artificial Immune Systems, 2004., 197-204.

[46]L. Li, T. Sun, Y. He, W. Li, Y. Fan and J. Zhang. Epitope-based peptide vaccine design and target site characterization against novel coronavirus disease caused by SARS-CoV-2[J]. 2020,