Supplementary material to

Identification and analysis of unstructured, linear B-cell epitopes in SARS-CoV-2 virion proteins for vaccine development

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Supplementary Data S1. Conservation of B-cell epitopes in S, E, M and N protein across coronavirus species. Independent sequence alignments between uBCELs/BCEH of SARS-CoV-2, and equivalent sequences in SARS-CoV and three bat coronavirus samples: bat-SL-CoVZXC21, bat-SL-CoVZC45 and RaTG13. For clarity, SARS-CoV and SARS-CoV-2 headers are in bold letters. Residues in uBCEs are in capital letters while the rest of the loop is in lowercase. Identical residues to SARS-CoV-2 sequences are highlighted in green. Deletions are indicated with dashes.

S protein

uBCEL-S1

```
SARS-CoV            20_ddvqaPNYTQHTS_32
Bat-SL-CoVZXC21     17_-dltGRTPLNPNY_28
Bat-SL-CoVZC45      17_vnltGRTPLNPNY_29
RaTG13              15_vnlttRTQLPPAY_27
SARS-CoV-2          15_vnlttRTQLPPAY_27
                         :
```

uBCEL-S2

```
SARS-CoV            72_in-------HTFGNpvip_82
Bat-SL-CoVZXC21     68_lttN-NAATKRTDNpild_84
Bat-SL-CoVZC45      69_lttN-NAATKRTDNpild_85
RaTG13              68_ihvSGTNGIKRFDNpvlp_85
SARS-CoV-2          68_ihvSGTNGTKRFDNpvlp_85
                       :         :  .**::
```

uBCEL-S3

```
SARS-CoV            389_vkGDDVRQIAPgqtgviadynyklpddf_416
Bat-SL-CoVZXC21     397_irFSEVRQVAPgqtgviadynyklpddf_424
Bat-SL-CoVZC45      398_irFSEVRQVAPgqtgviadynyklpddf_425
RaTG13              402_itGDEVRQIAPgqtgkiadynyklpddf_429
SARS-CoV-2          402_irGDEVRQIAPgqtgkiadynyklpddf_429
                        :  .:***:****** ************
```

uBCEL-S4

```
SARS-CoV            427_NIDATStgnyn_437
Bat-SL-CoVZXC21     435_KQDT-----gh_440
Bat-SL-CoVZC45      436_KQDV-----gn_441
RaTG13              440_HIDAKEggnfn_450
SARS-CoV-2          440_NLDSKVggnyn_450
                        : *       :
```

uBCEL-S5

```
SARS-CoV            442_ylrhGKLRPFERDISNVPFSPDGKPCtp-palncywp_477
Bat-SL-CoVZXC21     445_shrsTKLKPFERDLSSDENG--------------vrt_467
Bat-SL-CoVZC45      446_shrsTKLKPFERDLSSDENG--------------vrt_468
RaTG13              455_lfrkANLKPFERDISTEIYQAGSKPCngqtglncyyp_491
SARS-CoV-2          455_lfrkSNLKPFERDISTEIYQAGSTPCngvegfncyfp_491
                         *  :*:*****:*.
```

uBCEL-S6

```
SARS-CoV            601_VNCTDVSTAIHADQLTpawriystgnnv_628
Bat-SL-CoVZXC21     591_VNCTDVPTTIHADQLTpawriyaigtsv_618
Bat-SL-CoVZC45      592_VNCTDVPTTIHADQLTpawriyatgtnv_619
RaTG13              615_VNCTEVPVAIHADQLTptwrvystgsnv_642
SARS-CoV-2          615_VNCTEVPVAIHADQLTptwrvystgsnv_642
                        ****:* .:********:**:*: *..*
```

uBCEL-S7

```
SARS-CoV            662_TVSL----LRSTsq_671
Bat-SL-CoVZXC21     652_TASI----LRSTgq_661
Bat-SL-CoVZC45      653_TASI----LRSTsq_662
RaTG13              676_TQTNS----RSVas_685
SARS-CoV-2          676-TQTNSPRRARSVas-689
                        * :      **...
```

uBCEL-S8

```
SARS-CoV            765_AQVKQMYKTPTLKYFggfnfs_785
Bat-SL-CoVZXC21     755_AQVKQIYKTPPIKDFggfnfs_775
Bat-SL-CoVZC45      756_AQVKQIYKTPPIKDFggfnfs_776
RaTG13              779_AQVKQIYKTPPIKDFggfnfs_799
SARS-CoV-2          783_AQVKQIYKTPPIKDFggfnfs_803
                        *****:**** :* *******
```

uBCEL-S9

```
SARS-CoV           1107_NCDVVIG_1113
Bat-SL-CoVZXC21    1097_NCDVVIG_1103
Bat-SL-CoVZC45     1098_NCDVVIG_1104
RaTG13             1121_SCDVVIG_1127
SARS-CoV-2         1125_NCDVVIG_1131
                        .******
```

uBCEL-S10

```
SARS-CoV            1118_TVYDPLQPELDS_1129
Bat-SL-CoVZXC21     1108_TVYDPLQPELDS_1119
Bat-SL-CoVZC45      1109_TVYDPLQPELDS_1120
RaTG13              1132_TVYDPLQPELDS_1143
SARS-CoV-2          1136_TVYDPLQPELDS_1147
                         ************
```

uBCEL-S11

```
SARS-CoV            1220_tsCCSCLKG_1228
Bat-SL-CoVZXC21     1210_tsCCSCLKG_1218
Bat-SL-CoVZC45      1211_tsCCSCLKG_1219
RaTG13              1234_tsCCSCLKG_1242
SARS-CoV-2          1238_tsCCSCLKG_1246
                         *********
```

E protein

BCEH-E1

```
SARS-CoV              38_rlcayccnivnvslvkptvYVYSRVKNLNSSEgvpdllv_76
Bat-SL-CoVZXC21       38_rlcayccnivnvslvkpsfYVYSRVKNLNSSR-vpdllv_75
Bat-SL-CoVZC45        38_rlcayccnivnvslvkpsfYVYSRVKNLNSSR-vpdllv_75
RaTG13                38_rlcayccnivnvslvkpsfYVYSRVKNLNSSR-vpdllv_75
SARS-CoV-2            38_rlcayccnivnvslvkpsfYVYSRVKNLNSSR-vpdllv_75
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```

M protein

uBCEL-M1

SARS-CoV	208	DHAGSNDniallvq 221
Bat-SL-CoVZC45	209	DHSSSSDniallvq 222
Bat-SL-CoVZXC21	209	DHSSSSDniallvq 222
RaTG13	209	DHSSSSDniallvq 222
SARS-CoV-2	209	DHSSSSDniallvq 222
		:.*.******

N protein

uBCEL-N1

```
SARS-CoV              19 GGPTDSTDNNQNGGRNGARPKQRRPQGLPNntaswfta 56
Bat-SL-CoVZXC21       18 GGPSDSSDNSQNGERNGARPKQRRPQGLPNntaswfta 55
Bat-SL-CoVZC45        18 GGPSDSSDNSKNGERNGARPKQRRPQGLPNntaswfta 55
RaTG13                18 GGPSDSTGSNQNGERSGARPKQRRPQGLPNntaswfta 55
SARS-CoV-2            18 GGPSDSTGSNQNGERSGARSKQRRPQGLPNntaswfta 55
                         ***:**:...:** *.*** ******************
```

uBCEL-N2

```
SARS-CoV              60 HGKEELRFPRGQGVPINTNS 79
Bat-SL-CoVZXC21       59 HGKENLTFPRGQGVPINTNS 78
Bat-SL-CoVZC45        59 HGKENLTFPRGQGVPINTNS 78
RaTG13                59 HGKEDLKFPRGQGVPINTNS 78
SARS-CoV-2            59 HGKEDLKFPRGQGVPINTNS 78
                         ****:* ************
```

uBCEL-N3

```
SARS-CoV             136 tegalntpkdhigtrnpnnnaatVLQLPQGTTLPKG 171
Bat-SL-CoVZXC21      135 tegalntpkdhigtrnpannaaiVLQLPQGTTLPKG 170
Bat-SL-CoVZC45       135 tegalntpkdhigtrnpannaaiVLQLPQGTTLPKG 170
RaTG13               135 tegalntpkdhigtrnpannaaiVLQLPQGTTLPKG 170
SARS-CoV-2           135 tegalntpkdhigtrnpannaaiVLQLPQGTTLPKG 170
                         ***************** **** ************
```

uBCEL-N4

```
SARS-CoV             174 AEGSRGGSQASSRSSSRSRGNSRNSTPGSSRGNSPArmasg 214
Bat-SL-CoVZXC21      173 AEGSRGGSQASSRSSSRSRNSSRNSTPGSSRGTSPArmagn 213
Bat-SL-CoVZC45       173 AEGSRGGSQASSRSSSRSRNSSRNSTPGSSRGTSPArmagn 213
RaTG13               173 AEGSRGGSQASSRSSSRSRNSSRNSTPGSSRGTSPArmagn 213
SARS-CoV-2           173 AEGSRGGSQASSRSSSRSRNSSRNSTPGSSRGTSPArmagn 213
                         ******************..***********.******..
```

uBCEL-N5

```
SARS-CoV             236 SGKGQQQQGQTVT 248
Bat-SL-CoVZXC21      235 SGKGQQQQGQTVT 247
Bat-SL-CoVZC45       235 SGKGQQQQGQTVT 247
RaTG13               235 SGKGQQQQSQTVT 247
SARS-CoV-2           235 SGKGQQQQGQTVT 247
                         ********.****
```

uBCEL-N6

```
SARS-CoV            277_RRGPEQTQGNFG_288
Bat-SL-CoVZXC21     276_RRGPEQTQGNFG_287
Bat-SL-CoVZC45      276_RRGPEQTQGNFG_287
RaTG13              276_RRGPEQTQGNFG_287
SARS-CoV-2          276_RRGPEQTQGNFG_287
                        ************
```

uBCEL-N7

```
SARS-CoV            340_LDDKDP_345
Bat-SL-CoVZXC21     339_LDDKDP_344
Bat-SL-CoVZC45      339_LDDKDP_344
RaTG13              339_LDDKDP_344
SARS-CoV-2          339_LDDKDP_344
                        ******
```

uBCEL-N8

```
SARS-CoV            363_FPPTEPKKDKKKKTDEAQPLP_383
Bat-SL-CoVZXC21     363_FPPTEPKKDKKKKADELQALP_383
Bat-SL-CoVZC45      363_FPPTEPKKDKKKKADELQALP_383
RaTG13              363_FPPTEPKKDKKKKADETQALP_383
SARS-CoV-2          363_FPPTEPKKDKKKKADETQALP_383
                        **************:** * **
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Supplementary Table S1. References for databases and methods utilized in this study.

Method/database	Application	Reference
AAPPred	Prediction of linear B-cell epitopes	[1]
ABCPred	Prediction of linear B-cell epitopes	[2]
Bepipred	Prediction of linear B-cell epitopes	[3]
Bepipred 2.0	Prediction of linear B-cell epitopes	[4]
BLAST	Sequence database searching	[5]
CD-HIT 4.8.1	Sequence clustering	[6]
Clustal Omega 1.2.4	Sequence alignment	[7]
COILS	Prediction of coiled-coil regions	[8]
DISOPRED 3.1	Prediction of disordered regions	[9]
Emini	Prediction of accessibility	[10]
IUPRED2	Prediction of unstructured regions	[11]
Janin	Prediction of exposed surface	[12]
Karplus	Prediction of flexibility	[13]
Kolaskar	Prediction of antigenicity	[14]
LBEEP	Prediction of linear B-cell epitopes	[15]

Mega 7	Environment for phylogeny analysis	[16]
NCBI	Sequence database for searching	[17]
Neighbor-Joining	Calculation of phylogeny	[18]
NetMHCpan EL 4.0	Prediction of HLA-1 epitopes	[19]
NetMHCIIpan 3.2	Prediction of HLA-2 epitopes	[20]
Parker	Prediction of hydrophilicity	[21]
Pellenquer	Prediction of turns	[22]
Pfam 32.0	Identification of protein domains	[23]
Phobius	Prediction of transmembrane helices	[24]
Poison correction	Calculation of phylogenetic branch lengths	[25]
Ponnuswamy	Prediction of polarity	[26,27]
PSI-PRED 4.0	Prediction of secondary structure	[27]
SDPPred	Identification of SDPs	[28]
SignalP 5.0	Prediction of signal peptide	[29]
SVMtrip	Prediction of linear B-cell epitopes	[30]

Supplementary Table S2. Linear B-cell epitopes identified in spike (S), envelope (E), membrane (M), and nucleocapsid (N) proteins of SARS-CoV and SARS-CoV-2 that have been validated *in vivo*.

Structural proteins and subunits			Epitope		Coronavirus	Experiment type	Experimental evidence	Reference
			Location (residues)	Sequence				
S	S1	S1B	357-365	RISNCVADY	SARS-CoV-2	*In silico*	Not tested	[31]
			361-369	CVADYSVLY				
			369-391	YNSASFSTFKCYGVSPTKLNDLCF	SARS-CoV-2	*In vitro*	Not tested	[32]
			424-437	KLPDDFTGCVIAWN	SARS-CoV-2	*In silico*	Not tested	[33]
			447-458	NYNYLYRLFRK				
			92-96	ASTEK	SARS-CoV-2	*In silico*	Not tested	[34]
			110-115	LDSKTQ				
			352-357	AWNRKR				
			373-390	SFSTFKCYGVSPTKLNDL	SARS-CoV-2	*In silico*	Not tested	[35]
			434-467	GNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPC	SARS-CoV	*In vitro*	Sera contain neutralizing IgG antibody against peptides	[36]
			460-476	FSPDGKPCTPPALNCYW	SARS-CoV	*In vitro*	Monoclonal antibodies which neutralize the virus *in vitro*	[37]
			337-360	VYAWERKKISNCVADYSVLYNSTF	SARS-CoV	*In vitro*	Construction of mimotopes that reveal key amino acid residues involved in antibody binding	[38]
			380-399	SNVYADSFVVKGDDVRQIAP				
			491-510	YQPYRVVVLSFELLNAPATV	SARS-CoV	*In vitro*	Epitope recognized by monoclonal antibodies with virus neutralizing activity	[39]
			437-459	NYKYRYLRHGKLRPFERDISNVP	SARS-CoV	*In silico* *in vitro* *in vivo*	Induction of cellular and humoral responses. Epitope recognized by polyclonal sera	[40]

			336-352	SVYAWERKKISNCVADY	SARS-CoV	*In silico*	No tested	[41]
			424-435	NTRNIDATSTGN				
			442-458	YLKHGKLRPFERDISNV				
			459-470	PFSPDGKPCTPP				
			483-494	FYTTTGIGYQPY				
			424-435	NTRNIDATSTGN	SARS-CoV	*In silico* *in vitro* *in vivo*	Peptide recognized by antibodies in sera	[42]
			536-552	GVLTPSSKRFQPFQQFG	SARS-CoV	*In vitro* *in vivo*	Immunized mice produce antibodies with neutralizing activity	[43]
			335-352	SVYAWERKKISNCVADY	SARS-CoV	*In vitro*	Neutralizing antibodies that recognized epitopes in the RBD	[44]
			442-458	YLRHGKLRPFERDISNV				
			430–454	ATSTGNYNYKYRYLRHG KLRPFERD	SARS-CoV	*In silico* *in vitro*	Antigen recognized by monoclonal antibody	[45]
			447-458	LRPFERDISNV	SARS-CoV	*In silico* *in vitro*	Predicted epitope recognized by monoclonal antibody *in vitro*	[46]
			343-367	KKISNCVADYSVLYNSTF FSTFKCY	SARS-CoV	*In vitro* *in vivo*	Antigen recognized by antibodies with virus neutralizing activity	[47]
			373-390	KLNDLCFSNVYADSFVV K				
			411-428	KLPDDFMGCVLAWNTRN I				
			323-334	CPFGEVFNATKF	SARS-CoV	*In vitro*	Convalescent sera with high neutralizing activity against SARS-CoV recognized epitopes in the peptides	[48]
			467-480	CTPPALNCYWPLND				
			471-503	ALNCYWPLNDYGFYTTT GIGYQPYRVVVLSFEL	SARS-CoV-2	*In silico* *in vitro*	Antibodies against a peptide located in the receptor binding domain block binding and entrance of SARS-CoV into host cells in vitro	[49]
			287-317	DAVDCALDPLSETKCTLK SFTVEKGIYQTSN	SARS-CoV-2	*In silico*	Not tested	[50]

			524-598	VCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVI				
			815-823	RSFIEDLLF	SARS-CoV-2	*In silico*	Not tested	[31]
			1039-1047	RVDFCGKGY				
			1237-1245	MTSCCSCLK				
			1264-1272	VLKGVKLHY				
			144-153	YYHKNNKSWM	SARS-CoV-2	*In silico*	Not tested	[34]
			277-283	KYNENGT				
			15-30	CVNLTTRTQLPPAYTN	SARS-CoV-2	*In silico*	Not tested	[35]
			61-76	NVTWFHAIHVSGTNGT				
			175-201	KSGNFKHLREFVFKNKDGFLYVYKGY	SARS-CoV	*In vitro*	Sera contain neutralizing IgG against peptides	[36]
			174-195	EKSGNFKHLREFVFKNKDGFLY	SARS-CoV	*In silico* *in vitro*	Induction of cellular and humoral responses. Epitope recognized by polyclonal sera	[40]
			91-102	ATEKSNVVRGWV				
			291-308	KSFEIDKGIYQTSNFRVV	SARS-CoV	*In vitro* *in vivo*	Inoculation induces IgG and IgA in mice that exhibit potent neutralizing activity against SARS-CoV	[51]
			130-150	FELCDNPFFAVSKPMGTQTHT	SARS-CoV	*In vitro*	Antibodies block the binding of S protein to Vero E6 cells	[52]
			49–62	SDTLYLTQDLFLPF	SARS-CoV	*In vitro*	Convalescent sera with high neutralizing activity against SARS-CoV recognized epitopes in the peptides	[48]
			295–306	IDKGIYQTSNFR				
	S		601-640	GTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGS	SARS-CoV-2	*In silico*	Not tested	[21]
			802-819	FSQILPDPSKPSKRSFIE				

		888-909	FGAG LQIPFAMQMAYRFNG				
	2	814-826	KRSFIEDLLFNKV	SARS-CoV-2	*In silico*	Not tested	[53]
		560-571	LPFQQFGRDIAD	SARS-CoV-2	*In silico*	Not tested	[33]
		754-764	LQYGSFCTQLN				
		789-799	YKTPPIKDFGG				
		1139-1152	DPLQPELDSFKEEL				
		527-530	PKKS	SARS-CoV-2	*In silico*	Not tested	[34]
		601-606	GTNTSN				
		689-700	YQTQTNSPRRAR				
		771-779	EQDKNTQ				
		1154-1162	KYFKNHTSP				
		1141-1184	LQPELDSFKEELDKYFKN HTSPDVDLGDISGINASV VNIQKEID	SARS-CoV-2	*In vitro*	Neutralizing antibodies recognize the S2 domain of S protein and confers protection against a wide range of SARS-CoVs	[54]
		1128-1159	DSFKEELDKYFKNHTSPD VDLGDISGINASVV				
		958-966	VLNDILSRL	SARS-CoV	*In vitro*	Sera contained neutralizing IgG antibody against peptides	[36]
		1156−1178	ASVVNIQKEIDRLNEVAK NLNES	SARS-CoV	*In silico* *in vitro* *in vivo*	Sera from vaccinated mice contain IgG that exhibit virus neutralization activity	[55]
		556-568	SDFTDSVRDPKTS	SARS-CoV	*In silico* *in vitro*	Induction of cellular and humoral responses. Epitope recognized by polyclonal sera	[40]
		915-949	QIQESLTTTSTALGKLQD VVNQNAQALNTLVKQLS	SARS-CoV	*In silico*	Not tested	[41]
		1150-1184	ISGINASVVNIQKEIDRLN EVAKNLNESLIDLQE				
		1065-1076	HEGKAYFPREGV	SARS-CoV	*In silico* *in vitro* *in vivo*	Peptide recognized by antibodies in sera	[56]
		520-537	IKNQCVNFNFNGLTGTGV	SARS-CoV	*In vitro*	Inoculation in mice induces IgG	[51]

		564-581	DPKTSEILDISPCSFGGV		*in vivo*	and IgA that exhibit a potent neutralizing activity against SARS-CoV	
		540-554	PSSKRFQPFQQFGRD	SARS-CoV	*In silico* *in vitro*	Peptides at the N- the C-terminal regions of the N protein elicited strong antibody responses.	[57]
		553-570	RDVSDFTDSVRDPKTSEI				
		1236-1255	CKFDEDDSEPVLKGVKL HYT				
		1091-	NFFSPQIITTDNTFVSGNC DVVIGIINNTVYDPLQPEL DSFKEELDKYFKNHTSPD VDLGDISGINASVVNIQK EIDRLNEVAKNLNESLID LQELGKYEQYI	SARS-CoV	*In vitro*	Antibodies recognized HR2 domain and neutralize virus infection *in vitro*	[58]
		1143-1157	SPDVDLGDISGINAS	SARS-CoV	*In vitro*	Antibodies recognized HR2 domain	[59]
		539-559	TPSSKRFQPFQQFGRDVS DFT	SARS-CoV	*In vitro*	Four epitopes in S1 domain induce a humoral response in mice	[60]
		548-567	FQQFGRDVSDFTDSVRDP KT				
		583-606	VITPGTNASSEVAVLYQD VNCTDV				
		607-630	STAIHADQLTPAWRIYST GNNVFQ				
		927–937	GLGKLQDVVNQNGE	SARS-CoV	*In vitro*	Antibodies recognized SARS-CoV	[61]
		942–951	ALNTLVKQLSSNC				
		789-799	PDPLKPTKRSF	SARS-CoV	*In silico* *in vitro*	Epitope recognized by monoclonal antibody	[46]
		540-559	PSSKRFQPFQQFGRDVSD FT	SARS-CoV	*In silico* *in vitro* *in vivo*	Antibodies without neutralizing activity but inhibit syncytia formation	[62]
		731–753	CANLLLQYGSFCTQLNR ALSGIA				
		786-811	QILPDPLKPTKRSFIEDLL FNKVTLA	SARS-CoV	*In vitro*	Convalescent sera recognize S2 domain	[63]
		490-510	GYQPYRVVVLSFELLNAP	SARS-CoV	*In vitro*	Antibodies block the binding of S	[52]

			AT			protein to Vero E6 cells	
		599-620	QDVNCTDVSTAIHADQLTPAWR	SARS-CoV	*In silico* *in vitro*	Sera from patients with SARS-CoV react with peptides	[64]
		947-965	QLSSNFGAISSVLNDILSR				
		607-627	STAIHADQLTPAWRIYSTGN	SARS-CoV	*In vitro*	Peptide recognized by monoclonal antibodies which neutralize SARS-CoV	[65]
		599-620	QDVNCTDVSTAIHADQLTPAWR	SARS-CoV	*In silico* *in vitro*	Peptide recognized by antibodies in sera	[66]
		597-603	LYQDVNC	SARS-CoV	*In vitro*	Immunization with this peptide induces antibodies that enhance infection both *in vitro* and in non-human primate	[67]
		731-745	CANLLLQYGSFCTQL	SARS-CoV	*In vitro* *in vivo*	Antibodies recognize the cleavage site critical for SARS-CoV entry into host cells	[68]
		545-558	FQPFQQFGRDVSDF	SARS-CoV	*In vitro*	Convalescent sera with high neutralizing activity against SARS-CoV recognized epitopes in the peptides	[48]
		553-564	RDVSDFTDSVRD				
		651-662	PIGAGICASYHT				
		663-674	VSLLRSTSQKSI				
		695–708	AIPTNFSISITTEV				
		737–748	QYGSFCTQLNRA				
		879–890	PFAMQMAYRFNG				
		791-805	PLKPTKRSFIEDLLF	SARS-CoV	*In vitro*	Peptides recognized by convalescent sera	[69]
		1111-1130	VIGVINNTVYDPLQPELDSF	SARS-CoV	*In vitro*	Peptide recognized by neutralizing antibody that prevents viral	[70]
		60-76	SRVKNLNSSEGVPDLLV	SARS-CoV	*In silico* *in vitro*	Peptides elicit antibody responses	[57]

E	55-70	TVYVYSRVKNLNSSEG	SARS-CoV	*In vitro*	Convalescent sera with high neutralizing activity against SARS-CoV recognized epitopes in the peptides	[48]
M	1-24	MADSNGTITVEELKKLLEQWNLVI	SARS-CoV-2	*In silico*	No tested	[50]
	132-151	PLLESELVIGAVILRGHLRI				
	1-31	MADNGTITVEELKQLLEQWNLVIGFLFLAWI	SARS-CoV	*In silico* *in vitro*	Peptides react with convalescent sera and induce high antibody titers in rabbits	[44]
	132-161	LMESELVIGAVIIRGHLRMAGHSLGRCDIK				
	1-20	MADNGTITVEELKQLLEQWN	SARS-CoV	*In silico* *in vitro*	Peptide recognized by monoclonal antibody	[40]
	149-163	RMAGHSLGRCDIKDLP	SARS-CoV	*In silico* *in vitro* *in vivo*	Peptide recognized by monoclonal antibody	[42]
	173-185	PKEITVATSRTLS				
	204-221	KLNTDHAGSNDNIALLVQ				
	1-18	MADNGTITVEELKQLLEQ	SARS-CoV	*In silico* *in vitro*	Peptides elicit an antibody response	[57]
	1-15	MADNGTITVEELKQL	SARS-CoV	*In vitro*	Recognition by convalescent sera	[71]
	165–176	KEITVATSRTLS	SARS-CoV	*In vitro*	Convalescent sera with high neutralizing activity against SARS-CoV recognized epitopes in the peptides	[48]
	5–16	GTITVEELKQLL				
	137–158	LVIGAVIIRGHLRMAGHSLGR	SARS-CoV	*In silico* *in vitro*	Peptide recognized by antibodies in sera	[66]
N	42-62	RPQGLPNNTASWFTALTQHGK	SARS-CoV-2	*In silico*	Not tested	[50]
	153-172	NNN TVLQLPQGTTLPKGF				
	355-401	NKHIDAYKTFPPTEPKKDKKKKTDEAQPLPQRQKKQPTVTLLP DM				

	111-125	FYYLGTGPEASLPYG	SARS-CoV	*In vitro*	Peptide reacts with sera form mouse, rat, rabbit, civet, pig and horse	[72]
	1–17	MSDNGPQSNQRSAPRIT	SARS-CoV	*In silico* *in vitro*	Peptides elicit antibody responses	[57]
	13–30	APRITFGGPTDSTDNNQN				
	25–43	TDNNQNGGRNGARPKQRRP				
	38–55	PKQRRPQGLPNNIASWFT				
	341–360	DDKDPQFKDNVILLNKHIDA				
	356–375	KHIDAYKTFPPTEPKKDKKK				
	371–390	KDKKKKTDEAQPLPQRQKKQ				
	11-19	RSAPRITF	SARS-CoV	*In vitro*	Antibody binding in phage library screen	[73]
	17-32	TFGGPTDSTDNNQNGG	SARS-CoV	*In vitro*	Peptides recognized by antibodies	[74]
	135-150	ATEGALNTPKDHIGTR				
	117-132	GPEASLPYGANKEGIV				
	215-239	GGETALALLLLDRLNQLESKVSGKG				
	245-268	QTVTKKS EASKKPRQKRTATKQ				
	274-283	AFGRRGPEQT	SARS-CoV	*In vitro*	Monoclonal antibodies recognized epitopes	[75]
	286-295	NFGDQDLIRQ				
	316-325	FGMSRIGMEV				
	361-367	YKTFPPT				
	1-30	MSDNGPQSNQRSAPRITFGGPTDSTDNNQN	SARS-CoV	*In vitro*	Peptide recognition by antibodies	[76]
	81-95	PDDQIGYYRRATRRV				
	86-100	GYYRRATRRVRGGDG				
	156-175	TVLQLPQGTTLPK				
	300-320	HWPQIAQFAPSASAFFGM				

		SR				
	336-350	GAIKLDDKDPQFKDN				
	351-365	VILLNKHIDAYKTFP				
	1-69	MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQGLPNNIASWFTALTQHGKEELRFPR	SARS-CoV	*In vitro*	Recognition by monoclonal antibodies	[77]
	1-20	MSDNGPQSNQRSAPRITFGG	SARS-CoV	*In vitro*	Peptides react with convalescent sera. Antibody production after peptide immunization	[78]
	150-170	RNPNNNTVLQLPQGTTLPK				
	390-410	QPTVTLLPDMDDFSRQLQN				
	371-390	KDKKKKTDEAQPLPQRQKKQ	SARS-CoV		Peptides react with convalescent sera	[79]
	385-407	QRQKKQPTVTLLPDMDDFSRQ				
	52-59	SWFTALTQ	SARS-CoV	*In silico* *in vitro*	Synthetic peptides react with convalescent sera and antisera from mice immunized with inactivate SARS-CoV	[80]
	83-89	DQIGYYR				
	156-166	TVLQLPQGT				
	218-227	TALALLLLDR				
	347-363	FKDNVILLNKHIDAYKT				
	379-385	EAQPLPQ				
	389-398	KQPTVTLLPA				
	66-87	QLPQGTTLPKGFYAEGSRGGSQ	SARS-CoV	*In silico* *in vitro*	Peptide recognized by antibodies in sera	[66]
	371–390	KDKKKKTDEAQPLPQRQKKQ				

Abbreviations:

[a] IEDB: Immune Epitope Database

[b] PISA: Proteins, Interfaces, Structures and Assemblies

[c] ViPR: Virus Pathogen Database and Analysis Resource

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