

# **Title: Immunoinformatics based identification of B and T-Cell epitopes in RNA dependent RNA polymerase of SARS-CoV-2**

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**Supplementary Table S1.** B-cell epitopes predicted using the BCPREDS server along with their VaxiJen score.

<b>S No</b>	<b>Starting amino acid Position</b>	<b>Amino acid sequence of the Peptide epitope</b>	<b>BCPREDS server Score</b>	<b>VaxiJen score</b>
<b>1</b>	219	FGDFIQTPGSGVPVV	0.996	0.3090
<b>2</b>	908	TNDNTSRYWEPEFYEA	0.994	0.0979
<b>3</b>	677	PGGTSSGDATTAYANS	0.989	0.2651
<b>4</b>	443	AQDGNAAISDYDYRY	0.987	0.5716
<b>5</b>	20	TPCGTGTSTDVVYRAF	0.986	0.3946
<b>6</b>	794	MSEAKCWTETDLTKGP	0.981	0.5943
<b>7</b>	477	DKYFDCYDGGCINANQ	0.973	0.6443
<b>8</b>	821	KQGDDYVYLPYPDPSR	0.973	0.0896
<b>9</b>	866	AYPLTKHPNQEYADV	0.973	0.1365
<b>10</b>	283	FDRYFKYWDQTYHPNC	0.959	0.3082
<b>11</b>	135	DEGNCDTLKEILVTYN	0.942	-0.1097
<b>12</b>	347	HFRELGVVHNQDVNLH	0.938	1.4181
<b>13</b>	48	FLKTNCCRFQEKDEDD	0.919	0.5726

**Supplementary Table S2.** Top 40 HTL epitopes of RdRP predicted using IEDB server with their VaxiJen score.

S No	Amino acid (AA) sequence of the Peptide epitope	HLA allele to which epitope can bind	Starting AA Position	Percentile Rank	Vaxijen Score
1	AMPNMLRIMASLVLA	HLA-DRB1*15:01	205	0.01	0.096
2	MPNMLRIMASLVLAR	HLA-DRB1*15:01	206	0.01	0.1001
3	NMLRIMASLVLARKH	HLA-DRB1*15:01	208	0.01	0.4897
4	PNMLRIMASLVLARK	HLA-DRB1*15:01	207	0.01	0.4128
5	RAMPNMLRIMASVL	HLA-DRB1*15:01	204	0.01	0.0255
6	NEFYAYLRKHFSMMI	HLA-DRB1*11:01	323	0.02	0.2279
7	EFYAYLRKHFSMMIL	HLA-DRB1*11:01	324	0.05	0.39
8	VNEFYAYLRKHFSMM	HLA-DRB1*11:01	322	0.05	0.1645
9	QMNLKYAISAKNRAR	HLA-DPA1*02:01/DPB1*14:01	121	0.07	1.5044
10	MNLKYAISAKNRART	HLA-DPA1*02:01/DPB1*14:01	122	0.08	1.4377
11	FVNEFYAYLRKHFSM	HLA-DRB1*11:01	321	0.11	0.0518
12	TQMNLKYAISAKNRA	HLA-DPA1*02:01/DPB1*14:01	120	0.11	1.4529
13	QKLLKSIAATRGATV	HLA-DPA1*02:01/DPB1*14:01	153	0.12	0.0888
14	NMLRIMASLVLARKH	HLA-DPA1*02:01/DPB1*14:01	208	0.13	0.4897
15	PNMLRIMASLVLARK	HLA-DPA1*02:01/DPB1*14:01	207	0.14	0.4128
16	HQKLLKSIAATRGAT	HLA-DPA1*02:01/DPB1*14:01	152	0.15	0.0799
17	KLLKSIAATRGATVV	HLA-DPA1*02:01/DPB1*14:01	154	0.15	0.1825
18	NLKYAISAKNRARTV	HLA-DPA1*02:01/DPB1*14:01	123	0.15	1.3422
19	DSYSSLMPILTLTR	HLA-DRB1*01:01	25	0.16	0.5134
20	FHQKLLKSIAATRGA	HLA-DPA1*02:01/DPB1*14:01	151	0.16	0.2173
21	SYSSLMPILTLTRA	HLA-DRB1*01:01	26	0.16	0.5509
22	VDSYSSLMPILTLT	HLA-DRB1*01:01	24	0.16	0.5149
23	VVDSYSSLMPILTL	HLA-DRB1*01:01	23	0.16	0.4474
24	KELLVYAADPAMHAA	HLA-DRB3*01:01	159	0.2	0.1356
25	MLRIMASLVLARKHT	HLA-DPA1*02:01/DPB1*14:01	209	0.2	0.5283
26	DFVNEFYAYLRKHFS	HLA-DRB1*11:01	320	0.22	0.0385
27	MLRIMASLVLARKHT	HLA-DRB1*15:01	209	0.22	0.5283
28	PVVDYSSLMPILT	HLA-DRB1*01:01	22	0.24	0.4117
29	NFNVLFTVPPTSF	HLA-DPA1*01:03/DPB1*04:01	102	0.3	0.5021
30	FKELLVYAADPAMHA	HLA-DRB3*01:01	158	0.31	0.0669
31	PNMLRIMASLVLARK	HLA-DRB1*01:01	207	0.31	0.4128
32	LRIMASLVLARKHTT	HLA-DPA1*02:01/DPB1*14:01	210	0.32	0.6646
33	MPNMLRIMASLVLAR	HLA-DPA1*02:01/DPB1*14:01	206	0.34	0.1001
34	LPILTTLTRALTAES	HLA-DRB1*08:02	31	0.37	0.4225
35	VFHLYLQYIRKLHDE	HLA-DRB4*01:01	460	0.37	0.2814
36	DVFHLYLQYIRKLHD	HLA-DRB4*01:01	459	0.38	0.3189
37	MPILTTLTRALTAESH	HLA-DRB1*08:02	32	0.38	0.3258
38	FHLYLQYIRKLHDEL	HLA-DRB4*01:01	461	0.39	0.3059
39	ITQMNLKYAISAKNR	HLA-DPA1*02:01/DPB1*14:01	119	0.41	1.5061
40	MPNMLRIMASLVLAR	HLA-DRB1*01:01	206	0.41	0.1001

**Supplementary Table S3.** CTL epitopes predicted using NetCTL 1.2 server with their VaxiJen score and ToxinPred server report.

A2 supertype binding peptides	Start	VaxiJen score	A3 supertype binding peptides	Start	VaxiJen score	B7 supertype binding peptides	Start	VaxiJen score
TMADLVYAL	123	0.8208	RLYYDSMSY	513	-0.1146	FPPTSFGPL	321	1.6296
LMIERFVSL	854	-0.0605	HLYLQYIRK	882	0.492	VPHISRQRL	111	0.1685
FVNEFYAYL	741	-0.4788	KLFDRYFKY	281	-0.0533	KPYIKWDLL	263	0.4825
NLIDSYFVV	64	0.4282	RQFHQKLLK	569	-1.0437	AVTANVNAL	699	0.3733
ILHCANFNV	307	0.5385	KSAGFPFNK	500	1.1874	KARLYYDSM	511	-0.0551
MLDMYSVML	899	0.5626	TSFGPLVRK	324	1.7142	MPNMLRIMA	626	-0.2116
NMLRIMASL	628	-0.3326	MTNRQFHQK	566	0.5341	YVRNLQHRL	719	-0.4066
YTMADLVYA	122	1.0142	MVMCGGSLY	666	-0.259	IPTITQMNL	536	0.7997
FVDGVPFVV	334	0.1285	HISRQRLTK	113	-0.8467	ATRGTAVVI	581	0.5688
LLMPILTTL	240	0.5803	IMASLVLAR	632	0.5587	TPCGTGTST	20	0.7838
SLSHRFYRL	647	0.4779	AVAKHDFFK	95	-0.8254	LPYPDPSRI	829	-0.1931
SLAIDAYPL	861	0.7576	LVASIKNFK	775	0.8148	CPAVAKHDF	93	1.1025
RQLLFVVEV	467	0.816	HLMGWDPYK	613	-0.2495	YLRKHFSMM	748	0.4887
NLLKDCPAV	88	-0.5347	LIDSYFVVK	65	0.4939	RVRQALLKT	181	-0.5069
SVFNICQAV	692	-0.416	RVYANLGER	173	0.6654	MPILTTLRA	242	0.8061
MILSDDAVV	756	-0.1842	KNFKSVLYY	780	0.1643	IAATRGTATV	579	0.8883
SLLMPILTTL	239	0.2133	MASLVLARK	633	1.3011	AALTNNVAF	399	0.6381
VMCGGSLYV	667	-0.2332	CSQHTMLVK	813	0.1398	RAMPNMLRI	624	0.0566
RLANECAQV	654	0.9246	LSFKELLVY	366	0.7234	KPGNFNKDF	411	0.8932
KQGDDYVYL	821	0.4041	TVKPGNFNK	409	1.3778	GPLVRKIFV	327	-0.0569
QLLFVVEVV	468	0.821	AIDAYPLTK	863	0.5972	SAKNRARTV	549	0.9661
RIMASLVLA	631	0.1241	FAVSKGFFK	422	-0.2311	SIKNFKSVL	778	0.2414
SVLYYQNNV	784	0.5524	CSLSHRFYR	646	0.629	FAYTKRNV	528	1.0296
YADVFLHLY	877	0.0159	TITQMNLKY	538	1.6155	YIRKLHDEL	887	-0.2677
RLSFKELLV	365	0.8643	ISRQRLTKY	114	-0.6868	IERFVSLAI	856	0.1775
HMLDMYSVM	898	0.5853	LLKSIAATR	575	0.2055			
VVDSYYSLL	233	0.5381	RVCVSAAR	10	0.6078			
AMYTPHTVL	923	0.1196	ATVVIGTSK	585	0.7566			
SVAALTNNV	397	0.3839	RAFDIYNKD	33	0.5993			
MMILSDDAV	755	-0.1616	TLKEILVTY	141	0.1118			
KLLKSIAAT	574	-0.4372	LTNDNTSRY	907	-0.3497			
KLFDRYFKY	281	-0.0533	ASGNLLLDK	383	-0.4206			
RILGAGCFV	836	0.3846	NLKYAISAK	543	1.3508			
VTANVNALL	700	0.1708	VAGFAKFLK	42	-0.7456			
FMSEAKCWT	793	0.3756	ALLSTDGKN	706	-0.1557			
			MLTNDNTSR	906	-0.3109			
			SQGLVASIK	772	0.6336			
			VVIGTSKFY	587	0.7146			
			LMPILTLTR	241	0.9617			
			RLSFKELLV	365	0.8643			
			VVSTGYHFR	341	1.4741			
			VVYRAFDIY	30	0.7331			
			DVFHLYLQY	879	0.6321			
			MVPHISRQR	110	0.4279			
			SICSTMTNR	561	1.1164			
			RIMASLVLA	631	0.1241			
			YIKWDLLKY	265	-0.321			
			KLHDELTHG	890	0.4147			

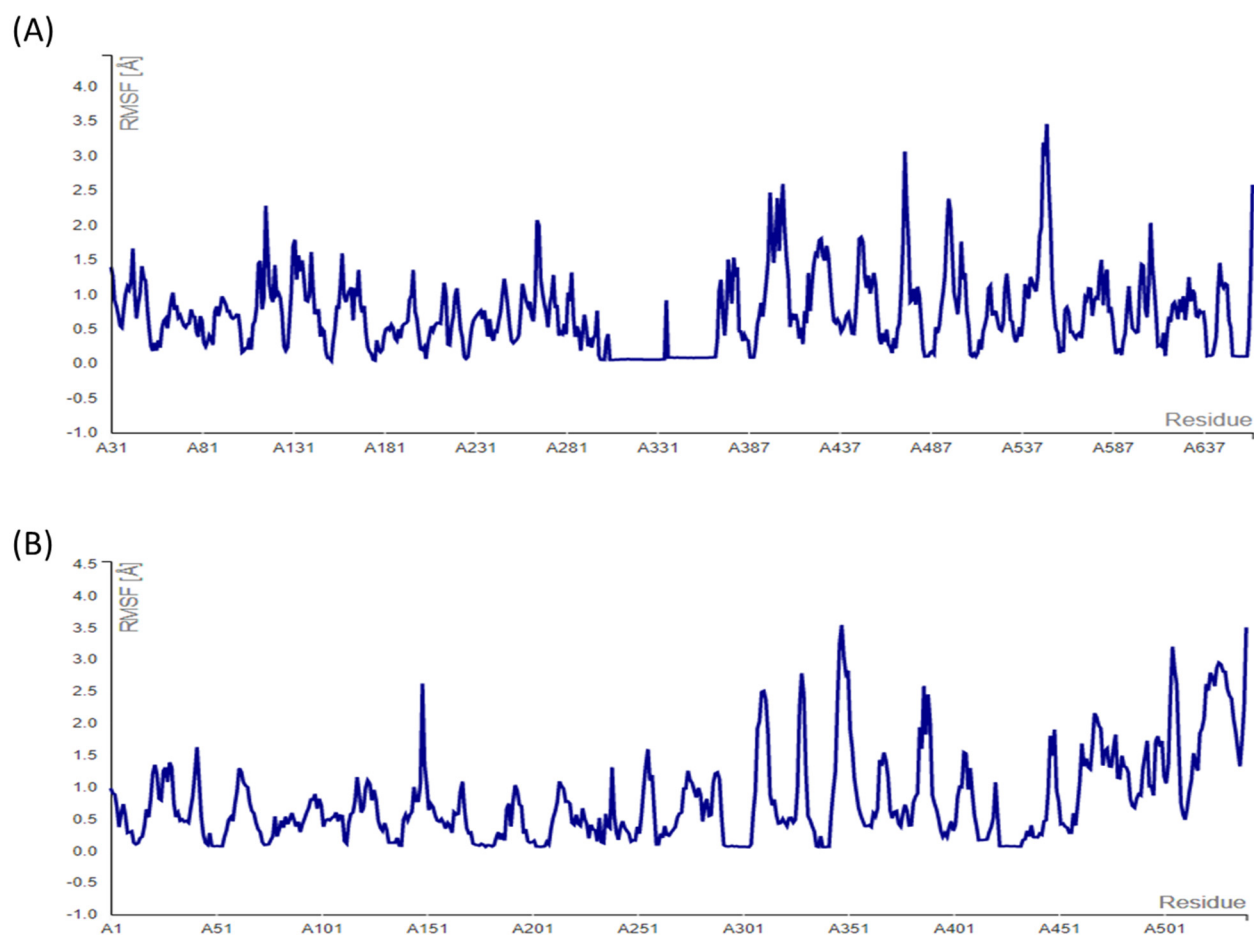
**Supplementary Table S4.** ToxinPred report for CTL epitopes having VaxiJen score above the threshold of 0.4

<b>A2 supertype binding peptides</b>			<b>A3 supertype binding peptides</b>			<b>B7 supertype binding peptides</b>		
<b>Amino acid sequence of the peptides</b>	<b>VaxiJen score</b>	<b>ToxinPred report</b>	<b>Amino acid sequence of the peptides</b>	<b>VaxiJen score</b>	<b>ToxinPred report</b>	<b>Amino acid sequence of the peptides</b>	<b>VaxiJen score</b>	<b>ToxinPred report</b>
<b>TMADLVYAL</b>	0.8208	Non-Toxin	<b>HLYLQYIRK</b>	0.492	Non-Toxin	<b>FPPTSFGPL</b>	1.6296	Non-Toxin
<b>NLIDSYFVV</b>	0.4282	Non-Toxin	<b>KSAGFPFNK</b>	1.1874	Non-Toxin	<b>KPYIKWDLL</b>	0.4825	Non-Toxin
<b>ILHCANFNV</b>	0.5385	Non-Toxin	<b>TSFGPLVRK</b>	1.7142	Non-Toxin	<b>IPITITQMNL</b>	0.7997	Non-Toxin
<b>MLDMYSVML</b>	0.5626	Non-Toxin	<b>MTNRQFHQK</b>	0.5341	Non-Toxin	<b>ATRGATVVI</b>	0.5688	Non-Toxin
<b>YTMADLVYA</b>	1.0142	Non-Toxin	<b>IMASLVLAR</b>	0.5587	Non-Toxin	<b>TPCGTGTST</b>	0.7838	Non-Toxin
<b>LLMPILTLT</b>	0.5803	Non-Toxin	<b>LVASIKNFK</b>	0.8148	Non-Toxin	<b>CPAVAKHDF</b>	1.1025	Non-Toxin
<b>SLSHRFYRL</b>	0.4779	Non-Toxin	<b>LIDSYFVVK</b>	0.4939	Non-Toxin	<b>YLRKHFSMM</b>	0.4887	Non-Toxin
<b>SLAIDAYPL</b>	0.7576	Non-Toxin	<b>RVYANLGER</b>	0.6654	Non-Toxin	<b>MPILTLTRA</b>	0.8061	Non-Toxin
<b>RQLLFVVEV</b>	0.816	Non-Toxin	<b>MASLVLARK</b>	1.3011	Non-Toxin	<b>IAATRGATV</b>	0.8883	Non-Toxin
<b>RLANECAQV</b>	0.9246	Non-Toxin	<b>LSFKELLVY</b>	0.7234	Non-Toxin	<b>AALTNNVAF</b>	0.6381	Non-Toxin
<b>KQGDDYVYL</b>	0.4041	Non-Toxin	<b>TVKPGNFNK</b>	1.3778	Non-Toxin	<b>KPGNFNKDF</b>	0.8932	Non-Toxin
<b>QLLFVVEVV</b>	0.821	Non-Toxin	<b>AIDAYPLTK</b>	0.5972	Non-Toxin	<b>SAKNRARTV</b>	0.9661	Non-Toxin
<b>SVLYYQNNV</b>	0.5524	Non-Toxin	<b>CSLSHRFYR</b>	0.629	Non-Toxin	<b>FAYTKRNVI</b>	1.0296	Non-Toxin
<b>RLSFKELLV</b>	0.8643	Non-Toxin	<b>TITQMNLKY</b>	1.6155	Non-Toxin			
<b>HMLDMYSVM</b>	0.5853	Non-Toxin	<b>RVCGVSAAR</b>	0.6078	Non-Toxin			
<b>VVDSYYSLL</b>	0.5381	Non-Toxin	<b>ATVVIGTSK</b>	0.7566	Non-Toxin			
			<b>RAFDIYNDK</b>	0.5993	Non-Toxin			
			<b>NLKYAISAK</b>	1.3508	Non-Toxin			
			<b>SQGLVASIK</b>	0.6336	Non-Toxin			
			<b>VVIGTSKFY</b>	0.7146	Non-Toxin			
			<b>LMPILTLTR</b>	0.9617	Non-Toxin			
			<b>RLSFKELLV</b>	0.8643	Non-Toxin			
			<b>VVSTGYHFR</b>	1.4741	Non-Toxin			
			<b>VVYRAFDIY</b>	0.7331	Non-Toxin			
			<b>DVFHLYLQY</b>	0.6321	Non-Toxin			
			<b>MVPHISRQR</b>	0.4279	Non-Toxin			
			<b>SICSTMTNR</b>	1.1164	Non-Toxin			
			<b>KLHDELTGH</b>	0.4147	Non-Toxin			

## Supplementary Figures:

MRTSYLLLF<sup>T</sup>LC<sup>L</sup>LLSEMASGGN<sup>F</sup>LTGLGHRSDHYNCVSSGGQCLYSACPIFTKI<sup>Q</sup>GTCYRGKAK<sup>C</sup>CK  
EAAAK<sup>M</sup>MLDMYSV<sup>M</sup>LAAY<sup>R</sup>QLLFVVEVAAYRLANECAQV<sup>A</sup>AYS<sup>V</sup>LYYQNNV<sup>A</sup>AY<sup>R</sup>LSFKELLVAA  
YLSFKELLV<sup>A</sup>AYTVKPGNFNKAAY<sup>R</sup>VCGVSAARAAYATV<sup>V</sup>IGTSKAAYNLKYAISAKAAY<sup>R</sup>LSFKEL  
LV<sup>A</sup>AYVVSTGYHFRAAYKLHDELTGH<sup>A</sup>AYATRGATV<sup>V</sup>IAAYMPILTLTRAAYIAATRGATV<sup>A</sup>AYA  
ALTNNVAF<sup>A</sup>AYFAYTKRNVIGPGPGNMLRIMASLV<sup>L</sup>LARKHGPGPGNMLRIMASLV<sup>L</sup>LARKGPGP  
GQMNLKYAISAKNRARGPGPGMNLKYAISAKNRARTGPGPGNLKYAISAKNRARTVGP<sup>G</sup>PGDSY  
YSLMPILTLTRGPGPGMLRIMASLV<sup>L</sup>LARKHTGPGPGLRIMASLV<sup>L</sup>LARKHTTGPGPGLMPILTLTRA  
LTAESGPGPGITQMNLKYAISAKNRKKAQDGNAAISDYDYRYKKDKYFDCYDGGCINANQKKHF  
RELGVVHNQDVNLH

**Supplementary Figure S1.** The designed vaccine construct sequence. The sequence of epitopes in the designed vaccine is: Adjuvant-CTL epitopes-HTL epitopes-B cell epitopes. The first 68 amino acids are occupied by the adjuvant,  $\beta$ -defensin 1 (Blue color), next 5 amino acids are of EAAAK linker (Orange color) and the amino acids from 74-286 constitute the CTL epitopes (Red color) whereas the amino acids from 287-486 and from 487-540 correspond to HTL (Green color) and B-cell epitopes (Black color), respectively. All the linkers, except EAAAK are represented in purple color.



**Supplementary Figure S2.** Molecular dynamics simulations of the docked complex (TLR3-Designed vaccine). (A) The root-mean-square fluctuation (RMSF) values of the amino acid residues of Chain A (TLR3) of the docked complex. (B) RMSF values of the amino acid residues of Chain B (designed vaccine) of the docked complex.