

**Designing a multi-epitope vaccine against Chickenpox Virus using
in Silico approach**

Supplementary Material

*Johnson Samuel, Madhushruti Borah, Filippo Castiglione,
Sharangouda J Patil**

SUPPLEMENTARY TABLES

<i>Herpesviridae</i> members	Accession numbers retrieved from NCBI			
	gB	gE	gH	gL
HHV-1 (Herpes Simplex virus - 1)	ABI63489	AFK50417	AAA45815	AAA99791
HHV-2 (Herpes Simplex virus - 2)	AFS18177	ABW83308	AIL27745	AIL27763
HHV-3 (Varicella zoster virus)	P09257	P09259	P09260	P09308
HHV-4 (Epstein Barr virus)	ALV83210	–	AKA28420	AFY97944
HHV-5 (Cytomegalo virus)	AFR55048	–	AAA45910	AHB20074
HHV-6 (Roseolovirus)	ALD88873	–	APO37231	AKZ18186
HHV-7 (Roseolovirus)	AAB63200	–	AAB64293	AAC54744
HHV-8 (Kaposi's sarcoma-associated herpesvirus)	ACY00399	–	AAB08395	ADB08193

Supplementary Table 1. Accession numbers of the target glycoproteins in VZV and other members of the *Herpesviridae* family, retrieved from the NCBI database. Blank spaces denote the absence of the glycoprotein in the corresponding organism.

Glycoprotein	Molecular weight (in Da)	Number of amino acids	Theoretical pI	Aliphatic Index	Instability Index	GRAVY	Antigenicity	Number of transmembrane helices
gB	105347.36	931	8.81	78.31	40.73	-0.351	0.5085	2
gE	69956.38	623	5.27	74.59	34.90	-0.392	0.5104	2
gH	93651.56	841	6.16	95.91	33.93	0.049	0.5135	1
gL	17617.29	159	5.05	98.68	32.81	0.118	0.4013	0

Supplementary Table 2. Physiochemical properties, antigenicity, and the number of transmembrane helices in the target glycoproteins as predicted by ExPASy Prototparam tool, VaxiJen v2.0 server, and hmmTOP server respectively.

Protein	Peptide Sequence	Overlapping CTL Epitopes	HLA Class II alleles	HLA Class II supertypes and alleles
gB	FAYRYVLKLKTSMPK	VLKLKTSPM AYRYVLKLK FAYRYVLKL VLKLKTSPM	DRB1*01:01, DRB1*04:01, DRB1*10:01, DRB1*11:01, DRB1*12:01, DRB1*14:01, DRB1*15:01	A2, B8, B39, B58, B62, HLA-A*30:01, HLA-B*08:01, HLA-B*15:01, HLA-B*51:01, HLA-B*53:01
	NLRFRRFFSSIHPNA	RFRRFFSSI LRFRRFFSS NLRFRRFFS RFFSSIHPN	DRB1*04:01, DRB1*10:01, DRB1*11:01, DRB1*15:01	A24, B7, B8, HLA-A*23:01, HLA-A*24:02, HLA-A*30:01, HLA-A*32:01, HLA-B*08:01

	NFRFTMKTLSTTFIS	TMKTLSTTF KTLSTTFIS	DRB1*04:01, DRB1*07:01, DRB1*10:01, DRB1*11:01,	A24, B8, B62, HLA-A*24:02, HLA-A*32:01, HLA-B*15:01, HLA-B*58:01
	YVLKLTSPMKALYP	VLKLTSPM KTSPMKALY VLKLTSPM	DRB1*11:01, DRB1*12:01, DRB1*14:01, DRB1*15:01	A3, A26, B8, B58 B62, HLA-A*01:01, HLA-A*03:01, HLA-A*11:01, HLA-A*30:01, HLA-B*08:01, HLA-B*15:01, HLA-B*57:01, HLA-B*58:01
	FFAYRYVLKLTSPM	VLKLTSPM AYRYVLKLK FAYRYVLKL FFAYRYVLK	DRB1*11:01, DRB1*12:01, DRB1*14:01, DRB1*15:01	A2, A3, A24, B8, B39, B58, B62, HLA-B*08:01, HLA-B*15:01, HLA-A*30:01, HLA-B*51:01, HLA-B*53:01, HLA-A*68:01
gE	TGTLRITNPVRASVL	ITNPVRASV GTLRITNPV	DRB1*08:03, DRB1*13:02, DRB1*14:01	A2, HLA-A*02:01, HLA-A*02:06, HLA-B*58:01, HLA-A*68:02
	ITGTLRITNPVRASV	ITNPVRASV GTLRITNPV	DRB1*08:03, DRB1*13:02, DRB1*14:01	A2, HLA-A*02:01, HLA-A*02:06, HLA-A*68:02, HLA-B*58:01
gH	SVFLRYLTGAIMDI	RYLTGAIM	DRB1*01:01, DRB1*04:01, DRB1*07:01, DRB1*08:03, DRB1*10:01, DRB1*15:01	A24, HLA-A*23:01, HLA-A*24:02
	RYHLSMAHTEALRM T	MAHTEALRM LSMAHTEAL SMAHTEALR	DRB1*04:01, DRB1*07:01, DRB1*10:01, DRB1*14:01	A3, B8, B58, B62, HLA-A*31:01, HLA-A*68:01, HLA-A*68:02, HLA-B*08:01, HLA-B*15:01, HLA-B*35:01, HLA-B*53:01, HLA-B*57:01
	HVNALSLARRVIMSI	HVNALSLAR LSLARRVIM LARRVIMSI NALSLARRV	DRB1*11:01, DRB1*12:01, DRB1*14:01	A3, B7, B8, HLA-A*03:01, HLA-A*11:01, HLA-A*30:01, HLA-A*31:01, HLA-A*68:01, HLA-B*08:01, HLA-B*51:01, HLA-B*57:01, HLA-B*58:01
gL	LQIVFLKTITIAYCL	IVFLKTITI KTITIAYCL FLKTITIAY LQIVFLKTI	DRB1*07:01, DRB1*08:03, DRB1*12:01, DRB1*15:01	A1, A2, A3, A24, A26, B8, B58, B62, HLA-A*01:01, HLA-A*02:06, HLA-A*26:01, HLA-A*32:01, HLA-B*15:01, HLA-B*35:01, HLA-B*51:01, HLA-B*57:01, HLA-B*58:01

Supplementary Table 3. Overlapping HTL and CTL epitopes.

Glycoprotein	Position	B Cell Epitopes	Score
gB	108	HKSQDAETKPTFYVCP	0.97
	263	AGTPGTYRTGTSVNCI	0.95
	212	KCSSKATYVRNNHKVE	0.92
	832	LPEGMDPFAEKP NATD	0.91
	7	YSKWRNRDRPEYRRNL	0.91
	398	TTFISETNEFNLNQIH	0.91
	674	HDVGMISTYVDLNLTL	0.90
	369	CSLVKWREVEDVVRDE	0.90
	200	VSEITDTIDKFGKCSS	0.90

	133	LEPTRTCPDYHLGKNF	0.90
	1	MSPCGYYSKWRNRDRP	0.90
	843	PNATDTPIEEIGDSQN	0.89
	84	EPTQSEDITRSAHLGD	0.89
	156	YKENIAAYKFKATVYY	0.89
	522	DHIQEHVNEMLARISS	0.88
	600	RVSGSTTRCYSRPLIS	0.87
	348	NFLVTPHLTVGWNWKP	0.87
	714	YSEIQRRNQMHSLRFY	0.86
	606	TRCYSRPLISIVSLNG	0.86
	426	INRIYTTRYNSSHVRT	0.86
	252	AWHTTNDTYMVAGTPG	0.86
	884	LVSAAERQESKARKKN	0.85
	863	VNSGFDPDKFREAQEM	0.85
	441	TGDIQTYLARGGFVVV	0.85
	298	GDIIYMSPFFGLRDGA	0.85
	850	IEEIGDSQNTEPSVNS	0.84
	590	DTRIILQNSMRVSGST	0.84
	549	LWSGLFPINPSALAST	0.84
	480	HSPQKHPTRNTRSRRS	0.84
	97	LGDGDEIREAIHKSQD	0.83
	902	SALLTSRLTGLALRNR	0.83
	624	TVEGQLGTDNELIMSR	0.83
	491	RSRRSVPVELRANRTI	0.83
	356	TVGWNWPKRTEVCSL	0.83
	35	AAAGSGFNGPGVFITS	0.83
	329	EGYRQRDLDTRALLEP	0.83
	515	AMLQFTYDHIQEHVNE	0.82
	142	YHLGKNFTEGIAVVYK	0.82
	126	TGSTIVRLEPTRTCPD	0.82
	869	PDKFREAQEMIKYMTL	0.81
	638	SRDLLEPCVANHKRYF	0.81
	463	NSLARLYLQELVRENT	0.81
	378	EDVVRDEYAHNFRFTM	0.81
	338	TRALLEPAARNFLVTP	0.81
	742	AIMQGMAQFFQGLGTA	0.80
	68	AVVSVSPSSFYESLQV	0.80
	576	GDVISVSNCPELGSDT	0.80
	391	FTMKTLSTTFISETNE	0.80
	308	GLRDGAYREHSNYAMD	0.80

	284	ARSIFPYDSFGLSTGD	0.80
	179	AWAGSSYTQITNRYAD	0.80
	877	EMIKYMTLVSAERQE	0.79
	757	AGQAVGHVVLGATGAL	0.79
	665	YRYVREIAVHDVGMIS	0.79
	694	EFMPLQVYTRDELRTD	0.78
	656	GHHYVYYEDYRYVREI	0.78
	416	QCVKEEARAIINRIYT	0.78
	223	NHKVEAFNEDKNPQDM	0.78
	704	DELRTDGLLDYSEIQR	0.77
	168	TVYYKDVIVSTAWAGS	0.77
	728	FYDIDKVVQYDSGTAI	0.76
	583	NCPELGSDTRILQNS	0.76
	44	PGVFITSVTGVWLCFL	0.76
	910	TGLALRNRRGYSRVRT	0.75
	800	LVAAFFAYRYVLKLKT	0.75
	535	ISSWCQLQNRERALW	0.75
	505	TITTSSVEFAMLQFT	0.75
	241	IASKYNSVGSKAWHTT	0.75
	120	YVCPPTGSTIVRLEP	0.75
	233	KNPQDMPLIASKYNSV	0.74
	15	RPEYRRNLRFRFFSS	0.74
	775	TVHGFTTFLSNPFGAL	0.73
	570	VKARILGDVISVSNCP	0.72
	892	ESKARKKNKTSALLTS	0.70
	818	MKALYPLTTKGLKQLP	0.70
	811	LKLKTSPMKALYPLTT	0.70
	185	YTQITNRYADRVPIPV	0.69
	649	HKRYFLFGHHYVYYED	0.68
	59	LCIFSMFVTAVVSVSP	0.68
	453	FVVVFQPLLSNSLARL	0.68
	432	TRYNSSHVRTGDIQTY	0.68
	316	EHSNYAMDRFHQFEGY	0.68
	562	ASTILDQRVKARILGD	0.67
	275	VNCIEEVEARSIFPY	0.66
	24	FRRFFSSIHPNAAAGS	0.65
	686	NLTLLKDREFMPLQVY	0.63
	543	QNRERALWSGLFPINP	0.63
	765	VLGATGALLSTVHGFT	0.62
	290	YDSFGLSTGDIIYMSP	0.60

gE	380	YVPIDPTCQPMRLYST	0.94
	207	TCTGDAAPAIQHICLK	0.93
	400	PNAPQCLSHMNSGCTF	0.92
	507	RGFPPTAGQPPATTKP	0.90
	277	DPPEIEPGVLKVL RTE	0.88
	149	VDQRQYGDVFKGDLNP	0.88
	193	GVRTYTETWSFLPSLTC	0.87
	555	IFLICTAKRMRVKAYR	0.86
	389	PMRLYSTCLYHPNAPQ	0.86
	69	ESSRKAYDHNSPYIWP	0.85
	515	QPPATTKPKEITPVNP	0.85
	342	HMWNYHSHVFSVGDTF	0.85
	263	IVVNTSTLFDELELDP	0.85
	245	LAEISYRFQGKKEADQ	0.85
	169	QRLIEVSVEENHPFTL	0.85
	105	GRGIDSGERLMQPTQM	0.85
	61	ESSWVNRGESSRKAYD	0.84
	584	GLPVDDFEDSESTDTE	0.84
	441	YCLGISHMEPSFGLIL	0.84
	175	SVEENHPFTLRAPIQR	0.84
	79	SPYIWPRNDYDGFLEN	0.83
	318	TWKGDEKTRNPTPAVT	0.83
	253	QGKKEADQPWIVVNTS	0.83
	304	RGSDGTSTYATFLVTW	0.82
	19	TGTLRITNPVRASVLR	0.82
	578	QSMYYAGLPVDDFEDS	0.81
	570	RVDKSPYNQSMYYAGL	0.81
	454	LILHDGGTTLKFV DTP	0.81
	328	PTPAVTPQPRGAEFHM	0.81
	201	SFLPSLTCTGDAAPAI	0.81
	425	ASTVYQNCEHADNYTA	0.80
	185	RAPIQRIYGVRYTETW	0.80
	563	RMRVKAYRVDKSPYNQ	0.79
	538	YAAWTGGLAAVVLLCL	0.79
	33	LR YDDFHTDEDKLDTN	0.79
	99	HGVYNQGRGIDSGERL	0.78
	90	GFLENAHEHHGVYNQG	0.78
	374	LLLEWLYVPIDPTCQP	0.78
	351	FSVGDTFSLAMHLQYK	0.78
	131	GIHVIPTLNGDDRHKI	0.78

	119	QMSAQEDLGDDTGIHV	0.78
	111	GERLMQPTQMSAQEDL	0.78
	448	MEPSFGLILHDGGTTL	0.77
	406	LSHMNSGCTFTSPHLA	0.77
	229	DVVVDVDCAENTKEDQ	0.77
	223	HTTCFQDVVVDVDCAE	0.77
	606	IGGSHGGSSYTVYIDK	0.76
	47	TNSVYEPYYHSDHAES	0.75
	522	PKEITPVNPGTSPLLR	0.74
	484	GHVEAVAYTVVSTVDH	0.74
	238	ENTKEDQLAEISYRFQ	0.74
	592	DSESTDTEEEFGNAIG	0.72
	528	VNPGTSPLLRYYAAWTG	0.71
	469	PESLSGLYVVFVVFNG	0.71
	432	CEHADNYTAYCLGISH	0.71
	477	VFVVYFNGHVEAVAYT	0.70
	297	GVYIWNMRGSDGTSTY	0.70
	1	MGTVNKPVVGVLMGFG	0.69
	490	AYTVVSTVDHFVNAIE	0.67
	54	YYHSDHAESSWVNRGE	0.65
	363	LQYKIHEAPFDLLEW	0.64
	357	FSLAMHLQYKIHEAPF	0.60
gH	819	FGIIGWMLCGNSRLRE	0.92
	737	TGAIMDIIIDSKDTE	0.92
	230	VWPIRYWATGSVLLTS	0.92
	567	TIPNVYSPCMGSLRTD	0.90
	11	LPLWTTANKSYVTPTP	0.90
	707	HGVIETVALPHPDNLK	0.88
	338	YHLSMAHTEALRMTTK	0.88
	119	FGFLSHPVPDVSFFD	0.88
	110	HRAPFPAGRFGFLSHP	0.88
	546	TQAALNIQEGLAYLNP	0.87
	407	LMRIGAGAHPTISGT	0.87
	667	HSYVITRNKPQRGLVY	0.86
	657	YVLILPAVQGHSYVIT	0.85
	49	KLEAFYPTGFDEELIK	0.85
	296	PPGPDPGPSYRVYLLG	0.85
	760	NSTIPPFNPDMHGDDS	0.84
	450	DYFISYDEARDQLKTA	0.84
	290	TWFQLNPPGPDGPSY	0.84

165	ETAATAERPFQVSLLP	0.84
743	IIIDSKDTERQLAAM	0.83
59	DEELIKSLHWGNDRKH	0.83
323	TVDICAYPEESLDYRY	0.83
678	RGLVYSLADVDVYNPI	0.82
128	PDVSFFDSSFAPYLTT	0.82
577	GSLRTDLTEEHVMNL	0.81
239	GSVLLTSDSGRVEVNI	0.81
701	DTCVSEHGVETVALP	0.80
593	LSAIPTRPGLNEVLHT	0.80
462	LKTAYALSRGQDQHVNA	0.80
377	ALSEMGRTEYFLLDE	0.80
348	LRMTTKADQHDINEES	0.80
537	TSMCTAAHATQAALNI	0.79
518	EGLNSSRVLDGRITL	0.79
722	KECLYCGSVFLRYLTT	0.78
36	ALLREYSDRNMSLKLE	0.78
249	RVEVNIGVGFMSLLIS	0.78
211	AEAITNSTLRIHVPL	0.78
622	TMMIFTTWTAKDLHIL	0.77
788	TLLGFERRQAIRMSGQ	0.76
527	LDGRITLLLMTSMCTA	0.76
330	PEESLDYRYHLSMAHT	0.76
184	TVPKNTILEHKAHFAT	0.76
145	HLVAFTTFPPNPLVWH	0.76
97	PKYLLSPYHFKAEHRA	0.75
88	EGDVGLVIFPKYLLSP	0.75
641	VPEVFTCQDAAARNGE	0.74
21	YVTPTPATRSIGHMSA	0.74
633	DLHILHTHVPEVFTCQ	0.73
507	FFASMILLNFREGLEN	0.73
196	HFATWDALARHTFFSA	0.73
80	VKVNPITHEGDVGLVI	0.72
607	HTQLDESEIFDAAFKT	0.72
552	IQEGLAYLNPSKHMFT	0.72
357	HDINEESYYHIAARIA	0.72
260	SSLISLSSGPPIELIV	0.72
753	RQLAAMGNSTIPPFNP	0.71
67	HWGNDRKHVFLVIVKV	0.71
482	RRVIMSIYKGLLVKQN	0.70

	414	AHPNTISGTSDLIFAD	0.70
	218	STLRIHVPLFGSVWPI	0.70
	688	DVYNPISVVYLSRDTC	0.69
	271	IELIVVPHTVKLNAVT	0.69
	154	PNPLVWHLERAETAAT	0.68
	825	MLCGNSRLREYNKIPL	0.67
	804	YLGASLGGAFLAVVGF	0.67
	387	YFLLDEIVDVQYQLKF	0.66
	714	ALPHPDNLKECLYCGS	0.65
	423	SDLIFADPSQLHDELS	0.65
	311	GRGLDMNFSKHATVDI	0.65
	174	FGVSLPARPTVPKNT	0.65
	728	GSVFLRYLTTGAIMDI	0.64
	137	FAPYLTTQHLVAFTTF	0.62
	766	FNPDMHGDDSKAVLLF	0.61
	648	QDAAARNGEYVLILPA	0.60
gL	133	DSTPSSTNIPENGCVW	0.92
	111	GEEHKSGDIRDALLDA	0.91
	53	YEAWDYAAPPVSNLSE	0.87
	127	LSGVWVDSTPSSTNIP	0.87
	41	SLIITEPCVSSVYEA	0.86
	23	HLQDDTPLFFGAKPLS	0.86
	84	VILWFKDKQMAYWTNP	0.85
	14	KTITIAYCLHLQDDTP	0.85
	144	NGCVWGADRLFQRVCQ	0.82
	104	KGLAQSVGEEHKSGDI	0.79
	91	KQMAYWTNPYVTLKGL	0.75
	73	IVVKTKCPVPEVILWF	0.73
	117	GDIRDALLDALSGVWV	0.73
	29	PLFFGAKPLSDVSLII	0.64
	63	VSNLSEALSGIVVTKTK	0.63
	1	MASHKWLLQIVFLKTI	0.61

Supplementary Table 4. Linear/continuous B cell epitopes in the target glycoprotein sequences as predicted by ABCPred 2.0 server. A total of 246 epitopes were predicted (gB-89, gE-62, gH-79 and gL-16).

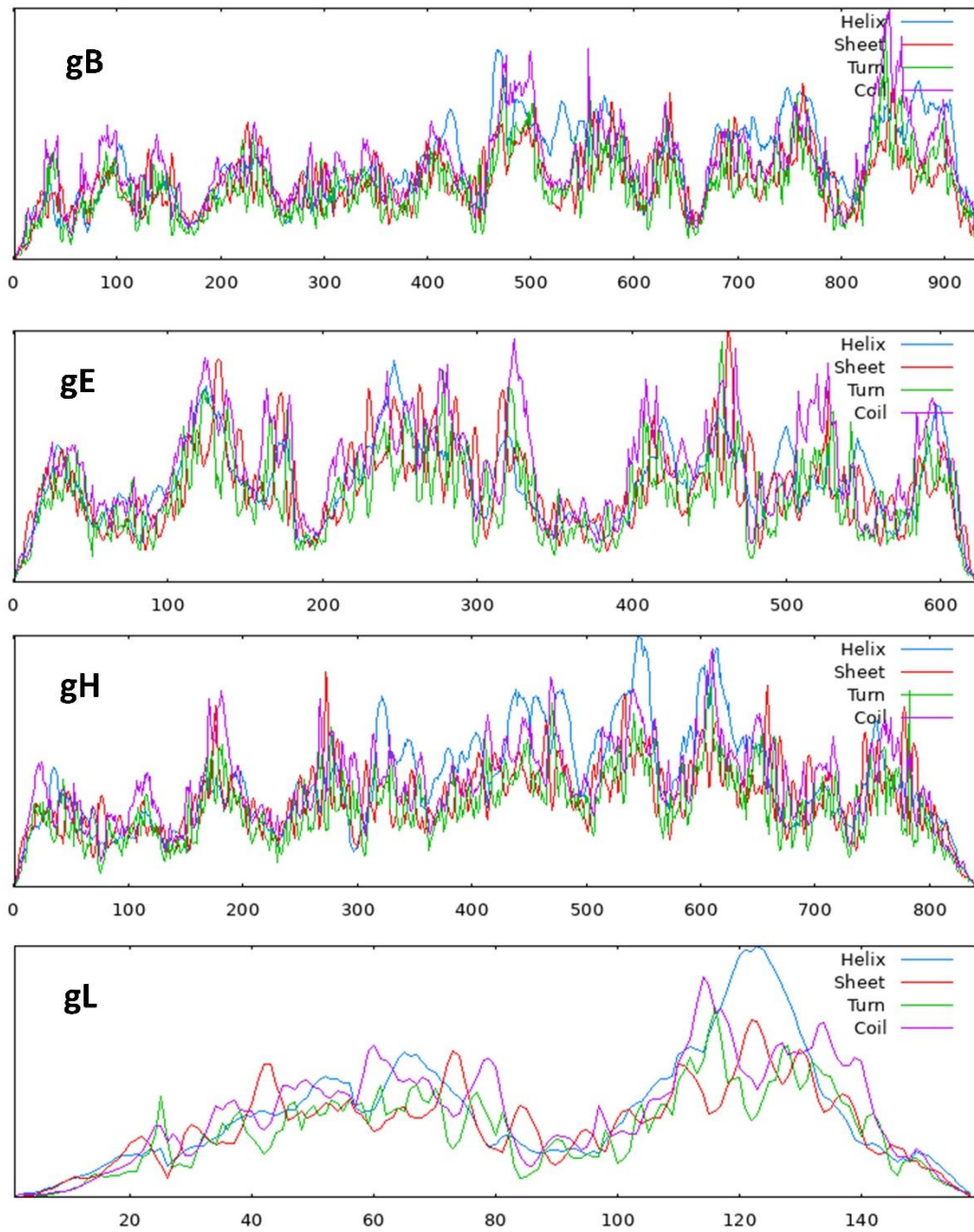
Protein	B Cell Epitopes	Residues	Score
gB	KTSPMKALYPLTTKGLKQLPEGMDPFAEKPNAATDTPIEEIGDSQNTEPSVNSGFDPDKFR EAQEMIKYMTLVSAAERQESKARKKNKTSALLTSRLTGLALRNRRGYSRVRTENVTGV (814-931)	118	0.863

	Q (568) NCPELGSDTRIILQNSMRVSGSTTRCYS (583-610) P (612) ISIVSLNGSGTVEGQLGT (614-631) NELIMSRDLLEPCVANHKRYFLFGHHYVYYEDYRYVREIAVHDVGM (633-679)	95	0.706
	MSPCG (1-5) YSKWRN(7-12) RPEYRR(15-20) LR (22-23) R (26) G (40) NGP (42-44) TAVVSVSPSSFYESLQVEPTQSEDI TRSAHLGDGDEIREAIHKS (67-110) DAETK (112-116) P (124) VYKE (155-166) IP (198-199) SE (201-202) TDTIDKFGKCS (204-214) D (232) Q (236) MPLIASKYNSVGSK (238-251) EARSIFPYD (283-291) Q (327) EGYRQRDL DTRALLEPAA (329-346) WPKRTEVCS (361-370) DEYAHN (383-388) ISETNEFNLNQIHLSQCVKEEARA (401-424) NR (427-428) T (431) NSSHVRTGDIQT (435-446) LARGGFV (448-454) Q (458) LLSNS (460-464) AR (466-467) LQ (470-471) VR (474-475) NTNHSPPQKHPTRNTRSRRSVPVELRANRTITTTSS (477-511)	254	0.661
	KD (691-692) EF (694-695)	4	0.595
	DTGLLD (708-713)	6	0.593
	FFGLRDGAYRE (306-316)	11	0.573
	HLGKN (143-147)	5	0.57
	AG (181-182) GTPGTY (264-269)	8	0.552
	PDY (140-142)	3	0.513
	MPL (696-698)	3	0.511
gE	TA (560-561) RMRVKAYRVD (563-572) SPYNQSMYYAGLPVDDFEDSESTDTEEEFGNAIGGSHGGSSYTVYIDKTR (574-623)	62	0.805
	MGFGIITGTLR (13-23) ASVL (30-33) YDDFHTDEDKLD TNSVYEPYHSDHAESSWVNRGESSRKAYDHNSPYIWPRNDYD (35-89) NQGRGIDSG (103-111) MQPT (115-118)	83	0.752
	IQRIYGVRYTETW (188-200) P (204) L (206) AIQHICLKHTTCFQD (215-229) VVDVDCAENTKEDQLAEISYRFQGKKEADQPWIVVNTSTLFDE (231-273) LDPPEIEPGVLKVL RTE (276-292) N (302) RDS DGTS (304-310)	98	0.667
	NYHSHVFSVGDTFS (345-358) PIDPTCQPM (382-390) G (453) KFVDTPELSG (464-474) VSTVDHFVNAIE (494-505) PATTKPKEITPVNPGTSPLLR YAA (517-540) T (542)	72	0.655
	SHMN (407-410) STVYQNCEHADN (426-437) CLGISH (442-447)	22	0.544
	MGT (1-3)	3	0.519
	MEPSF (448-452)	5	0.514
gH	QAIR (796-799)	4	0.904
	MSGQYL GASLGGAFLAVVGFGIIGWMLCGNSRLREYNKIPLT (800-841)	42	0.899
	T (546) AL (549-550) EGLAYLNPSKHM (554-565) L (579) PSKHMFTIPNVYSPCMGSLRTDLTEEIHVMNLLSAIPTRPGLNEVLHTQLDESEIFDAAFK TMMIFTTWTAKDLHILH THVPEVFTCQDAAARNGEY (581-657) AVQGH (663-667) RNKPQRGLVYS (673-684) VDVYNPISTCVSEHGVETVALPHPDNLKECLYCGSVFLR (687-733) L (735) AIMDIIIDSKDTERQLAAMGNSTIPPFPNPD MHGDDS (739-775) AVLLFPNGTVV (777-787) LLGFERR (789-795)	214	0.728
	K (49) F (58) EE (60-61) KS (64-65) HWGNDRKHV (67-75) PKYLLSPYHFKA EHRAPFPAGRFGFLSHPVTPDV SF (97-132)	166	0.66

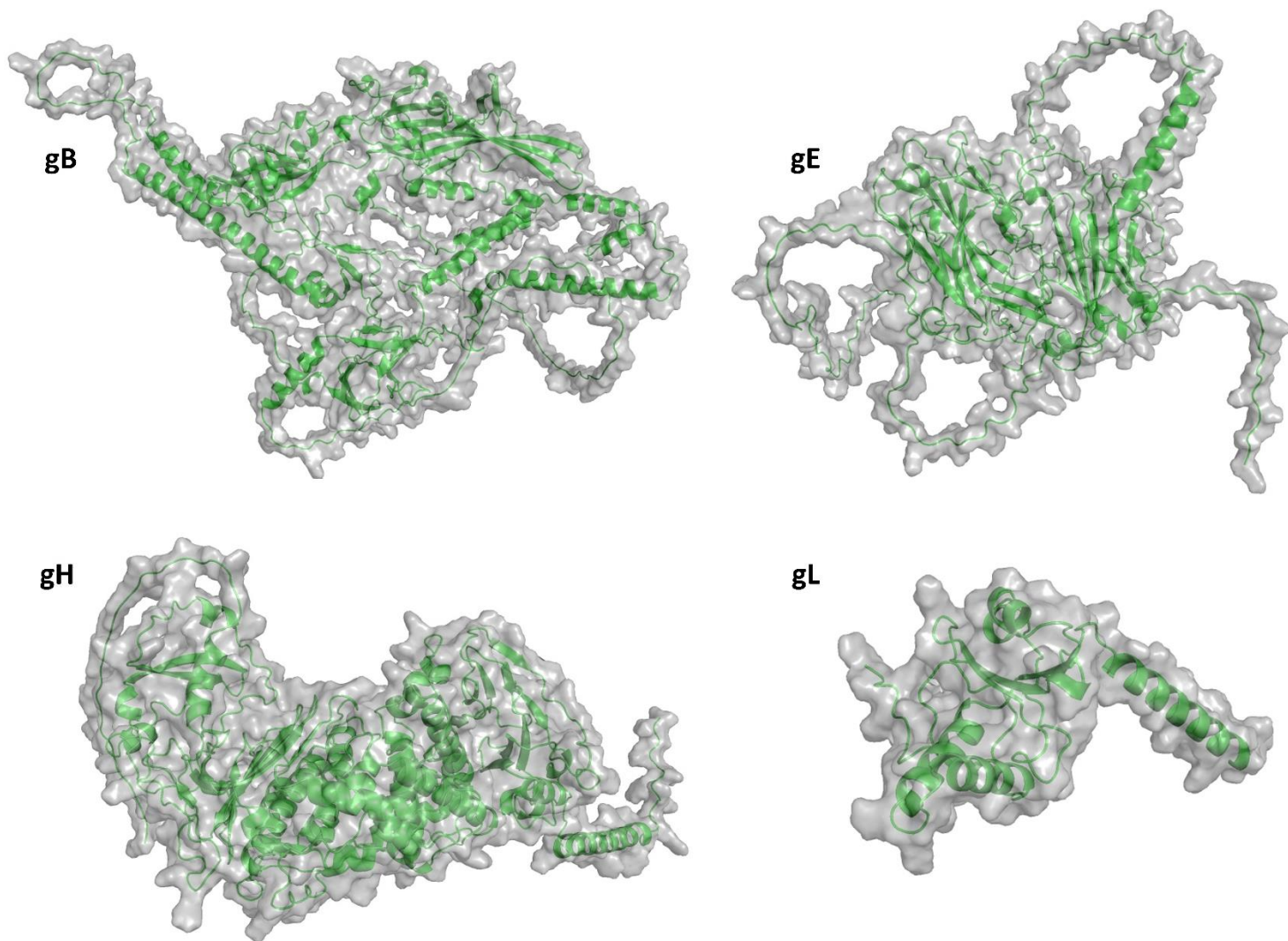
	DSSFAPYLTTQHLVAFITTFPPNPLVWHLERAETAATAERPFGVSLLPARPTVPKNTILEH KAHFAT (134-199) DA (201-202) ARHTFF (204-209) NST (217-219) WATG (236-239) IGVGF (254-258) VPHTVKLNAVTSDDTTWFQLNPPGPDGPS (276-304)		
	LGRGLDMNFSKH (310-321) N (360)	13	0.593
	TTANKSYVT (15-23) E (40) SDRNM (42-46) D (90)	16	0.565
	S (247) SSGP (266-269)	5	0.51
gL	RVCQ (156-159)	4	0.819
	MASH (1-4) WL (6-7) Q (108) VGEEHKSGDIRDA (110-122) D (125)	21	0.763
	LSDVSL (37-42) TEPCVSSVYEAWDYAAPPVSN (45-65) SEA (67-69) TKC (77-79) FKDK (88-91) M (93)	38	0.636
	LHLQDDTPLF (22-31) VDSTPSSTNIPENGCVW (132-148)	27	0.608

Supplementary Table 5. Conformational/discontinuous B cell epitopes in the target glycoprotein structures as predicted by Ellipro server of the IEDB website. A total of 28 epitopes were predicted (gB-10, gE-7, gH-7, and gL-4)

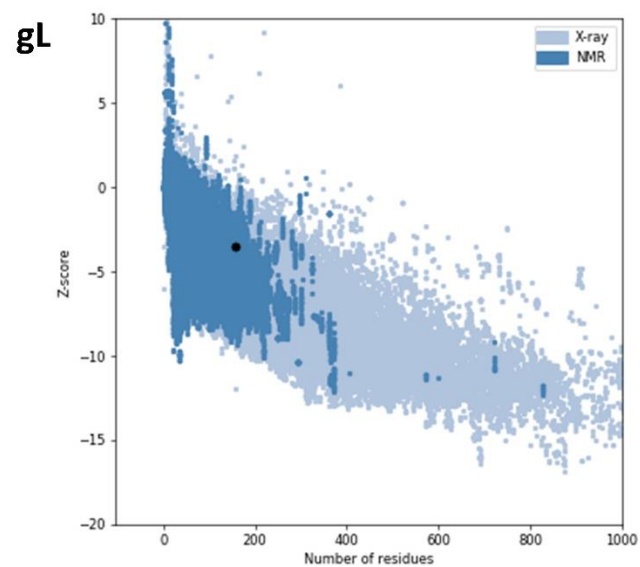
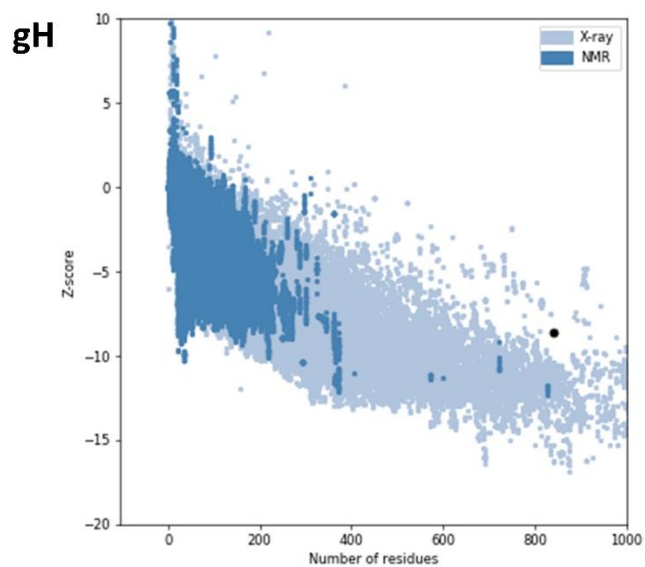
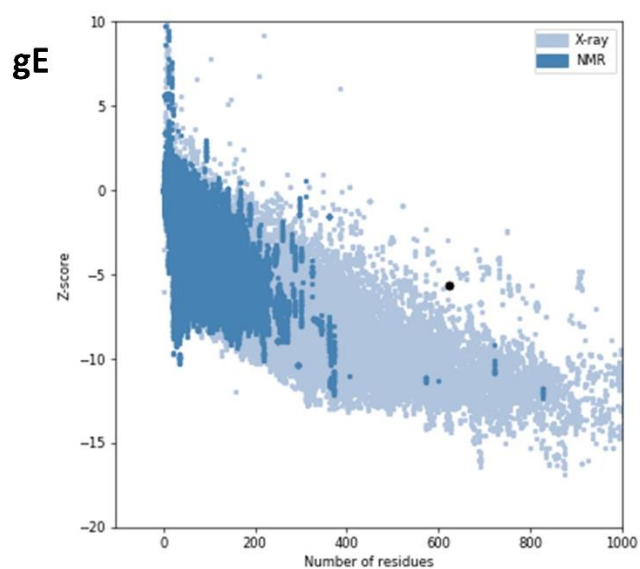
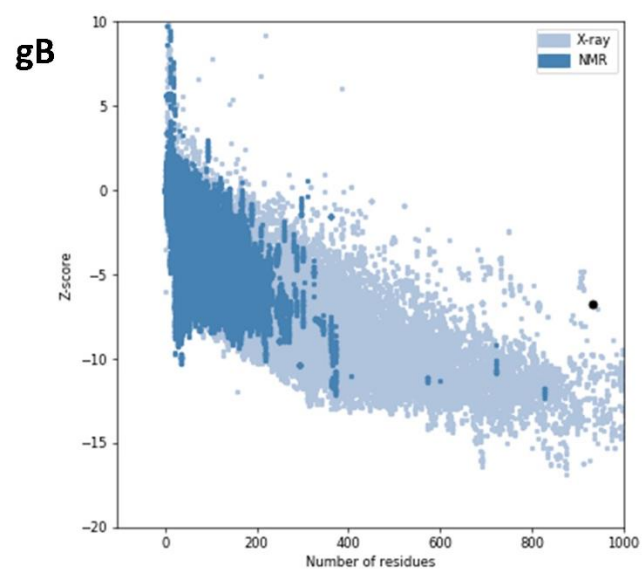
SUPPLEMENTARY FIGURES



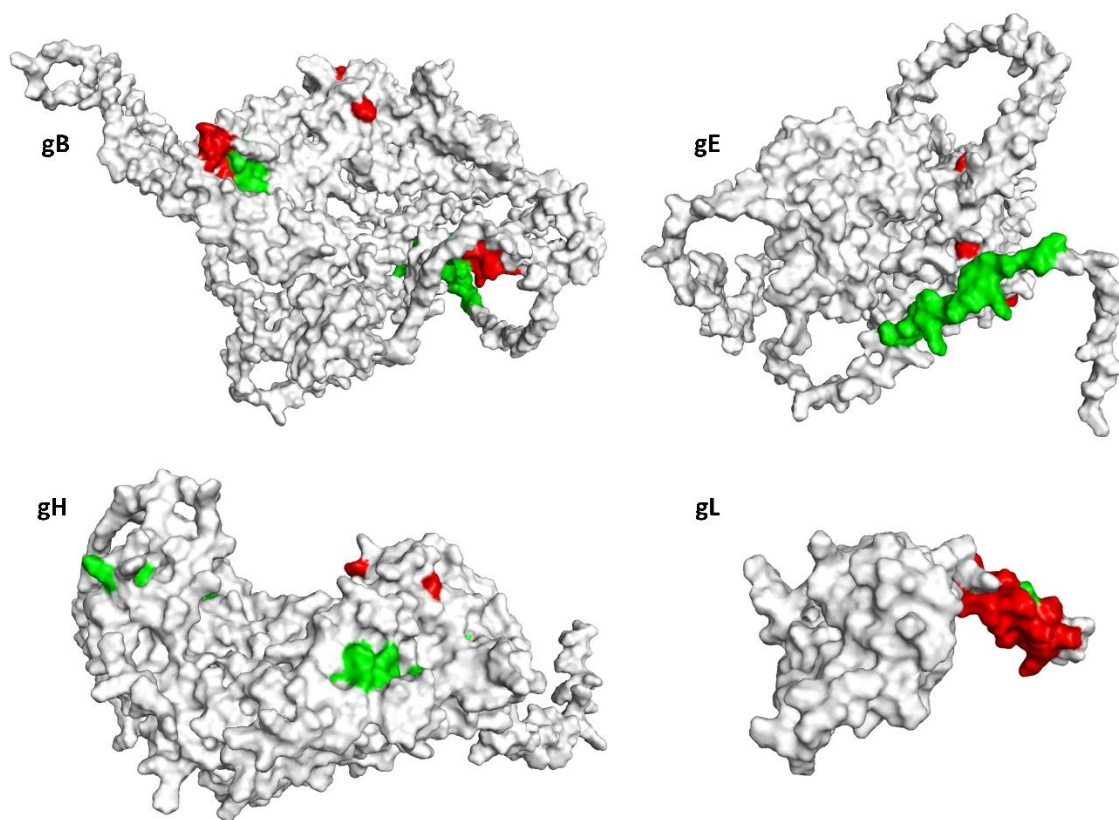
Supplementary figure S1. Secondary structural properties of the target proteins (a) glycoprotein gB (b) glycoprotein gE (c) glycoprotein gH and (d) glycoprotein gL as predicted by the SOPMA webserver



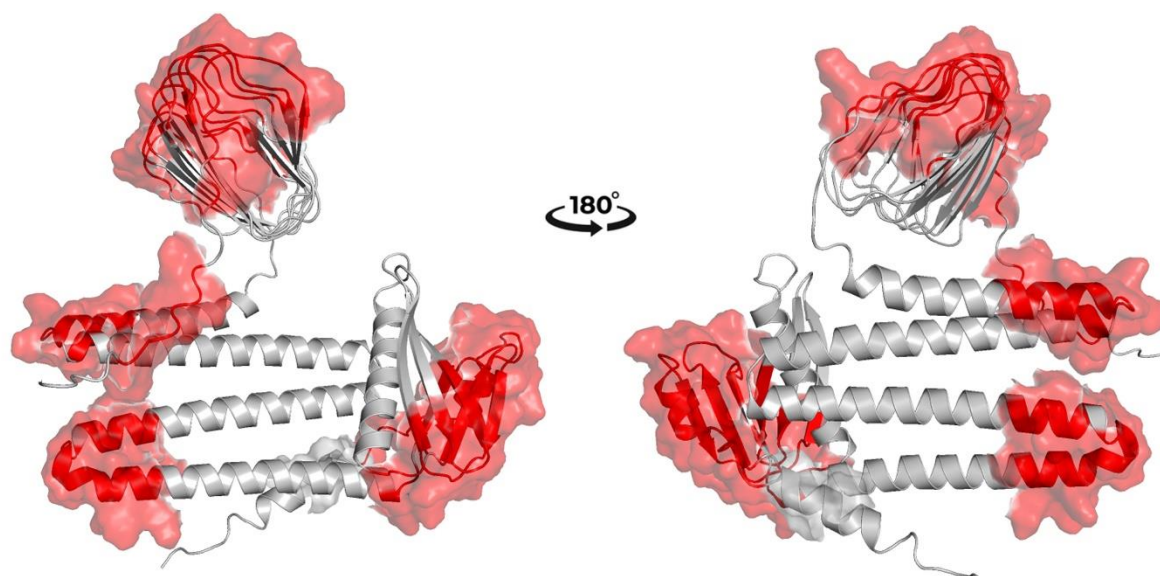
Supplementary figure S2. 3D structures of the Glycoproteins were obtained using Alphafold for the target proteins (a) glycoprotein gB (b) glycoprotein gE (c) glycoprotein gH and (d) glycoprotein gL



Supplementary figure S3. Validation of the modeled glycoprotein structures as predicted by ProSA-web server; the Z scores for (a) glycoprotein gB (b) glycoprotein gE (c) glycoprotein gH and (d) glycoprotein gL were found to be -6.76, -5.66, -8.65, and -3.54 respectively.



Supplementary figure S5. The finalized epitopes mapped on the surface of the glycoproteins for (a) glycoprotein gB (b) glycoprotein gE (c) glycoprotein gH and (d) glycoprotein gL. CTL and HTL epitopes are represented using red and green colors respectively.



Supplementary figure S6. all the conformational B cell epitopes predicted are mapped on the surface of the vaccine molecule. The epitopes are shown as surface representation colored in red on the vaccine molecule which is represented as cartoons colored in white