

**Supplementary Table 1: Details of identified 43 GPI-anchored antigenic protein containing signal peptides**

Accession no.	PredGPI Score	VaxiJen Score	No. of TM helice(s)
RO3G_04553-T26_1-P1	1	1.2318	0
RO3G_02456-T26_1-P1	0.999	1.2021	0
RO3G_14327-T26_1-P1	0.999	1.1372	0
RO3G_05587-T26_1-P1	0.999	1.0931	0
RO3G_07776-T26_1-P1	0.999	1.0783	0
RO3G_06224-T26_1-P1	1	1.0661	0
RO3G_01173-T26_1-P1	0.999	1.0467	0
RO3G_11619-T26_1-P1	1	0.9706	0
RO3G_01770-T26_1-P1	1	0.9297	0
RO3G_03817-T26_1-P1	0.999	0.8911	0
RO3G_00641-T26_1-P1	0.999	0.8847	2
RO3G_09529-T26_1-P1	1	0.8256	1
RO3G_06182-T26_1-P1	0.999	0.8188	0
RO3G_01922-T26_1-P1	1	0.7699	0
RO3G_02887-T26_1-P1	0.999	0.7634	0
RO3G_14139-T26_1-P1	1	0.7633	0
RO3G_03352-T26_1-P1	1	0.7371	1
RO3G_08029-T26_1-P1	1	0.7133	0
RO3G_16597-T26_1-P1	1	0.6959	0
RO3G_07500-T26_1-P1	0.999	0.6856	0
RO3G_02640-T26_1-P1	0.999	0.6739	0
RO3G_12363-T26_1-P1	1	0.6668	0
RO3G_15470-T26_1-P1	1	0.6634	0
RO3G_11882-T26_1-P1	1	0.6632	0
RO3G_07649-T26_1-P1	1	0.6505	0
RO3G_06116-T26_1-P1	1	0.6458	0
RO3G_11699-T26_1-P1	0.999	0.6448	0
RO3G_01479-T26_1-P1	1	0.6382	1
RO3G_16395-T26_1-P1	1	0.6381	0
RO3G_14221-T26_1-P1	0.999	0.6178	0
RO3G_10385-T26_1-P1	0.999	0.609	0
RO3G_11684-T26_1-P1	0.999	0.5991	0
RO3G_10160-T26_1-P1	0.999	0.5967	0
RO3G_13663-T26_1-P1	1	0.5915	0
RO3G_08263-T26_1-P1	0.999	0.5544	0
RO3G_15084-T26_1-P1	0.999	0.5469	1
RO3G_11245-T26_1-P1	1	0.526	0
RO3G_01628-T26_1-P1	1	0.5186	0
RO3G_15122-T26_1-P1	1	0.5161	0
RO3G_06080-T26_1-P1	1	0.5155	0

RO3G_01485-T26_1-P1	1	0.5112	0
RO3G_05018-T26_1-P1	1	0.5096	0
RO3G_16531-T26_1-P1	0.999	0.5028	0

**Supplementary Table 2 : Details of predicted linear B cell epitopes from 4 randomly selected experimentally reported antigens (ERA) and 4 genome derived predicted antigens (GDPA)**

<b>B-cell epitopes from ERA</b>				
<b>S.No.</b>	<b>Antigen name</b>	<b>Start position</b>	<b>Epitope sequence</b>	<b>Score</b>
1	Hypothetical protein RO3G_11882 (EIE87171.1)	542	GTAAAPAPAAGNSTG	1
		269	NGKPPATLGPLYDGAS	1
		495	QGV TAPNNNGGAAFG	1
		565	SSSASSNK TSAQSTSG	1
		302	VANTANPNGEAYEALD	0.999
		321	KAWNETTYTDNTAIAN	0.999
		367	TNDGAYRDPTDNNKWY	0.995
		45	ASDANVPYFTGSAEVG	0.981
		109	EKDPQWTRSGSKADIF	0.979
		66	SSKPDPTPTPTPPGG	1
2	Hypothetical protein RO3G_17119 (EIE92521.1)	126	TTTTKTTTATATATPG	1
		179	EVNPNPNPGKCIPGYK	1
		17	QAAVNPKAAAASKCIS	0.996
		38	GNGDGYKGYCCKDSDD	0.987
		151	KNGDGYKGDCCTSDD	0.984
3	Hypothetical protein G6F43_000212 (KAG1057968.1)	229	PPMPPLNPGSYDL DHP	0.999
		190	TYDNP KPLPTLNSST	0.994
		406	SVIREALEYDPKYQDD	0.989
		353	LRTVTPFTTYFGPGFS	0.976
		212	VVEGHATHPMHKARKS	0.973
4	Endopeptidase (EIE89256.1)	359	SGFMGM DIPEPAGPLW	0.998
		128	RYDSASSRTYSENGTE	0.981
		63	ETFKLNPDG SANHGVP	0.979
		273	IKFGDDYVDIDPVGAA	0.976
<b>B-cell epitopes from GDPA</b>				
<b>S.No.</b>	<b>Antigen name</b>	<b>Start position</b>	<b>Epitope sequence</b>	<b>Score</b>
1	Hypothetical proteins RO3G_04553	339	GAPGAGASGAGASGAG	1
		34	GAAAASSSTAAGGSTG	1
		159	AASTSNSTASASTSPD	1
		244	ADSAGASADSGDASGS	1
		190	SDDASGSGDASADSGD	1
		210	SGDASADSGDASASAG	1
		227	DDTSGSGDASADSGDA	1
		424	SGSGASSSSSATSGSS	1
		371	GAAASGVPSAAGGSAA	1
		17	EAAPQPSSASASASPS	1
		276	SGSEDASGSTDSSSAS	1
		319	GSSGSGASGSGASGSG	1
		301	AAAAAPAKRQESTGAS	0.986
		111	TQVDVPNNVTAGNDYS	0.983

2	Hypothetical proteins RO3G_02456	164	AASSAASSAASSSSST	1
		117	ASGSSASSSSSTTAAS	1
		139	AAAASGSSTSKTSSAS	1
		75	VDASSLSYTWIPSDT	0.977
3	Hypothetical proteins RO3G_14327	121	SSSAAASSAASSSTSL	1
		163	ATSAAASAASSAASSI	1
		193	ATSSAAAQASSTSSGF	1
		82	YTNWIPADITPANNYA	0.973
4	Hypothetical proteins RO3G_05587	127	GGAAPGTTNNTAASSA	1
		22	AAAANAGVAVNKPFG	1
		161	SSGSASSTASASQTTS	1
		46	YTITWTVTDTNAKTIN	0.998
		183	AGMVG VAGVAGVVALF	0.996
		84	PINVNPPQYTNWNPAT	0.991

**Supplementary Table 3: Details of predicted antigenic and immunogenic epitopes predicted for 4 ERA and 4 GDPA**

**Details of predicted antigenic and immunogenic epitopes predicted for 4 ERA**

Antigen	Epitope	Allele	PPC Value	Vaxijen score (Fungal)	Immunogenic score
E3	TLVAHVWNL	HLA-A*02:01, HLA-A*02:06	40.60%	1.5476	0.30629
E1	VLALHNFL	HLA-A*02:01	39.08%	1.0572	0.11927
E1	NLPQLPWPI	HLA-A*02:01	39.08%	0.96	0.03906
E1	KMFDLDRFM	HLA-A*02:01	39.08%	2.13	0.18248
E1	TMGNRNFFK	HLA-A*03:01, HLA-A*11:01, HLA-A*31:01	35.36%	0.8758	0.216
E1	ISAAFLVAITHAASI	HLA-DRB1*01:01, HLA-DRB1*07:01, HLA-DRB1*08:02	30.59%	0.94	0.40566
E1	AFLVAITHAASIKFN	HLA-DRB1*01:01, HLA-DRB1*07:01, HLA-DRB1*08:02	30.59%	1.29	0.20172
E1	AAFLVAITHAASIKF	HLA-DRB1*01:01, HLA-DRB1*07:01, HLA-DRB1*08:02	30.59%	1.21	0.21083
E3	TYFGPGFSF	HLA-A*23:01, HLA-A*24:02, HLA-C*14:02	28.43%	2.7741	0.09534
E4	SVYDLGNNR	HLA-A*11:01, HLA-A*31:01, HLA-A*68:01	25.64%	1.0009	0.03298
E1	LAAPEGNAF	HLA-B*15:01, HLA-B*35:01, HLA-C*03:03	23.27%	0.7	0.14834
E1	LVAITHAASIKFNVI	HLA-DRB1*07:01, HLA-DRB1*08:02	20.33%	0.99	0.17948

E1	FLVAITHAASIKFNV	HLA-DRB1*07:01, HLA-DRB1*08:02	20.33%	1.65	0.18839
E2	ATATATPGK	HLA-A*11:01, HLA-A*30:01	19.09%	1.9045	0.13684
E1	TLTFIGSNYVYSFQN	HLA-DRB1*15:01	18.41%	0.83	0.03399
E1	SGTLTFIGSNYVYSF	HLA-DRB1*15:01	18.41%	1.5	0.08392
E1	RISGTLTFIGSNYVY	HLA-DRB1*15:01	18.41%	1.22	0.17561
E1	ISGTLTFIGSNYVYS	HLA-DRB1*15:01	18.41%	1.27	0.21546
E1	GTLTFIGSNYVYSFQ	HLA-DRB1*15:01	18.41%	1.47	0.10656
E1	VAITHAASIKFNVA	HLA-DRB1*07:01	18.23%	1.0601	0.16897
E4	LSLVVSAAFSVFTDA	HLA-DRB1*07:01	18.23%	1.0725	0.14226
E4	ALSLVVSAAFSVFTD	HLA-DRB1*07:01	18.23%	1.3679	0.04388
E3	VAHVWNLDTKKEKRV	HLA-DRB1*03:01, HLA-DRB1*03:09	17.84%	1.9249	0.06234
E3	LVAHVWNLDTKKEKRV	HLA-DRB1*03:01, HLA-DRB1*03:09	17.84%	1.8915	0.07594
E3	HVWNLDTKKEKRVFL	HLA-DRB1*03:01, HLA-DRB1*03:09	17.84%	1.5374	0.03365
E3	AHVWNLDTKKEKRVF	HLA-DRB1*03:01, HLA-DRB1*03:09	17.84%	1.8094	0.09815
E1	GLVEYIAAKAQAVAK	HLA-DRB1*01:01, HLA-DRB1*09:01	17.55%	0.64	0.12618
E2	QIQAAVNP	HLA-A*11:01	15.53%	0.7099	0.06679
E1	SAAFLVAITHAASIK	HLA-DRB1*01:01, HLA-DRB1*08:02	13.72%	1.16	0.40997
E1	FPSRYPGAV	HLA-B*07:02	12.78%	2.14	0.0358
E4	GSLEGFISQDTLSVG	HLA-DRB1*04:01, HLA-DRB1*04:21	11.21%	1.2521	0.03331
E4	SENGTEFAI	HLA-B*40:01, HLA-B*40:02	11.13%	2.8358	0.28571

E1	MGQTNDGAY	HLA-A*30:02, HLA-B*35:01	10.64%	0.55	0.0675
E3	YSGEGWEIV	HLA-C*12:03	10.31%	1.599	0.51552
E1	VAKEFNISI	HLA-C*12:03	10.31%	3.4889	0.15432
E1	TMVRLFINNQGFQTF	HLA-DRB1*04:04, HLA-DRB1*04:08, HLA-DRB1*04:10, HLA-DRB1*04:23, HLA-DRB1*11:02, HLA-DRB1*11:21, HLA-DRB1*13:04, HLA-DRB1*13:22, HLA-DRB1*15:02, HLA-DRB1*15:06	10.24%	0.7748	0.36736
E1	DATMVRLFINNQGFQ	HLA-DRB1*04:04, HLA-DRB1*04:08, HLA-DRB1*04:10, HLA-DRB1*04:23, HLA-DRB1*11:02, HLA-DRB1*11:21, HLA-DRB1*13:04, HLA-DRB1*13:22, HLA-DRB1*15:02, HLA-DRB1*15:06	10.24%	1.14	0.13466
E1	ATMVRLFINNQGFQ	HLA-DRB1*04:04, HLA-DRB1*04:08, HLA-DRB1*04:10, HLA-DRB1*04:23, HLA-DRB1*11:02, HLA-DRB1*11:21, HLA-DRB1*13:04, HLA-DRB1*13:22, HLA-DRB1*15:02, HLA-DRB1*15:06	10.24%	1.45	0.29284

E1	ANDATMVRLFINNQG	HLA-DRB1*04:04, HLA-DRB1*04:08, HLA-DRB1*04:10, HLA-DRB1*04:23, HLA-DRB1*11:02, HLA-DRB1*11:21, HLA-DRB1*13:04, HLA-DRB1*13:22, HLA-DRB1*15:02, HLA-DRB1*15:06	10.24%	0.75	0.15754
E4	LVDEPLFSF	HLA-A*02:06, HLA-C*05:01	9.65%	0.6127	0.08885
E3	LKGFVIRDFGGVKAH	HLA-DRB1*13:01, HLA-DRB1*13:27, HLA-DRB1*13:28	8.77%	0.8042	0.43032
E4	VVSAAFSVF	HLA-B*15:01	8.44%	1.2962	0.01847
E4	STKEPGLTF	HLA-B*15:01	8.44%	2.382	0.06517
E3	LIRVLDLHY	HLA-B*15:01	8.44%	1.7212	0.07796
E1	TAIANFEKM	HLA-C*03:03	8.12%	0.72	0.14497
E4	KEPGLTFAF	HLA-A*32:01, HLA-B*40:02	7.90%	2.6364	0.1779
E1	TADWDGYWM	HLA-C*05:01	7.85%	1.54	0.40989
E1	ASDANVPYF	HLA-C*05:01	7.85%	0.86	0.06761
E4	GEIEIGTPP	HLA-B*40:01	7.81%	1.4944	0.33173
E1	LTADWDGYW	HLA-B*57:01, HLA-B*58:01	7.26%	3.52	0.29804
E1	FGLVEYIAAKAQAVA	HLA-DRB1*09:01	6.40%	0.87	0.11384
E1	AFGLVEYIAAKAQAV	HLA-DRB1*09:01	6.40%	0.77	0.09167
E1	YLTADWDGY	HLA-A*29:02, HLA-B*15:02	6.25%	3.0022	0.3206
E1	RVLALHNFL	HLA-A*02:06, HLA-A*30:01	5.80%	1.56	0.11836
E1	KWYFLDQDF	HLA-A*23:01	5.43%	1.94	0.04188
E1	GNRNFFKLR	HLA-A*31:01	5.36%	1.77	0.04601
E3	TASDILTVV	HLA-A*02:06, HLA-A*68:02	4.43%	1.2457	0.14466



E1	LTFIGSNYV	HLA-A*02:06, HLA-A*68:02	4.43%	1.01	0.04157
E3	FVIRDFGGV	HLA-A*02:06, HLA-A*68:02	4.43%	0.9032	0.27548
E1	VRLFINNQGFGTFNM	HLA-DRB1*04:08, HLA-DRB1*04:10, HLA-DRB1*04:23, HLA-DRB1*15:02, HLA-DRB1*15:06	4.42%	0.5276	0.42996
E2	TTKTTTATA	HLA-A*30:01	3.89%	1.6475	0.0991
E1	TLTFIGSNY	HLA-A*29:02	3.89%	0.95	0.1485
E1	RSKTAPIVL	HLA-A*30:01	3.89%	1.01	0.13316
E4	KVHETATEK	HLA-A*30:01	3.89%	0.5834	0.27714
E4	TEFAIQYGT	HLA-B*40:02	3.45%	0.9147	0.11461
E3	KSAGVELDI	HLA-B*58:01	3.42%	4.5347	0.18485
E3	DIRAQYQNYVFIAIH	HLA-DRB1*15:02	3.09%	0.5036	0.20733
E4	TYSENGTEF	HLA-C*14:02	3.04%	0.8415	0.16391
E3	TYDHEVLAI	HLA-C*14:02	3.04%	0.8161	0.18961
E4	RYSHTGEYL	HLA-C*14:02	3.04%	0.9016	0.13089
E3	EHQLNVEAL	HLA-B*39:01	2.75%	1.547	0.09116
E1	YANDATMVRLFINNQ	HLA-DRB1*03:09, HLA-DRB1*04:08, HLA-DRB1*04:10, HLA-DRB1*04:21, HLA-DRB1*04:23, HLA-DRB1*11:02, HLA-DRB1*11:21, HLA-DRB1*13:04, HLA-DRB1*13:22	2.52%	1.4183	0.23496
E1	TTYTDNTAI	HLA-A*68:02	2.50%	0.5792	0.10899
E1	TTAAAPAPA	HLA-A*68:02	2.50%	0.5517	0.10627
E1	NVSFGIHGA	HLA-A*68:02	2.50%	2.3	0.26948
E4	MGMDIPEPA	HLA-A*68:02	2.50%	1.6599	0.1625
E2	LVAAVQIQA	HLA-A*68:02	2.50%	0.5701	0.02787
E1	ISAAFLVAI	HLA-A*68:02	2.50%	0.89	0.21333
E1	RISGTLTFI	HLA-A*02:06	1.95%	1.31	0.10892

E3	NQFIGLCLL	HLA-A*02:06	1.95%	0.7054	0.1425
E1	FLDQDFDGT	HLA-A*02:06	1.95%	1.58	0.06096
E4	AQYYGEIEI	HLA-A*02:06	1.95%	0.5436	0.29315
E3	RLIRVLDLHYSGEGW	HLA-DRB1*11:02, HLA-DRB1*11:21, HLA-DRB1*13:22	0.95%	0.7326	0.13848
E3	QRLIRVLDLHYSGEG	HLA-DRB1*11:02, HLA-DRB1*11:21, HLA-DRB1*13:22	0.95%	1.28	0.18019
E3	QLQRLIRVLDLHYSG	HLA-DRB1*11:02, HLA-DRB1*11:21, HLA-DRB1*13:22	0.95%	0.6419	0.15455
E3	LQRLIRVLDLHYSGE	HLA-DRB1*11:02, HLA-DRB1*11:21, HLA-DRB1*13:22	0.95%	0.8725	0.13404
E3	LIRVLDLHYSGEGWE	HLA-DRB1*11:02, HLA-DRB1*11:21, HLA-DRB1*13:22	0.95%	0.6255	0.21041
E3	IRVLDLHYSGEGWEI	HLA-DRB1*11:02, HLA-DRB1*11:21, HLA-DRB1*13:22	0.95%	2.0968	0.28768
E3	CQLQRLIRVLDLHYS	HLA-DRB1*11:02, HLA-DRB1*11:21, HLA-DRB1*13:22	0.95%	1.1153	0.16514
E3	VELDILPDSCVEAHS	HLA-DRB1*11:07	0.04%	0.6946	0.12109
E3	SAGVELDILPDSCVE	HLA-DRB1*11:07	0.04%	1.8487	0.11333
E3	LKKSAGVELDILPDS	HLA-DRB1*11:07	0.04%	1.8865	0.10589
E3	KSAGVELDILPDSCV	HLA-DRB1*11:07	0.04%	1.5967	0.15306
E3	KKSAGVELDILPDSC	HLA-DRB1*11:07	0.04%	2.1636	0.19759
E3	GVELDILPDSCVEAH	HLA-DRB1*11:07	0.04%	1.7375	0.10516
E3	AGVELDILPDSCVEA	HLA-DRB1*11:07	0.04%	1.5648	0.13604

E4	MGMDIPEPAGPLWIV	HLA-DRB1*03:06, HLA-DRB1*03:07, HLA-DRB1*03:08	0.02%	0.8471	0.48538
E4	ISGFMGMDIPEPAGP	HLA-DRB1*03:06, HLA-DRB1*03:07, HLA-DRB1*03:08	0.02%	0.8057	0.10008
E4	CISGFMGMDIPEPAG	HLA-DRB1*03:06, HLA-DRB1*03:07, HLA-DRB1*03:08	0.02%	1.5554	0.03355
E3	WNLDTKEKRVEFLDR	HLA-DRB1*03:09	0.00%	1.1033	0.03592
E1	TYANDATMVRLFINN	HLA-DRB1*03:09, HLA-DRB1*04:21	0.00%	1.552	0.23123
E3	TLVAHVWNLDTKEKR	HLA-DRB1*03:09	0.00%	1.6599	0.13797
E1	MGTYANDATMVRLFI	HLA-DRB1*03:09, HLA-DRB1*04:21	0.00%	1.32	0.11514
E1	HAMGTYANDATMVRL	HLA-DRB1*03:09, HLA-DRB1*04:21	0.00%	1.31	0.04038
E1	GTYANDATMVRLFIN	HLA-DRB1*03:09, HLA-DRB1*04:21	0.00%	1.01	0.21509
E4	EPLFSFWLNDANKDQ	HLA-DRB1*04:26	0.00%	1.0473	0.15027
E1	EKMFDLDRFMRFMVI	HLA-DRB3*01:01	0	0.62	0.12312
E1	AMGTYANDATMVRLF	HLA-DRB1*03:09, HLA-DRB1*04:21	0.00%	1.52	0.08082

#### Details of predicted antigenic and immunogenic epitopes predicted for 4 GDPA

Antigen	Epitope	PPC value	Allele name	Vaxijen 2.0 score	Immunogenic score
P4	YTNVNPATV	HLA-A*02:01, HLA-A*02:06, HLA-A*68:02, HLA-C*12:03, HLA-C*15:02	50.86%	1.7415	0.15085
P4	GSSNNLQISIANILS	HLA-DRB1*07:01, HLA-DRB1*07:03, HLA-DRB1*13:02	24.29%	2.0937	0.04584

P2	ISKIVLAQGAATSLQ	HLA-DRB1*01:01, HLA-DRB1*09:01	17.55%	0.6153	0.01826
P2	YTAGQDAII	HLA-A*03:01	16.81%	2.2939	0.06566
P2	SAQTNIVSITSPLTG	HLA-DRB1*04:01, HLA-DRB1*04:04	15.70%	2.764	0.01304
P2	AQTNIVSITSPLTGT	HLA-DRB1*04:01, HLA-DRB1*04:04	15.70%	2.1266	0.05241
P2	QTNIVSITSPLTGTV	HLA-DRB1*04:01, HLA-DRB1*04:04	15.70%	1.762	0.08344
P2	TNIVSITSPLTGTVY	HLA-DRB1*04:01, HLA-DRB1*04:04	15.70%	1.2808	0.03492
P3	SAQTNIVSITSPLTG	HLA-DRB1*04:01, HLA-DRB1*04:04	15.70%	2.764	0.01304
P3	AQTNIVSITSPLTGT	HLA-DRB1*04:01, HLA-DRB1*04:04	15.70%	2.1266	0.05241
P3	QTNIVSITSPLTGTV	HLA-DRB1*04:01, HLA-DRB1*04:04	15.70%	1.762	0.08344
P3	TNIVSITSPLTGTVY	HLA-DRB1*04:01, HLA-DRB1*04:04	15.70%	1.2808	0.03492
P4	ATVEVGSAY	HLA-A*26:01, HLA-B*15:01	13.77%	1.1302	0.06949
P1	SPSTGAAAA	HLA-B*07:02	12.78%	1.7801	0.11107
P1	GPVSITAPL	HLA-B*07:02	12.78%	1.2476	0.03961
P1	TPAAAAAPA	HLA-B*07:02	12.78%	0.7416	0.15354
P2	SYTALFTIQAASGSS	HLA-DRB1*01:01	11.53%	0.9443	0.06218
P2	VSYTALFTIQAASGS	HLA-DRB1*01:01	11.53%	0.6802	0.18887
P2	NVSYTALFTIQAASG	HLA-DRB1*01:01	11.53%	0.6559	0.14947

P4	MKVSIAAIFAAAVST	HLA-DRB1*01:01	11.53%	0.5533	0.34754
P2	VSYTALFTI	HLA-B*35:01	8.42%	0.5619	0.187
P1	AATPAAAAA	HLA-C*03:03	8.12%	0.7672	0.13225
P1	VALAIPAAL	HLA-C*03:03	8.12%	0.5975	0.21081
P2	GQDAIISWI	HLA-C*03:03	8.12%	2.2272	0.29125
P2	DTAAGTDYA	HLA-C*03:03	8.12%	1.9701	0.13817
P2	AAVAVAAMM	HLA-C*03:03	8.12%	0.5288	0.06022
P3	PANNYAEL	HLA-C*03:03	8.12%	2.9639	0.07376
P3	LAQGDPTAL	HLA-C*03:03	8.12%	2.2987	0.06328
P4	AAANAGVAV	HLA-C*03:03	8.12%	1.6982	0.13389
P1	MISGVALAI	HLA-A*32:01, HLA-A*68:02	7.05%	1.2196	0.07093
P4	SSNNLQISIANILSG	HLA-DRB1*07:03, HLA-DRB1*13:02	6.71%	1.8076	0.01695
P3	TVYTAGQSAIISWIN	HLA-DRB1*09:01	6.40%	1.1043	0.24133
P3	TGTVYTAGQSAIISW	HLA-DRB1*09:01	6.40%	0.9164	0.06458
P3	GTVYTAGQSAIISWI	HLA-DRB1*09:01	6.40%	0.8803	0.12746
P3	LTGTVYTAGQSAIIS	HLA-DRB1*09:01	6.40%	0.7876	0.14857
P4	VNPPQYTWNVPATVE	HLA-DRB1*09:01	6.40%	1.5751	0.23915
P4	PQYTWNVPATVEVGS	HLA-DRB1*09:01	6.40%	1.5485	0.54165
P4	NVNPPQYTWNVPATV	HLA-DRB1*09:01	6.40%	1.5233	0.1922
P4	NPPQYTWNVPATVEV	HLA-DRB1*09:01	6.40%	1.4837	0.32082
P4	PPQYTWNVPATVEVG	HLA-DRB1*09:01	6.40%	1.4532	0.45866
P1	LATGIEASK	HLA-A*68:01	5.83%	1.1687	0.20691
P2	TAAGTDYAL	HLA-A*02:06, HLA-B*39:01	4.64%	2.5848	0.12522
P2	ITSPLTGTV	HLA-C*15:02	4.41%	1.0116	0.01216
P4	KVSIAAIFA	HLA-A*30:01	3.89%	0.8436	0.33587

P3	VSYTALFTI	HLA-B*58:01	3.42%	0.5619	0.187
P3	ITPANNYAL	HLA-C*14:02	3.04%	2.2275	0.04312
P4	TYSTYFTIL	HLA-C*14:02	3.04%	1.6147	0.20248
P2	TAAGTDYAL	HLA-B*39:01	2.75%	2.5848	0.12522
P4	LQISIANIL	HLA-B*39:01	2.75%	0.6152	0.11546
P1	SVAATPAAA	HLA-A*68:02	2.50%	0.8642	0.13531
P2	TSAGFKVTV	HLA-A*68:02	2.50%	1.365	0.01532
P3	ITSPLTGTV	HLA-A*68:02	2.50%	1.0116	0.01216
P4	WNVPATVEV	HLA-A*68:02	2.50%	1.2605	0.17022
P4	VSIAAIFAA	HLA-A*02:06	1.95%	0.6645	0.36761
P3	GDPTALQPVSTIAEN	HLA-DRB1*04:10	0.30%	0.9216	0.07286
P3	LQPVSTIAENVDASA	HLA-DRB1*04:10	0.30%	0.7238	0.17098
P3	ALQPVSTIAENVDAS	HLA-DRB1*04:10	0.30%	0.59	0.20748
P3	TALQPVSTIAENVDA	HLA-DRB1*04:10	0.30%	0.5228	0.09285
P4	NLQISIANILSGPIN	HLA-DRB1*07:03	0.02%	1.2116	0.15462
P4	LQISIANILSGPINV	HLA-DRB1*07:03	0.02%	1.0394	0.12693

**Supplementary Table 4: Details of prediction of cytokines responses induction of epitope ensemble of experimentally reported antigens (ERA) and genome derived predicted antigens (GDPA)**

<b>ERA</b>				
<b>Epitope ensemble</b>	<b>IL-4</b>	<b>IL-10</b>	<b>IFN-<math>\gamma</math></b>	<b>IL-17</b>
TMGNRNFFK	Inducer	Non-inducer	Non-inducer	Non-inducer
LAAPEGNAF	Non-inducer	Non-inducer	Non-inducer	Non-inducer
FPSRYPGAV	Inducer	Non-inducer	Inducer	Inducer
MGQTNDGAY	Non-inducer	Non-inducer	Non-inducer	Inducer
VAKEFNISI	Inducer	Non-inducer	Non-inducer	Inducer
LTADWDGYW	Inducer	Non-inducer	Non-inducer	Non-inducer
YLTADWDGY	Inducer	Non-inducer	Non-inducer	Non-inducer
AFLVAITHAASIKFN	Inducer	Non-inducer	Inducer	Inducer
SGTLTFIGSNVYVSF	Non-inducer	Inducer	Non-inducer	Inducer
GLVEYIAAKAQAVAK	Non-inducer	Non-inducer	Inducer	Inducer
ATMVRLFINNQGFGT	Non-inducer	Non-inducer	Non-inducer	Inducer
ATATATPGK	Non-inducer	Non-inducer	Inducer	Inducer
TLVAHVWNL	Non-inducer	Non-inducer	Inducer	Inducer
TYFGPGFSF	Inducer	Non-inducer	Non-inducer	Inducer
TASDILTVV	Non-inducer	Non-inducer	Non-inducer	Non-inducer
EHQLNVEAL	Non-inducer	Non-inducer	Non-inducer	Inducer
VAHVWNLDTKEKRVE	Inducer	Non-inducer	Non-inducer	Inducer
LKGFVIRDFGGVKAH	Inducer	Inducer	Inducer	Inducer
SVYDLGNRR	Inducer	Non-inducer	Non-inducer	Non-inducer
SENGTEFAI	Inducer	Non-inducer	Non-inducer	Non-inducer
LVDEPLFSF	Inducer	Non-inducer	Non-inducer	Non-inducer
KEPGLTFAF	Inducer	Non-inducer	Non-inducer	Non-inducer
GSLEGFISQDTLSVG	Inducer	Inducer	Inducer	Inducer
<b>GDPA</b>				
<b>Epitope ensemble</b>	<b>IL-4</b>	<b>IL-10</b>	<b>IFN-<math>\gamma</math></b>	<b>IL-17</b>
YTWNVPATV	Inducer	Non-inducer	Non-inducer	Inducer
YTAGQDAII	Non-inducer	Non-inducer	Inducer	Non-inducer
ATVEVGSAY	Non-inducer	Non-inducer	Non-inducer	Non-inducer
SPSTGAAAA	Non-inducer	Non-inducer	Inducer	Non-inducer
VSYTALFTI	Inducer	Non-inducer	Non-inducer	Non-inducer
GQDAIISWI	Inducer	Non-inducer	Inducer	Inducer
MISGVALAI	Non-inducer	Non-inducer	Non-inducer	Non-inducer
LATGIEASK	Inducer	Non-inducer	Non-inducer	Inducer
TAAGTDYAL	Non-inducer	Non-inducer	Non-inducer	Inducer
KVSIAAIFA	Inducer	Non-inducer	Non-inducer	Non-inducer
VSYTALFTI	Inducer	Non-inducer	Non-inducer	Non-inducer
ITPANNYAL	Inducer	Non-inducer	Non-inducer	Inducer
GSSNNLQISIANILS	Non-inducer	Inducer	Non-inducer	Inducer
ISKIVLAQGAATSLQ	Inducer	Non-inducer	Non-inducer	Inducer
SAQTNIVSITSPLTG	Non-inducer	Non-inducer	Non-inducer	Inducer
GDPTALQPVSTIAEN	Non-inducer	Non-inducer	Non-inducer	Inducer

**Supplementary Table 5: Details of predicted discontinuous B-cell epitopes from the 3D structure of designed vaccines ERAMV1 and GDPAMV1**

S. No.	ERAMV1 Amino acid residues	Number of amino acid residues	Score
1	A:E1, A:A2, A:A3, A:A4, A:K5, A:M6, A:I7, A:K8, A:L9, A:K10, A:F11, A:G12, A:V13, A:F14, A:F15, A:T16, A:V17, A:L18, A:L19, A:S20, A:S21, A:A22, A:Y23, A:A24, A:N25, A:G26, A:T27, A:P28, A:Q29, A:N30, A:I31, A:T32, A:D33, A:L34, A:C35, A:A36, A:E37, A:Y38, A:H39, A:N40, A:T41, A:Q42, A:I43, A:H44, A:T45, A:L46, A:N47, A:D48, A:K49, A:I50, A:F51, A:S52, A:Y53, A:T54, A:E55, A:S56, A:L57, A:A58, A:G59, A:K60, A:R61, A:E62, A:M63, A:A64, A:I65, A:I66, A:T67, A:F68, A:N70, A:G71, A:A72, A:T73, A:F74, A:Q75, A:V76, A:E77, A:V78, A:P79, A:G80, A:S81, A:Q82, A:H83, A:I84, A:D85, A:S86, A:Q87, A:K88, A:K89	88	0.896
2	A:A495, A:P496, A:A497, A:A498, A:G499, A:N500, A:S501, A:T502, A:G503, A:G504, A:P505, A:G506, A:P507, A:G508, A:Q509, A:G510, A:V511, A:T512, A:A513, A:P514, A:N515, A:N516, A:N517, A:G518, A:G519, A:G520, A:A521, A:A522, A:F523, A:G524, A:G525, A:P526, A:G529, A:T530, A:T531, A:K534, A:T535, A:T536, A:T537, A:A538, A:T539, A:A540, A:T541, A:A542, A:T543, A:P544, A:G545, A:G546, A:P547, A:G548, A:P549, A:G550, A:E551, A:V552, A:N553, A:P554, A:N555, A:P556, A:N557, A:P558, A:G559, A:K560, A:C561, A:I562, A:P563, A:G564, A:Y565, A:K566, A:G567, A:P568, A:G569, A:P570, A:G571, A:Y572, A:T573, A:Y574, A:D575, A:N576, A:P577, A:K578, A:P579, A:L580, A:P581, A:T582, A:L583, A:N584, A:S585, A:S586, A:T587, A:G588, A:P589, A:G590, A:P591, A:G592, A:L593, A:R594, A:T595, A:V596, A:F603, A:G604, A:P605, A:G606, A:F607, A:S608, A:G609, A:P610, A:G611, A:P612, A:G613, A:R614, A:Y615, A:D616, A:S617, A:A618, A:S619, A:S620, A:R621, A:T622, A:S624, A:E625, A:N626, A:G627, A:T628, A:E629, A:G630, A:P631, A:G632, A:P633, A:G634, A:E635, A:T636, A:F637, A:K638, A:L639, A:N640, A:P641, A:D642, A:G643, A:S644, A:A645, A:N646, A:H647, A:G648, A:V649, A:P650, A:G651, A:P652, A:G653, A:P654, A:G655	150	0.671



3	A:G223, A:S229, A:S230, A:E231, A:N232, A:G233, A:T234, A:E235, A:Q245, A:T246, A:N247, A:D248, A:G249, A:A250, A:Y251, A:G252, A:G253, A:G254, A:S255, A:V256, A:A257, A:K258, A:P273, A:L274, A:F275, A:S276, A:F277, A:G278, A:G279, A:G280, A:S281, A:K282, A:E283, A:P284, A:G285, A:D298, A:W299, A:D300, A:G301, A:Y302, A:W303, A:G304, A:G305, A:G306, A:S307, A:Y308, A:L309, A:T310, A:L326, A:T327, A:V328, A:V329, A:G330, A:G331, A:G332, A:S333, A:E334, A:H335, A:Q336, A:H355, A:A357, A:S358, A:I359, A:K360, A:F361, A:N362, A:G363, A:P364, A:G365, A:P366, A:G367, A:S368, A:G369, A:T370, A:L371, A:T372, A:F373, A:L394, A:D395	79	0.656
4	A:A90, A:I91, A:E92, A:R93, A:M94, A:K95, A:D96, A:T97, A:L98, A:R99, A:Y102	11	0.636
<b>GDPAMV1</b>			
<b>S. No.</b>	<b>Amino acid residues</b>	<b>Number of amino acid residues</b>	<b>Score</b>
1	A:E1, A:A2, A:A3, A:A4, A:K5, A:M6, A:I7, A:K8, A:L9, A:K10, A:F11, A:G12, A:V13, A:F14, A:F15, A:T16, A:V17, A:L18, A:L19, A:S20, A:S21, A:A22, A:Y23, A:A24, A:N25, A:G26, A:T27, A:P28, A:Q29, A:N30, A:I31, A:T32, A:D33, A:L34, A:C35, A:A36, A:E37, A:Y38, A:H39, A:N40, A:T41, A:Q42, A:I43, A:H44, A:T45, A:L46, A:N47, A:D48, A:K49, A:I50, A:F51, A:S52, A:Y53, A:T54, A:E55, A:S56, A:L57, A:A58, A:G59, A:K60, A:R61, A:E62, A:M63, A:A64, A:I65, A:I66, A:T67, A:F68, A:K69, A:N70, A:A72, A:F74, A:Q75, A:V76, A:E77, A:V78, A:P79, A:G80, A:S81, A:Q82, A:H83, A:I84, A:D85, A:S86, A:Q87, A:K88, A:K89, A:A90, A:I91, A:E92, A:R93, A:M94, A:K95	93	0.818

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A:S403, A:S404, A:T405, A:A406, A:A407, A:G408,  
A:G409, A:S421, A:A422, A:A423, A:A426, A:S427,  
A:S428, A:T429, A:S430, A:S431, A:G432, A:F433,  
A:S442, A:S443, A:A444, A:S445, A:S446, A:S447,  
A:S448, A:S449, A:T450, A:T451, A:A452, A:A453,  
A:S454, A:G455, A:G457, A:P458, A:G459, A:S460,  
A:S461, A:S462, A:A463, A:A464, A:A465, A:S466,  
A:S467, A:A468, A:A469, A:S470, A:S471, A:S472,  
A:T473, A:S474, A:L475, A:G478, A:P479, A:G480,  
A:A481, A:T482, A:S483, A:A484, A:A485, A:A486,  
A:S487, A:A488, A:A489, A:S490, A:S491, A:A492,  
A:A493, A:S494, A:S495, A:I496, A:G497, A:P498,  
A:G499, A:P500, A:G501, A:A502, A:G503, A:M504,  
A:V505, A:G506, A:V507, A:A508, A:G509, A:V510,  
A:A511, A:G512, A:V513, A:V514, A:A515, A:L516,  
A:F517, A:G518, A:P519, A:G520, A:P521, A:G522,  
A:A523, A:A524, A:A525, A:A526, A:N527, A:A528,  
A:G529, A:V530, A:A531, A:V532, A:N533, A:K534,  
A:P535, A:G536, A:F537, A:G538, A:G539, A:P540,  
A:G541, A:P542, A:G543

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0.707

**Supplementary Table 6: Result of MHC Class I processing of designed vaccine.**

<b>MHC Class I processing result of ERAMV1</b>					
<b>S.No.</b>	<b>Peptide</b>	<b>Allele</b>	<b>Proteasome Score</b>	<b>TAP Score</b>	<b>Processing Score</b>
1	LAAPEGNAF (E2)	HLA-B*15:01, HLA-B*15:02, HLA-B*15:25, HLA-B*35:01, HLA-C*03:02, HLA-C*03:03, HLA-C*03:04, HLA-C*12:02, HLA-C*12:03, HLA-C*16:01	1.44	1.16	2.6
2	MGQTNDGAY (E4)	HLA-A*30:02, HLA-B*15:02, HLA-B*15:25, HLA-B*35:01, HLA-C*03:02	1.33	1.18	2.51
3	VAKEFNISI (E5)	HLA-A*30:01, HLA-C*03:03, HLA-C*03:04, HLA-C*12:03	1.25	0.3	1.56
4	LTADWDGYW (E6)	HLA-B*53:01, HLA-B*57:01, HLA-B*58:01	1.37	0.41	1.78
5	YLTADWDGY (E7)	HLA-A*29:02, HLA-B*35:01	1.32	1.28	2.6
6	TLVAHVWNL (E13)	HLA-A*02:01, HLA-A*02:06, HLA-A*32:01, HLA-A*68:02, HLA-B*08:01	1.56	0.47	2.03
7	TYFGPGFSF (E14)	HLA-A*23:01, HLA-A*24:02, HLA-A*29:02, HLA-A*32:01, HLA-C*03:02, HLA-C*07:02, HLA-C*12:03, HLA-C*14:02, HLA-C*16:01	1.39	1.28	2.67
8	EHQLNVEAL (E16)	HLA-B*38:01, HLA-B*39:01	1.58	0.34	1.92
9	SVYDLGNNR (E19)	HLA-A*11:01, HLA-A*31:01, HLA-A*33:03, HLA-A*68:01	1.22	0.83	2.05
10	LVDEPLFSF (E21)	HLA-B*35:01, HLA-C*05:01, HLA-C*16:01	1.32	1.11	2.43
11	KEPGLTFAF (E22)	HLA-B*13:01, HLA-B*18:01, HLA-B*40:01, HLA-B*40:02	1.37	1.1	2.47

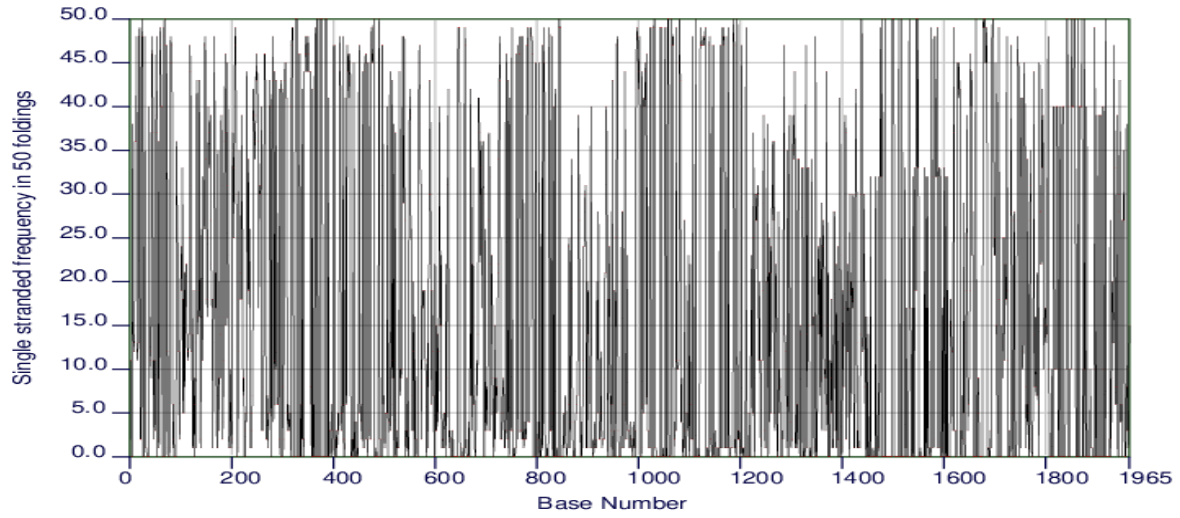
**MHC Class I processing result of GDPAMV1**

	<b>Peptide</b>	<b>Allele</b>	<b>Proteasome Score</b>	<b>TAP Score</b>	<b>Processing Score</b>
1	MISGVALAI (G2)	HLA-A*02:01, HLA-A*02:06, HLA-A*32:01, HLA-A*68:02, HLA-B*15:25, HLA-B*35:01, HLA-C*02:02, HLA-C*02:09, HLA-C*03:02, HLA-C*03:03, HLA-C*03:04, HLA-C*12:02, HLA-C*12:03, HLA-C*15:02, HLA-C*16:01	1.28	0.33	1.61
2	VSYTALFTI (G5)	HLA-A*02:06, HLA-A*23:01, HLA-A*30:01, HLA-A*32:01, HLA-B*13:02, HLA-B*52:01, HLA-B*58:01, HLA-C*03:02, HLA-C*03:03, HLA-C*03:04, HLA-C*12:03, HLA-C*15:02, HLA-C*16:01	1.34	0.38	1.72
3	TAAGTDYAL (G7)	HLA-A*68:02, HLA-B*35:01, HLA-B*39:01, HLA-C*03:02, HLA-C*03:03, HLA-C*03:04, HLA-C*08:01, HLA-C*16:01	1.59	0.46	2.05
4	VSYTALFTI (G10)	HLA-A*02:06, HLA-A*23:01, HLA-A*30:01, HLA-A*32:01, HLA-B*13:02, HLA-B*52:01, HLA-B*58:01, HLA-C*03:02, HLA-C*03:03, HLA-C*03:04, HLA-C*12:03, HLA-C*15:02, HLA-C*16:01	1.34	0.38	1.72
5	ITPANNYAL (G11)	HLA-A*02:06, HLA-C*03:03, HLA-C*03:04, HLA-C*16:01, HLA-G*01:01, HLA-G*01:02, HLA-G*01:03, HLA-G*01:04, HLA-G*01:06	1.53	0.43	1.97

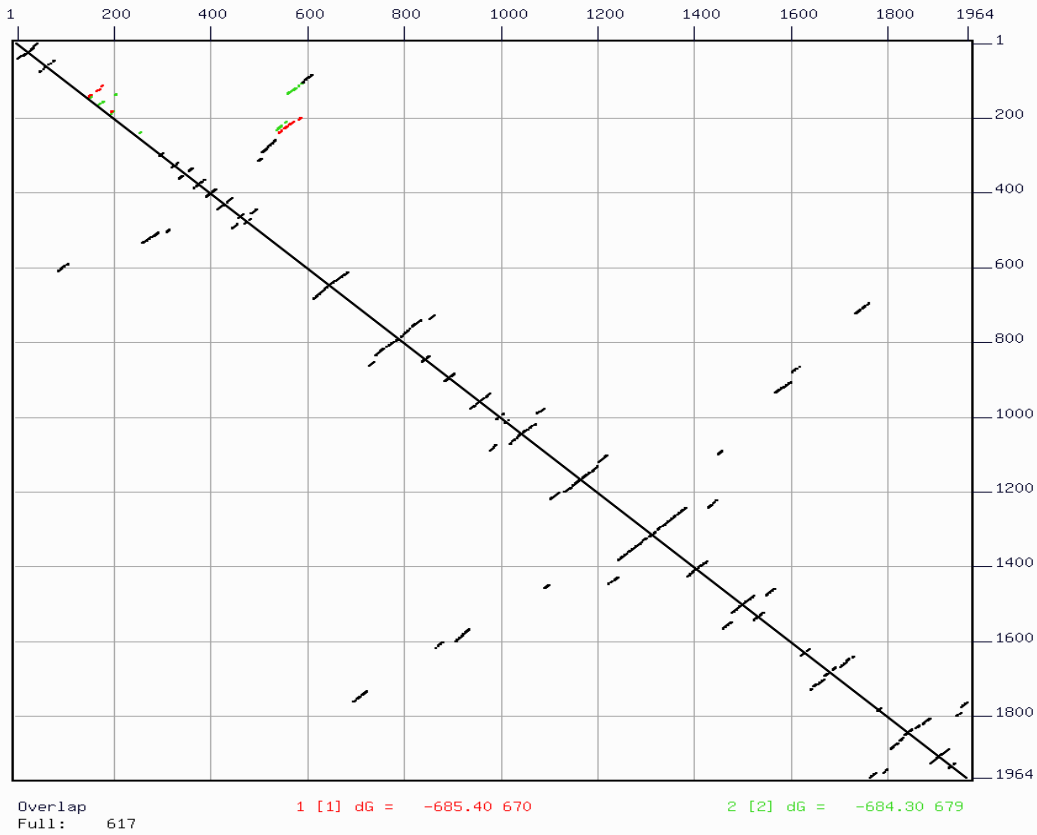
6	ATVEVGSAY (G14)	HLA-A*11:01, HLA-A*25:01, HLA-A*26:01, HLA-A*29:02, HLA-A*68:01, HLA-B*15:01, HLA-B*15:02, HLA-B*15:25, HLA-B*35:01, HLA-C*02:02, HLA-C*02:09, HLA-C*03:02, HLA-C*12:02, HLA-C*12:03, HLA-C*16:01	1.26	1.38	2.65
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**Supplementary Table 7 : Details of prediction of Disulfide engineering of designed vaccine candidates (ERAMV1 and GDPAMV1)**

<b>ERAMV1</b>								
<b>Res1 Chain</b>	<b>Res1 Seq #</b>	<b>Res1 AA</b>	<b>Res2 Chain</b>	<b>Res2 Seq #</b>	<b>Res2 AA</b>	<b>Chi3</b>	<b>Energy</b>	<b>Sum B-Factors</b>
A	177	SER	A	206	ALA	-66.06	1.13	17.64
A	8	LYS	A	44	HIS	80.02	1.86	34.33
A	300	ASP	A	329	VAL	85.12	2.3	16.12
A	496	PRO	A	540	ALA	90.56	0.78	26.14
A	289	ALA	A	294	SER	91.69	0.7	13.76
A	501	SER	A	522	ALA	94.71	0.55	20.16
<b>GDPAMV1</b>								
<b>Res1 Chain</b>	<b>Res1 Seq #</b>	<b>Res1 AA</b>	<b>Res2 Chain</b>	<b>Res2 Seq #</b>	<b>Res2 AA</b>	<b>Chi3</b>	<b>Energy</b>	<b>Sum B-Factors</b>
A	376	ALA	A	399	ALA	-85.83	1.99	19.52
A	501	GLY	A	517	PHE	-79.83	2.4	40.48
A	236	ALA	A	261	ALA	77.98	2.09	18.45
A	348	LEU	A	360	ALA	84.19	2.24	20.28
A	439	ALA	A	452	ALA	93.25	1.74	20.16
A	385	SER	A	388	THR	94.4	0.71	16.77
A	82	GLN	A	86	SER	96.08	0.9	45.52
A	160	ILE	A	164	SER	96.33	2.31	25.75



**Supplementary Figure 1a:** SS-Count plot of mRNA of ERAMV1.

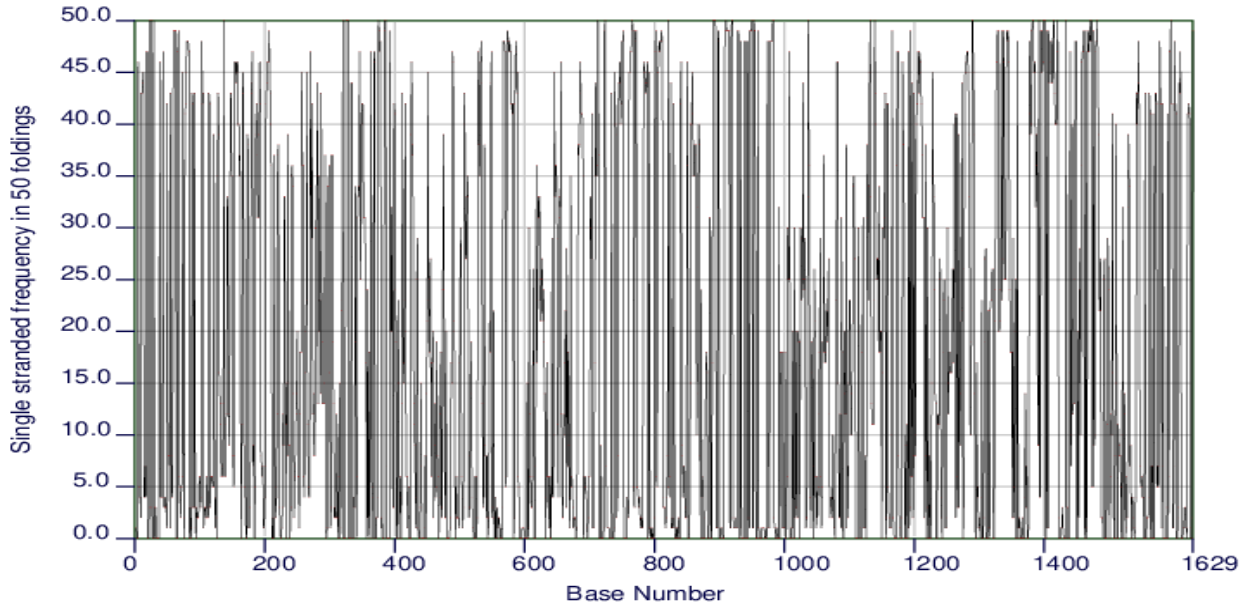


**Supplementary Figure 1b:** Structure dot plot of mRNA of ERAMV1 for 2 folding (Structure 1 and Structure 2).

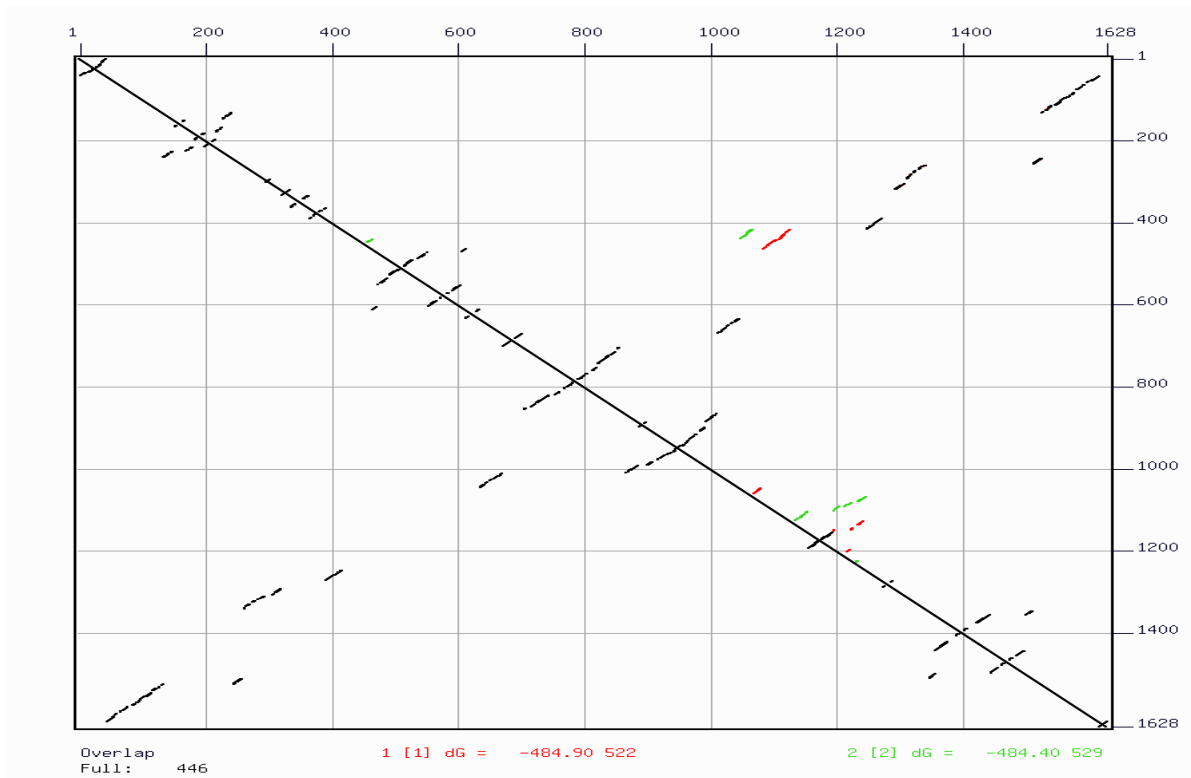


**Supplementary Figure 1c:** The folding structure of mRNA of ERAMV1.

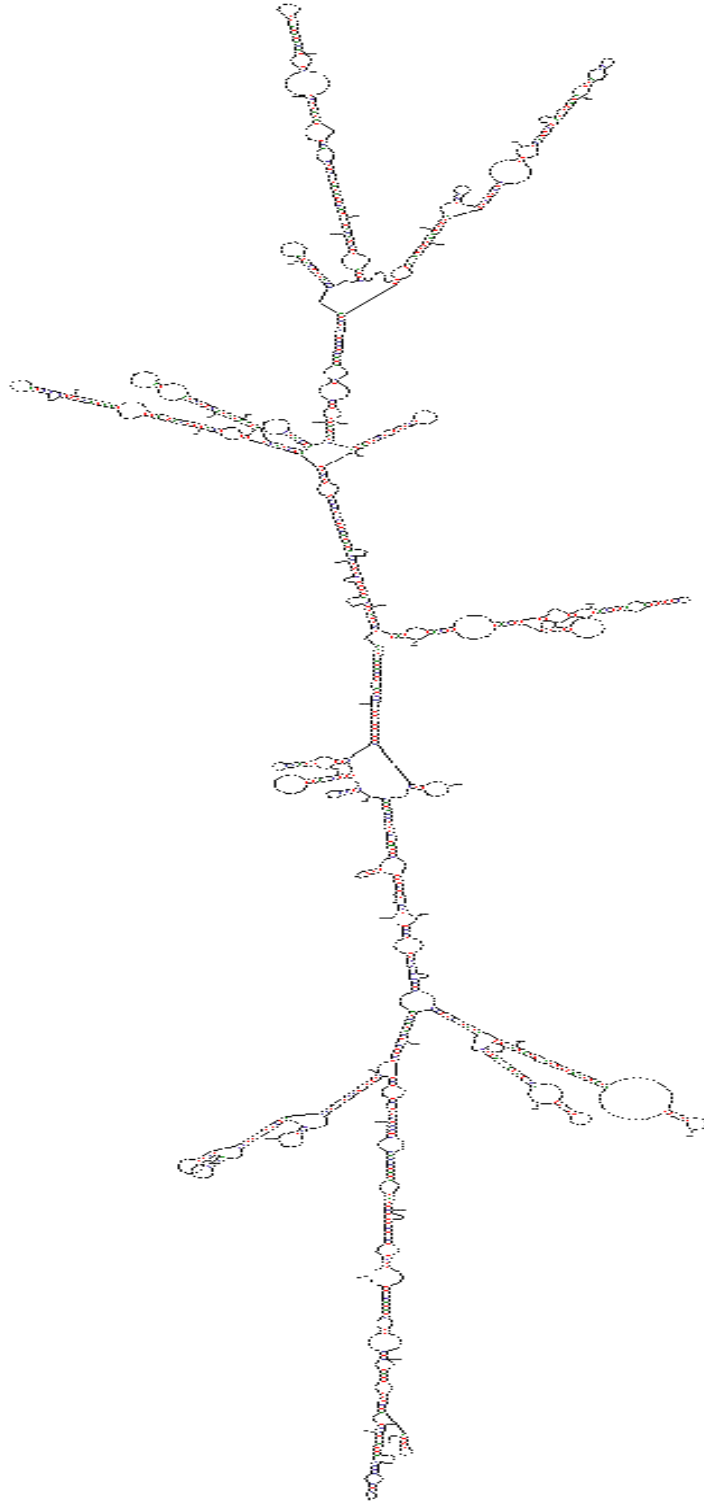




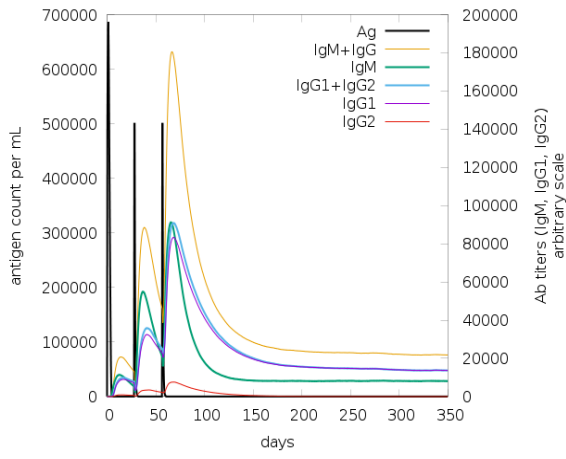
**Supplementary Figure 2a:** SS-Count plot of mRNA of GDPAMV1.



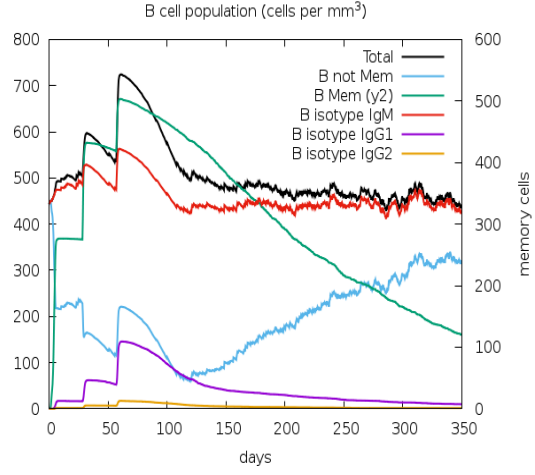
**Supplementary Figure 2b:** Structure dot plot of mRNA of GDPAMV1 for 2 folding (Structure 1 and Structure 2).



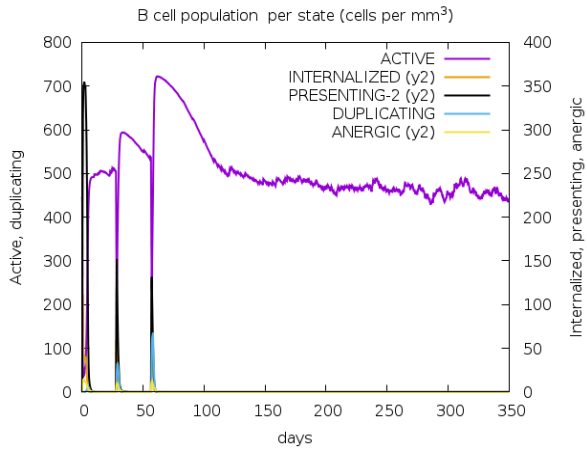
**Supplementary Figure 2c:** The folding structure of mRNA of GDPAMV1.



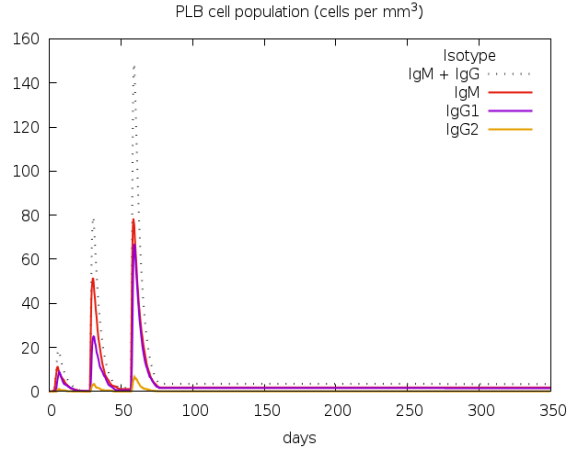
(a)



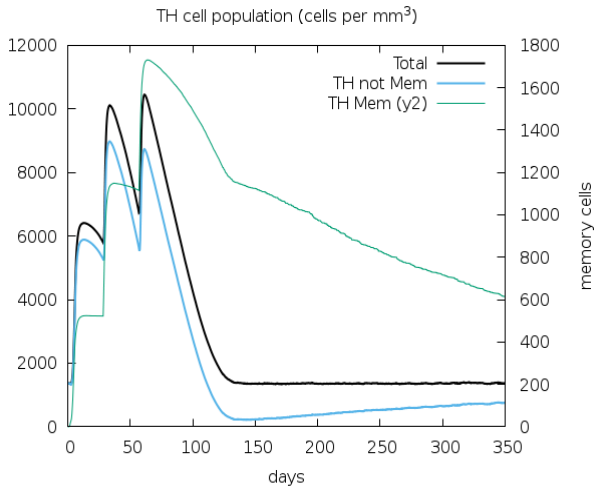
(b)



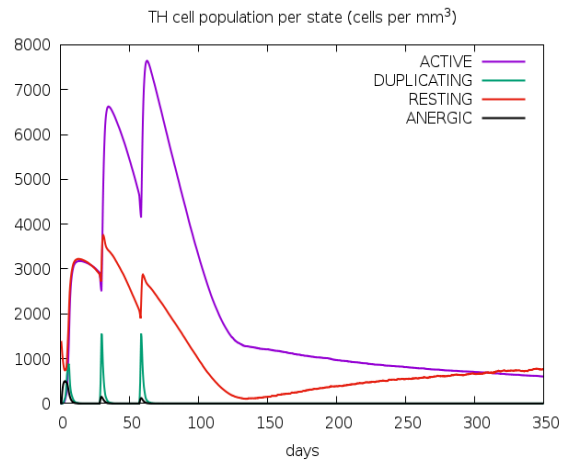
(c)



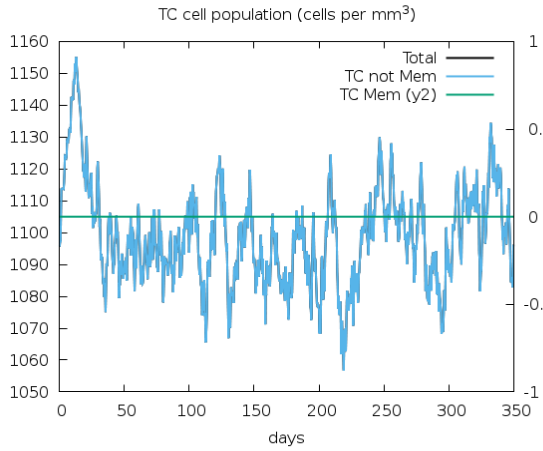
(d)



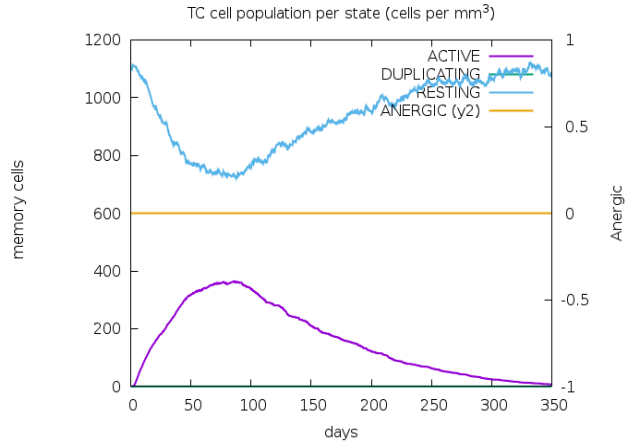
(e)



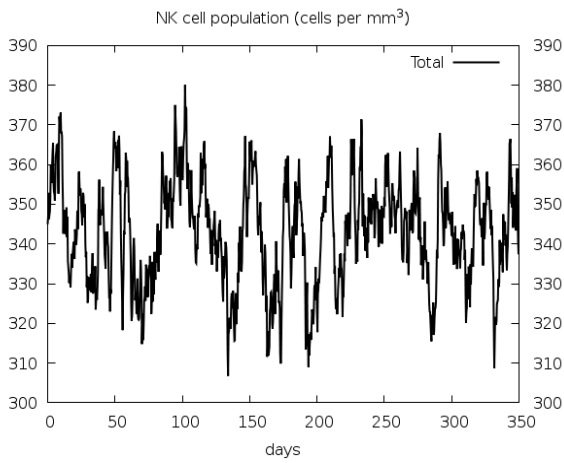
(f)



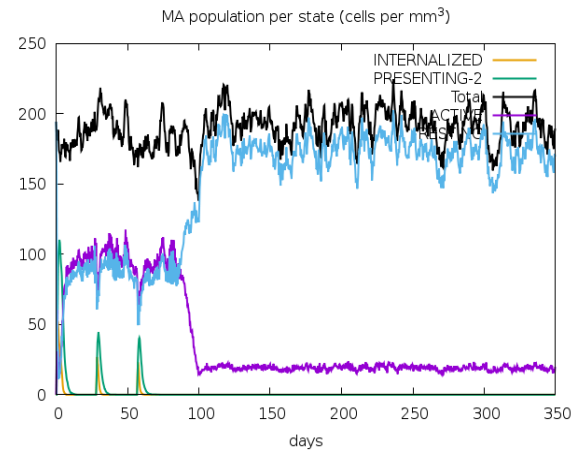
(g)



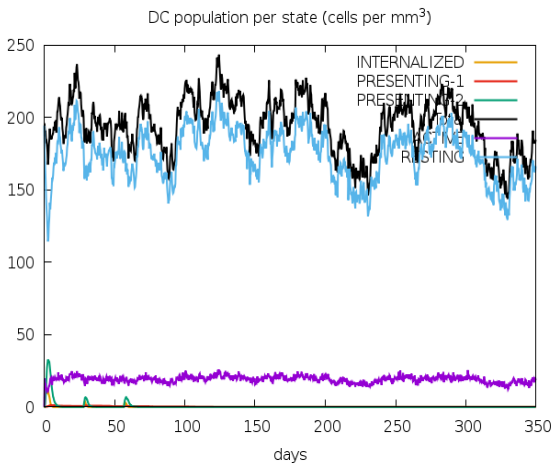
(h)



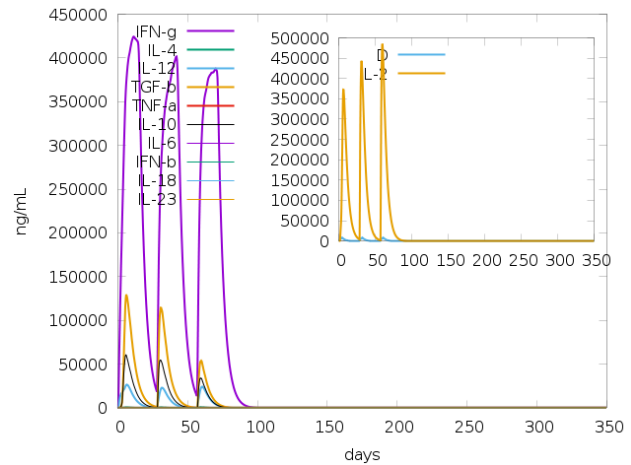
(i)



(j)



(k)



(l)

**Supplementary figure 3:** Result obtained by immune simulation of control vaccine (C2). The section a, represents antigen profile and antibody titration; b, c, represent the B cell population; d, represents plasma B lymphocytes count sub-divided per isotype (IgM, IgG1 and IgG2); e, f, represents CD4+ T-helper lymphocytes; g, h, represents CD8+ T-cytotoxic lymphocytes count per entity-state; i, represents natural killer cells (total count); j, represents macrophages: total count, internalized, presenting on MHC class-II, active and resting macrophages; k, represents Dendritic cells (DC) that can present antigenic peptides on both MHC class-I and class-II molecules; l, represent concentration of cytokines and interleukins titration.