Table S1. Predicted B-cell epitopes from FimD protein.

S. No.	BCPred Epitopes			FCPred			ABCPred		
	Position	Epitopes	Sores	Position	Epitopes	Scores	Position	Epitopes	Scores
1	649	YSVQTGYAGGGEGSNGNSGY	1	654	GYAGGGEGSNGNSG	1	718	AVLIKAPGAKDAKVEN	0.9
2	223	RDNTTWSYSSGANSSGSKNK	1	224	DNTTWSYSSGANSS	1	169	ARGYIPPELWDSGINA	0.9
3	805	NNKPLPFGAMVTSDSSQSSG	0.99	816	TSDSSQSSGIVADN	1	87	GYMATRDVTFNAGDSE	0.9
4	379	TAGEYRSGNAQQEKPRFFQS	0.98	321	YNSTVPPGPFTIND	1	848	GEGENAHCVADYKLPP	0.9
5	64	LSNFENGQELPPGTYRVDIY	0.98	760	LDTNSLADNVDLDN	1	506	DGVIQVKPKFTDYYNL	0.89
6	312	SIKQNGYDIYNSTVPPGPFT	0.96	192	TGNSVQNSIGGDSH	1	818	DSSQSSGIVADNGQVY	0.88
7	184	AGLLNYNFTGNSVQNSIGGD	0.95	66	NFENGQELPPGTYR	0.99	747	LPYATEYRENRVALDT	0.88
8	402	HGLPAGWTIYGGMQLADRYR	0.94	445	NATLPDDSEHEGQS	0.99	658	GGEGSNGNSGYAALNY	0.88
9	532	SVTQQLGRTSTLYLSGSHQT	0.93	801	TLTRNNKPLPFGAM	0.99	414	MQLADRYRAFNFGVGK	0.88
10	261	LTLGDGYTQGDIFDGINFRG	0.92	844	QVKWGEGENAHCVA	0.99	730	KVENQTGVRTDWRGYA	0.89
11	766	ADNVDLDNAVANVVPTRGAI	0.85	336	YAAGNSGDLQVTIK	0.99	802	LTRNNKPLPFGAMVTS	0.88
12	745	AVLPYATEYRENRVALDTNS	0.84	170	RGYIPPELWDSGIN	0.99	570	FEDINWTLSYSLTKNA	0.88
13	163	AFMSNHARGYIPPELWDSGI	0.83	360	VPYSSVPLLQREGH	0.99	374	TRYSITAGEYRSGNAQ	0.88
14	284	ASDDNMLPDSQRGFAPVIHG	0.83	381	GEYRSGNAQQEKPR	0.99	345	QVTIKEADGSTQIFTV	0.88

15	722	KAPGAKD AKVENQT GVRTDW	0.83	675	GGYGNA NIGYSHS D	0.99	214	GLNIGAWRL RDNTTWS	0.88
16	88	YMATRDVT FNAGDSEQ GIVP	0.81	93	DVTFNAG DSEQGIV	0.98	648	SYSVQTGYAG GGEGSN	0.87
17	139	TSMINEATS HLDVGQQ RLNL	0.81	707	GVTLGQP LNDTAVL	0.98	635	AGLYGTLLED NNLSYS	0.87
18	841	GKVQVKW GEGENAH CVADYK	0.80	482	STSGYFNF ADTTYK	0.98	611	KSLWRHANA SYSMSHD	0.87
19	573	INWTLSYSL TKNAWQK GRDR	0.77	460	RFLYNKSL NESGTN	0.97	498	SGYNIETQDG VIQVKP	0.87
20				567	NTAFEDI NWTLSYS	0.97	77	TYRVDIYLNN GYMATR	0.85
21				264	GDGYTQG DIFDGIN	0.95	583	KNAWQKGR DRMLALNV	0.85
22				284	ASDDNM LPDSQRG F	0.94	454	HEGQSVRFLY NKSLNE	0.85
23				402	HGLPAG WTIYGGM Q	0.92	40	APFSYADLYF NPRFLA	0.85
24				564	SGSHQTY WGTNNID	0.85	309	AQVSIKQNGY DIYNST	0.85
25				40	APFSYAD LYFNPRF	0.84	140	SMINEATSHL DVGQQR	0.85
26				690	IKQFYYGI SGGVLA	0.83	675	GGYGNANIG YSHSDDI	0.85
27				722	KAPGAKD AKVENQT	0.80	478	GYRYSTSGYF NFADTT	0.85
28				775	VANVVPT RGAIVRA	0.79	184	AGLLNYNFT GNSVQNS	0.84
29				531	FSVTQQL GRTSTLY	0.78	129	LLAVDACVPL TSMINE	0.84
30				134	ACVPLTS MINEATS	0.72	842	KVQVKWGEG ENAHCVA	0.83
31				512	KPKFTDY YNLAYNK	0.72	71	QELPPGTYRV DIYLNN	0.83
32				4	LNLSVYQ RNTQCLH	0.70	619	ASYSMSHDLK GRMTNL	0.83
33							196	VQNSIGGDSH YAYLNL	0.83
34							808	PLPFGAMVTS DSSQSS	0.82
35							629	GRMTNLAGL YGTLLED	0.82

36	333	NDLYAAGNS GDLQVTI	0.82
37	248	TWLERDIIPLR SRLTL	0.82
38	114	LASMGLNTAS VPGMNL	0.82
39	724	PGAKDAKVE NQTGVRT	0.81
40	549	HQTYWGTNN IDEQLQA	0.81
41	537	LGRTSTLYLSG SHQTY	0.8
42	487	FNFADTTYKR MSGYNI	0.8
43	221	RLRDNTTWSY SSGANS	0.8
44	175	PELWDSGINA GLLNYN	0.79
45	856	VADYKLPPES QHQLLT	0.79
46	791	KARVGMKLL MTLTRNN	0.79
47	694	YYGISGGVLA HADGVT	0.79
48	404	LPAGWTIYGG MQLADR	0.79
49	293	SQRGFAPVIH GIARGT	0.79
50	229	SYSSGANSSGS KNKWQ	0.79
51	160	IPQAFMSNHA RGYIPP	0.79
52	664	GNSGYAALN YRGGYGN	0.78
53	32	VACVFAAQA PFSYADL	0.78
54	261	LTLGDGYTQG DIFDGI	0.78
55	832	VYLSGMPLAG KVQVKW	0.77
56	684	YSHSDDIKQF YYGISG	0.77
57	526	RGKLQFSVTQ QLGRTS	0.77
58	269	QGDIFDGINF RGAELA	0.77
59	763	NSLADNVDL DNAVAN	0.76

60	564	AGLNTAFEDI NWTLSY	0.76
61	707	GVTLGQPLN DTAVLIK	0.75
62	517	DYYNLAYNK RGKLQFS	0.75
63	102	EQGIVPCLTR AQLASM	0.75
64	824	GIVADNGQV YLSGMPL	0.74
65	95	TFNAGDSEQG IVPCLT	0.73
66	701	VLAHADGVT LGQPLND	0.73
67	446	ATLPDDSEHE GQSVRF	0.73
68	440	DMTQANATL PDDSEHE	0.73
69	431	MGALGALSV DMTQANA	0.73
70	353	GSTQIFTVPYS SVPLL	0.73
71	757	RVALDTNSLA DNVDLD	0.72
72	51	PRFLADDPQA VADLSN	0.72
73	318	YDIYNSTVPP GPFTIN	0.72
74	9	YQRNTQCLH NRKLRLA	0.71
75	302	HGIARGTAQ VSIKQNG	0.71
76	279	RGAELASDD NMLPDSQ	0.71
77	202	GDSHYAYLN LQSGLNI	0.71
78	737	VRTDWRGYA VLPYATE	0.71
79	384	RSGNAQQEK PRFFQST	0.7
80	555	TNNIDEQLQA GLNTAF	0.68
81	58	PQAVADLSNF ENGQEL	0.66
82	25	GFFVRLSVAC VFAAQA	0.66
83	393	PRFFQSTLLH GLPAGW	0.65

84	468	NESGTNIQLV GYRYST	0.64
85	360	VPYSSVPLLQ REGHTR	0.64
86	285	SDDNMLPDS QRGFAPV	0.62
87	425	FGVGKNMGA LGALSVD	0.61
88	1	MSYLNLSVYQ RNTQCL	0.6
89	146	TSHLDVGQQ RLNLTIP	0.56
90	18	NRKLRLAGFF VRLSVA	0.54

Table S2. Common Identified B-cells Epitopes from all three tools.

S. No	Position	Epitopes	Scores
1	163	AFMSNHARGYIPPELWDSGI	0.84
2	223	RDNTTWSYSSGANSSGSKNK	1
3	801	TLTRNNKPLPFGAM	0.99
4	844	QVKWGEGENAHCVA	0.9
5	64	LSNFENGQELPPGTYRVDIY	0.9
6	87	GYMATRDVTFNAGDSE	0.9
7	816	TSDSSQSSGIVADN	1
8	841	GKVQVKWGEGENAHCVADYK	0.8
9	184	AGLLNYNFTGNSVQNS	0.9
10	129	LLAVDACVPLTSMINE	0.8
11	318	YDIYNSTVPPGPFTIN	0.7
12	374	TRYSITAGEYRSGNAQ	0.8
13	88	YMATRDVTFNAGDSEQGIVP	0.8
14	649	YSVQTGYAGGGEGSNGNSGY	1
15	760	LDTNSLADNVDLDN	1
16	402	HGLPAGWTIYGGMQ	0.9
17	32	VACVFAAQAPFSYADL	0.7
18	284	ASDDNMLPDSQRGF	0.9
19	722	KAPGAKDAKVENQTGVRTDW	0.8
20	570	FEDINWTLSYSLTKNA	0.8
21	169	ARGYIPPELWDSGINA	0.9
22	4	LNLSVYQRNTQCLH	08
23	393	PRFFQSTLLHGLPAGW	0.9
24	64	LSNFENGQELPPGTYRVDIY	0.9
25	77	TYRVDIYLNNGYMATR	0.8
26	531	FSVTQQLGRTSTLY	0.7

Table S3. Comparative analysis of B Cell, MHC-I and MHC-II epitopes.

S. No	B-cell epitopes	MHC-I	MHC-II	Scores
1	LNLSVYQRNTQCLHNRKLRLAGFF VRLSVA	YQRNTQCLH	NRKLRLAGFFVRLSV RKLRLAGFFVRLSVA	0.6
2	TAGEYRSGNAQQEKPRFFQSTLLHG LPAGWTIYGGMQLADRYR	--	KPRFFQSTLLHGLPA EKPRFFQSTLLHGLP QEKPRFFQSTLLHGL	0.8
3	LSNFENGQELPPGTYRVDIYLNNGY MATRDVTFNAGDSE	--	YRVDIYLNNGYMATR RVDIYLNNGYMATRD	0.9

Table S4. Vaccine model Constructs.

S. No	Vaccine construct	Vaccine composition	Sequence
1	V1	FimD, HBHA adjuvant, (4-33, 64-102 and 379-421)	EAAAKMAENPNIDDLPAPLLAALGAADLALATVNDLIANLRERAEETRA ETRTRVEERRARLTKFQEDLPEQFIELRDKFTTEELRKAAEGYLEAATNRY NELVERGEAALQRLRSQTAFEDASARAEGYVDQAVELTQEALGTVASQT RAVGERAAKLVGIELEAAAK*AKFVAAWTLKAAA*GGGS**LNLSVYQRNTQC LHNRKLRLAGFFVRLSVA**GGGS**LSNFENGQELPPGTYRVDIYLNNGYM ATRDVTFNAGDSE**GGGSHEYGAEALERAG**TAGEYRSGNAQQEKPRFF QSTLLHGLPAGWTIYGGMQLADRYR**HEYGAEALERAG*AKFVAAWTLKA AA*GGGS
2	V2	FimD, HBHA conserved adjuvant, (4-33, 64-102 and 379-421)	EAAAKMAENSNIDDIKAPLLAALGAADLALATVNELITNLRERAEETRRS RVEESRARLTKLQEDLPEQLTELREKFTAEELRKAAEGYLEAATSELVERGE AALERLRSQQSFEEVSARAEGYVDQAVELTQEALGTVASQVEGRAAKLVG IELEAAAK*AKFVAAWTLKAAA*GGGS**LNLSVYQRNTQCLHNRKLRLAGFF VRLSVA**GGGS**LSNFENGQELPPGTYRVDIYLNNGYMATRDVTFNAGD SE**GGGSHEYGAEALERAG**TAGEYRSGNAQQEKPRFFQSTLLHGLPAGW TIYGGMQLADRYR**HEYGAEALERAG*AKFVAAWTLKAAA*GGGS
3	V3	FimD, Beta defensin adjuvant, (4-33, 64-102 and 379-421)	EAAAKGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKE AAAK*WTLKAAA*GGGS**LNLSVYQRNTQCLHNRKLRLAGFFVRLSVA**GG GS**LSNFENGQELPPGTYRVDIYLNNGYMATRDVTFNAGDSE**GGGSHEY GAEALERAG**TAGEYRSGNAQQEKPRFFQSTLLHGLPAGWTIYGGMQL ADRYR**HEYGAEALERAG*AKFVAAWTLKAAA*GGGS
4	V4	FimD, Ribosomal adjuvant adjuvant, (4-33, 64-	EAAAKMAKLSTDELLDAFKEMTLLELSDFVKKFEETFEVTAAAPVAVAAA GAAPAGAAVEAAEEQSEFDVILEAAGDKKIGVIKVVREIVSGLGLKEAKDL VDGAPKPLLEKVAKEAADEAKAKLEAAGATVTVK**EAAAK***AKFVAAWTL KAAA*GGGS**LNLSVYQRNTQCLHNRKLRLAGFFVRLSVA**GGGS**LSNFEN GQELPPGTYRVDIYLNNGYMATRDVTFNAGDSE**GGGSHEYGAEALER AG**TAGEYRSGNAQQEKPRFFQSTLLHGLPAGWTIYGGMQLADRYR**HE YGAEALERAG*AKFVAAWTLKAAA*GGGS

		102 and 379-421)	
5	V5	FimD, HBHA adjuvant (379-421, 64-102, and 4-33)	EAAAKMAENPNIDDLPAPLLAALGAADLALATVNDLIANLRERAEETRA ETRTRVEERRARLTKFQEDLPEQFIELRDKFTTEELRKAAEGYLEAATNRY NELVERGEAALQRLRSQTAFEDASARAEGYVDQAVELTQEALGTVASQT RAVGERAAKLVGIELEAAAK*AKFVAAWTLKAAA*GGGS**TAGEYRSGNAQ QEKPRFFQSTLLHGLPAGWTIYGGMQLADRYR**GGGS**LSNFENGQELPP GTYRVDIYLNNGYMATRDVTFNAGDSE**HEYGAEALERAG**LNLSVYQR NTQCLHNRKLRLAGFFVRLSVA**HEYGAEALERAG*AKFVAAWTLKAAA*G GGS
6	V6	FimD, HBHA conserved adjuvant (379-421, 64-102, and 4-33)	EAAAKMAENSNIDDIKAPLLAALGAADLALATVNELITNLRERAEETRRS RVEESRARLTKLQEDLPEQLTELREKFTAEELRKAAEGYLEAATSELVERGE AALERLRSQQSFEEVSARAEGYVDQAVELTQEALGTVASQVEGRAAKLVG IELEAAAK*AKFVAAWTLKAAA*GGGS**TAGEYRSGNAQQEKPRFFQSTLLH GLPAGWTIYGGMQLADRYR**GGGS**LSNFENGQELPPGTYRVDIYLNNG YMATRDVTFNAGDSE**HEYGAEALERAG**LNLSVYQRNTQCLHNRKLRL AGFFVRLSVA**HEYGAEALERAG*AKFVAAWTLKAAA*GGGS
7	V7	FimD, Beta defensin adjuvant (379-421, 64-102, and 4-33)	EAAAKGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKE AAAK*AKFVAAWTLKAAA*GGGS**TAGEYRSGNAQQEKPRFFQSTLLHGLP AGWTIYGGMQLADRYR**GGGS**LSNFENGQELPPGTYRVDIYLNNGYMA TRDVTFNAGDSE**HEYGAEALERAG**LNLSVYQRNTQCLHNRKLRLAGFF VRLSVA**HEYGAEALERAG*AKFVAAWTLKAAA*GGGS
8	V8	FimD, Ribosomal adjuvant (379-421, 64-102, and 4-33)	EAAAKMAKLSTDELLDAFKEMTLLELSDFVKKFEETFEVTAAAPVAVAAA GAAPAGAAVEAAEEQSEFDVILEAAGDKKIGVIKVVREIVSGLGLKEAKDL VDGAPKPLLEKVAKEAADEAKAKLEAAGATVTVKEAAAK*AKFVAAWTL KAAA*GGGS**TAGEYRSGNAQQEKPRFFQSTLLHGLPAGWTIYGGMQLA DRYR**GGGS**LSNFENGQELPPGTYRVDIYLNNGYMATRDVTFNAGDSE **HEYGAEALERAG**LNLSVYQRNTQCLHNRKLRLAGFFVRLSVA**HEYGAE ALERAG*AKFVAAWTLKAAA*GGGS
9	V9	FimD, HBHA adjuvant, (64-102, 4-33, and 379-421)	EAAAKMAENPNIDDLPAPLLAALGAADLALATVNDLIANLRERAEETRA ETRTRVEERRARLTKFQEDLPEQFIELRDKFTTEELRKAAEGYLEAATNRY NELVERGEAALQRLRSQTAFEDASARAEGYVDQAVELTQEALGTVASQT RAVGERAAKLVGIELEAAAK*AKFVAAWTLKAAA*GGGS**LSNFENGQELPP GTYRVDIYLNNGYMATRDVTFNAGDSE**GGGS**LNLSVYQRNTQCLHNR KLRLAGFFVRLSVA**HEYGAEALERAG**TAGEYRSGNAQQEKPRFFQSTLL HGLPAGWTIYGGMQLADRYR**HEYGAEALERAG*AKFVAAWTLKAAA*GG GS
10	V10	FimD, HBHA conserved	EAAAKMAENSNIDDIKAPLLAALGAADLALATVNELITNLRERAEETRRS RVEESRARLTKLQEDLPEQLTELREKFTAEELRKAAEGYLEAATSELVERGE AALERLRSQQSFEEVSARAEGYVDQAVELTQEALGTVASQVEGRAAKLVG IELEAAAK*AKFVAAWTLKAAA*GGGS**LSNFENGQELPPGTYRVDIYLNNG**

		adjuvant, (64-102, 4-33, and 379-421)	**YMATRDVTFNAGDSE**GGGS**LNLSVYQRNTQCLHNRKLRLAGFFVRLS VA**HEYGAEALERAG**TAGEYRSGNAQQEKPRFFQSTLLHGLPAGWTIYG GMQLADRYR**HEYGAEALERAG*AKFVAAWTLKAAA*GGGS
11	V11	FimD, Beta defensin adjuvant (64-102, 4-33, and 379-421)	EAAAKGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKE AAAK*AKFVAAWTLKAAA*GGGS**LSNFENGQELPPGTYRVDIYLNNGYMA TRDVTFNAGDSE**GGGS**LNLSVYQRNTQCLHNRKLRLAGFFVRLSVA**HE YGAEALERAG**TAGEYRSGNAQQEKPRFFQSTLLHGLPAGWTIYGGMQ LADRYR**HEYGAEALERAG*AKFVAAWTLKAAA*GGGS
12	V12	FimD, Ribosomal adjuvant (64-102, 4-33, and 379-421)	EAAAKMAKLSTDELLDAFKEMTLLELSDFVKKFEETFEVTAAAPVAVAAA GAAPAGAAVEAAEEQSEFDVILEAAGDKKIGVIKVVREIVSGLGLKEAKDL VDGAPKPLLEKVAKEAADEAKAKLEAAGATVTVK**EAAAK*AKFVAAWTL *KAAA*GGGS**LSNFENGQELPPGTYRVDIYLNNGYMATRDVTFNAGDSE**G GGS**LNLSVYQRNTQCLHNRKLRLAGFFVRLSVA**HEYGAEALERAG**TAG EYRSGNAQQEKPRFFQSTLLHGLPAGWTIYGGMQLADRYR**HEYGAEA LERAG*AKFVAAWTLKAAA*GGGS

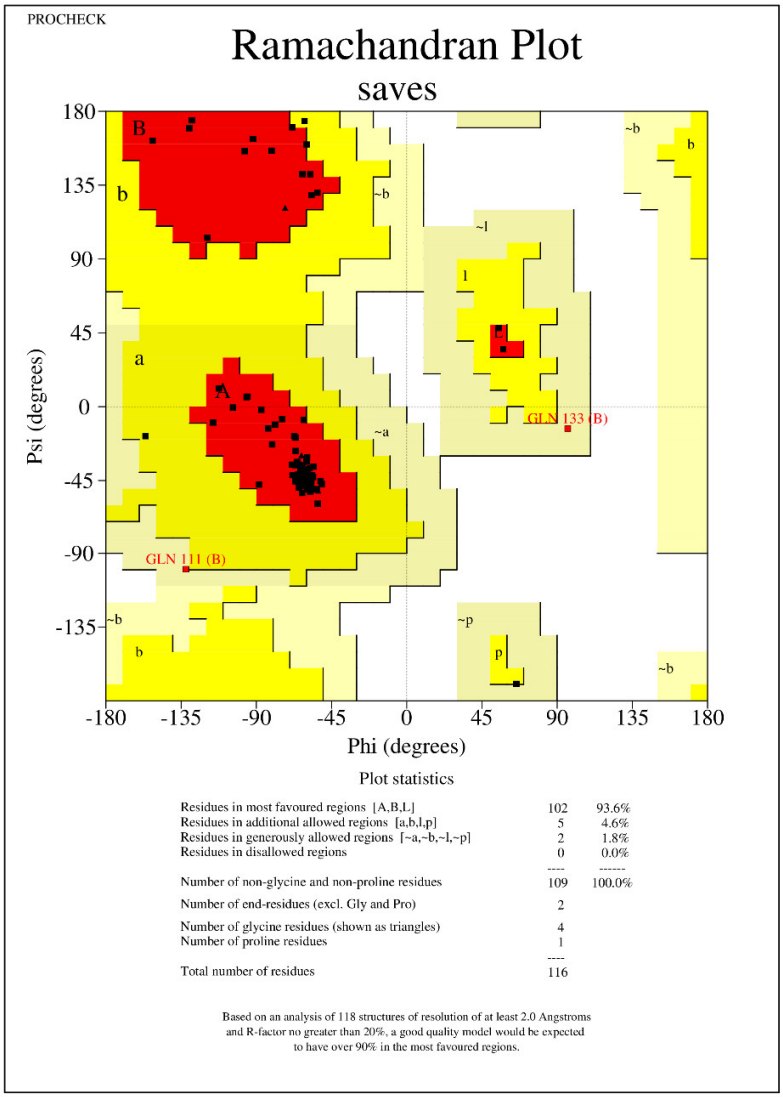


Figure S1A. Ramachandran plot of V6.

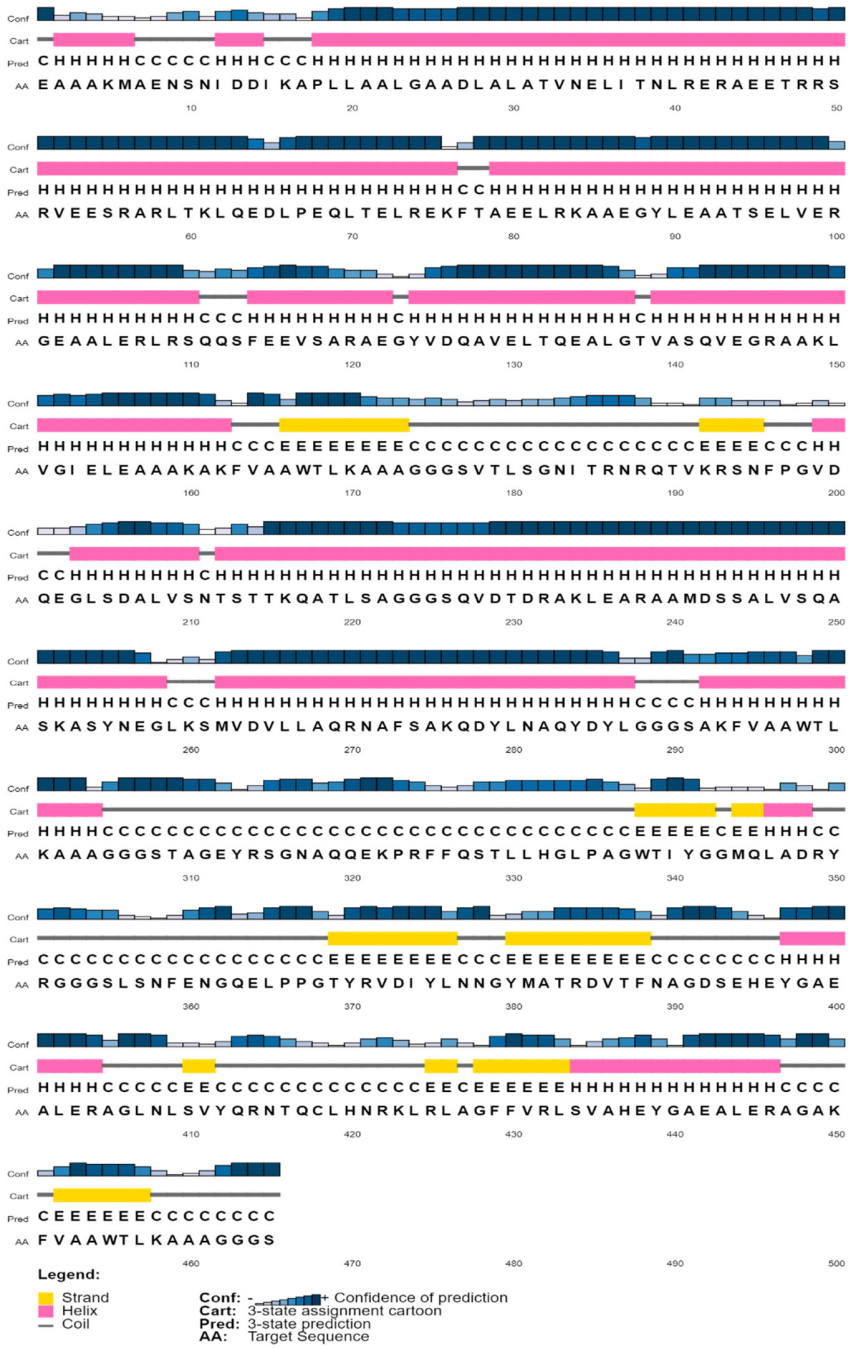


Figure S1B. Secondary structure of V6 construct.

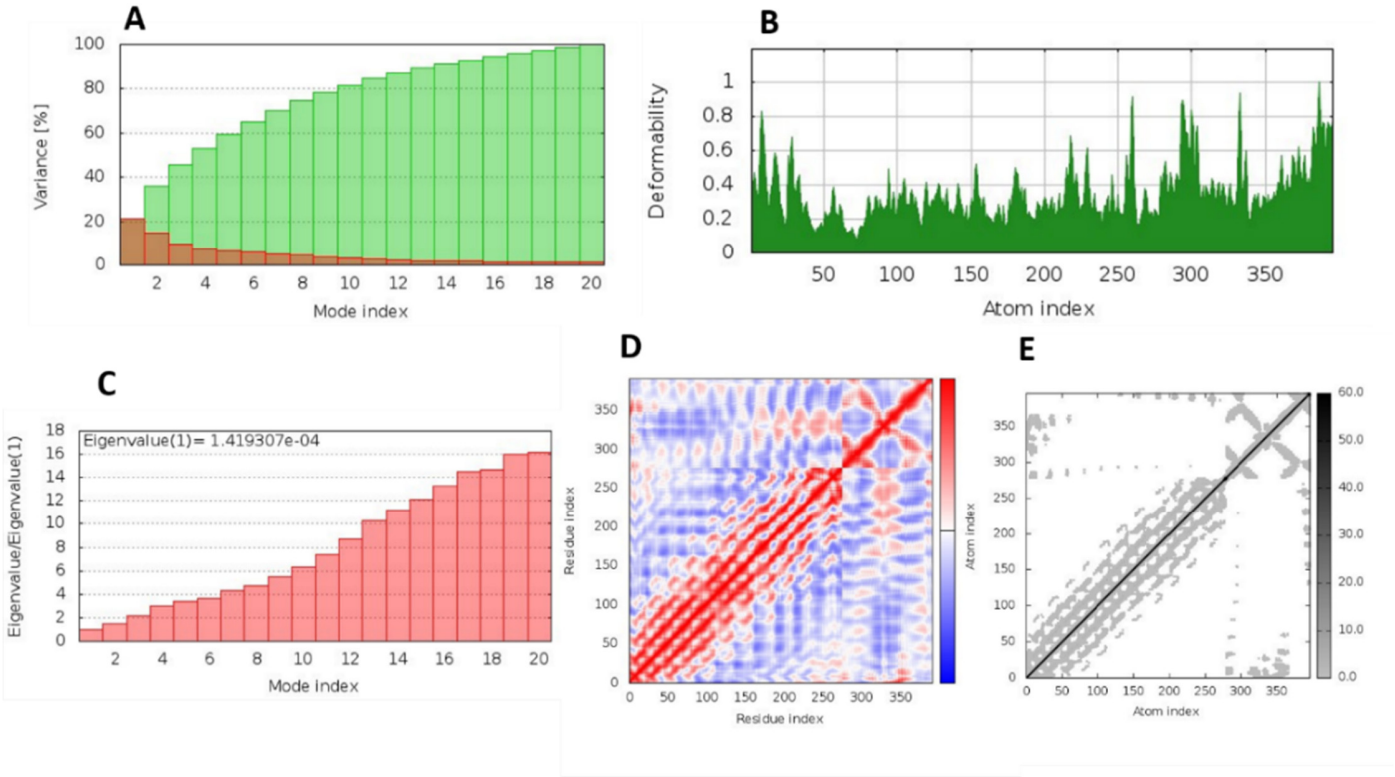


Figure S2. Secondary structure of V6 construct.