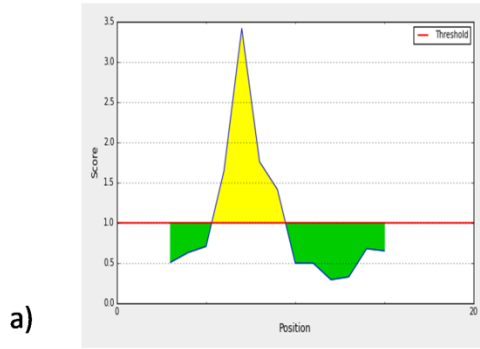
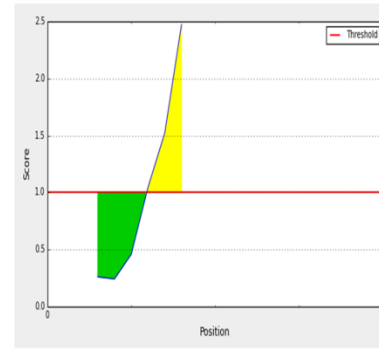


**Supplementary Fig 1: Consensus sequences of all serotypes of Dengue virus visualization with Jal View.**



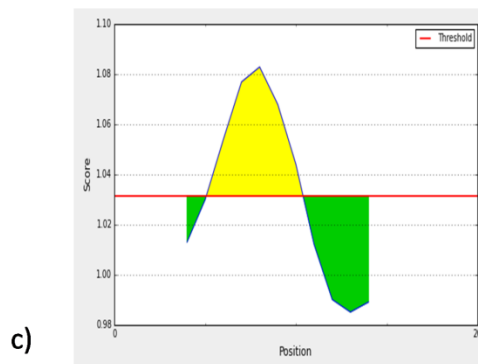
Epitope sequence: NPVVTKKEEPVNIEAEP

Average score: 1 (range: 0.289 – 3.420)



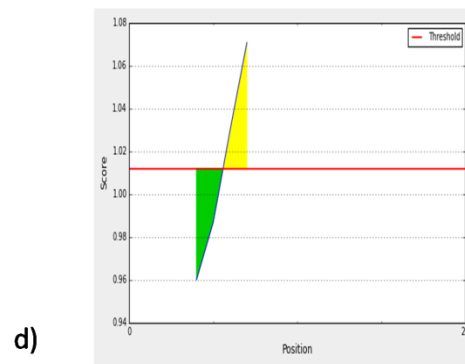
Epitope sequence: TWIGLNSKNTS

Average score: 1 (range: 0.240 – 2.477)



Epitope sequence: NPVVTKKEEPVNIEAEP

Average score: 1.031 (range: 0.985 – 1.083)

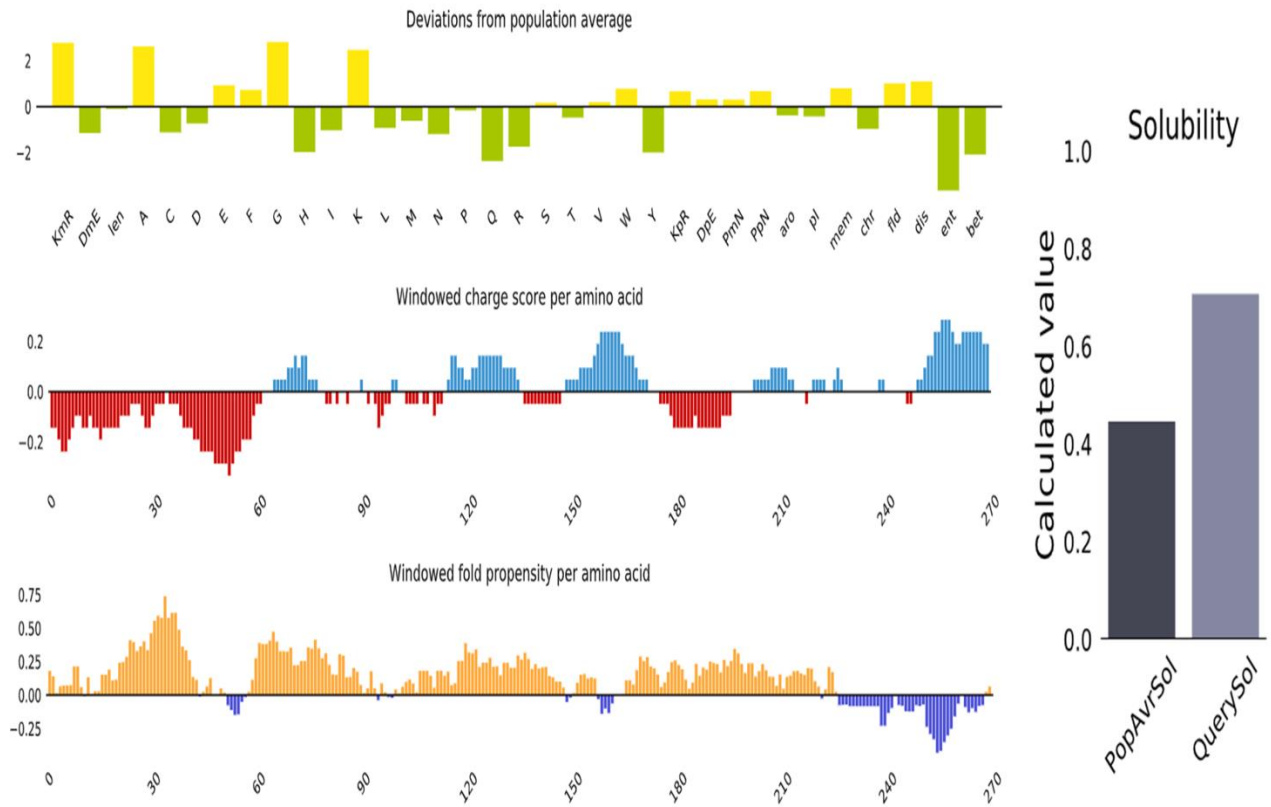


Epitope sequence: TWIGLNSKNTS

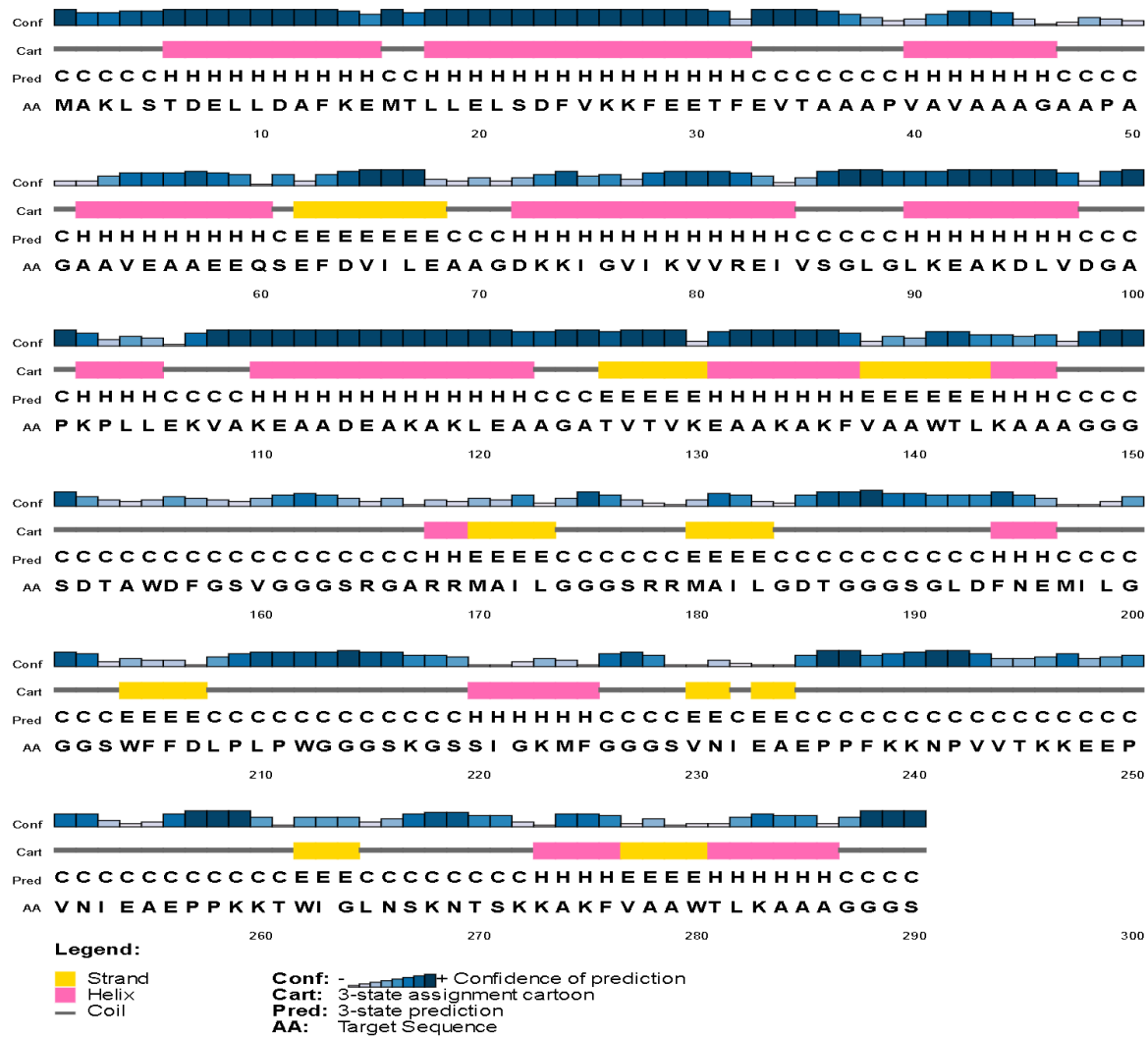
Average score: 1.012 (range: 0.960 - 1.071)

**Supplementary Fig 2:** Surface accessibility (a & b) and Flexibility (c & d) of the B cell epitopes.

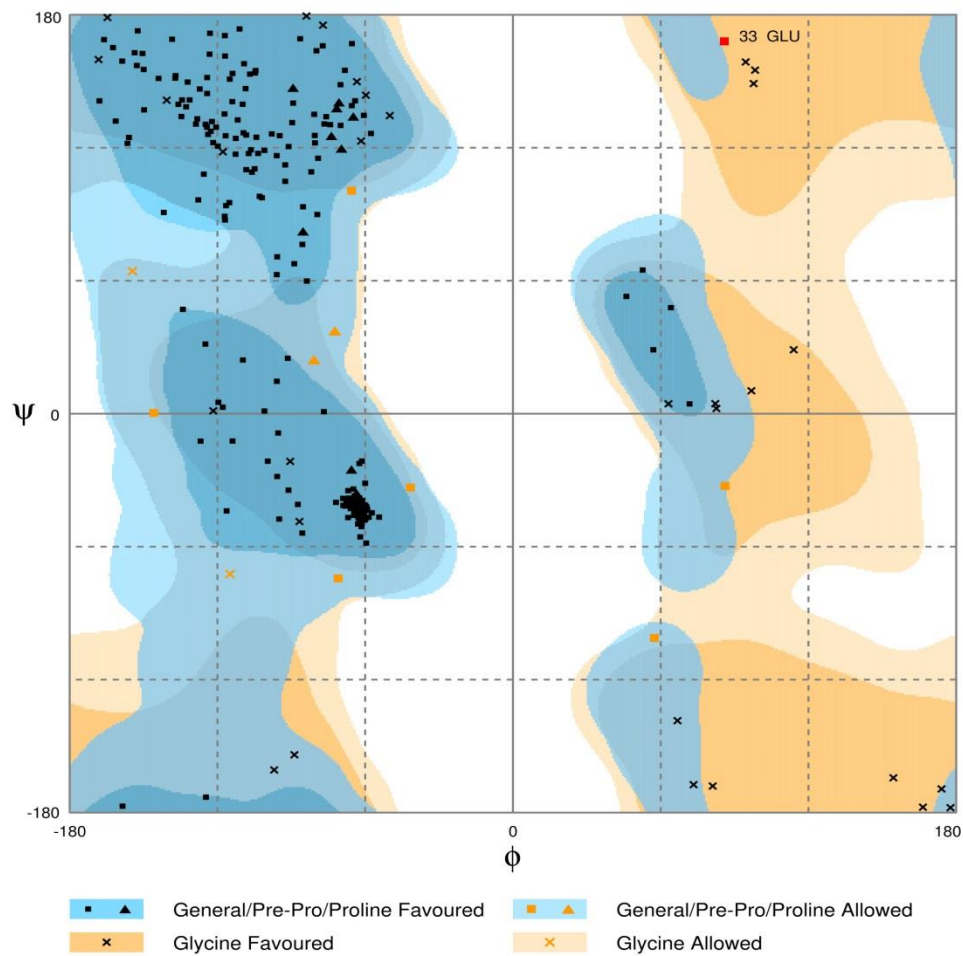
Most of the amino acid residues of both of the epitope were above the cut-off (horizontal red line, denoting the threshold value) is in the yellow region.



**Supplementary Fig 3:** Solubility prediction of designed vaccine constructs V2 using Protein-sol server.



**Supplementary Fig 4:** Secondary structure analysis of vaccine protein V2 using PESIPRED server. Alpha helix-25%, strand-17% and coil regions-56%.



Number of residues in favoured region (~98.0% expected) : 277 (96.2%)  
 Number of residues in allowed region (~2.0% expected) : 10 (3.5%)  
 Number of residues in outlier region : 1 (0.3%)

RAMPAGE by Paul de Bakker and Simon Lovell available at <http://www-cryst.bioc.cam.ac.uk/rampage/>  
 Please cite: S.C. Lovell, I.W. Davis, W.B. Arendall III, P.I.W. de Bakker, J.M. Word, M.G. Prisant, J.S. Richardson & D.C. Richardson (2002)  
 Structure validation by C $\alpha$  geometry:  $\phi/\psi$  and C $\beta$  deviation. *Proteins: Structure, Function & Genetics*. **50**: 437-450

**Supplementary Fig 5:** Ramachandran plot analysis of refined vaccine construct-2.

**Supplementary Table 1:** Potential Cytotoxic T cell epitopes (CTL) predicted by NetCTL 1.2.

<b>Super type</b>	<b>Epitope</b>	<b>NetCTL score</b>
A1	TTEAILPEY	3.0728
	VVQYENLKY	1.7164
	KLELKGMSY	1.3769
	CTNTFVLKK	1.0143
	GTILIKVEY	1.1196
	VSETQHGTI	0.895
	GTSIFAGHL	0.8474
	KTEATQLAT	0.6114
	IAIGITLY	0.9308
	TTETPTWNR	0.7093
	WMVHRQWFF	0.8018
	PIEGKVVQY	0.7988
	YAMCTNTFV	0.6164
	ATQLATLRK	0.6076
	CSPRTGLDF	0.6323
	ILGDTAWDF	0.62
	NSKNTSMSF	0.6101
	LPEEQDQNY	0.6101
A2	ALFSGVSWV	1.3184
	YAMCTNTFV	1.2194
	RLITANPVV	1.2235
	RQWFFDLPL	1.1523
	WVMKIGIGV	0.9885
	AMCTNTFVL	1.0751
	SMSFSCIAI	0.9362
	AMHTALTGA	0.9577
	GLFGKGSV	0.9761
	AIGITLYL	0.9707
	SLGKMVHQI	0.8513
	VTAEITPQA	0.7599
	LKYTVIITV	0.7946
	ITLYLGAVV	0.7368
	IITLYLGAV	0.6935
	TMAKNKPTL	0.7521
	TMKNKAWMV	0.6848
	GLNSKNTSM	0.6978



	QIFGSAYTA	0.6457
	GLDFNEMIL	0.6663
	CIAIGITL	0.6663
A3	ITANPVVTK	1.4887
	CTNTFVLKK	1.4107
	MILLTMKNK	1.2118
	VTFKNAHAK	1.2517
	KLELKGMSY	1.3080
	TQHGTILIK	1.3080
	TANPVVTKK	1.3080
	TSIFAGHLK	1.1493
	ATQLATLRK	1.0789
	ALKINWYKK	1.0488
	FSGVSWVMK	1.1037
	KVVQYENLK	0.8568
	TILIKVEYK	0.9214
	LTWIGLNSK	0.9430
	IAIGITLY	0.9429
	CVTTMAKNK	1.0139
	MCTNTFVLK	0.7186
	VVQYENLKY	0.7751
	NALKINWYK	0.7355
	KGSLVTCAK	0.6558
	TFKNAHAKK	0.6299
A24	SYAMCTNTF	2.0168
	AWMVHRQWF	1.6308
	IFGSAYTAL	1.1031
	QYENLKYTV	0.9088
	NWYKKGSSI	0.8465
	WMVHRQWFF	0.9875
	TWNRKELLV	0.7597
	NYVCKHTYV	0.8785
	AYTALFSGV	0.7771
	LFSGVSWVM	0.7966
	WFFDLPLPW	0.7734
	GWGNGCGLF	0.7544
	AMCTNTFVL	0.6813
A26	IAIGITLY	1.521
	ELKGMSYAM	1.2681

	TTEAILPEY	1.3586
	ETQGVTAEI	1.0908
	DTAWDFGSV	1.0395
	ETQHGTLI	0.9998
	LTMKNKAWM	0.8399
	EVSETQHGT	0.7108
	DNALKINWY	0.9708
	ATARGARRM	0.7823
	GVLNSLGKM	0.7479
	GTILIKVEY	0.9171
	SVGGVLNSL	0.784
	WMVHRQWFF	0.7867
	NSKNTSMSF	0.7531
B7	TPTWNRKEL	1.6889
	LPEYGTGLGL	1.4946
	CPTQGEAVL	1.3113
	LPWASGATT	1.15
	TPQASTTEA	1.1442
	APCKIPFST	0.9513
	TARGARRMA	0.8742
	RGARRMAIL	0.8405
	SVGGVLNSL	0.6999
	RGWGNGCGL	0.7061
B8	RGARRMAIL	1.6713
	ELKGMSYAM	1.6923
	HAKKQEVVV	1.4005
	LGKMHQIF	1.2598
	VMKIGIGVL	1.1465
	YENLKYTVI	0.8736
	RLKMDKLEL	0.9087
	NRKELLVTF	0.9805
	NWYKKGSSI	0.7219
	NAHAKKQEV	0.6841
	FGSAYTALF	0.6941
	TPTWNRKEL	0.6298
	WMVHRQWFF	0.677
	VHRQWFFDL	0.6
	NSKNTSMSF	0.6
B27	RQWFFDLPL	1.6461



	NRKELLVTF	1.4773
	RRMAILGDT	1.1053
	YKKGSSIGK	0.966
	RKELLVTFK	0.8805
	ARGARRMAI	0.8685
	LRKLCIEGK	0.7794
	GRLITANPV	0.8729
	RKLCIEGKI	0.6665
	TQHGTILIK	0.7266
	MKIGIGVLL	0.6215
	MRCVGVGNR	0.6268
B39	TMAKNKPTL	1.5632
	VHRQWFFDL	1.3347
	EHGGCVTTM	1.0927
	AMCTNTFVL	0.9923
	TEATQLATL	0.9685
	AKKQEVVVL	0.9474
	QEGAMHTAL	0.8615
	AHAKKQEVV	0.8022
	CIAIGITL	0.8286
	GLDFNEMIL	0.7579
	SYAMCTNTF	0.8233
	SETQHGTIL	0.6379
B44	SETQHGTIL	1.8525
	QEGAMHTAL	1.7207
	LECSPRTGL	1.4858
	GESNIVIGI	1.2891
	TEATQLATL	1.2029
	RQWFFDLPL	1.2238
	PEEQDQNYV	0.9534
	YENLKYTVI	0.9981
	LEHGGCVTT	0.8577
	KEEPVNIEA	0.8072
	MKIGIGVLL	0.7434
	LDFNEMILL	0.6926
	LEPIEGKVV	0.6164
B58	IGIGVLLTW	1.9499
	KAWMVHRQW	1.9475
	GATTETPTW	1.6885

	MAILGDTAW	1.6874
	TALFSGVSW	1.5662
	IAIGITLY	1.5304
	WFFDLPLPW	1.1137
	KGSSIGKMF	1.061
	FGSAYTALF	0.9208
	GSLVTCAKF	0.9584
	WMVHRQWFF	0.908
	KHTYVDRGW	0.7182
	LFGVSWVM	0.7809
	ILGDTAWDF	0.8265
	CSPRTGLDF	0.64
	GATWVDVVL	0.6216
	GTILIKVEY	0.7121
B62	RQWFFDLPL	1.288
	VMKIGIGVL	1.2157
	WMVHRQWFF	1.2543
	IQNSGGTSI	1.1376
	NSKNTSMSF	1.2336
	KLELKGMSY	1.2421
	IAIGITLY	1.253
	VVQYENLKY	1.0358
	VNIEAEPPF	0.9816
	QNSGGTSIF	1.0617
	LQKTEATQL	0.948
	HQIFGSAYT	0.7435
	FGSAYTALF	0.9471
	SMSFSCIAI	0.7314
	GTILIKVEY	0.9482
	AMCTNTFVL	0.8516
	QNYVCKHTY	0.9019
	ILGDTAWDF	0.8929
	MAILGDTAW	0.8296
	ELKGMSYAM	0.7485
	LGKMHQIF	0.749
	RLITANPVV	0.7487
	VHQIFGSAY	0.8246
	TQLATLRKL	0.7449
	TTEAILPEY	0.8201

	GLNSKNTSM	0.6741
	GSLVTCAKF	0.7177

**Supplementary Table 2: Seven shortlisted T-cell epitopes MHC I and binding predictions.**

<b>Epitope</b>	<b>MHC- I Allele</b>	<b>IC-50 value</b>
DTAWDFGSV	HLA-A*26:02	22.50
	HLA-C*12:03	32.00
	HLA-B*27:20	42.50
	HLA-A*32:07	48.98
	HLA-A*69:01	53.43
	HLA-C*15:02	95.59
	HLA-B*40:13	158.82
RGARRMAIL	HLA-B*27:20	5.158
	HLA-C*03:03	15.12
	HLA-A*32:07	22.64
	HLA-B*40:13	49.30
	HLA-A*02:50	95.54
	HLA-B*15:02	141.98
	HLA-C*12:03	143.61
RRMAILGDT	HLA-B*27:20	3.29
	HLA-A*32:07	18.11
	HLA-C*12:03	26.86
	HLA-B*40:13	53.94

	HLA-C*14:02	66.46
	HLA-B*27:05	101.99
	HLA-C*07:01	114.86
GLDFNEMIL	HLA-B*27:20	9.53
	HLA-A*02:50	11.59
	HLA-A*32:07	21.38
	HLA-A*02:12	24.36
	HLA-C*12:03	29.45
	HLA-C*05:01	32.63
	HLA-A*02:16	47.80
WFFDLPLPW	HLA-B*40:13	4.644
	HLA-C*12:03	13.81
	HLA-C*14:02	24.98
	HLA-A*32:07	25.06
	HLA-A*02:50	27.11
	HLA-A*32:15	34.93
KGSSIGKMF	HLA-A*32:07	12.59
	HLA-B*27:20	21.15
	HLA-B*40:13	32.50
	HLA-A*02:50	44.28
	HLA-C*12:03	80.57
	HLA-C*03:03	105.83
	HLA-C*07:02	112.50
	HLA-B*27:20	9.71

VNIEAEPPF	HLA-A*32:07	30.69
	HLA-C*03:03	40.98
	HLA-C*12:03	71.48
	HLA-C*14:02	83.10
	HLA-B*40:13	125.00
	HLA-A*02:50	169.51