

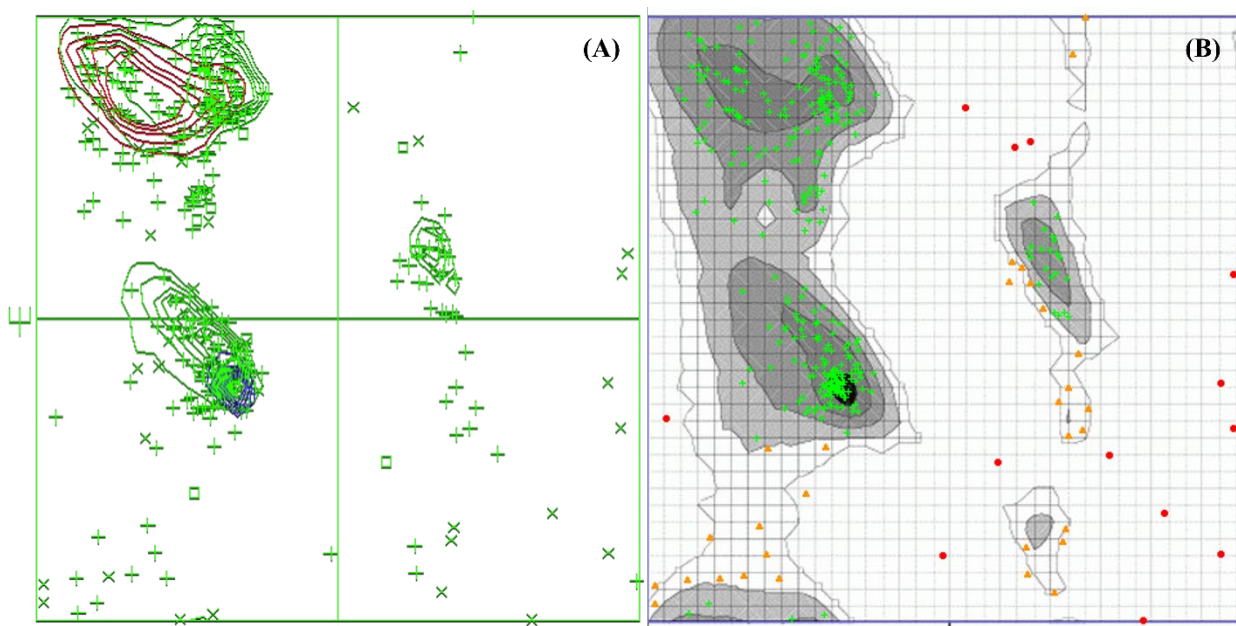
**Figure S1:** Graphical representation of the immunogenic epitopes. (A) B-turn prediction; (B) Surface accessibility; (C) Flexibility; (D) Antigenicity.

Query= FVC2			(A)			Query= FVC2			(B)		
Length=386						Length=386					
Sequences producing significant alignments:			Score	E		Sequences producing significant alignments:			Score	E	
			(Bits)	Value					(Bits)	Value	
drugbank_target P03200	Envelope glycoprotein GP350 (D800632)		128	1e-032		tr B4DLN1 B4DLN1_HUMAN	cDNA FLJ60124, highly similar to Mitochondrial		53.9	2e-007	
drugbank_target P68344	Envelope glycoprotein GP340 (D800632)		127	3e-032		sp P52815 RM12_HUMAN	39S ribosomal protein L12, mitochondrial O...		49.3	1e-006	
T23459 VGP3_EBVP3			127	3e-032		sp O60244 MED14_HUMAN	Mediator of RNA polymerase II transcripti...		33.5	0.62	
T69200 SIMCA4_HUMAN			29.3	2.3		tr H3BQK9 H3BQK9_HUMAN	Microtubule-actin cross-linking factor 1...		33.1	0.82	
drugbank_target Q8IC05	Heat shock protein 90 (D811638)		28.9	2.6		tr H3BPE1 H3BPE1_HUMAN	Microtubule-actin cross-linking factor 1...		33.1	0.83	
drugbank_target Q04609	Glutamate carboxypeptidase 2 (D800089; D...		28.1	4.4		sp Q9UL36 ZN236_HUMAN	Zinc finger protein 236 OS=Homo sapiens O...		31.2	2.8	
T97071 FOLH1_HUMAN			28.1	4.4		tr J9JID5 J9JID5_HUMAN	Zinc finger protein 236 OS=Homo sapiens ...		31.2	3.1	
						tr H3BP71 H3BP71_HUMAN	E3 ubiquitin protein ligase OS=Homo sapi...		30.4	4.9	
						tr A0A804HI87 A0A804HI87_HUMAN	Alstrom syndrome protein 1 (Frag...		30.4	5.3	
						sp O75150 BRE1B_HUMAN	E3 ubiquitin-protein ligase BRE1B OS=Homo...		30.4	5.5	
						tr A0A804HKP4 A0A804HKP4_HUMAN	Alstrom syndrome protein 1 (Frag...		30.0	7.6	
						tr H3BUR1 H3BUR1_HUMAN	Protein 4.2 (Fragment) OS=Homo sapiens O...		28.5	8.5	
						tr A0A2R8Y4P4 A0A2R8Y4P4_HUMAN	Transcription activator BRG1 OS=...		29.6	8.5	
						tr A0A2R8Y7S2 A0A2R8Y7S2_HUMAN	Transcription activator BRG1 OS=...		29.6	8.6	

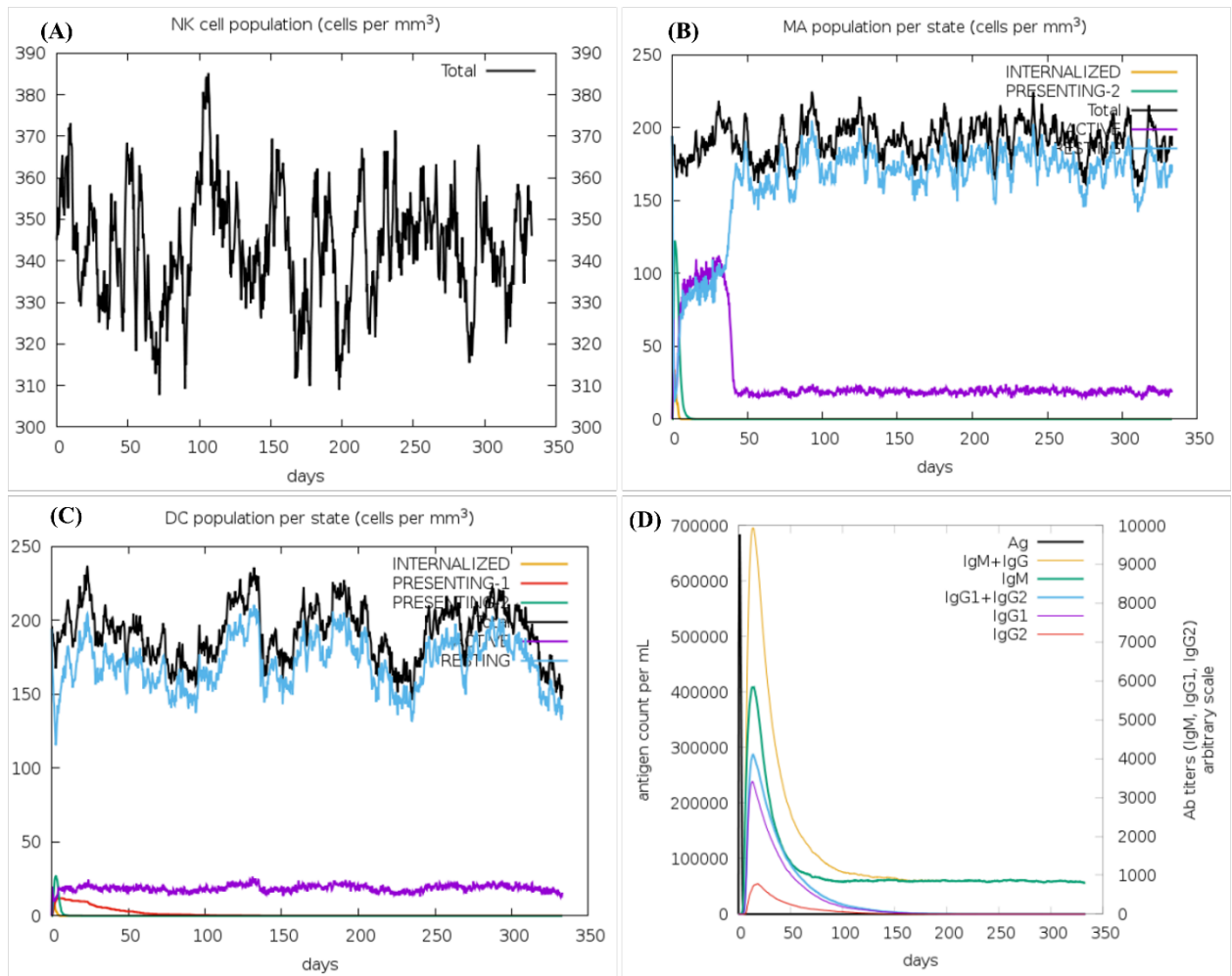
  

			Score	E (C)		Serial No.			Epitope Name	Sequence	Method	Result	Score (D)
Sequences producing significant alignments:			(Bits)	Value									
sp Q32AF8 RL7_SHIDS	50S ribosomal protein L7/L12 OS=Shigella dy...		228	5.00E-74		1	E1	LRLTPRPVS	SVM	POSITIVE	0.31056275		
sp Q31U11 RL7_SHIBS	50S ribosomal protein L7/L12 OS=Shigella bo...		228	5.00E-74		2	E2	VLQWASLAV	SVM	POSITIVE	0.16185077		
tr F1XJ52 F1XJ52_ECO57	50S ribosomal protein L7/L12 OS=Escheric...		228	5.00E-74		3	E3	VVRAQGLDV	SVM	POSITIVE	0.5550728		
sp P0A7K5 RL7_SHIFL	50S ribosomal protein L7/L12 OS=Shigella fl...		228	5.00E-74		4	E4	WASLAVLTL	SVM	POSITIVE	0.1626063		
sp P0A7K5 RL7_SHIFL	50S ribosomal protein L7/L12 OS=Shigella fl...		228	5.00E-74		5	E5	WTFTSPPVV	SVM	NEGATIVE	-0.80908108		
sp A8AKU0 RL7_CITK8	50S ribosomal protein L7/L12 OS=Citrobacter...		226	4.00E-73									
sp A6TGN9 RL7_KLEP7	50S ribosomal protein L7/L12 OS=Klebsiella ...		226	6.00E-73									
tr D0ZQV3 D0ZQV3_SALT1	50S ribosomal protein L7/L12 OS=Salmonel...		224	3.00E-72									

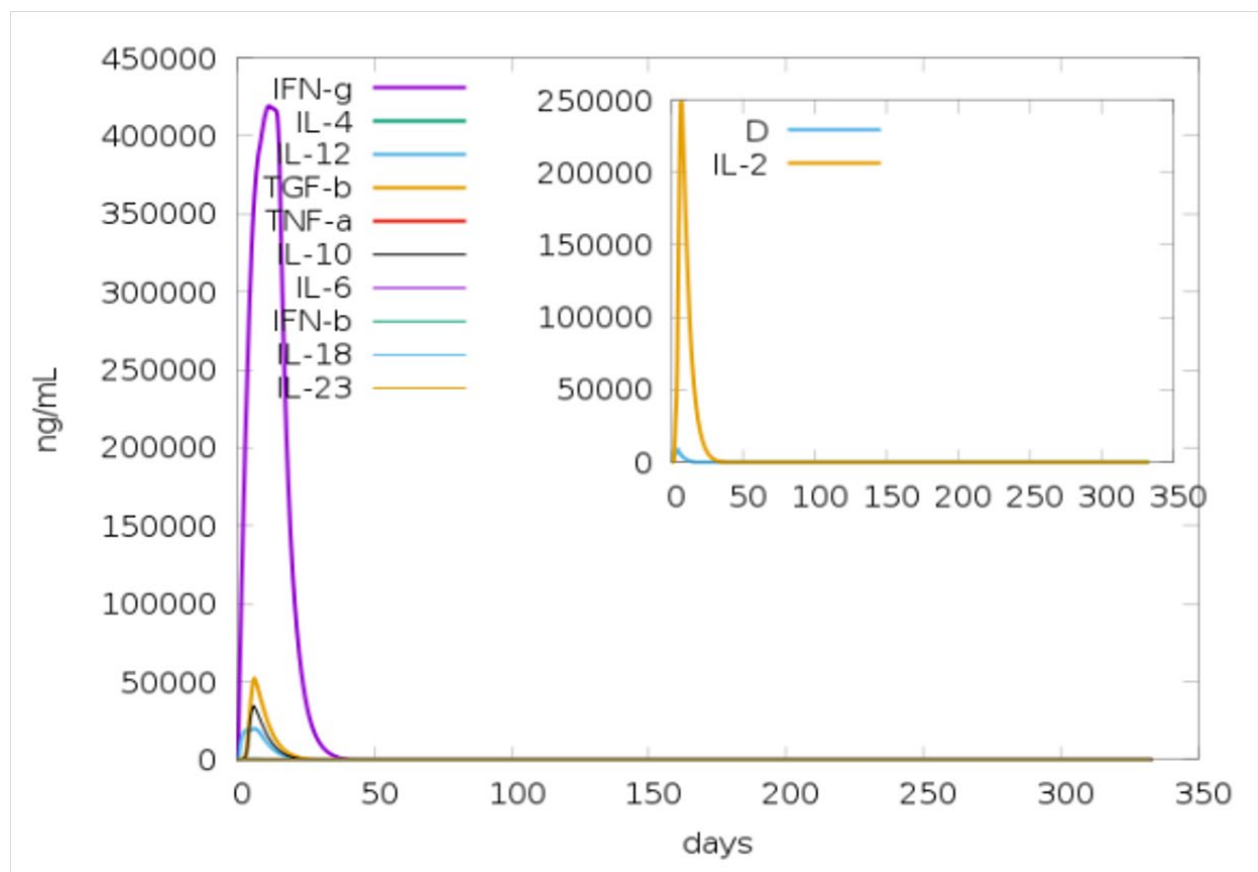
**Figure S2:** (A) Druggability blast of the vaccine candidate. (B) homology analysis of the vaccine candidate with gut microbiota. (C) homology analysis of the vaccine candidate with the human host. (D) IFN-gamma stimulation potential of the MHC-II-restricted epitopes.



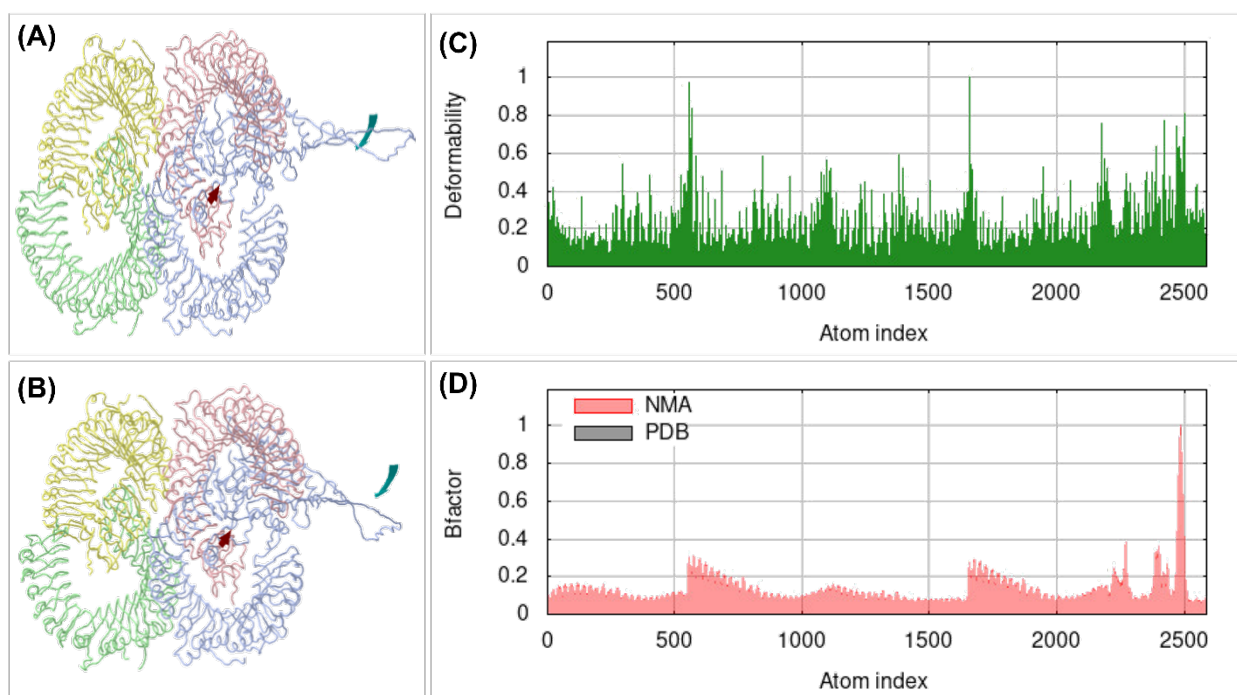
**Figure S3:** (A) Ramachandran plot computed using the WHAT IF server illustrating the most preferred region amino acids as +, and preferred region amino acids as x; (B) Ramachandran plot computed using the Z-lab server showing green residues in the most preferred regions, yellow in the preferred regions, and red in the questionable regions.



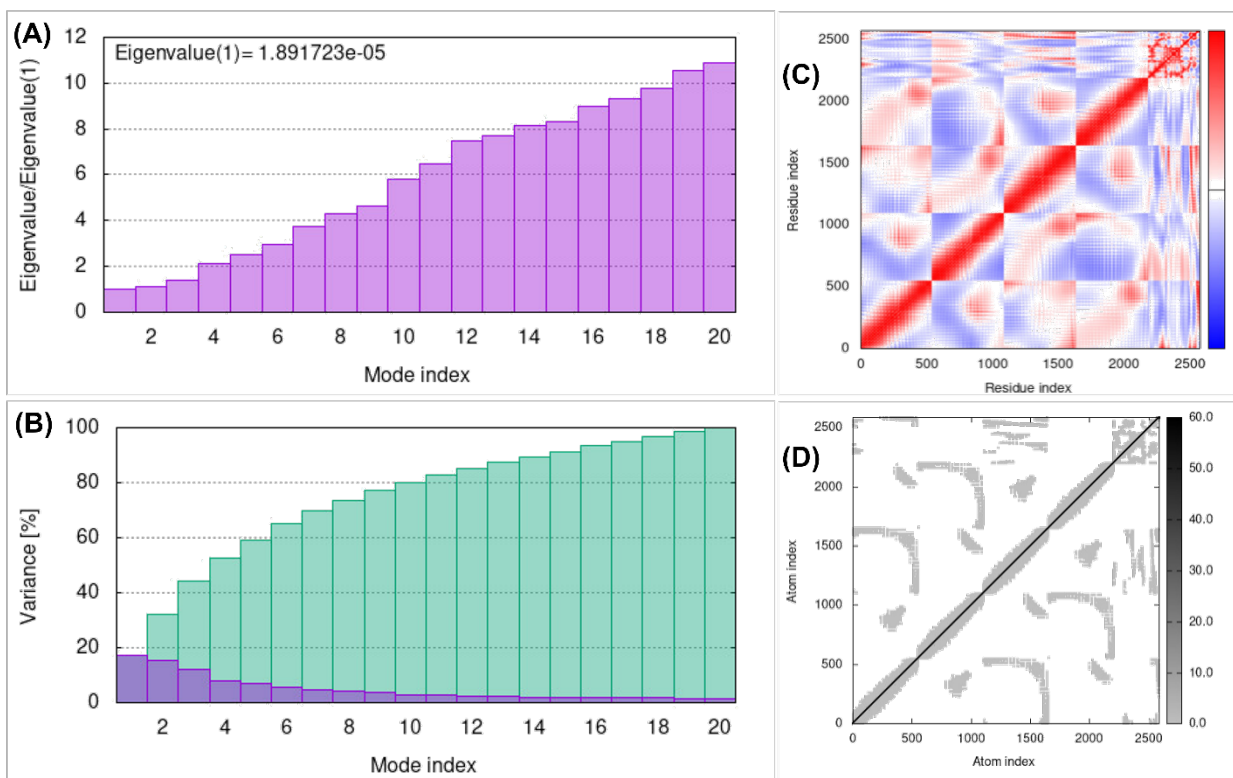
**Figure S4:** (A) NK cell population; (B) Macrophage (MA) cell population; (C) Dendritic cell (DC) population; (D) Antigen and Immune complex stimulation.



**Figure S5:** Danger signal and Cytokine stimulation.

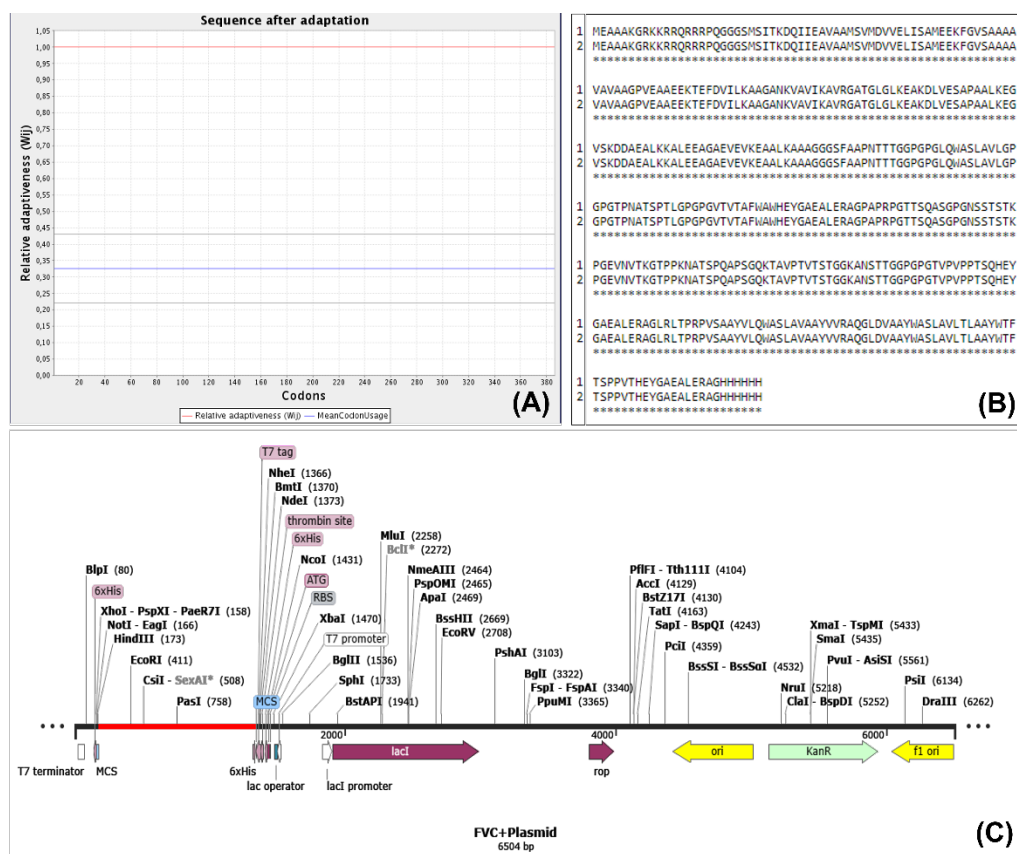


**Figure S6:** Molecular dynamics simulation of the docked complex. (A) MD simulation in the initial mode; (B) MD simulation in the final mode. A slight deformability is seen in the vaccine candidate with the green arrow showing downward movement and the red arrow showing upward movement of the residues; (C) deformability graph of the complex; (D) B-factor plot.



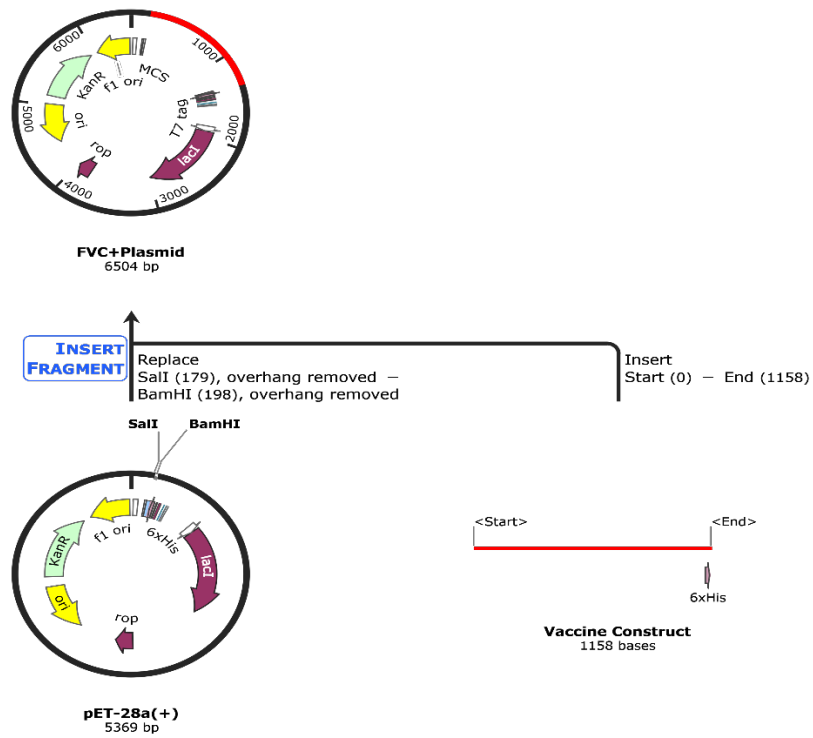
**Figure S7:** (A) eigenvalue plot. (B) variance % plot. (C) the covariance map; (D) the elastic network map of the docked complex





**Figure S8:** Expression analysis of the vaccine construct. (A) optimized codons with CAI 1.000 showing the maximum optimization; (B) CLUSTAL-W analysis showing 100% similarity between the pre-optimization (depicted as 1) and post-optimization (depicted as 2) vaccine constructs; (C) the linear map of cloned plasmid.





**Figure S9:** The history of *insilico* cloning.