Supplementary Materials

Table S1. Four vaccine constructs with antigenicity and allergenicity score.

Vaccine construct	Adjuvant	Construct	Allergenicity	Antigenpro	Vaxijen	Solubility
V1	Hbha adjuvant	EAAAKMAENPNIDDLPAPLLAALGAADL ALATVNDLIANLRERAEETRAETRTRVEE RRARLTKFQEDLPEQFIELRDKFTTEELRK AAEGYLEAATNRYNELVERGEAALQRLR SQTAFEDASARAEGYVDQAVELTQEALGT VASQTRAVGERAAKLVGIELEAAAKTLNL FPLNFAYYAKAKYPFSYAYYYSNIGFLLY AYYSSRPTILIRAYYRLSPVPSVKAYYIYIK NIDELAYYEAKDIATTYAYYAHYRNLVSL GPGPGNLFPLNFKSITNKRFGPGPGHYIRA GYNHKYPFRIGPGPGENTDSFYSNIGFLLY GPGPGKLPFRSSRPTILIRNGPGPGPMNDIL RLSPVPSVKGPGPGGPLQYIYIKNIDELKK KDIATTYNFTQHLSFVKKAAFAHYRNLVS LIRLKKNTLNLFPLNFKSITNKKKHKYPFRI CSIAKGTDLKKVELPEGLYCPRTEINLKKK LPFRSSRPTILIRNTKKYSTKNTGPMPVLR VLKKKLQNIYEKHMFFTNLTFGGGSAKFV AAWTLKAAAGGGSKKAKDIATTYNFTQH LSFHEYGAEALERAGKKVSLIRLVKRTISIS NLHEYGAEALERAGAKFVAAWTLKAAA GGGS	NON-ALLERGEN	**0.6842**	Probable ANTIGEN	
V2	Beta definsin adjuvant	EAAAKGIINTLQKYYCRVRGGRCAVLSCL PKEEQIGKCSTRGRKCCRRKKEAAAKTLN LFPLNFAYYAKAKYPFSYAYYYSNIGFLL YAYYSSRPTILIRAYYRLSPVPSVKAYYIYI KNIDELAYYEAKDIATTYAYYAHYRNLVS LGPGPGNLFPLNFKSITNKRFGPGPGHYIR AGYNHKYPFRIGPGPGENTDSFYSNIGFLL YGPGPGKLPFRSSRPTILIRNGPGPGPMNDI LRLSPVPSVKGPGPGGPLQYIYIKNIDELK KKDIATTYNFTQHLSFVKKAAFAHYRNLV SLIRLKKNTLNLFPLNFKSITNKKKHKYPF RICSIAKGTDLKKVELPEGLYCPRTEINLK KKLPFRSSRPTILIRNTKKYSTKNTGPMPV LRVLKKKLQNIYEKHMFFTNLTFGGGSAK FVAAWTLKAAAGGGSKKAKDIATTYNFT QHLSFHEYGAEALERAGKKVSLIRLVKRTI SISNLHEYGAEALERAGAKFVAAWTLKA AAGGGS	NON-ALLERGEN	**0.7289**	Probable ANTIGEN	
V3	Hbha cons rved adjuvant	EAAAKMAENSNIDDIKAPLLAALGAADLA LATVNELITNLRERAEETRRSRVEESRARL TKLQEDLPEQLTELREKFTAEELRKAAEG YLEAATSELVERGEAALERLRSQQSFEEVS ARAEGYVDQAVELTQEALGTVASQVEGR AAKLVGIELEAAAKTLNLFPLNFAYYAKA KYPFSYAYYYSNIGFLLYAYYSSRPTILIRA YYRLSPVPSVKAYYIYIKNIDELAYYEAKD IATTYAYYAHYRNLVSLGPGPGNLFPLNF KSITNKRFGPGPGHYIRAGYNHKYPFRIGP GPGENTDSFYSNIGFLLYGPGPGKLPFRSS RPTILIRNGPGPGPMNDILRLSPVPSVKGPG PGGPLQYIYIKNIDELKKKDIATTYNFTQH LSFVKKAAFAHYRNLVSLIRLKKNTLNLFP LNFKSITNKKKHKYPFRICSIAKGTDLKKV ELPEGLYCPRTEINLKKKLPFRSSRPTILIRN TKKYSTKNTGPMPVLRVLKKKLQNIYEKH MFFTNLTFGGGSAKFVAAWTLKAAAGGG SKKAKDIATTYNFTQHLSFHEYGAEALER AGKKVSLIRLVKRTISISNLHEYGAEALER AGAKFVAAWTLKAAAGGGS	NON-ALLERGEN	**0.6838**	Probable ANTIGEN	

Continued.

Vaccine construct	Adjuvant	Construct	Allergenicity	Antigenpro	Vaxijen	Solubility
V4	Ribosomal protein adjuvant	EAAAKMAENSNIDDIKAPLLAALGAADL ALATVNELITNLRERAEETRRSRVEESRA RLTKLQEDLPEQLTELREKFTAEELRKAA EGYLEAATSELVERGEAALERLRSQQSFE EVSARAEGYVDQAVELTQEALGTVASQV EGRAAKLVGIELEAAAKTLNLFPLNFAYY AKAKYPFSYAYYYSNIGFLLYAYYSSRPT ILIRAYYRLSPVPSVKAYYIYIKNIDELAY YEAKDIATTYAYYAHYRNLVSLGPGPGN LFPLNFKSITNKRFGPGPGHYIRAGYNHK YPFRIGPGPGENTDSFYSNIGFLLYGPGPG KLPFRSSRPTILIRNGPGPGPMNDILRLSPV PSVKGPGPGGPLQYIYIKNIDELKKKDIAT TYNFTQHLSFVKKAAFAHYRNLVSLIRLK KNTLNLFPLNFKSITNKKKHKYPFRICSIA KGTDLKKVELPEGLYCPRTEINLKKKLPF RSSRPTILIRNTKKYSTKNTGPMPVLRVLK KKLQNIYEKHMFFTNLTFGGGSAKFVAA WTLKAAAGGGSKKAKDIATTYNFTQHLS FHEYGAEALERAGKKVSLIRLVKRTISISN LHEYGAEALERAGAKFVAAWTLKAAAG GGS	NON-ALLERGEN	**0.6706**	Probable ANTIGEN	

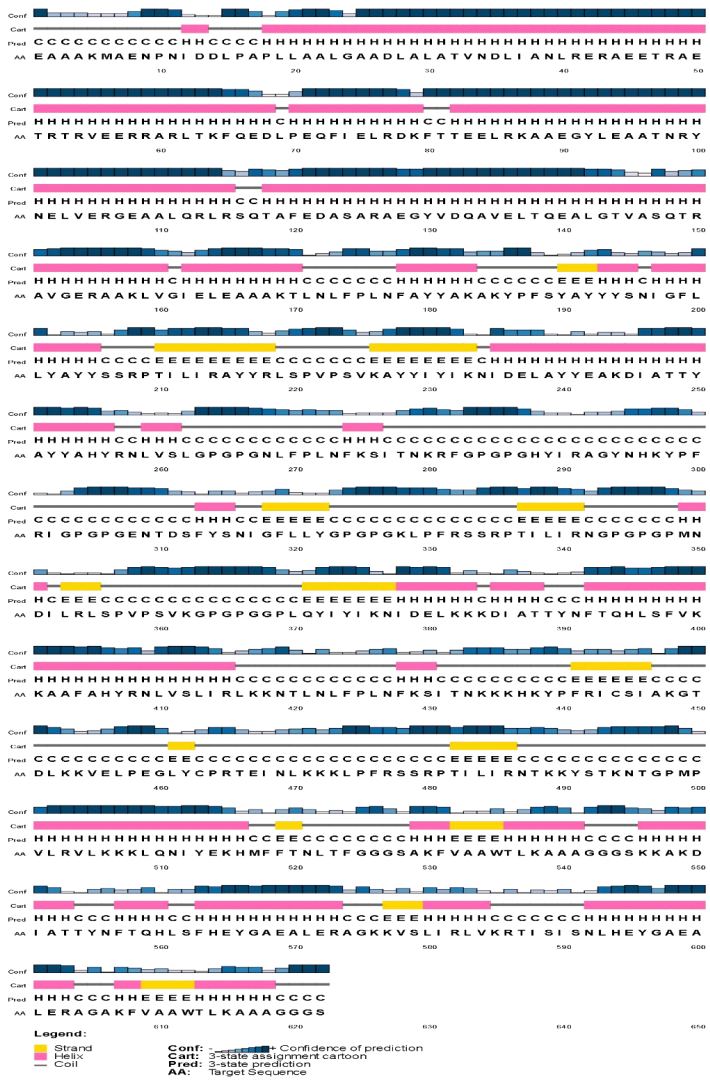

Figure S1. 2D structure of V1 construct, Yellow color in the structure represents Beta strands, the pinks color represents Alpha Helix and the black represents random coils in the structure.

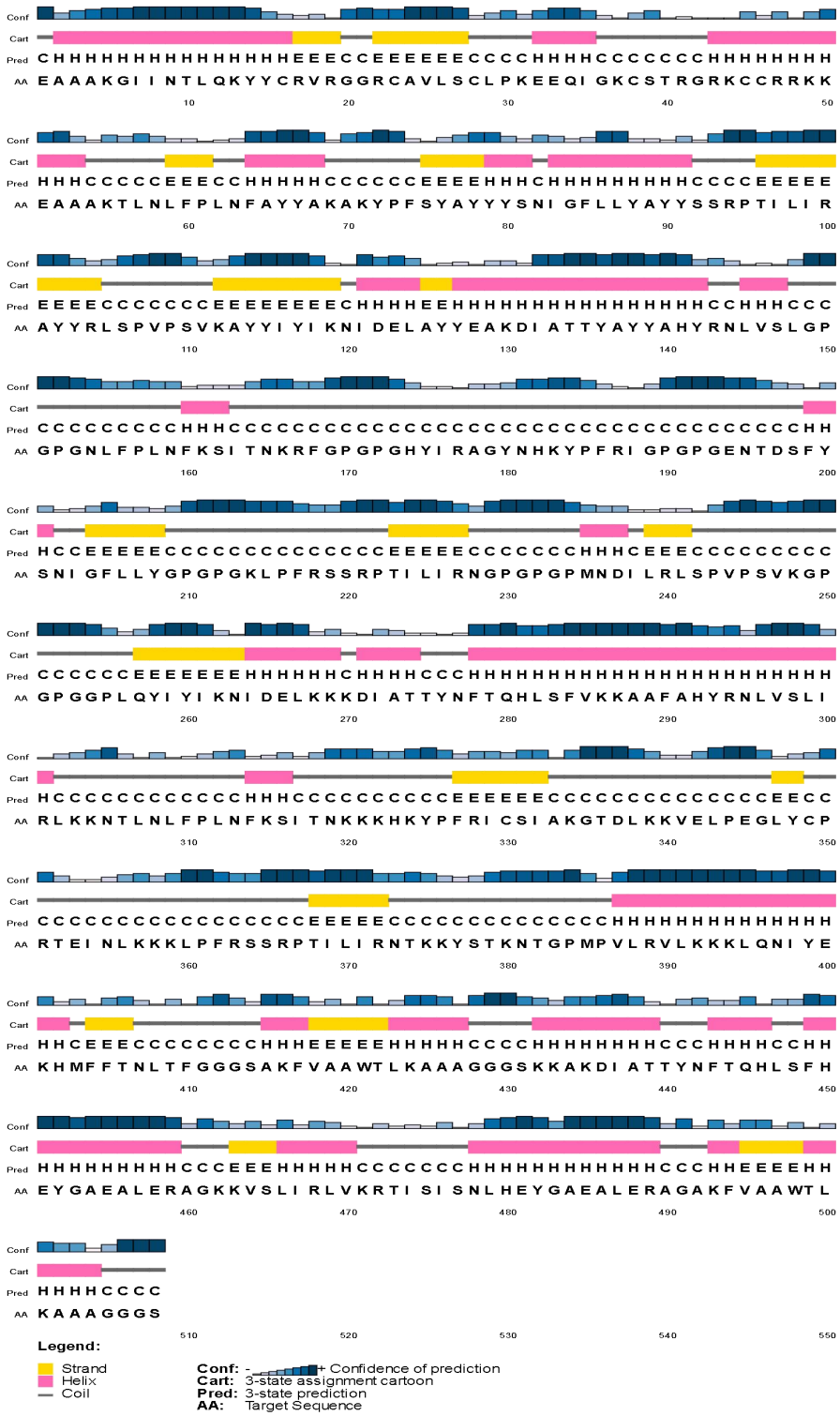

Figure S2. 2D structure of V2 construct, yellow color in the structure represents Beta strands, the pinks color represents Alpha Helix and the black represents random coils in the structure.

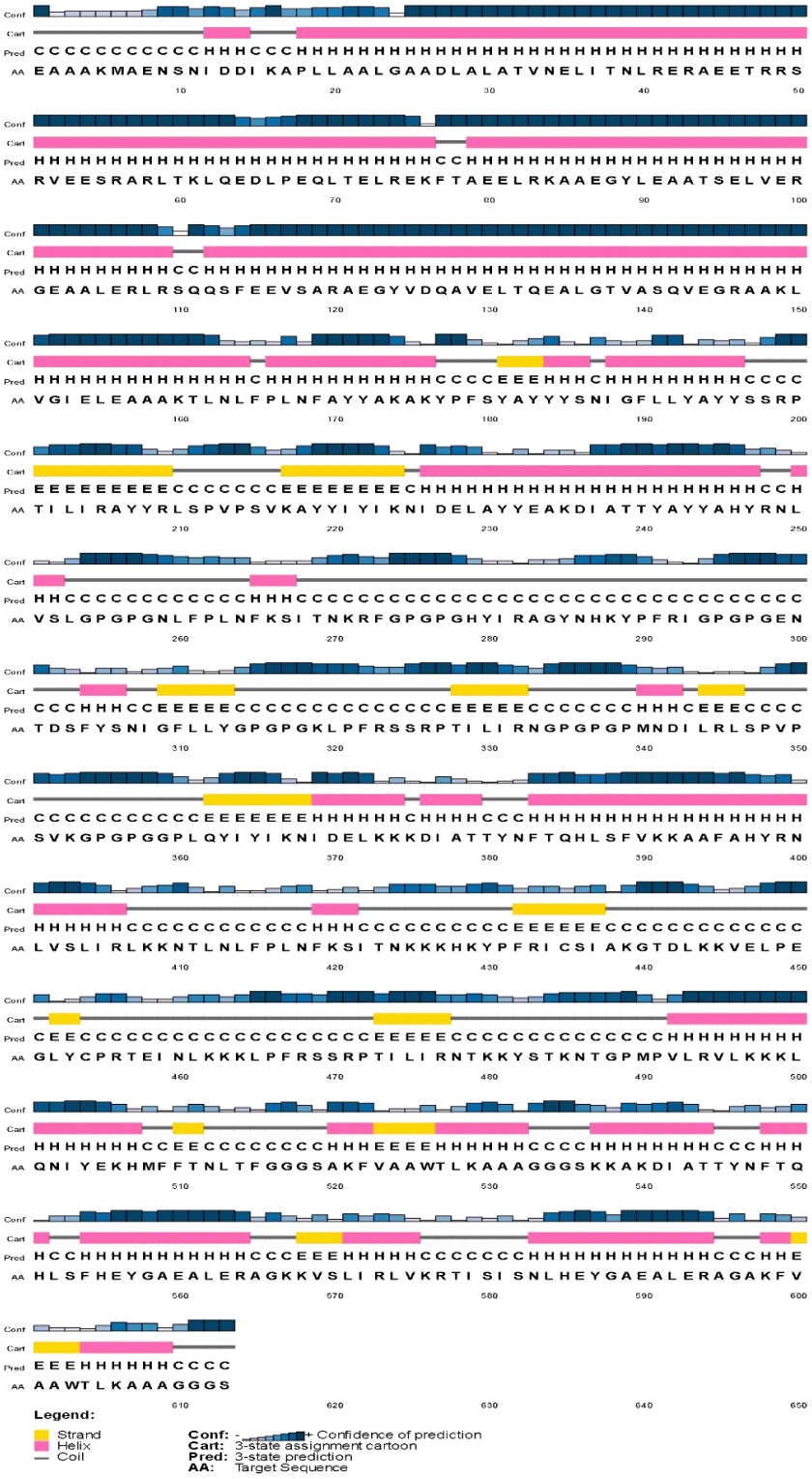

Figure S3. 2D structure of V4 construct, yellow color in the structure represents beta strands, the pinks color represents Alpha Helix and the black represents random coils in the structure.

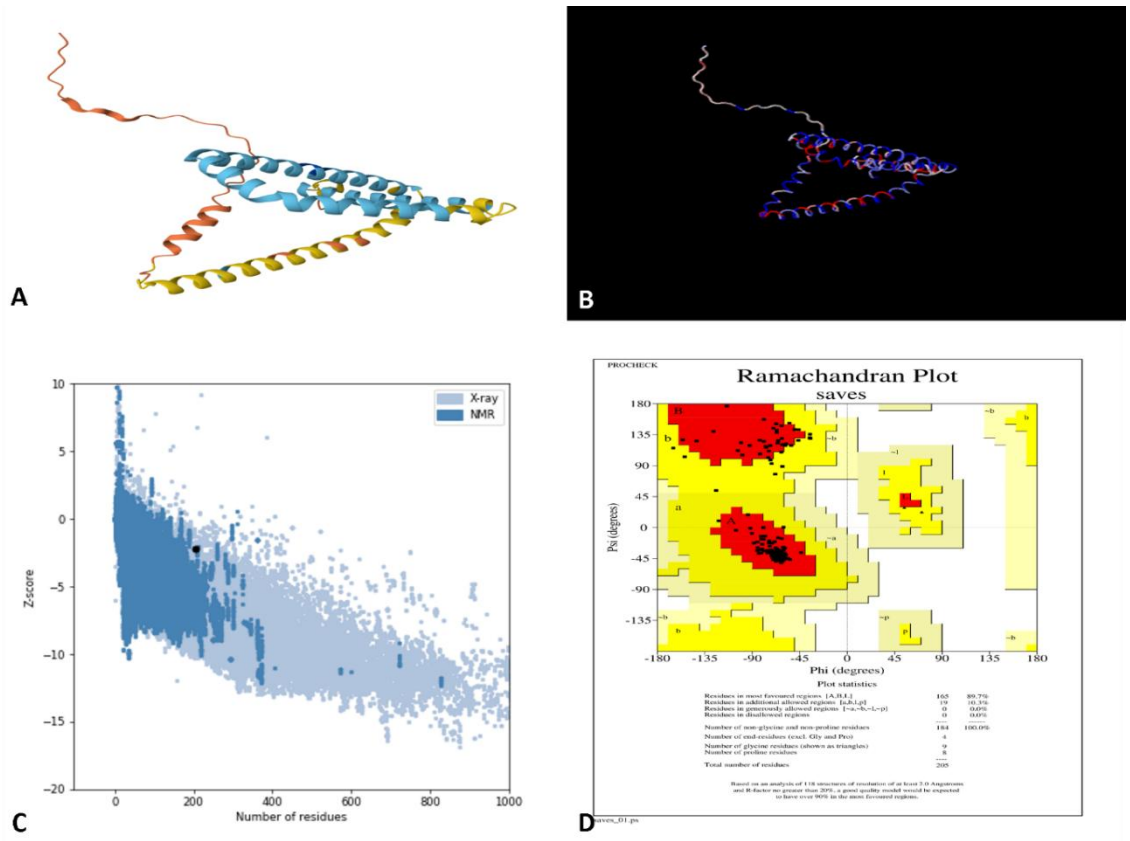

Figure S4. Vaccine construct V1. (A)3D structure predicted on Alphafold server. (B) Validated Structure of V1. (C) Z-score of V1 construct. (D) Ramachandran Plot of V1 construct scoring 89.7% of residues in most favored region, 10.3% of residues in additional allowed region, 0% in generously allowed region and 0% in disallowed regions.

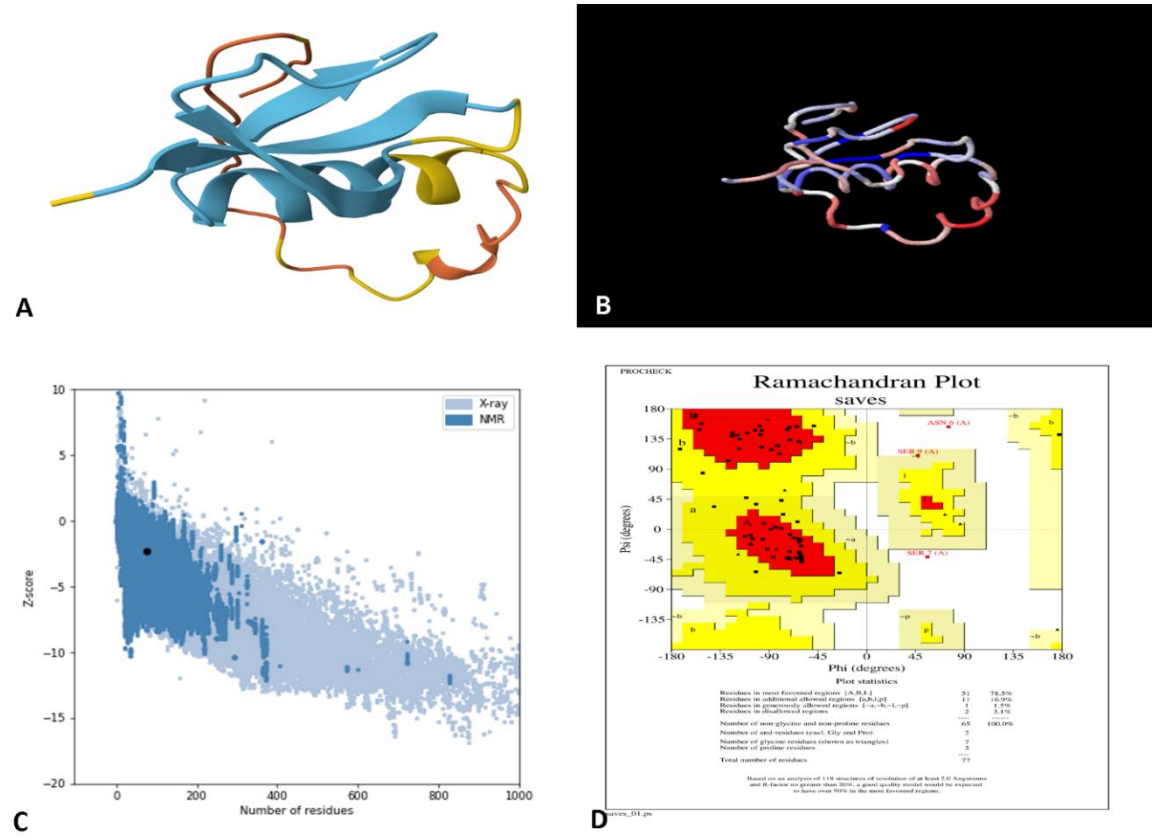

Figure S5. Vaccine construct V2. (A)3D structure predicted on Alphafold server. (B) Validated Structure of V2. (C) Z-score of V2 construct. (D) Ramachandran Plot of V2 construct scoring 78.5% of residues in most favored region, 16.9% of residues in additional allowed region, 1.5% in generously allowed region and 3.1% in disallowed regions.

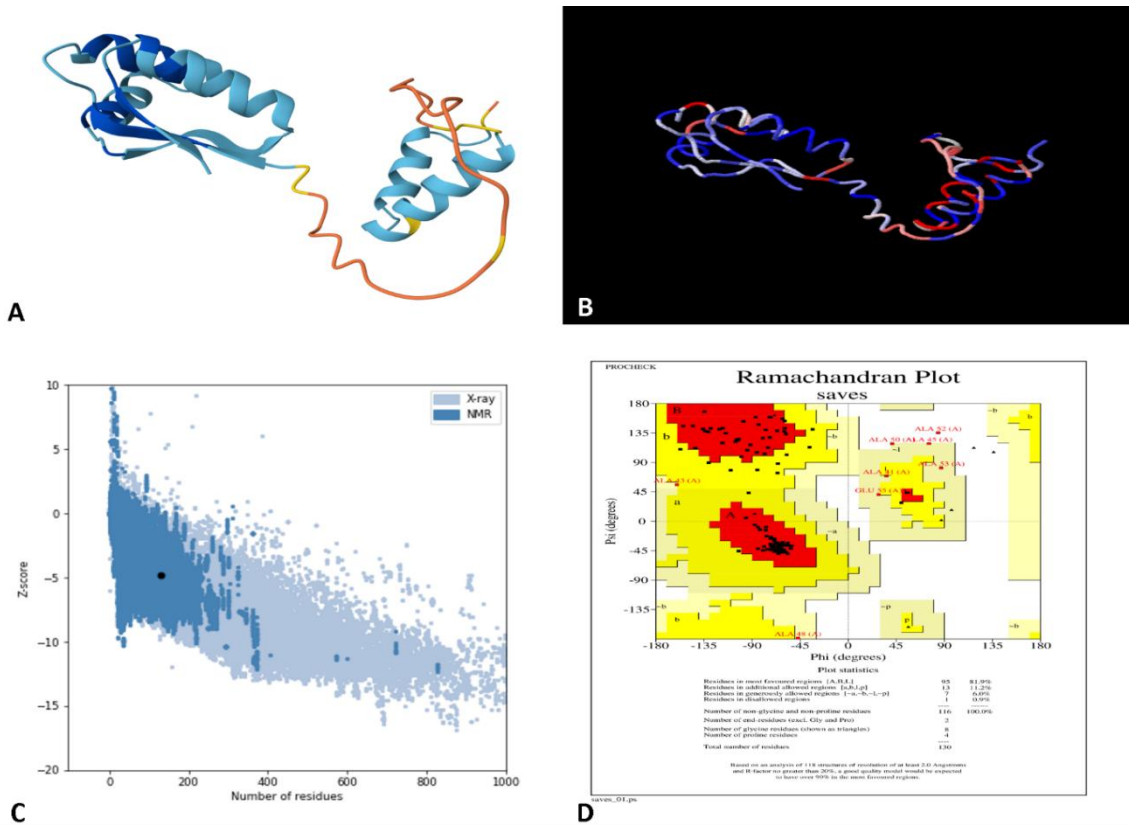

Figure S6. Vaccine construct V4. (A)3D structure predicted on Alphafold server. (B) Validated Structure of V4. (C) Z-score of V4 construct. (D) Ramachandran Plot of V4 construct scoring 81.9% of residues in most favored region, 11.2% of residues in additional allowed region, 6.0% in generously allowed region and 0.9% in disallowed regions.