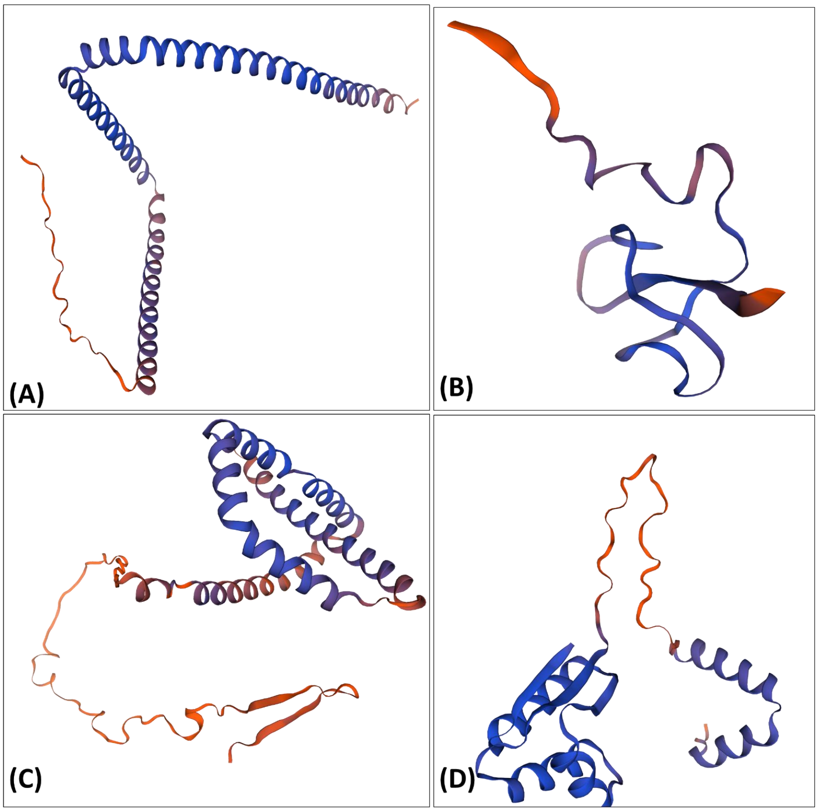

Figure S1. 3D structure of vaccine constructs. (A) YEZV-V1 with HBHA adjuvant. (B) YEZV-V2 with β- adjuvant. (C) YEZV-V3 with HBHA conserved adjuvant. (D) YEZV-V4 with ribosomal protein adjuvant.

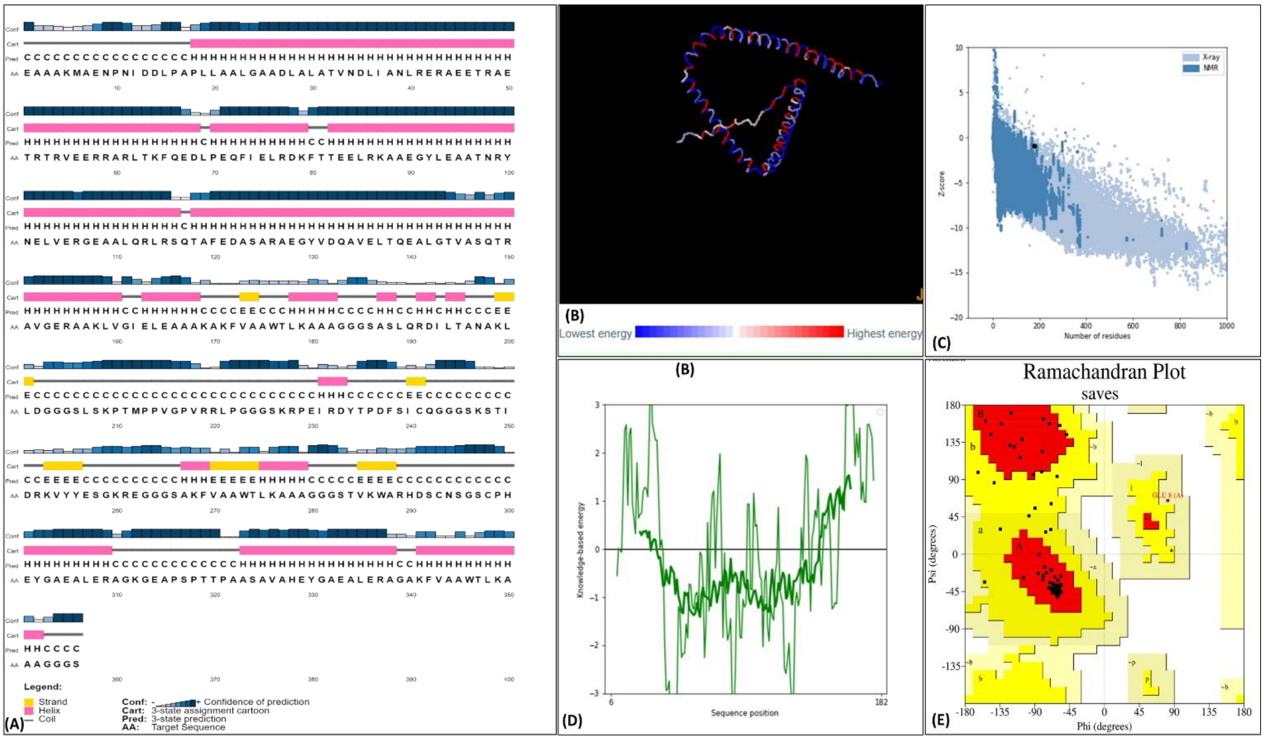

Figure S2. Development and validation of a tertiary structure model for YEZV-V1 construct. (A) 2D structure presentation of vaccine construct. (B) The refined 3D structure showing energies of construct. (C) Evaluation of the Refined 3D Structure having -0.88 Z-Score using the ProSA-Web server. (D) Quality of the model on a local scale by displaying energy variations across the amino acid sequence. (E) Ramachandran plot analysis of the MEV constructs.

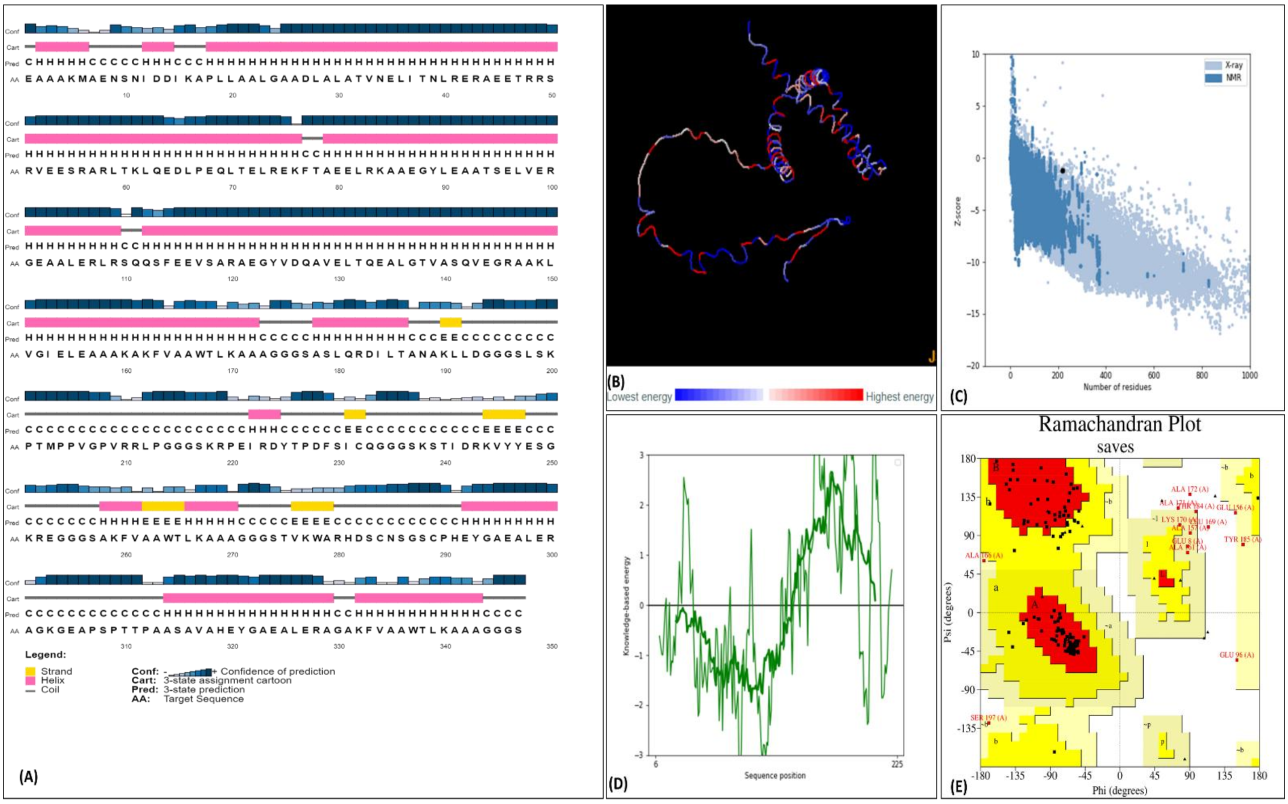

Figure S3. Development and validation of a tertiary structure model for YEZV-V3 construct. (A) 2D structure presentation of vaccine construct. (B) The refined 3D structure showing energies. (C) Evaluation of the refined 3D structure having -1.2 Z-Score using the ProSA-Web server. (D) Quality of the model on a local scale by displaying energy variations across the amino acid sequence. (E) Ramachandran plot analysis of the MEV construct.

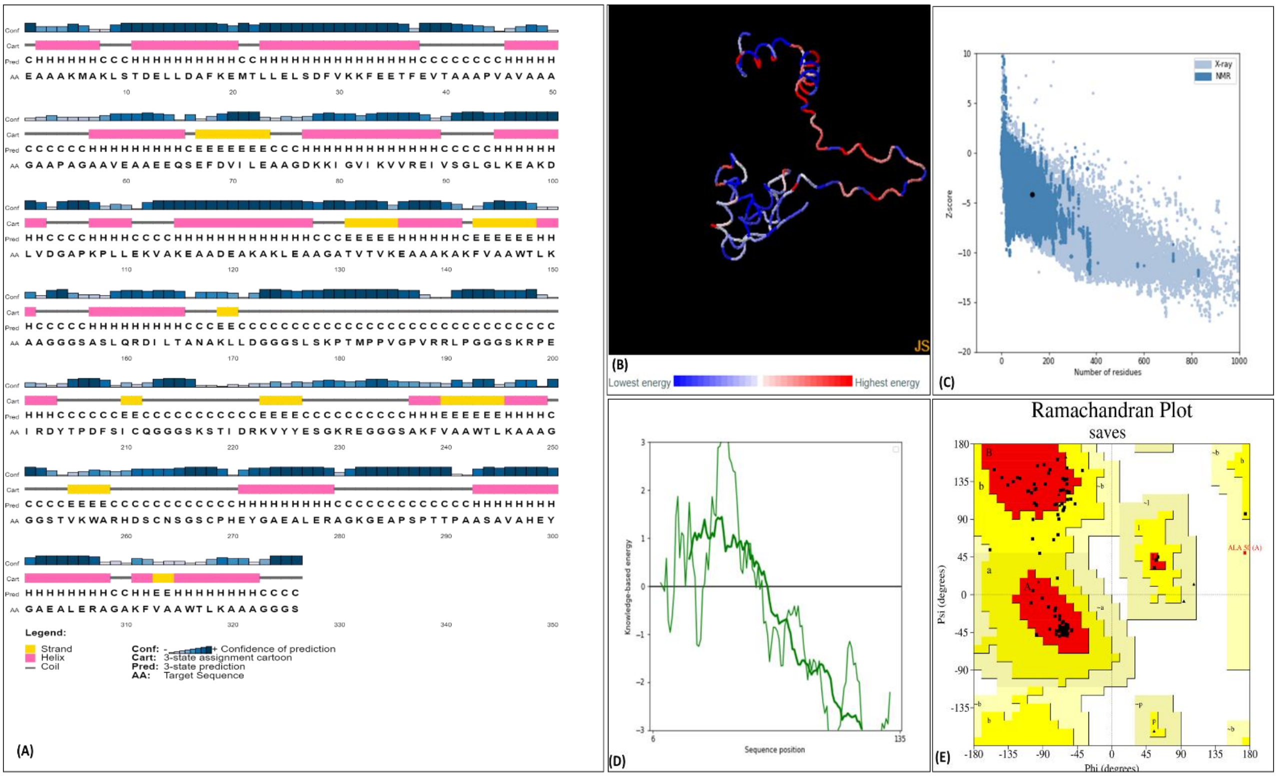

Figure S4. Development and validation of a tertiary structure model for YEZV-V4 construct. (A) 2D structure presentation of vaccine construct. (B) The refined 3D structure YEZV-V4 showing energies. (C) Evaluation of the Refined 3D Structure having-4.11 Z-Score using the ProSA-Web server. (D) Quality of the model on a local scale by displaying energy variations across the amino acid sequence. (E) Ramachandran Plot Analysis of the MEV construct.

Table S1. Conservancy analysis performed by IEDB on chosen B and T cell epitopes.

Protein IDs	MHC-I Epitopes	Conservation	MHC-II Epitopes	Conservation	B Cell Epitopes	Conservation
YP_010840880.1*	ASLQRDILT	50.00% (1/2)	SLQRDILTANAKLLD	50.00% (1/2)	ASLQRDILTANAKLLD	50.00% (1/2)
	LSKPTMPPV	50.00% (1/2)	MPPVGPVRRLPARLE	50.00% (1/2)	LSKPTMPPVGPVRRLP	50.00% (1/2)
	KRPEIRDYT	50.00% (1/2)	RPEIRDYTPDFSICQ	50.00% (1/2)	KRPEIRDYTPDFSICQ	50.00% (1/2)
YP_010840879.1*	KSTIDRKVY	50.00% (1/2)	DRKVYYESGKRELER	50.00% (1/2)	KSTIDRKVYYESGKRE	50.00% (1/2)
	TVKWARHDS	50.00% (1/2)	GEFVDHTVKWARHDS	50.00% (1/2)	TVKWARHDSCNSGSCP	50.00% (1/2)
	KGEAPSPTT	50.00% (1/2)	TTVKGEAPSPTTPAA	50.00% (1/2)	KGEAPSPTTPAASAVA	50.00% (1/2)

YP_010840880.1*: RNA-dependent RNA-polymerase.

YP_010840879.1*: glycoprotein precursor.

Table S2. Characteristics of vaccine constructs and adjuvants: Allergenicity, antigenicity, toxicity, and solubility.

Vaccine Construct	Adjuvant	Construct	Allergenicity	Antigenicity	Toxicity	Solubility
V1	Hbha adjuvant	EAAAKMAENPNIDDLPAPLLAALGAADLALATVNDLIANLRERAEETRAETRTRVEERRARLTKFQEDLPEQFIELRDKFTTEELRKAAEGYLEAATNRYNELVERGEAALQRLRSQTAFEDASARAEGYVDQAVELTQEALGTVASQTRAVGERAAKLVGIELEAAAKAKFVAAWTLKAAAGGGSASLQRDILTANAKLLDGGGSLSKPTMPPVGPVRRLPGGGSKRPEIRDYTPDFSICQGGGSKSTIDRKVYYESGKREGGGSAKFVAAWTLKAAAGGGSTVKWARHDSCNSGSCPHEYGAEALERAGKGEAPSPTTPAASAVAHEYGAEALERAGAKFVAAWTLKAAAGGGS	PROBABLE NON-ALLERGEN	0.4102 (Probable ANTIGEN).	Non-Toxin	Protein: Protein-sol Predicted scaled solubility: 0.591 pI: 6.330
V2	Beta defensin adjuvant	EAAAKGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKEAAAKAKFVAAWTLKAAAGGGSASLQRDILTANAKLLDGGGSLSKPTMPPVGPVRRLPGGGSKRPEIRDYTPDFSICQGGGSKSTIDRKVYYESGKREGGGSAKFVAAWTLKAAAGGGSTVKWARHDSCNSGSCPHEYGAEALERAGKGEAPSPTTPAASAVAHEYGAEALERAGAKFVAAWTLKAAAGGGS	PROBABLE NON-ALLERGEN	0.3744 (Probable NON-ANTIGEN)	Non-Toxin	Protein: Protein-sol Predicted scaled solubility: 0.812 pI: 10.580
V3	Hbha cons rved adjuvant	EAAAKMAENSNIDDIKAPLLAALGAADLALATVNELITNLRERAEETRRSRVEESRARLTKLQEDLPEQLTELREKFTAEELRKAAEGYLEAATSELVERGEAALERLRSQQSFEEVSARAEGYVDQAVELTQEALGTVASQVEGRAAKLVGIELEAAAKAKFVAAWTLKAAAGGGSASLQRDILTANAKLLDGGGSLSKPTMPPVGPVRRLPGGGSKRPEIRDYTPDFSICQGGGSKSTIDRKVYYESGKREGGGSAKFVAAWTLKAAAGGGSTVKWARHDSCNSGSCPHEYGAEALERAGKGEAPSPTTPAASAVAHEYGAEALERAGAKFVAAWTLKAAAGGGS	PROBABLE NON-ALLERGEN	0.4024 (Probable ANTIGEN).	Non-Toxin	Protein: Protein-sol Predicted scaled solubility: 0.628 pI: 5.820
V4	Ribosomal protein adjuvant	EAAAKMAKLSTDELLDAFKEMTLLELSDFVKKFEETFEVTAAAPVAVAAAGAAPAGAAVEAAEEQSEFDVILEAAGDKKIGVIKVVREIVSGLGLKEAKDLVDGAPKPLLEKVAKEAADEAKAKLEAAGATVTVKEAAAKAKFVAAWTLKAAGGGSASLQRDILTANAKLLDGGGSLSKPTMPPVGPVRRLPGGGSKRPEIRDYTPDFSICQGGGSKSTIDRKVYYESGKREGGGSAKFVAAWTLKAAAGGGSTVKWARHDSCNSGSCPHEYGAEALERAGKGEAPSPTTPAASAVAHEYGAEALERAGAKFVAAWTLKAAAGGGS	PROBABLE ALLERGEN	0.3580 (Probable NON-ANTIGEN).	Non-Toxin	Protein: Protein-sol Predicted scaled solubility: 0.672 pI: 6.750