

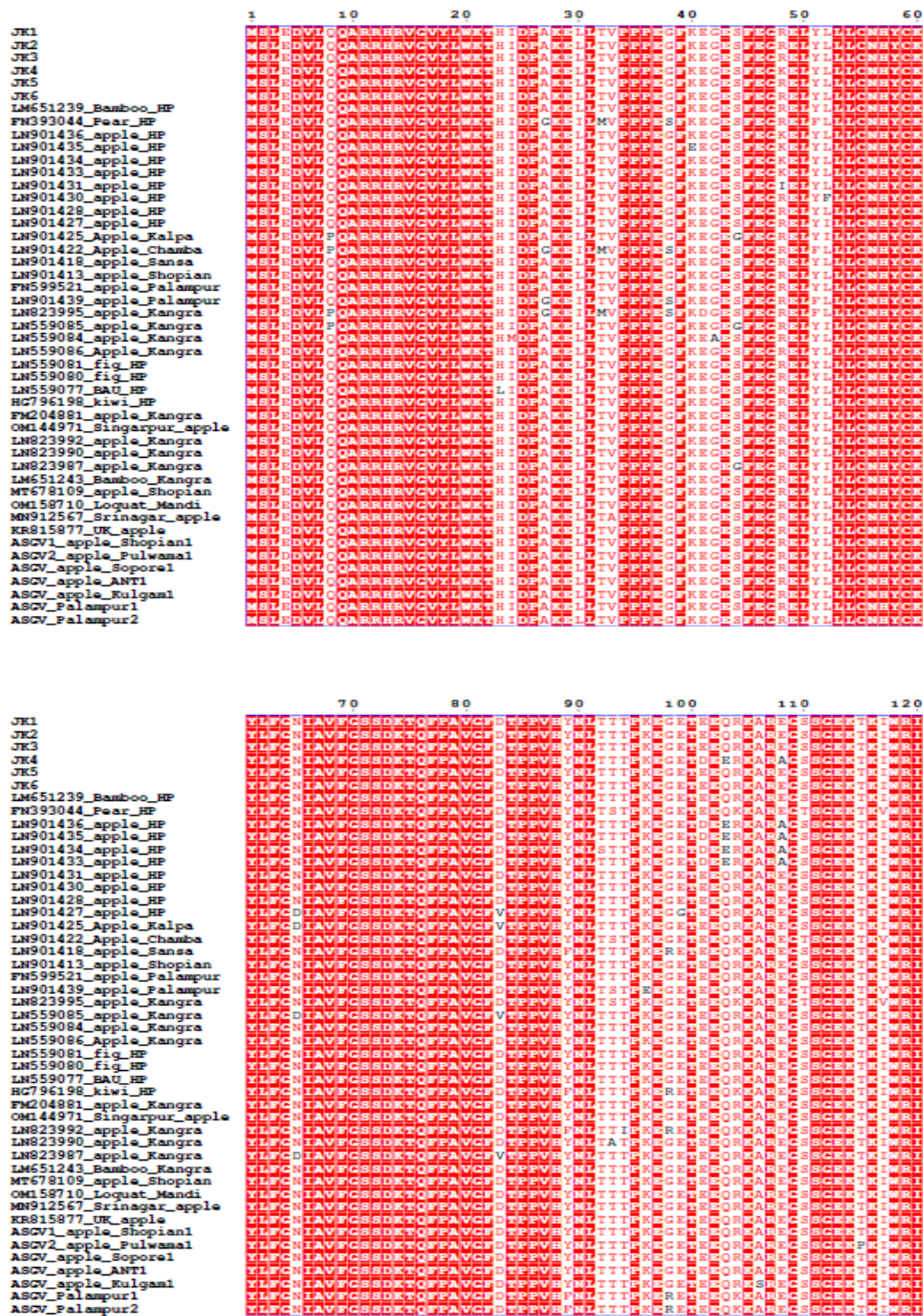
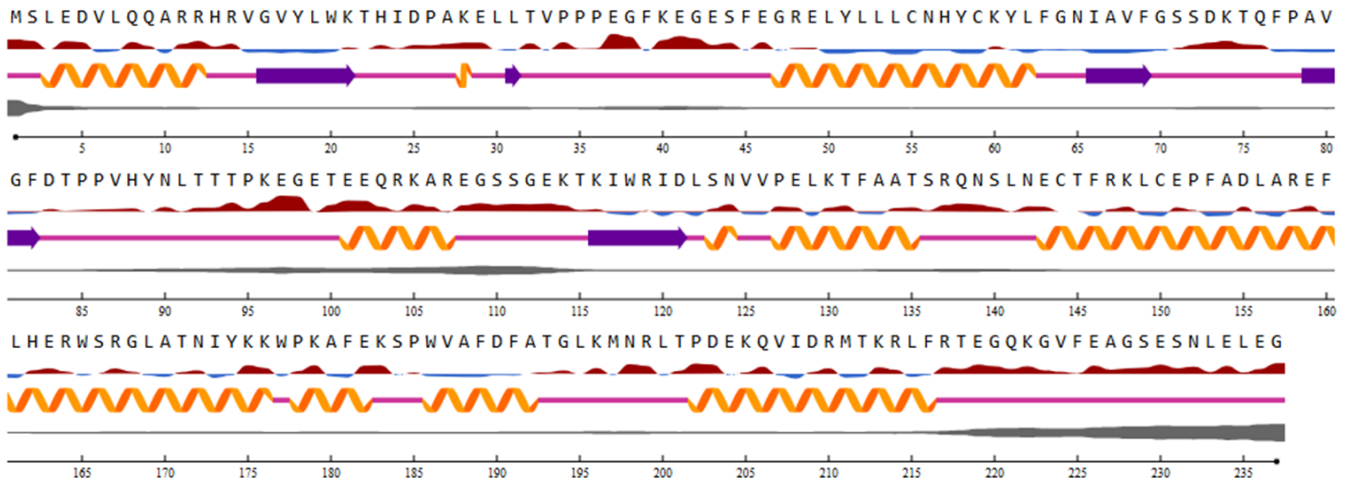


Figure S1: Multiple sequence alignment of coat protein (CP) amino acid sequences of ASGV isolates from different geographical regions, including Indian isolates from Himachal Pradesh (HP) and Jammu & Kashmir (J&K), along with representative Indian isolates retrieved from GenBank. Conserved residues are highlighted in red, demonstrating high sequence conservation across the CP region. Alignment analysis indicates limited variability among Indian isolates, supporting the conserved structural organization of the ASGV coat protein.

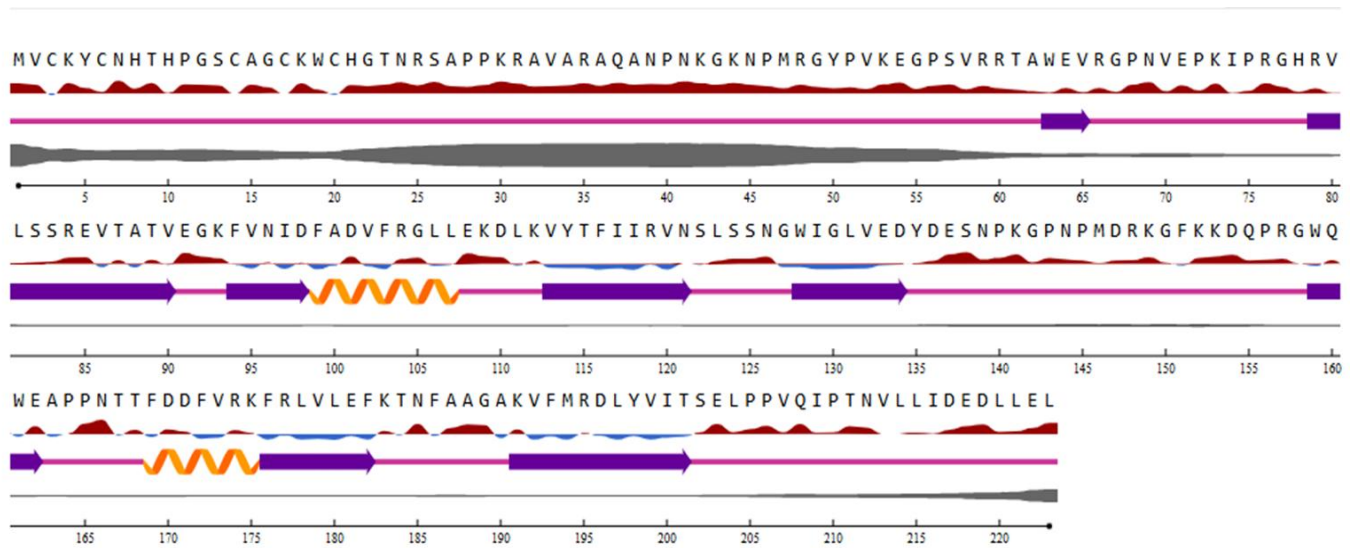
Relative Surface Accessibility: ▲ Red is exposed and blue is buried, thresholded at 25%.
Secondary Structure: 🌀 Helix, ➡ Strand, — Coil.
Disorder: — Thickness of line equals probability of disordered residue.

gv

Export gv



ASGV



ApMV

Figure S2. Secondary structure and surface accessibility analysis of ASGV and ApMV coat proteins. Predicted α -helices, β -strands, coil regions, disorder propensity, and relative surface accessibility are shown across the amino acid sequences. Red regions indicate surface-exposed residues, whereas blue regions represent buried residues. The analyses reveal several structurally exposed and flexible regions that were considered during epitope selection.

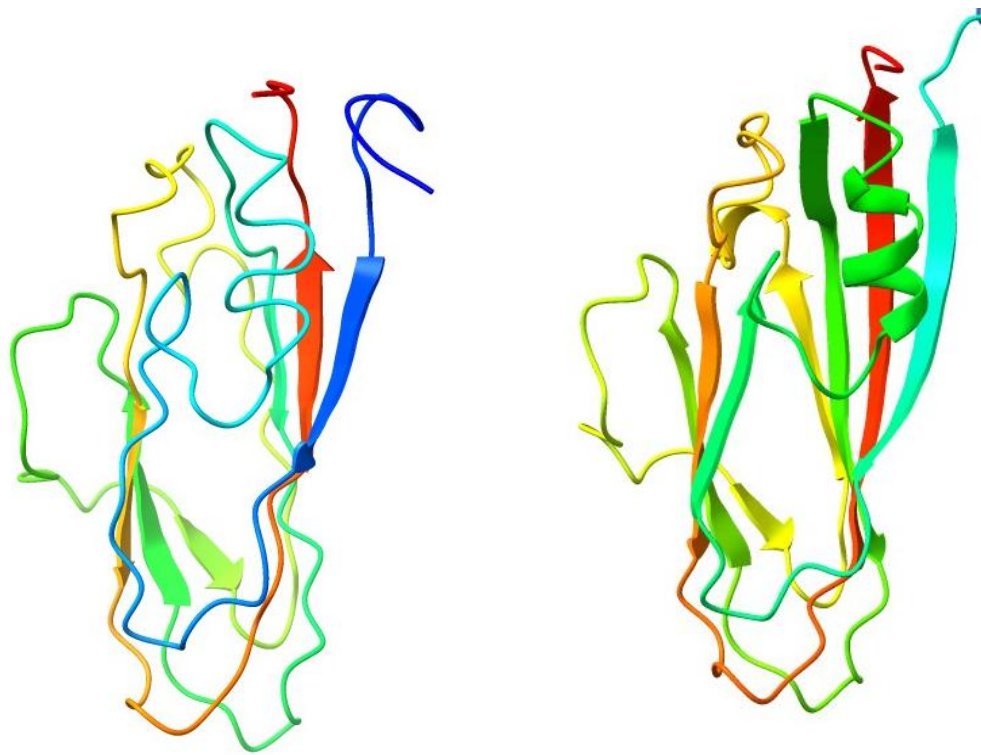


Figure S3: Structural comparison between the potato leaf roll virus (PLRV) coat protein models predicted using AlphaFold3 (left) and the experimentally resolved X-ray crystallographic structure (right). The overall similarity between the two structures supports the reliability of AlphaFold3-based structural predictions for plant viral coat proteins.

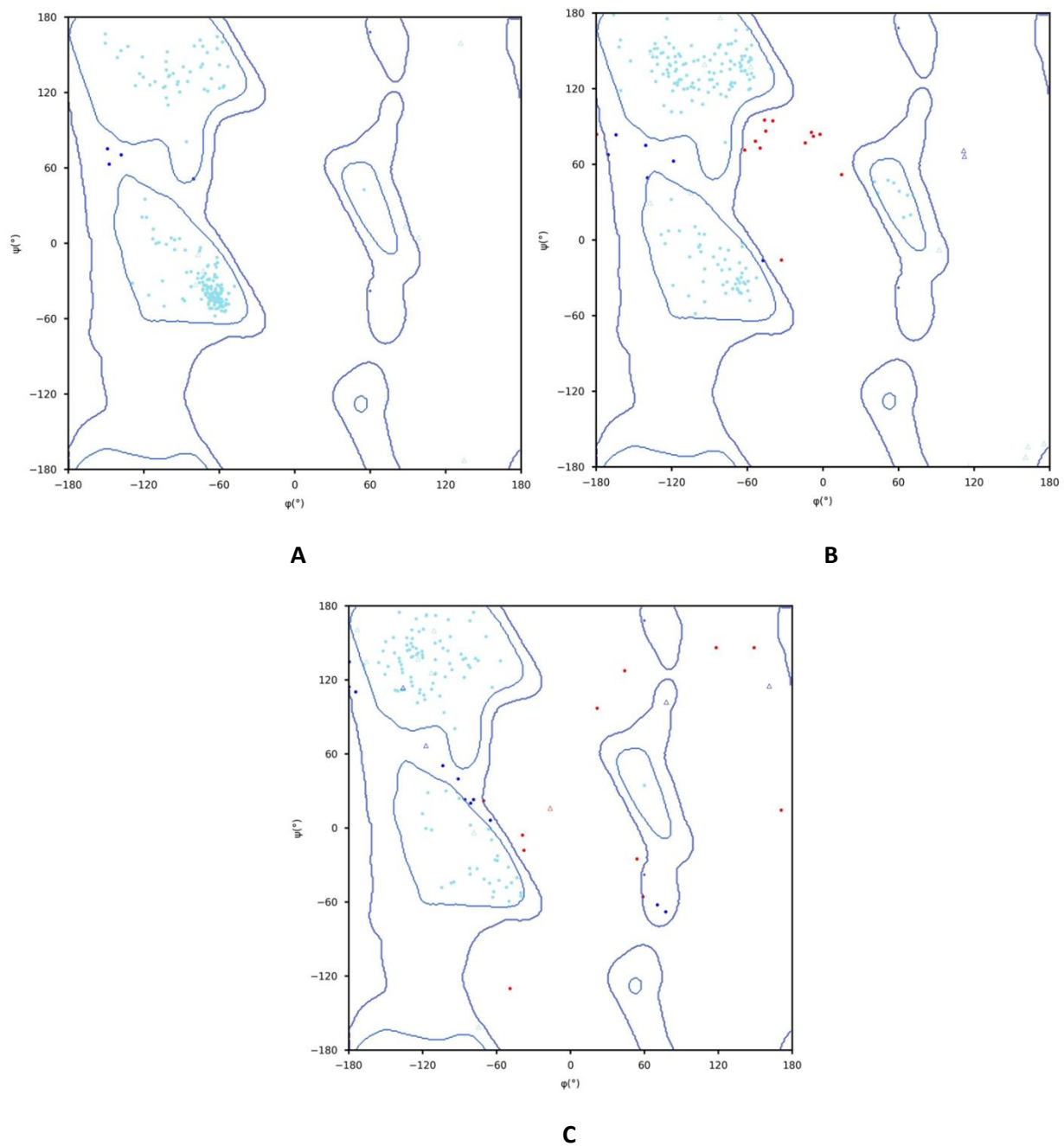


Figure S4. Ramachandran (R-plot) analysis of predicted coat protein structures of (A) ASGV, (B) ApMV, and (C) PLRV. Most residues were localized within favored and additionally allowed regions, indicating good stereochemical quality and structural reliability of the predicted models.

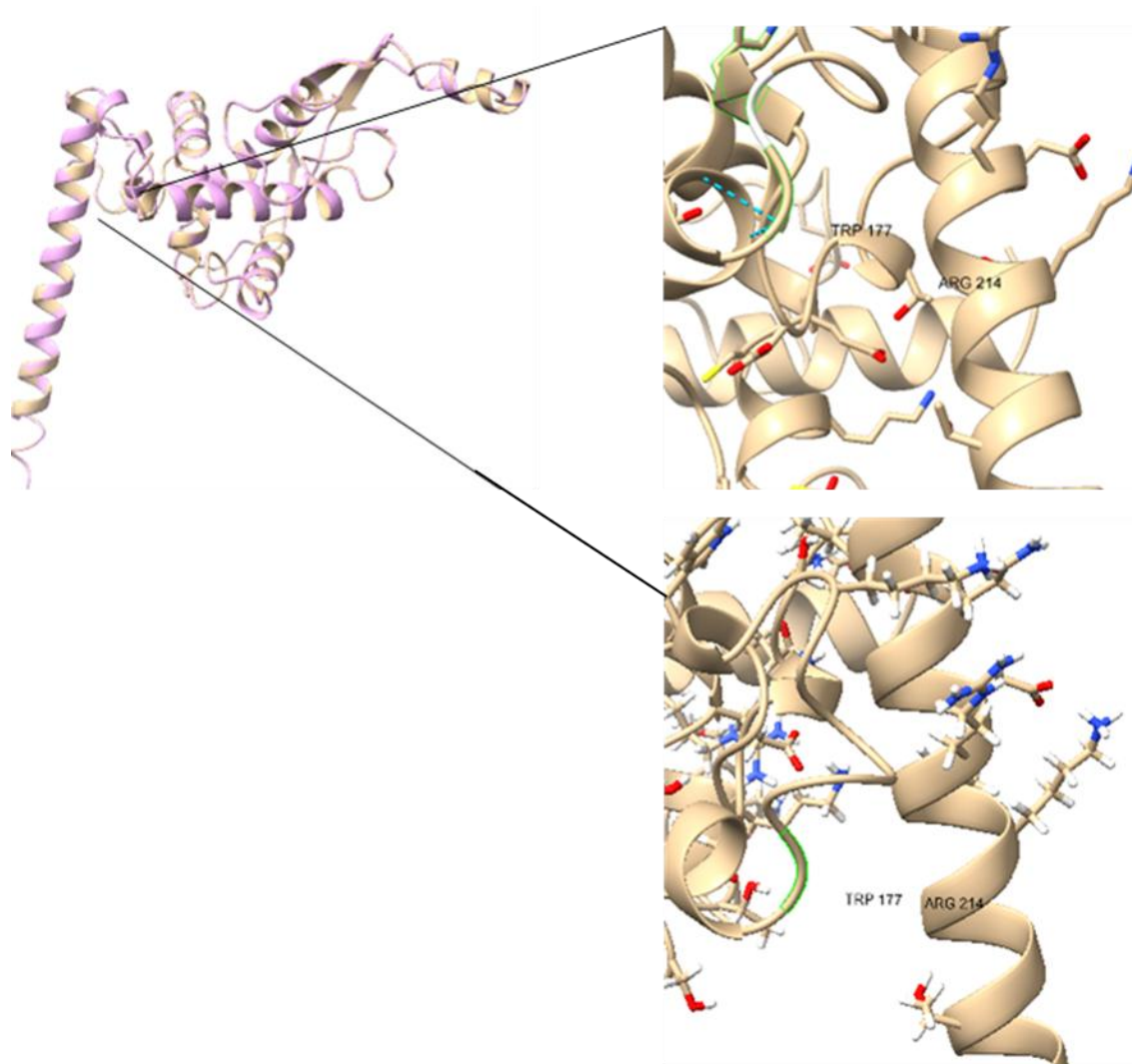
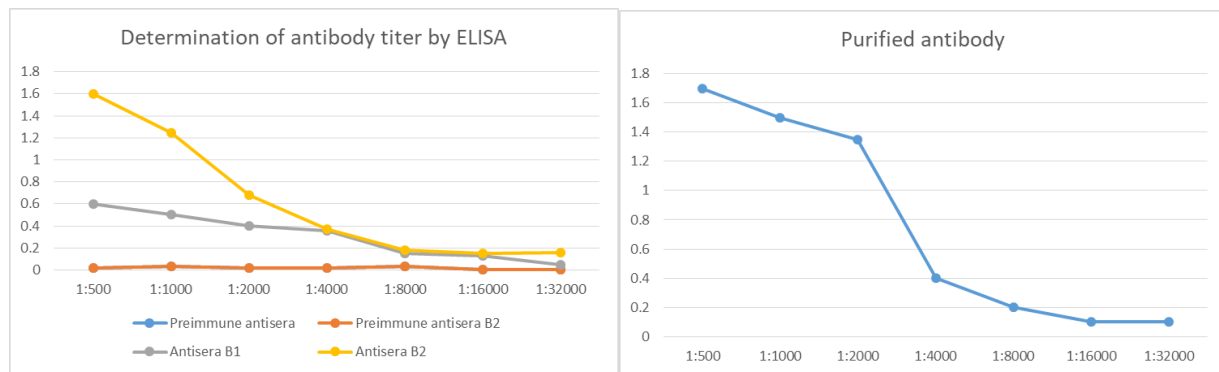
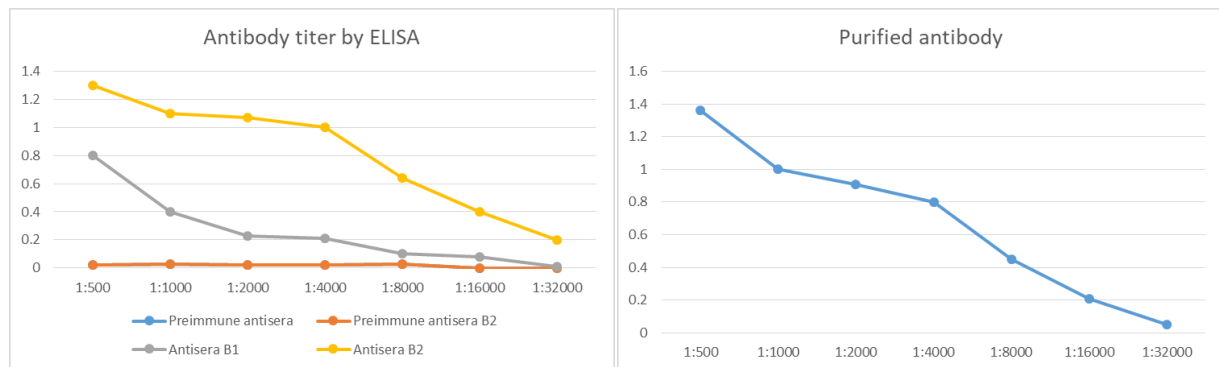


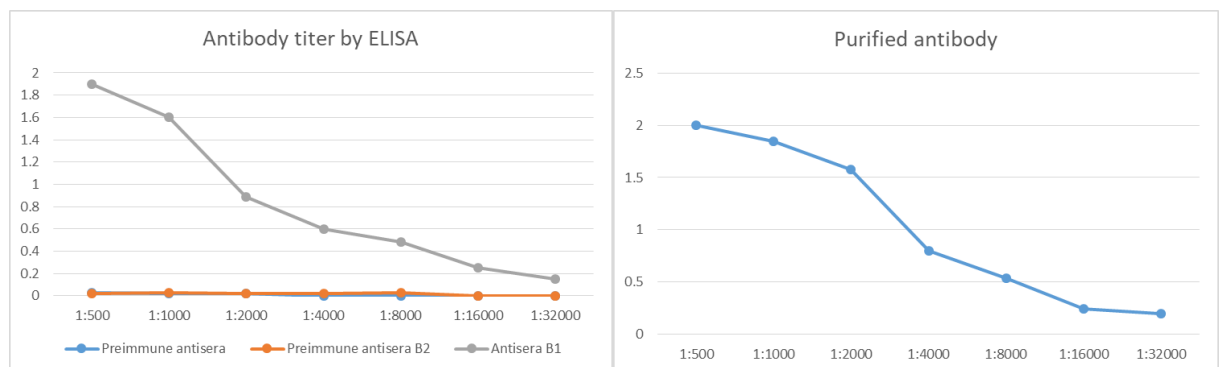
Figure S5 Refined ASGV coat protein (CP) structure (pink) superimposed on the unrefined AlphaFold-predicted structure (gold) reveals minimal differences in the overall protein conformation. The Ramachandran plot (bottom center) of the refined model indicates improved stereochemical quality, with 0% of residues located in generously allowed regions. The upper-right panel highlights steric clashes between Trp177 (W177) and Arg214 (R214) in the unrefined structure (enlarged view shown). The lower-right panel shows the refined model, in which steric hindrance between W177 and R214 has been substantially reduced, resulting in improved local geometry and structural stability.



ASGV Peptide 1 antibody



ASGV Peptide 2 antibody



ApMV antibody

Figure S6 Determination of antibody titer and characterization of purified antibodies by ELISA. ELISA-based antibody titration of the pre-immune and post-immunization antisera and the corresponding purified antibody preparations. Top row: ASGV Pep1-derived antibody; middle row: ASGV Pep2-derived antibody; and low row: ApMV Pep1 derived antibody. Left panels show ELISA reactivity of pre-immune sera B1/B2 and antisera B1/B2 across serial antibody dilutions (1:500-1:32,000). Right panels show the ELISA reactivity of the corresponding purified antibody preparations across the same dilution series. O.D. values were measured at 450 nm.

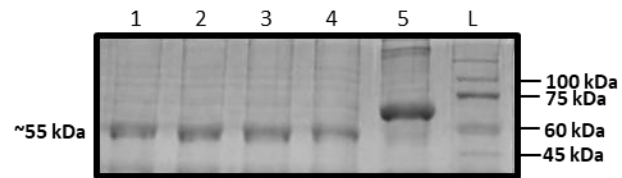
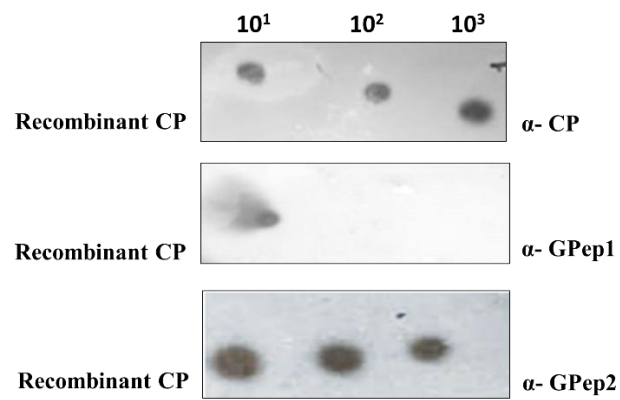


Figure S7: SDS-PAGE analysis of purified peptide-derived antibody preparations. SDS-PAGE profiles of purified peptide-derived antibodies used in the study. Lanes 1 and 2: α -GPep1 antibody; lanes 3 and 4: α -GPep2 antibody; lane 5: BSA control; L: Tri-Color Protein Marker (G Biosciences). The predominant protein (IgG heavy chain) band was observed at approximately 55 kDa



Supplementary Figure S8 DIBA analysis of ASGV CP recognition by the generated antibodies. DIBA was performed using purified recombinant ASGV coat protein (CP) at the indicated concentrations with α -CP (top), α -GPep1 (middle), and α -GPep2 (bottom) antibodies. α -GPep2 showed stronger and more consistent immunoreactive signals across the tested CP concentrations.

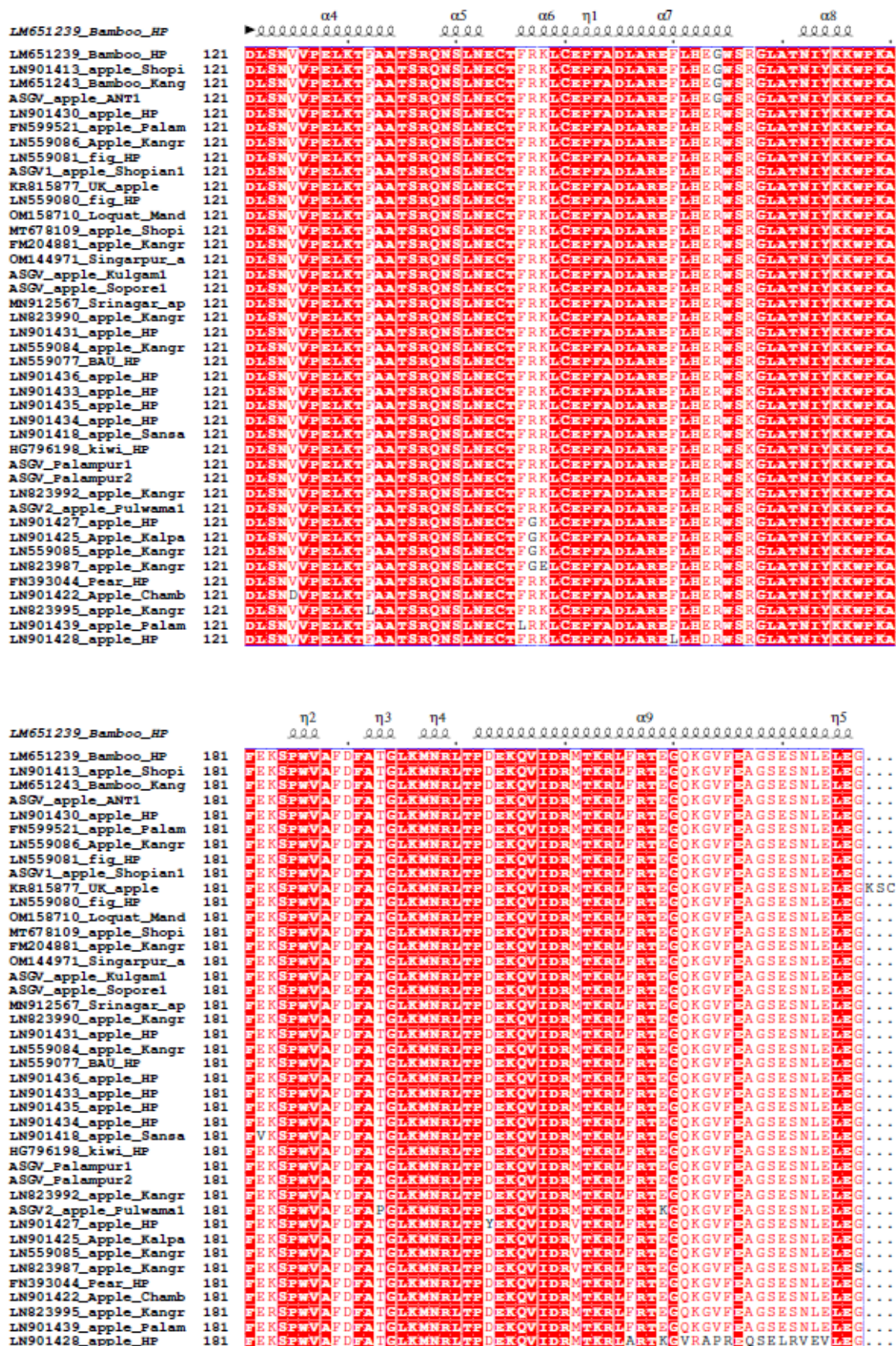


Figure S9: Multiple sequence alignment of ASGV CP sequences showing predominance of type II (E-A) variants among Indian isolates, with a few type III (Q-E) variants identified from Himachal Pradesh and Jammu & Kashmir.

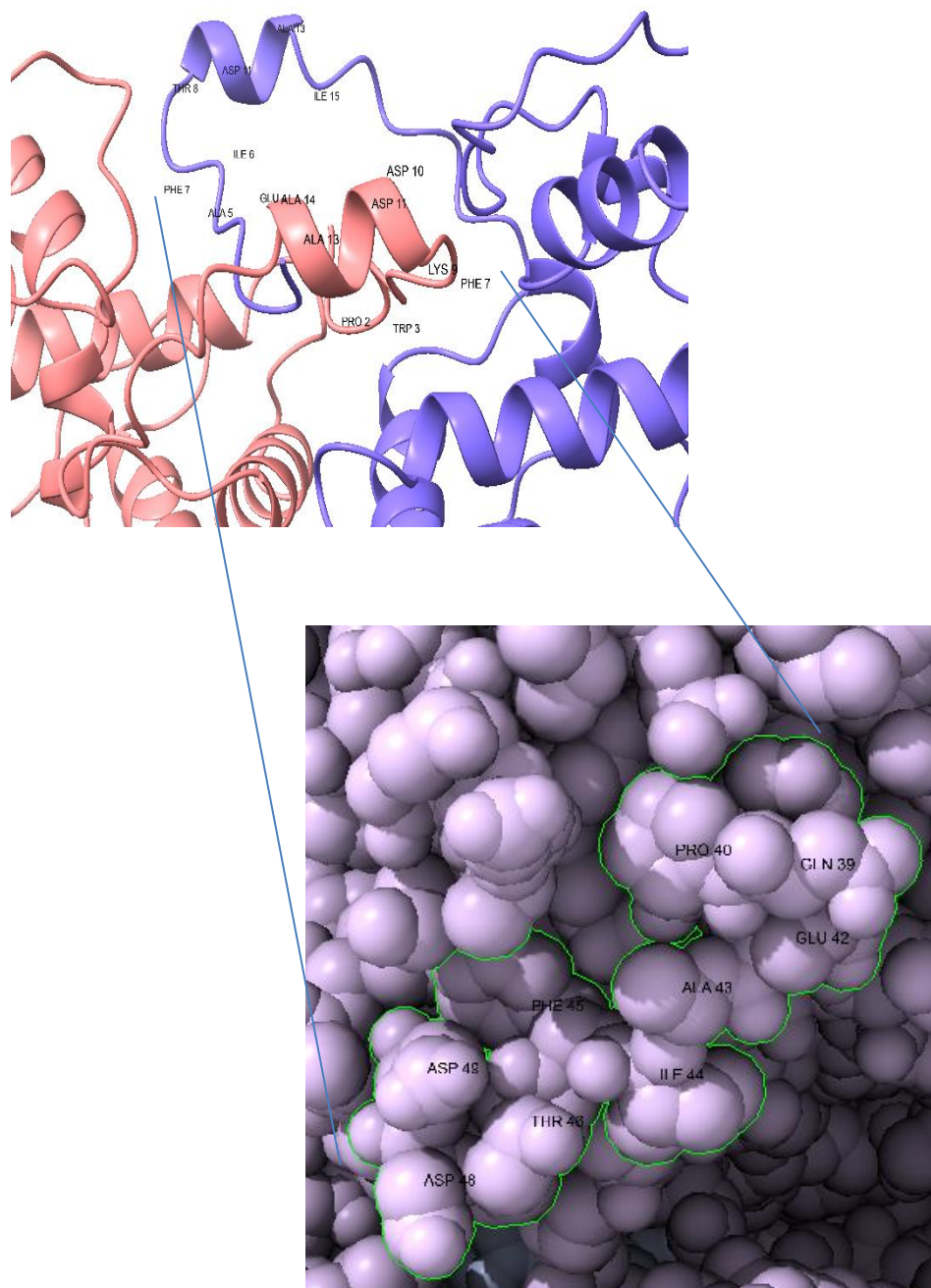


Figure S10: Structural localization of bamboo mosaic virus (BaMV) coat protein residues 36-48 within the assembled virion architecture. Surface-rendered and magnified views demonstrate that residues corresponding to this region remain externally exposed during CP-CP interactions, supporting their accessibility and potential antigenic relevance.

CP region*	Interaction propensity (catRAPID#)	Interaction
ASGV		
1-50	17.86	High
16-66	12.74	Low
51-100	13.85	Intermediate
101-150	12.24	Low
151-200	16.63	High
168-218	18.01	Highest
ApMV		
1-50	6.85	High
51-100	3.5	Low
101-150	5.75	Intermediate
151-200	5.47	Intermediate
168-217	8.97	Highest
35-85	2.98	Lowest

Supplementary Table S1 catRAPID interaction propensity analysis of ASGV and ApMV coat protein (CP) regions. The predicted interaction propensity scores and corresponding interaction strengths are shown for different CP regions of ASGV and ApMV. Higher catRAPID propensity scores indicate greater predicted protein-protein interaction potential. A minimum of 50 amino acids is required for catRAPID propensity analysis.*

ASGV

Sample No.	ELISA (α -CP)	ELISA (GPep1)	ELISA (GPep2)	RT-PCR
1	+	+	+	+
2	+	+	+	+
3	-	+	+	+
4	+	+	+	+
5	-	-	+	+
6	+	+	+	+
7	-	+	+	+
8	-	-	-	-
9	+	+	+	+
10	-	-	-	-
11	-	-	-	-
12	+	+	+	+
13	-	-	-	-
14	-	-	-	-
15	+	+	-	+
16	-	-	-	-
17	-	-	-	-
18	+	+	+	+
19	+	-	-	+
20	-	+	+	-
21	+	+	+	+
22	-	+	+	-
23	+	+	-	-
24	+	+	-	-
25	+	+	-	-
26	-	+	+	+
27	+	-	+	+
28	-	-	+	+
29	+	+	+	+
30	+	+	+	-
31	+	+	+	+
32	+	+	+	+
33	-	+	-	-
34	-	-	+	-
35	-	-	+	-
36	-	-	+	-
37	+	+	+	+
38	+	-	-	-
39	+	-	-	+
40	-	+	-	-
41	+	+	+	+
42	-	-	+	-
43	+	+	+	+
44	+	+	+	+
45	-	+	-	+
46	+	+	-	-
47	-	+	+	+
48	+	-	+	-
49	+	-	-	+
50	-	+	-	+
True Positive	20	20	22	
True Negative	14	13	15	
False Positive	9	10	8	
False Negative	7	7	5	

ApMV

Sample No.	ELISA (α -CP)	ELISA (GPep1)	RT-PCR
1	+	+	+
2	+	+	+
3	-	+	+
4	+	+	+
5	+	+	-
6	+	+	+
7	-	+	+
8	+	-	-
9	+	+	+
10	-	+	+
11	-	+	+
12	+	-	-
13	+	+	-
14	+	+	+
15	+	+	+
16	+	+	+
17	-	-	-
18	-	-	-
19	-	-	-
20	-	-	-
21	-	-	-
22	+	-	-
23	-	-	-
24	-	-	-
25	-	-	-
26	-	-	-
27	-	-	+
28	-	+	+
29	+	+	+
30	-	+	+
31	+	+	+
32	-	+	-
33	+	+	-
34	-	+	+
35	-	-	-
True Positive	10	17	
True Negative	11	14	
False Positive	5	3	
False Negative	9	1	

Supplementary Table S2 Comparison of ASGV and ApMV ELISA and RT-PCR results. The tables summarizes the ELISA results obtained using α -CP, α -GPep1, and α -GPep2 antibodies in comparison with RT-PCR detection for ASGV-positive and negative samples, and similarly ELISA results obtained using α -mCP and α -mPep1 antibodies in comparison with RT-PCR detection for ApMV positive and negative samples. The numbers of true-positive, true-negative, false-positive, and false-negative results are provided for each ELISA antibody configuration.

Condition	Pep1 Ab	Pep2 Ab
No peptide	0.549	1.242
Pep1/Pep2 0.1 µg/mL	0.400	0.338
0.5 µg/mL	0.192	0.257
1 µg/mL	0.183	0.308
5 µg/mL	0.276	0.273
10 µg/mL	0.270	0.312
25 µg/mL	0.136	0.152
50 µg/mL	0.124	0.153

Supplementary Table S3 Peptide competition ELISA. ELISA reactivity of α -GPep1 and α -GPep2 antibodies was evaluated in the presence of increasing concentrations of the corresponding peptides. OD values at 450 nm are shown for each peptide concentration.

Concentration	CP antibody	GPep1 antibody	GPep2 antibody
100 mg	8.7	7.64	11.1
1 mg	12.63	13.2	14.34
100 ng	12.68	11.54	15.17
100 pg/ml	12.31	14.3	11.74
10 pg/ml	9.93	12.32	9.49
Buffer only	5.25	4.83	0

Supplementary Table S4 Trigit scores of ASGV LFIA test lines across an antigen dilution series. Test-line intensity was assessed using Trigit scoring for the CP antibody, α -GPep1, and α -GPep2 antibody configurations at the indicated ASGV antigen concentrations. Buffer-only samples were included as negative controls.

Fig. 4D

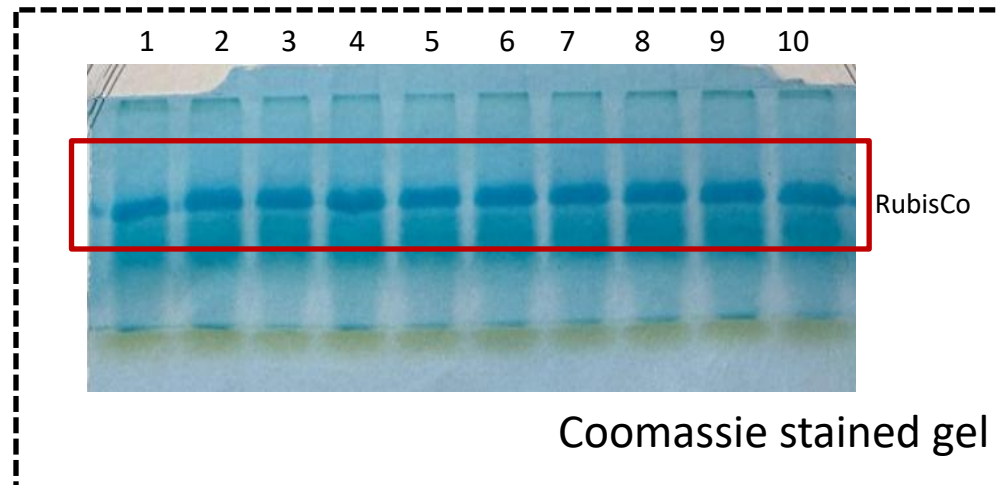
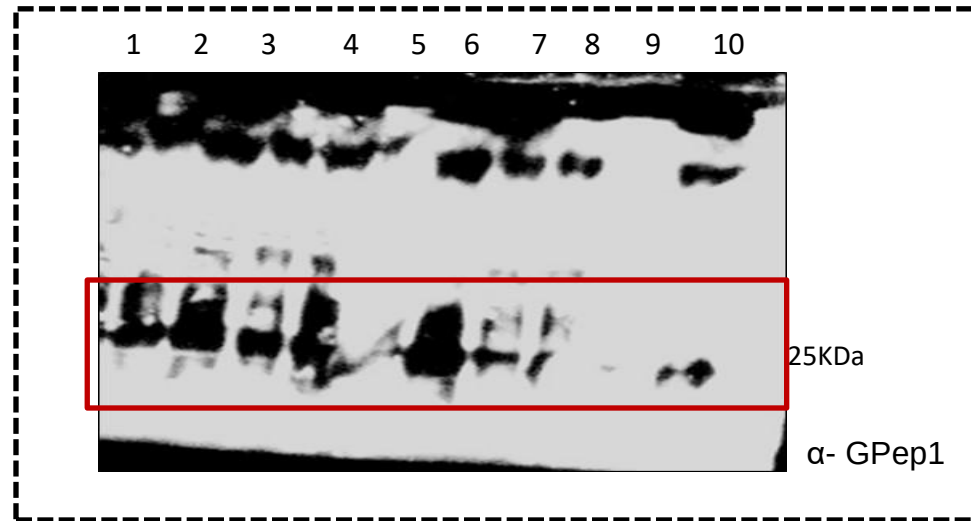


Fig. 4D

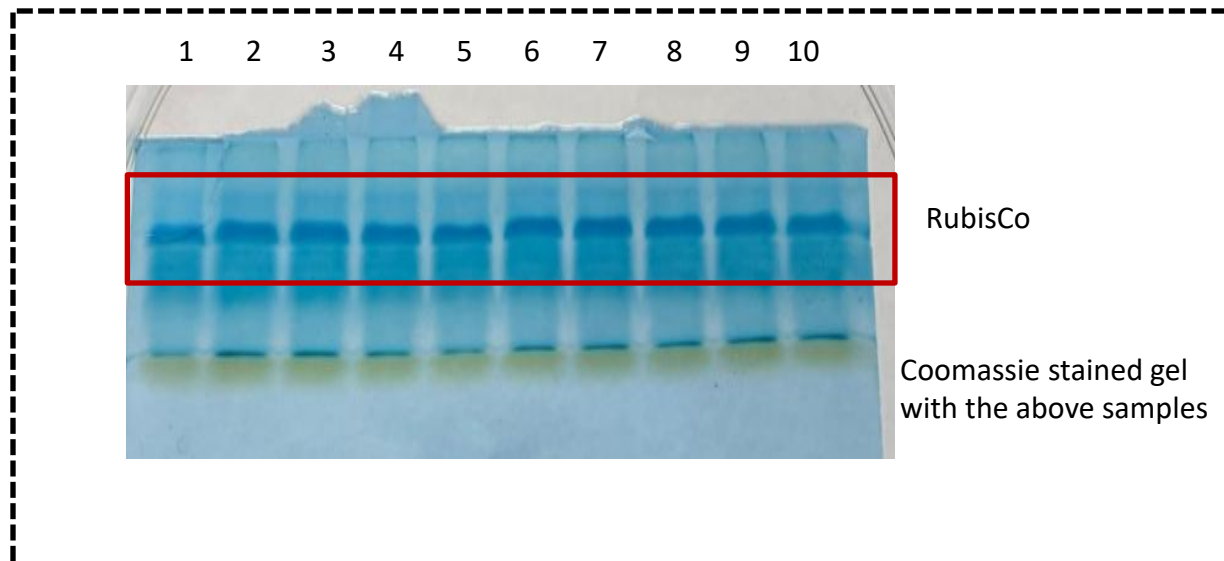
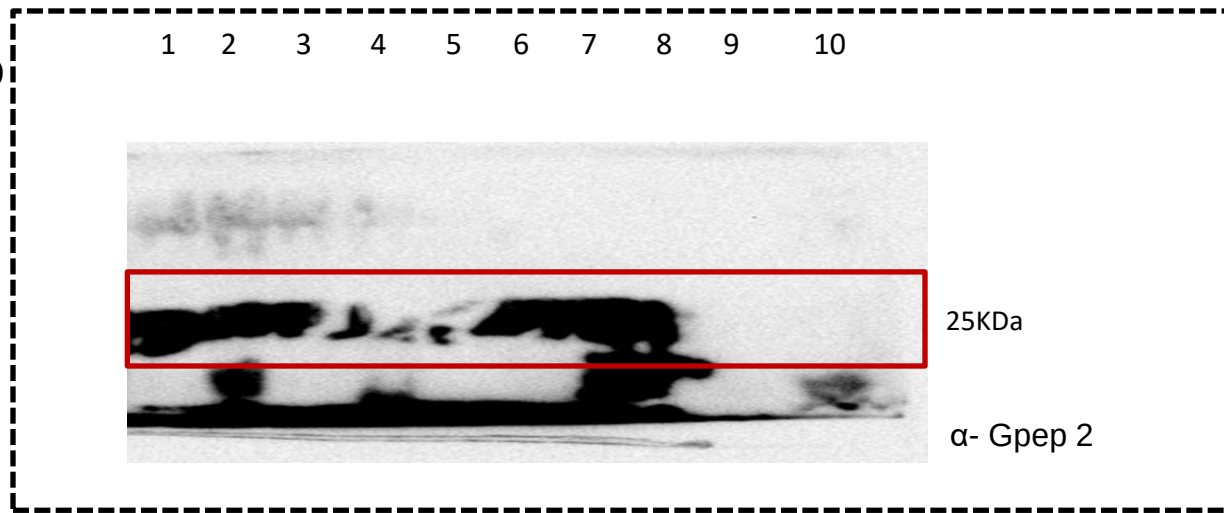


Fig. 4D

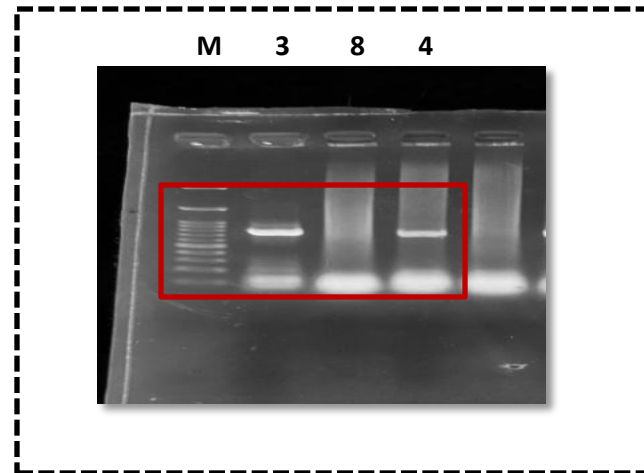
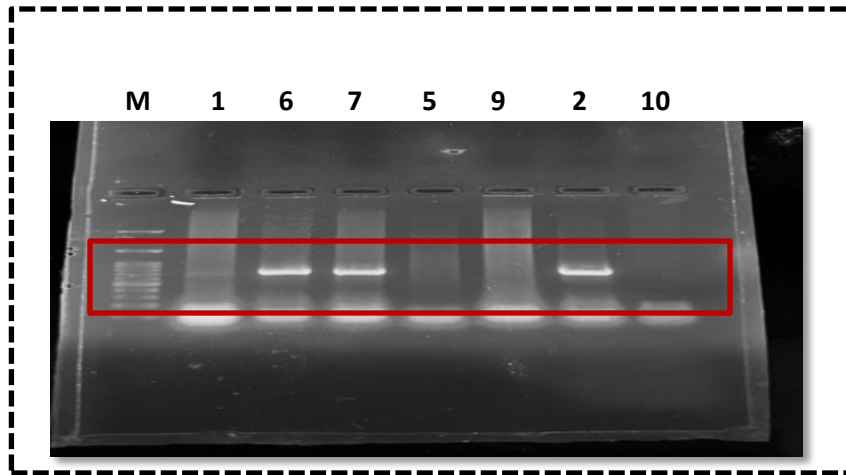


Fig. 4E

