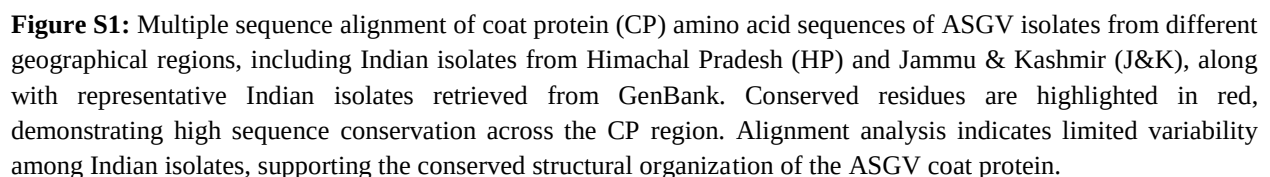


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JK3	DLSNVVFELK	FAATSRQMSLN	ECTFRK	LCFFADL	ARF	LBERWS
JK4	DLSNVVFELK	FAATSRQMSLN	ECTFRK	LCFFADL	ARF	LBERWS
JK5	DLSNVVFELK	FAATSRQMSLN	ECTFRK	LCFFADL	ARF	LBERWS
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FN393044_Fear_HF	DLSNVVFELK	FAATSRQMSLN	ECTFRK	LCFFADL	ARF	LBERWS
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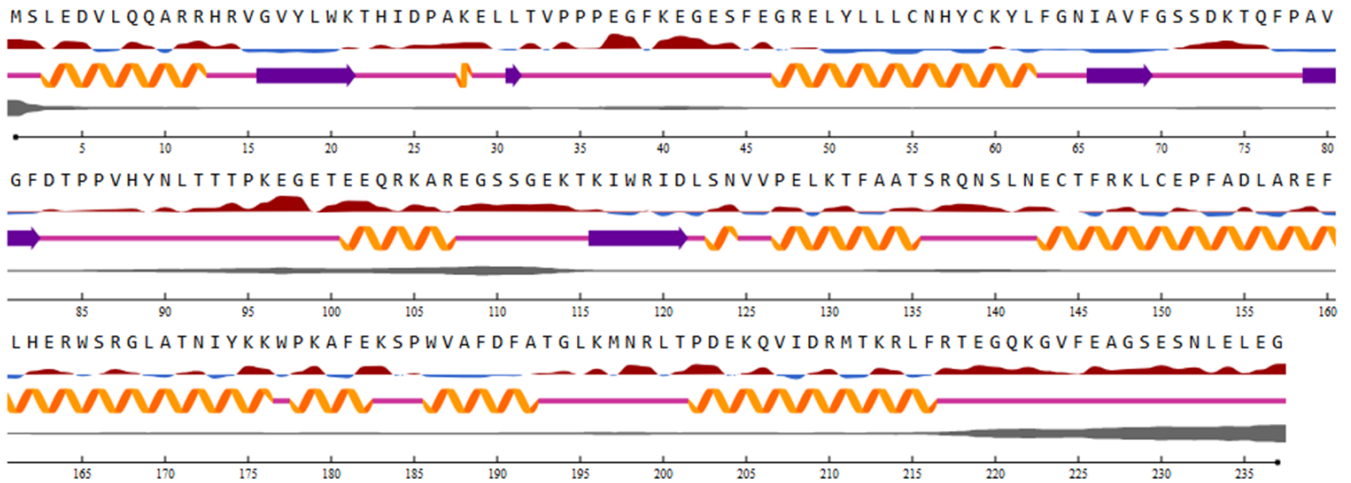
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ASGV_Palampur1	EKSPVVA	FDFA	CLKMMRLTF	EKQVIDR	FEET
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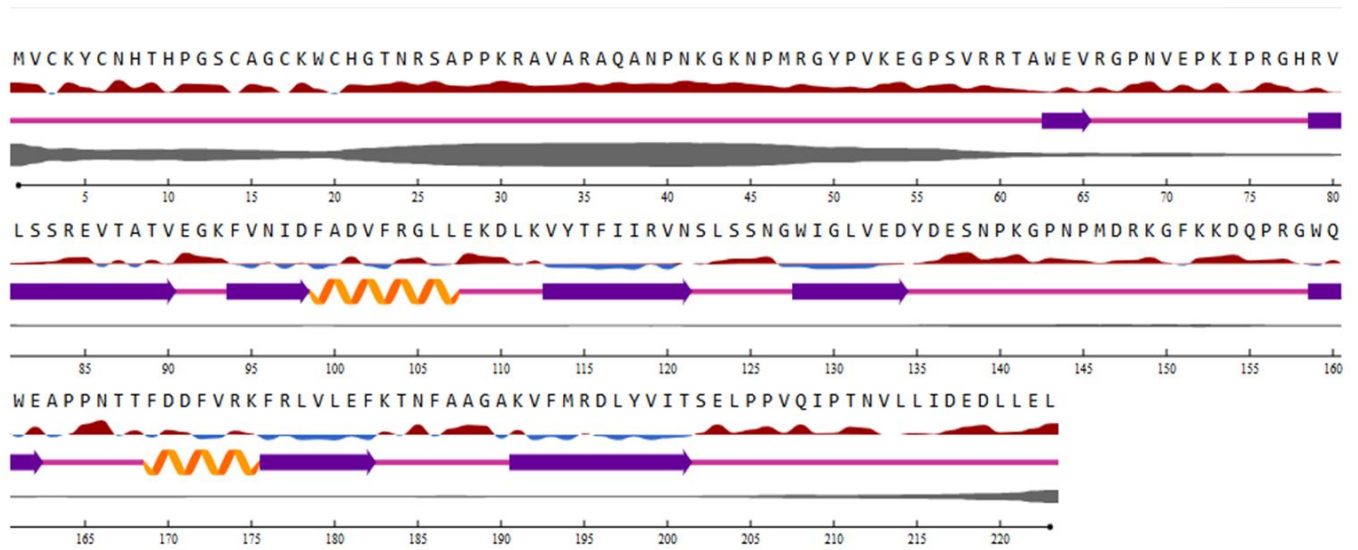
Relative Surface Accessibility: ▲ Red is exposed and blue is buried, thresholded at 25%.
Secondary Structure: 🌀 Helix, ➡ Strand, — Coil.
Disorder: 📏 Thickness of line equals probability of disordered residue.

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.

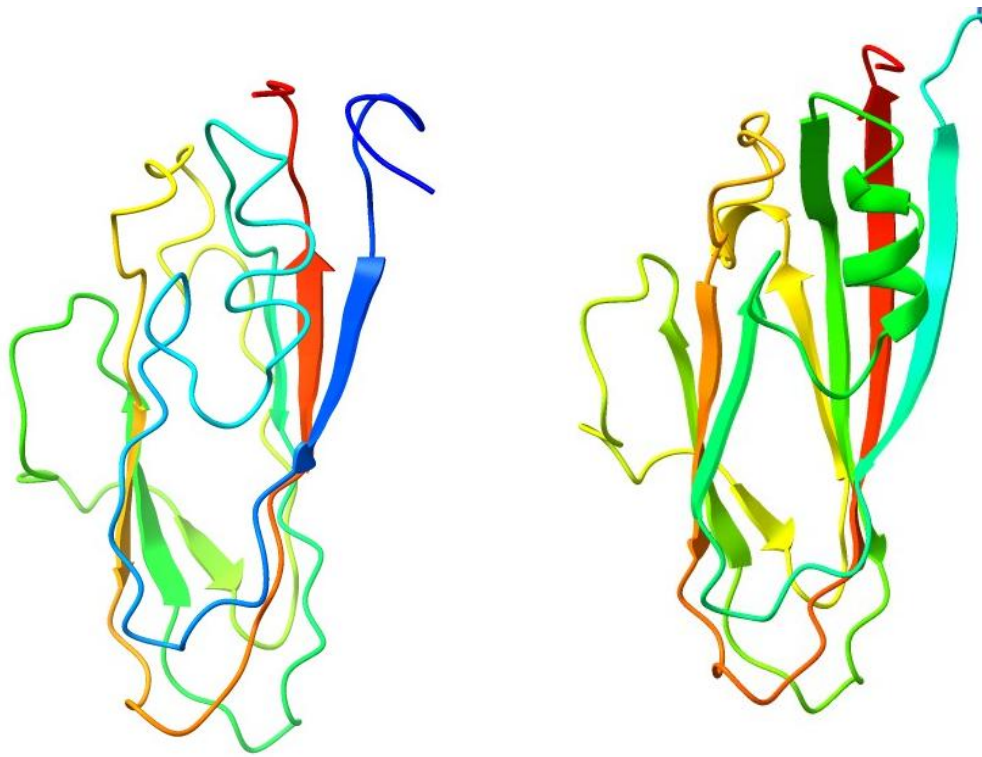


Figure S3: Structural comparison between the potato leaf roll virus (PLRV) coat protein models predicted using AlphaFold3 (left) and the experimentally resolved X-ray crystallographic structure (right). The overall similarity between the two structures supports the reliability of AlphaFold3-based structural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

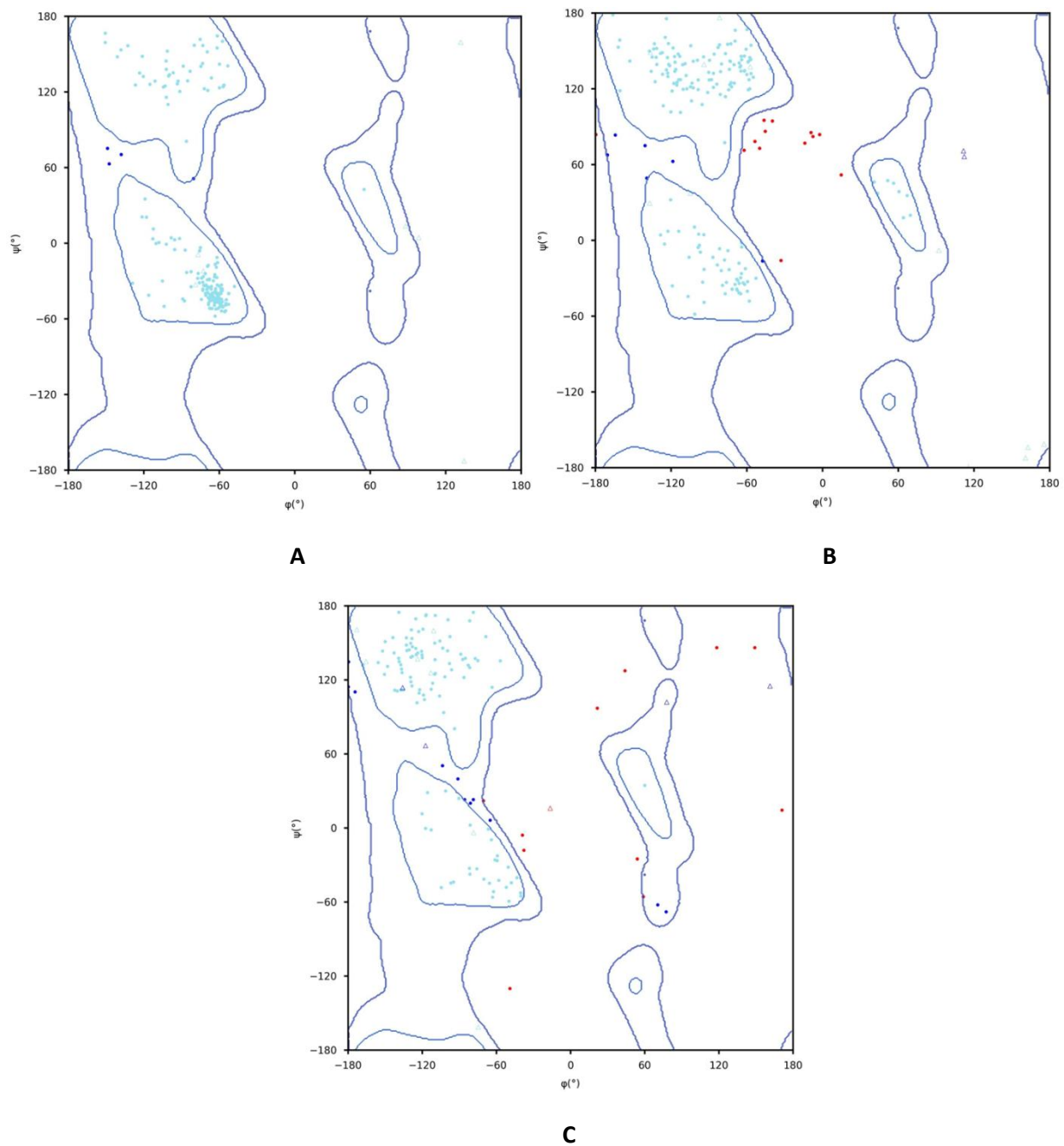


Figure S4. Ramachandran (R-)plot analysis of predicted coat protein structures of (A) ASGV, (B) ApMV, and (C) PLRV. Most residues were localized within favored and additionally allowed regions, indicating good stereochemical quality and structural reliability of the predicted models.

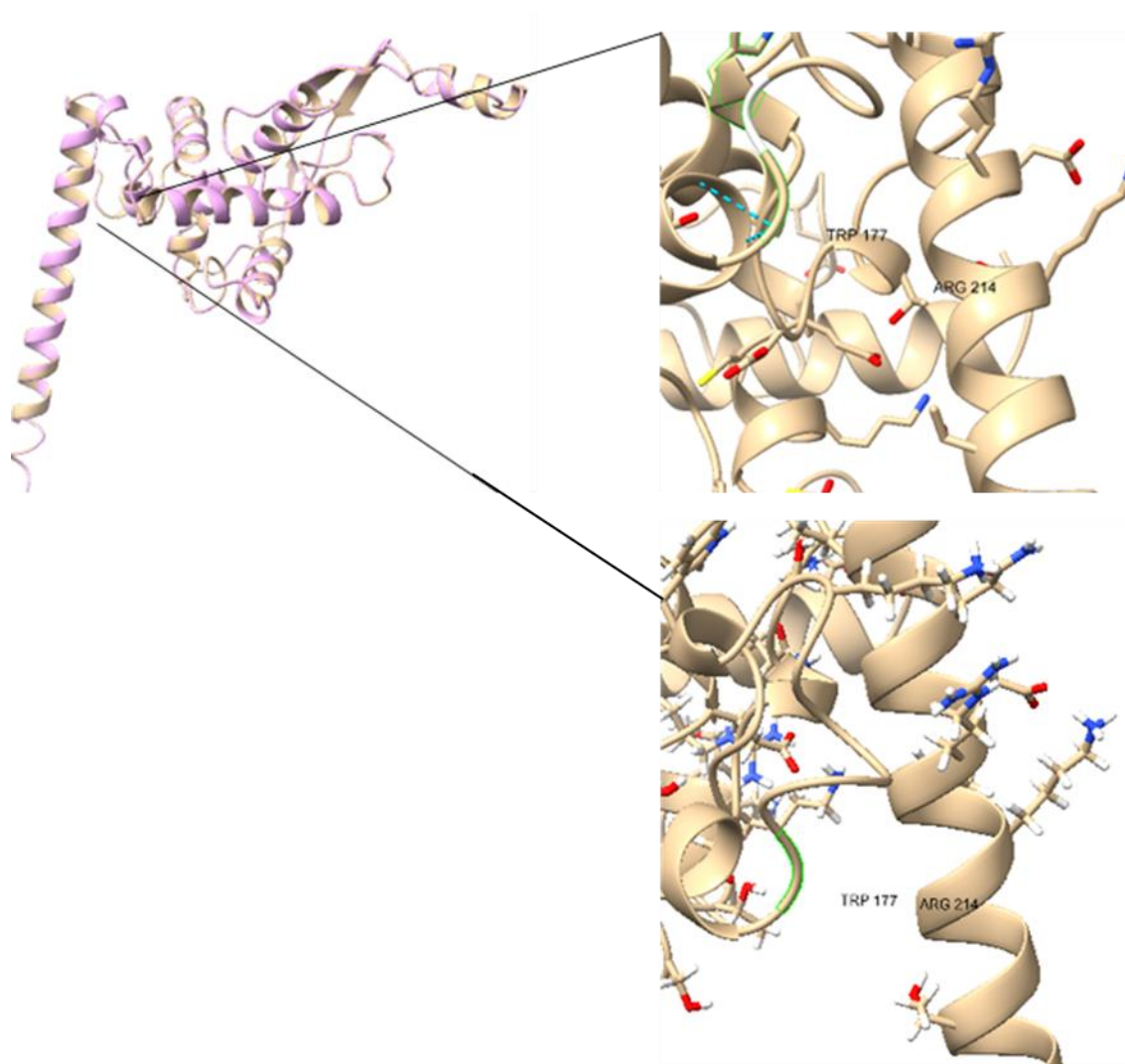


Figure S5 Refined ASGV coat protein (CP) structure (pink) superimposed on the unrefined AlphaFold-predicted structure (gold) reveals minimal differences in the overall protein conformation. The Ramachandran plot (bottom center) of the refined model indicates improved stereochemical quality, with 0% of 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.

			$\alpha 1$				$\alpha 2$
LM651239_Bamboo_HP					TT		
LM651239_Bamboo_HP	1	MSLEDV	IQARRHRVG	VLLMKT	HIDPAK	LLTVFPFEG	KEGESFECRELYLLLCNHYCK
LN901413_apple_Shopi	1	MSLEDV	IQARRHRVG	VLLMKT	HIDPAK	LLTVFPFEG	KEGESFECRELYLLLCNHYCK
LM651243_Bamboo_Kang	1	MSLEDV	IQARRHRVG	VLLMKT	HIDPAK	LLTVFPFEG	KEGESFECRELYLLLCNHYCK
ASGV_apple_ANT1	1	MSLEDV	IQARRHRVG	VLLMKT	HIDPAK	LLTVFPFEG	KEGESFECRELYLLLCNHYCK
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				$\beta 1$	$\beta 2$		$\alpha 3$	$\beta 3$	$\beta 4$
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LN901413_apple_Shopi	61	YLFGN	IAVFGSSDK	QFFAVGF	DTPPVHYNLT	TTTPE	KEGESFECRELYLLLCNHYCK		
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ASGV_Palampur1	61	YLFGN	IAVFGSSDK	QFFAVGF	DTPPVHYNLT	TTTPE	KEGESFECRELYLLLCNHYCK		
ASGV_Palampur2	61	YLFGN	IAVFGSSDK	QFFAVGF	DTPPVHYNLT	TTTPE	KEGESFECRELYLLLCNHYCK		
LN823992_apple_Kangr	61	YLFGN	IAVFGSSDK	QFFAVGF	DTPPVHYNLT	TTTPE	KEGESFECRELYLLLCNHYCK		
ASGV2_apple_Fulwamal	61	YLFGN	IAVFGSSDK	QFFAVGF	DTPPVHYNLT	TTTPE	KEGESFECRELYLLLCNHYCK		
LN901427_apple_HP	61	YLFGN	IAVFGSSDK	QFFAVGF	DTPPVHYNLT	TTTPE	KEGESFECRELYLLLCNHYCK		
LN901425_Apple_Kalpa	61	YLFGN	IAVFGSSDK	QFFAVGF	DTPPVHYNLT	TTTPE	KEGESFECRELYLLLCNHYCK		
LN559085_apple_Kangr	61	YLFGN	IAVFGSSDK	QFFAVGF	DTPPVHYNLT	TTTPE	KEGESFECRELYLLLCNHYCK		
LN823987_apple_Kangr	61	YLFGN	IAVFGSSDK	QFFAVGF	DTPPVHYNLT	TTTPE	KEGESFECRELYLLLCNHYCK		
FN393044_Pear_HP	61	YLFGN	IAVFGSSDK	QFFAVGF	DTPPVHYNLT	TTTPE	KEGESFECRELYLLLCNHYCK		
LN901422_Apple_Chamb	61	YLFGN	IAVFGSSDK	QFFAVGF	DTPPVHYNLT	TTTPE	KEGESFECRELYLLLCNHYCK		
LN823995_apple_Kangr	61	YLFGN	IAVFGSSDK	QFFAVGF	DTPPVHYNLT	TTTPE	KEGESFECRELYLLLCNHYCK		
LN901439_apple_Palam	61	YLFGN	IAVFGSSDK	QFFAVGF	DTPPVHYNLT	TTTPE	KEGESFECRELYLLLCNHYCK		
LN901428_apple_HP	61	YLFGN	IAVFGSSDK	QFFAVGF	DTPPVHYNLT	TTTPE	KEGESFECRELYLLLCNHYCK		

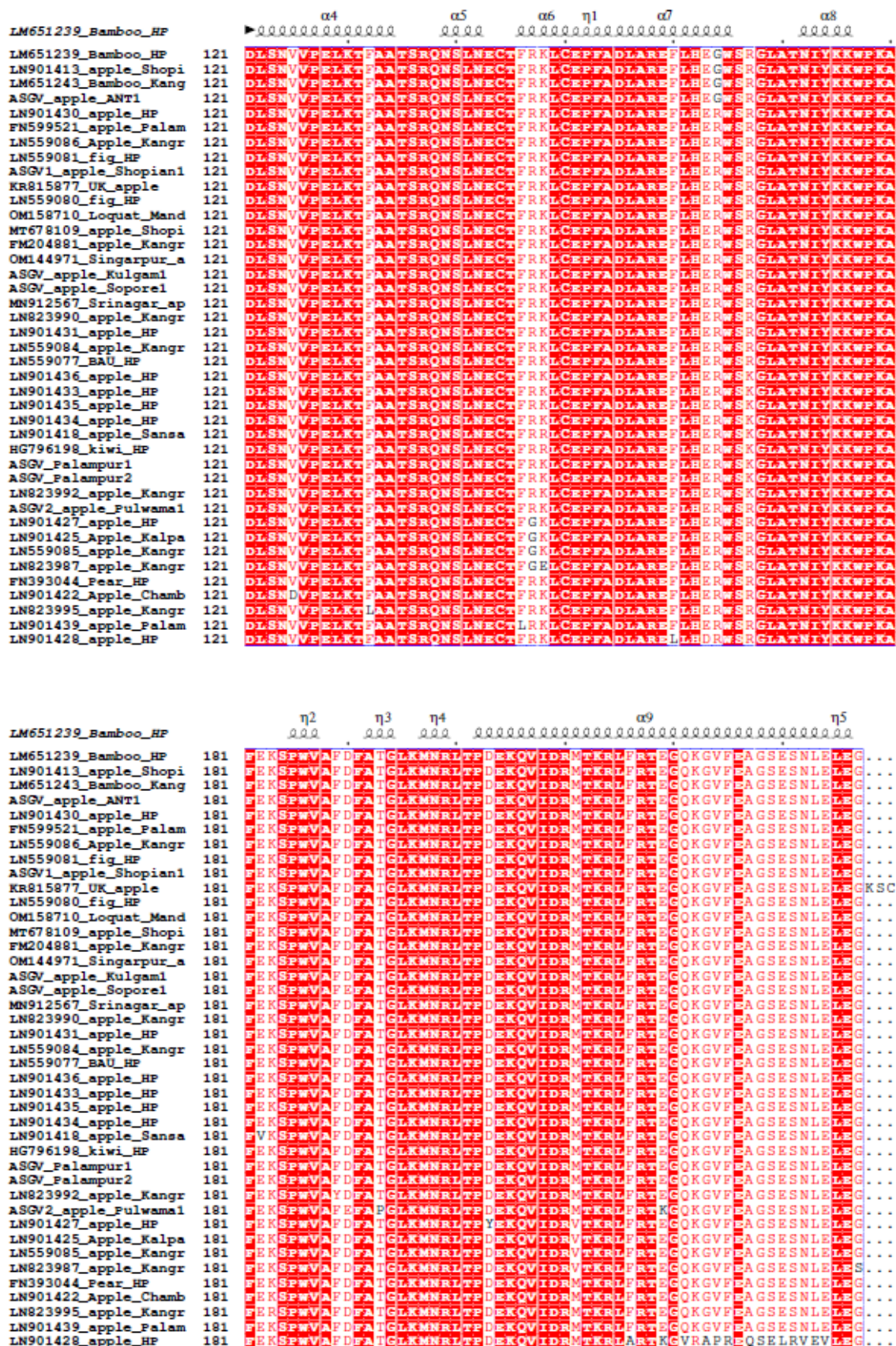


Figure S6: Multiple sequence alignment of ASGV CP sequences showing predominance of type II (E-A) variants among Indian isolates, with a few type III (Q-E) variants identified from Himachal Pradesh and Jammu & Kashmir.

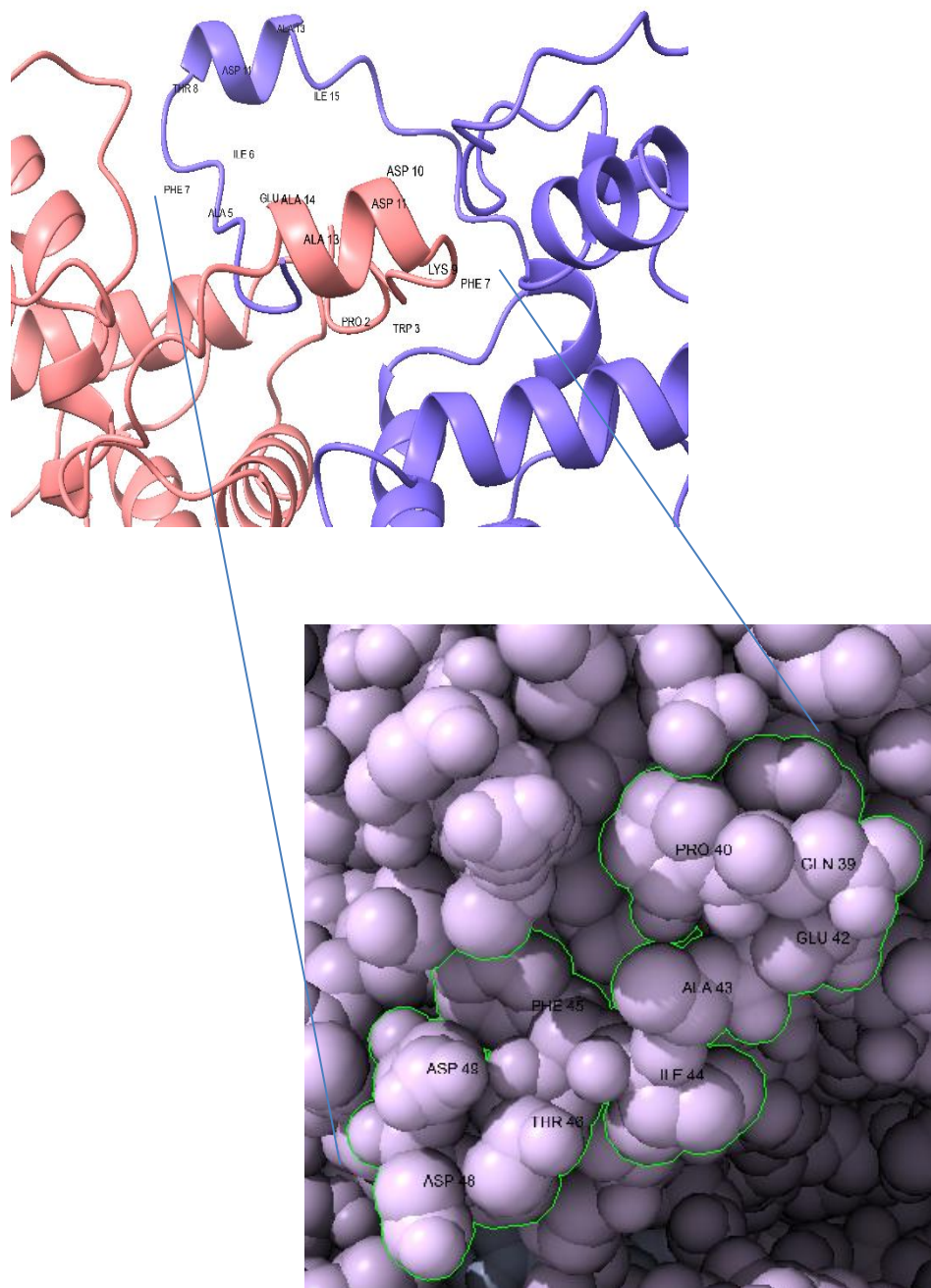


Figure S7: Structural localization of bamboo mosaic virus (BaMV) coat protein residues 36-48 within the assembled virion architecture. Surface-rendered and magnified views demonstrate that residues corresponding to this region remain externally exposed during CP-CP interactions, supporting their accessibility and potential antigenic relevance.