Indian Journal of Biochemistry & Biophysics
Vol. 63, June 2026, pp. 700-710
DOI: 10.56042/ijbb.v63i6.9407

Conformational and docking analyses of the frenatin 3 peptide, an inhibitor of nNOS enzyme and a ligand for Ca^{2+}-calmodulin

Mohd Shafique*

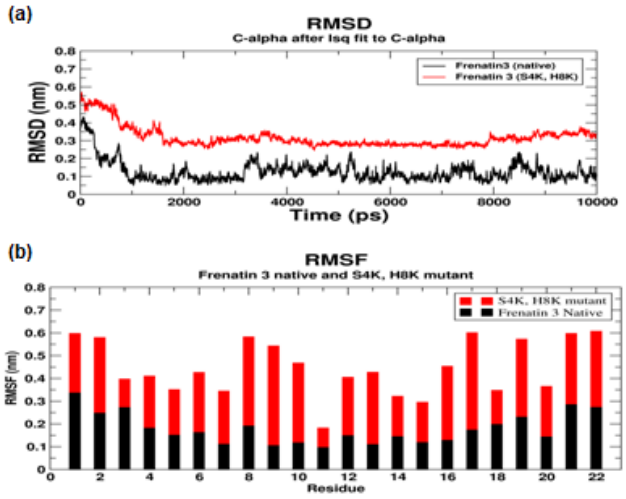
Department of Biophysics, Panjab University, U.T.-160 014, Chandigarh, India

Received 08 April 2024; *revised 29 April 2026*

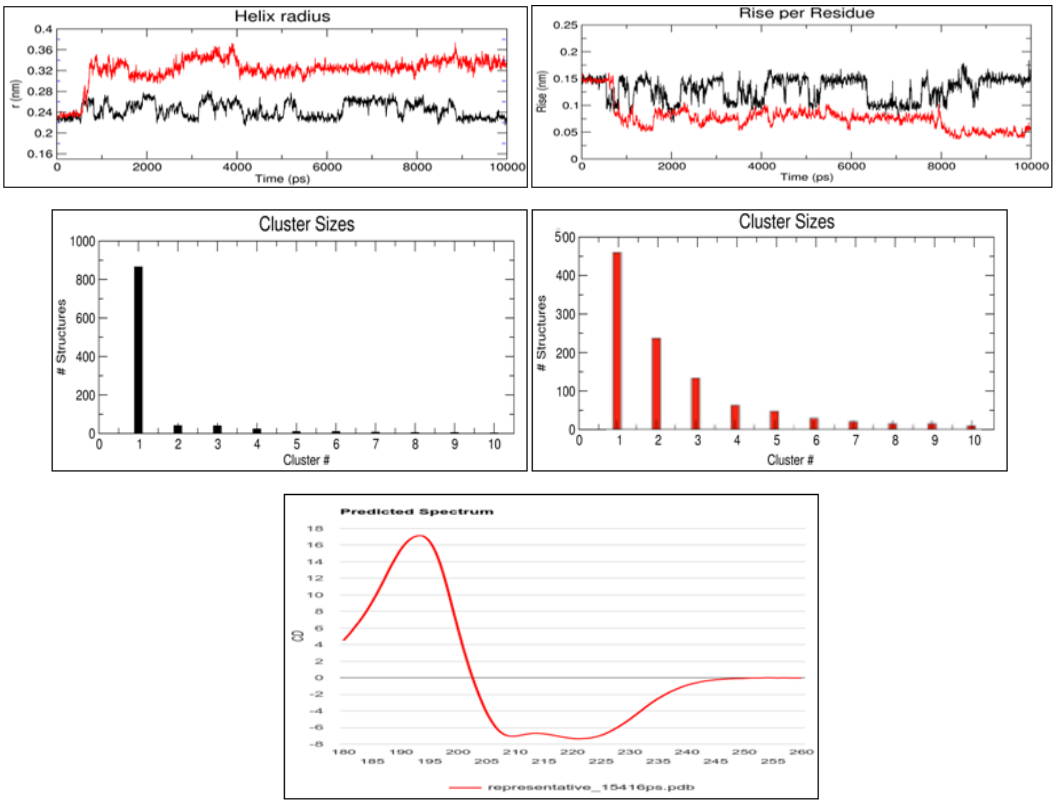
Supplementary data

Suppl. Table 1 — The data depicted the solvation free energy change for frenatin 3 and all studied peptides calculated from ProWaVE sever. The change in solvation free energy for the Lys rich peptide has found to be high among all the studied systems

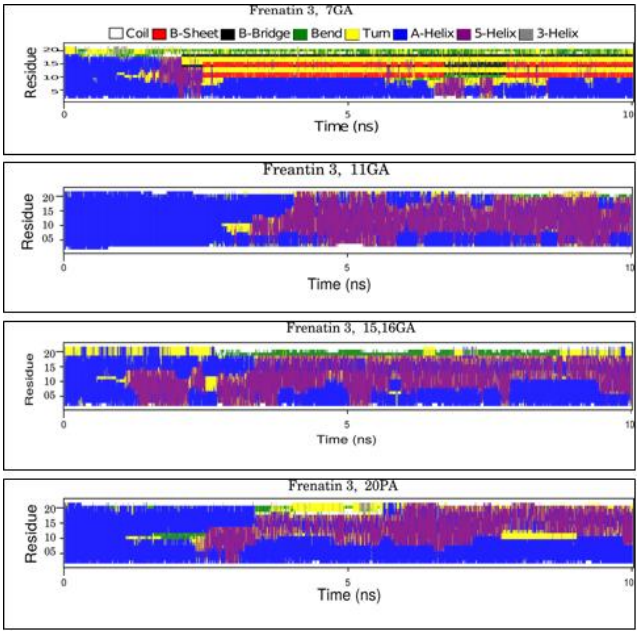
Peptide	Solvation Free Energy change (ΔG_{solv})
Freantin 3 native	-7.5386
Lys rich mutant (S4K, H8K)	-264.5713
G7A	2.5534
G11A	-10.8234
G16A	-0.3215
G15,16A	7.8040
P20A	-15.9304



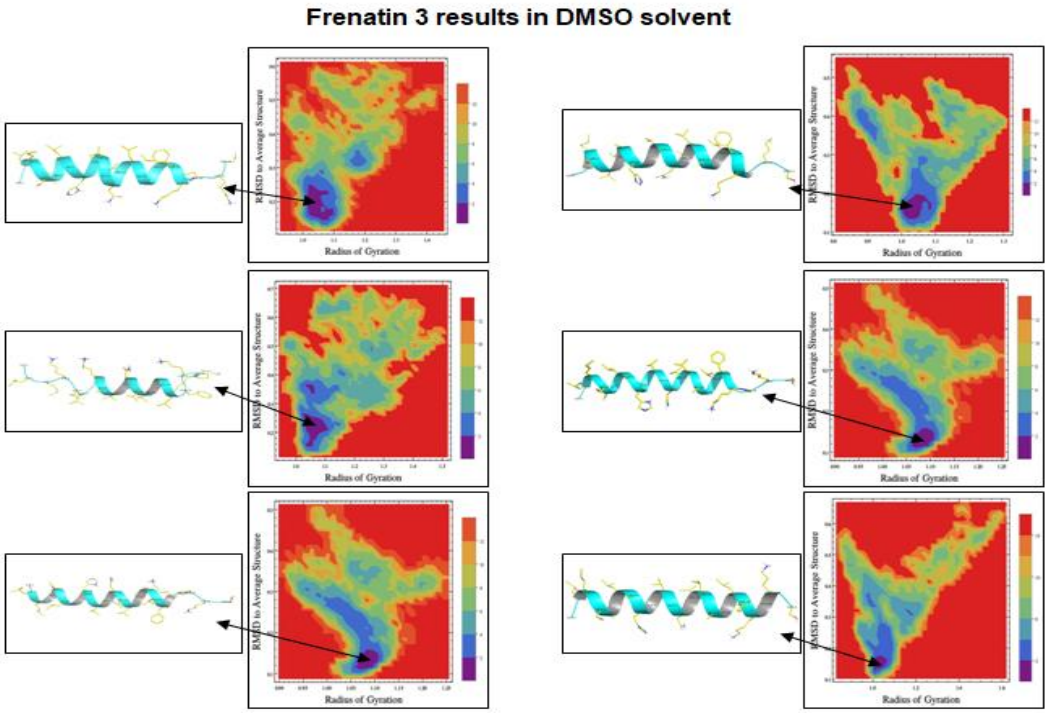
Suppl. Fig S1 — (a) The RMSD of native and frenatin 3 peptide (S4K, H8K) peptides and the simulated trajectory, seems more stable as compared to the trajectory for native peptide, b) the root means square fluctuations) revealed that the native frenatin 3 peptide (black) has lower fluctuations than Lys rich mutant (red)



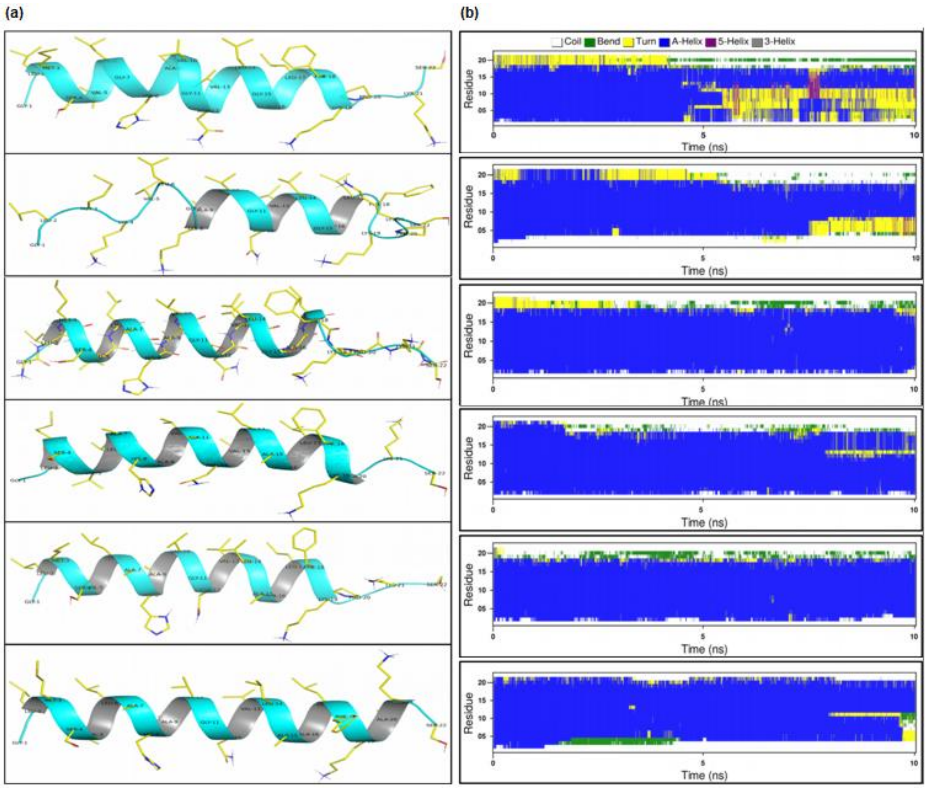
Suppl. Fig S2 — (*Upper left to right*) Evolution of helix during simulations, the rise per residue plot for frenatin 3 and S4K, H8K mutant. (lower panel) Cluster size plots for frenatin 3 (Black) and S4K, H8K mutant (Red). The predicted CD spectra of native peptide



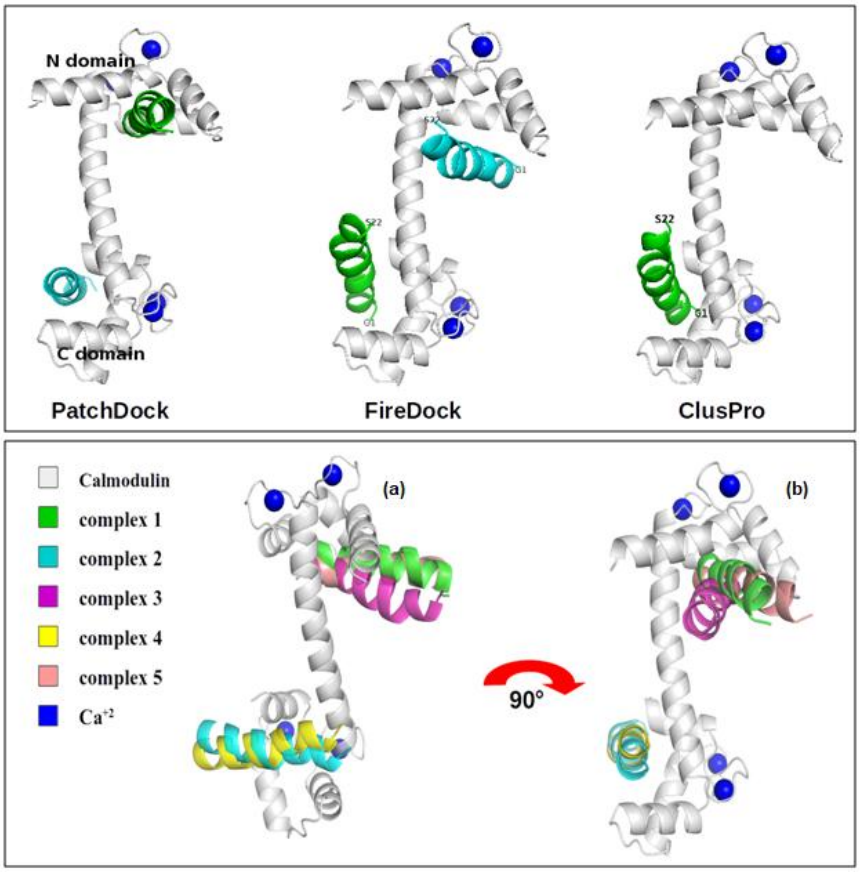
Suppl. Fig. S3 — The DSSP plots results (in explicit water) shown for frenatin 3 with mutations 7GA, 11 GA, 15-16 GA, 16GA, 20PA (up side to downward). It is clear that helical content increases with increase in alanine content, hence the flexibility in the conformation provided by glycine residues. Interestingly, the π-helix (purple in colour) content increased with Ala residues in the peptide



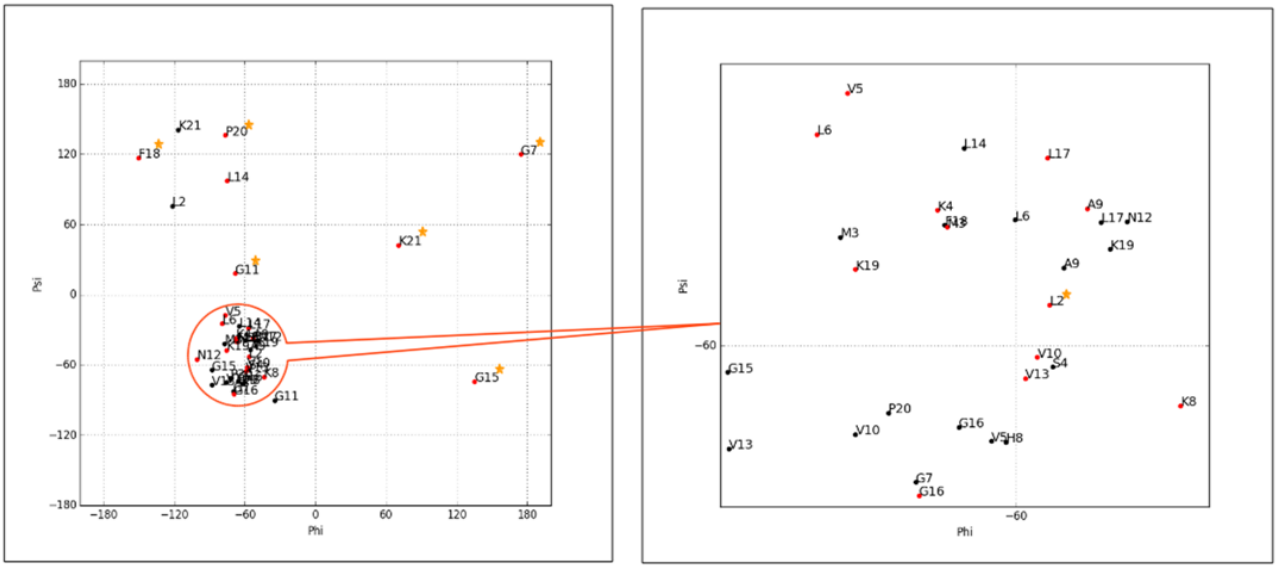
Suppl. Fig. S4 — FEL for the frenatin 3 native, S4K, H8K mutant, 7GA, 15,16GA, 16GA and 20PA mutants in DMSO solvent (at low dielectric constant, ε)



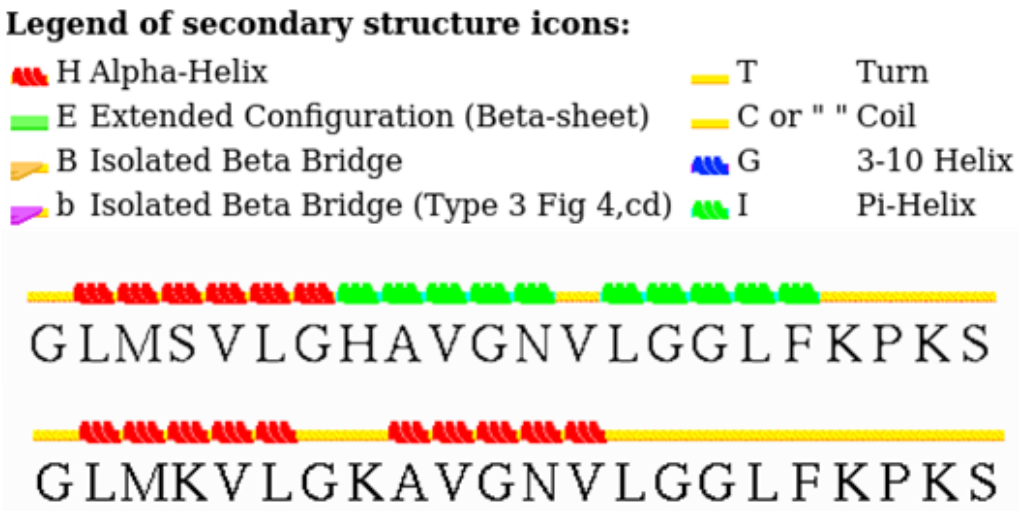
Suppl. Fig. S5: — (a) The cartoon diagrams for representative conformations of frenatin 3 peptide and its studied mutants (upside to lower; see table 1); and (b) DSSP plot. The results belong to molecular dynamics study in low dielectric solvent, DMSO



Suppl. Fig. S6 — The graphical representation for the docked results obtained from online docking servers. The cartoon diagrams shown in green (rank 1) and cyan (rank 2) for native frenatin 3 - calmodulin complex



Suppl. Fig. S7 — Ramachandran plot for representative structures of frenatin 3 native and its S4K, H8K mutant after 10 ns of simulation in water. The most occupied region is expanded for clarity and the plot shows the preference of individual residues in both of peptides. The residues with asterisk have changed their location in the Ramachandran map

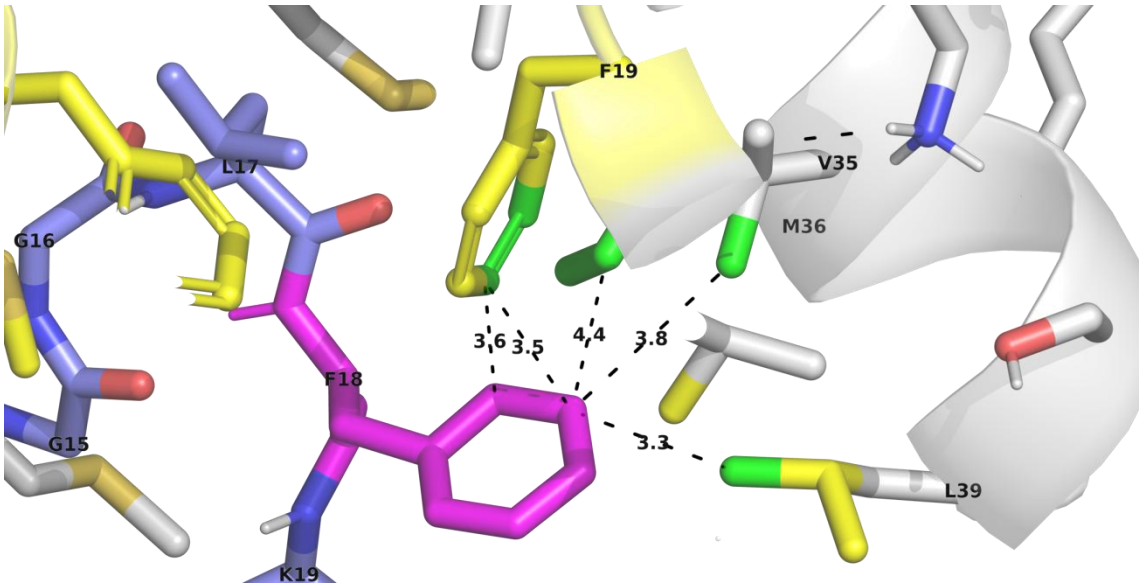


Suppl. Fig. S8 — Stride analysis

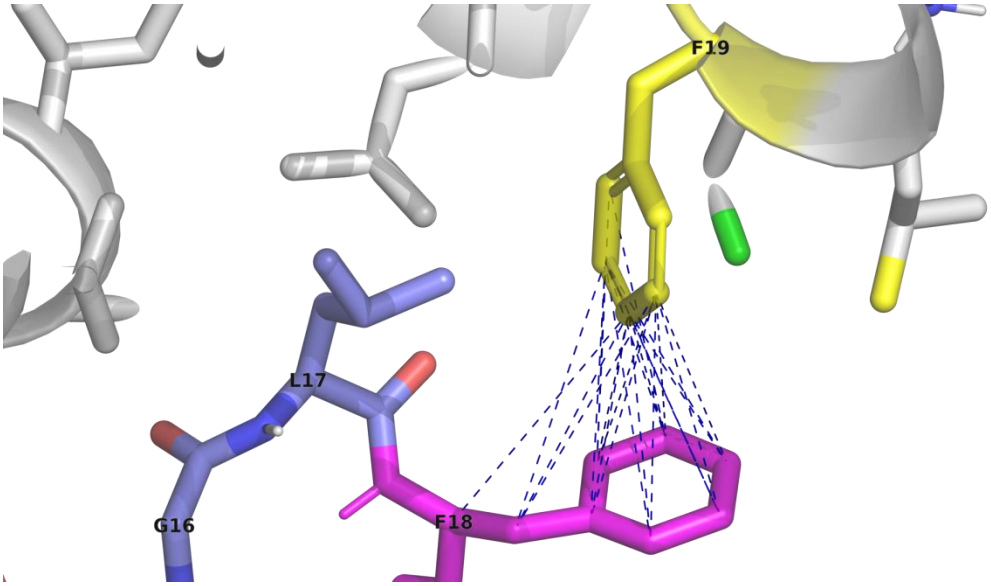
Results for docking studies

The molecular docking was performed to study the peptide-calmodulin interactions. The study was done by using various online available tools viz. Z-dock, PatchDock, FireDock, HawkDock, ClusPro, and Gramm-X. The multiple docking tools were used to support the docking results and the favoured docking site at the receptor (calmodulin). It is clear from the figure given below, the binding site for frenatin 3 peptide lies at the EF hand motif C-domain of calmodulin.

(a)



(b)



Suppl. Fig. S9: (a) the hydrophobic interactions between aromatic ring of F^{18} (magenta) with residues of Ca+-calmodulin protein residues viz. F^{19}, V^{35}, and L^{39}; and (b) pi-pi interactions between F^{18} of frenatin 3 and F^{19} of calmodulin protein