

Different terminal capping of tau PHF6 displays distinct effects on the structural stability of membrane-bound PHF6 fibril and fibril-induced membrane disruption

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1 | Introduction

Abnormal aggregation of tau into amyloid fibrils is closely linked to Alzheimer's disease and other neurodegenerative diseases [1]. Tau interacting with membranes is experimentally reported to promote protein fibrillization and disrupt membrane integrity [2], thus causing neurotoxicity. The hexapeptide PHF6 is the crucial fibril-nucleating core and widely serves as a model system to study the aggregation of tau proteins [3], while the effect of terminal capping on its interaction with membranes and the underlying mechanisms remain elusive. Herein, we perform extensive all-atom molecular dynamics simulations to investigate the interactions between four capping variants of PHF6 fibrils and membranes, as well as the resulting fibril stabilization and membrane disruption.

2 | Materials & Methods

Four capping variants of PHF6 peptides:

System 1: Ac-PHF6

System 2: Ac-PHF6-NH₂

System 3: PHF6

System 4: PHF6-NH₂

System: Fibril | Fibril + Membrane

Method: MD in NPT ensemble, 1 μ s

Force Field: AMBER99SB-ILDN

3 | Results

The fibrillar structures of PHF6 capping variants display different stability in solution

Ranking of stability:

Ac-PHF6-NH₂ > Ac-PHF6
 >>> PHF6 ~ PHF6-NH₂
 (2 > 1 >>> 3 ~ 4)

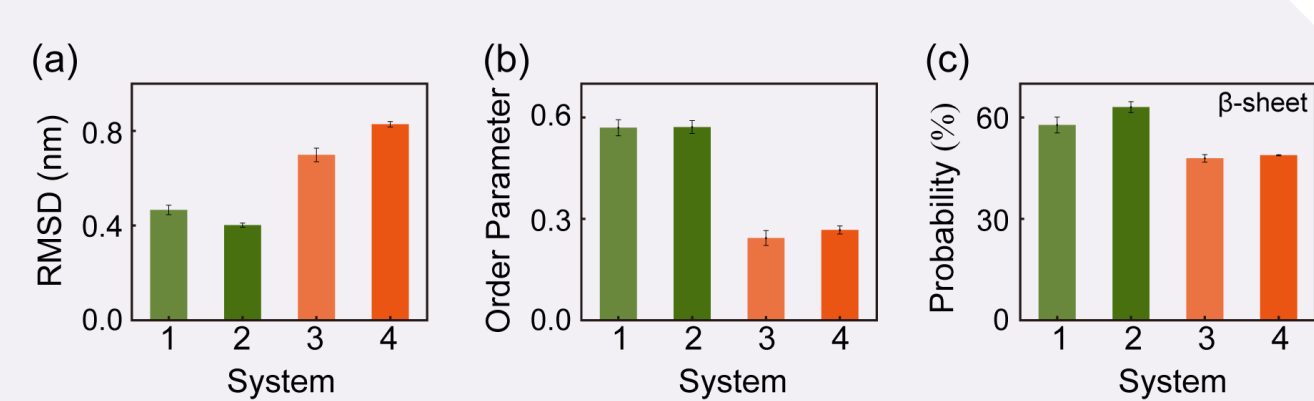


Fig. 1. Structural stability of four performed PHF6 fibrils in solution.

The structural stability and order of all capping variants increase in the presence of membrane

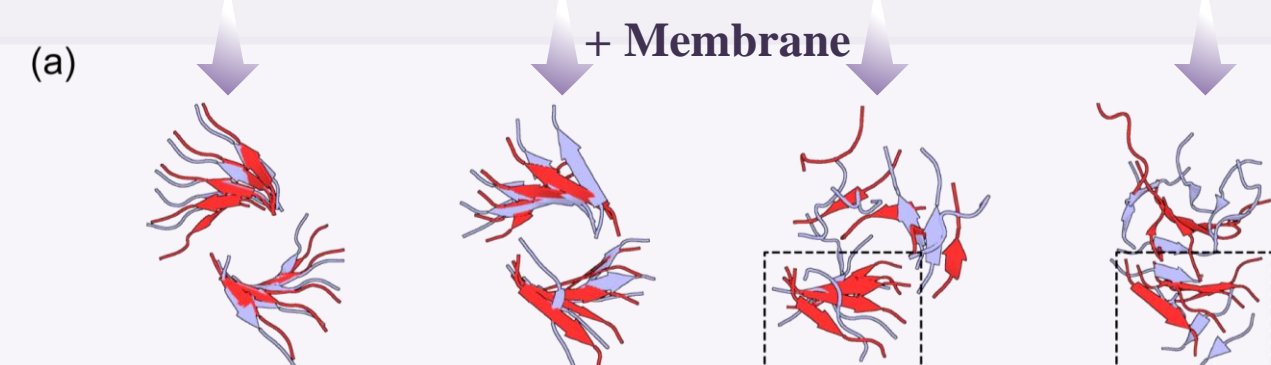


Fig. 2. Comparison of fibril stability in solution (blue) and in the membrane environment (red).

System	RMSD (nm)	β -sheet probability (%)	Order parameter	
Ac-PHF6	\	0.4660 \pm 0.0007	57.8 \pm 3.2	0.5695 \pm 0.0996
	+membrane	0.3729 \pm 0.0006	60.2 \pm 2.5	0.5715 \pm 0.0822
Ac-PHF6-NH ₂	\	0.4020 \pm 0.0007	63.1 \pm 2.6	0.5715 \pm 0.0848
	+membrane	0.3556 \pm 0.0005	63.5 \pm 1.4	0.6352 \pm 0.0597
PHF6	\	0.6986 \pm 0.0007	47.9 \pm 4.9	0.2430 \pm 0.0858
	+membrane	0.5872 \pm 0.0004	54.4 \pm 2.5	0.3043 \pm 0.1568
PHF6-NH ₂	\	0.8281 \pm 0.0033	48.8 \pm 4.7	0.2669 \pm 0.0689
	+membrane	0.6000 \pm 0.0017	49.8 \pm 2.6	0.3817 \pm 0.1736

Table 1. Stability for each capping variant of Tau₃₀₆₋₃₁₁ fibril in the absence/presence of membrane.

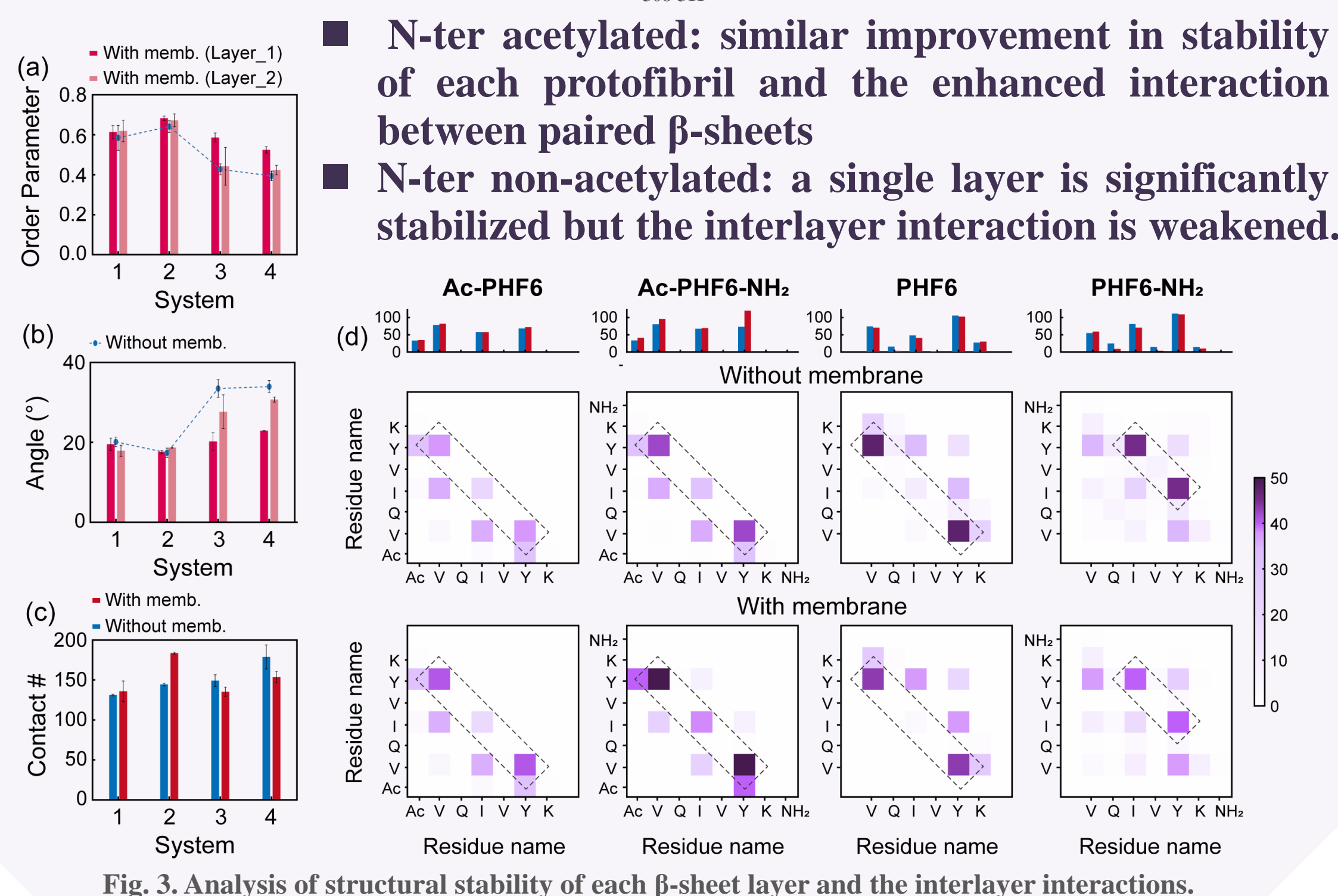


Fig. 3. Analysis of structural stability of each β -sheet layer and the interlayer interactions.

N-terminal modification determines the Distinct Binding Modes of PHF6 on lipid bilayers

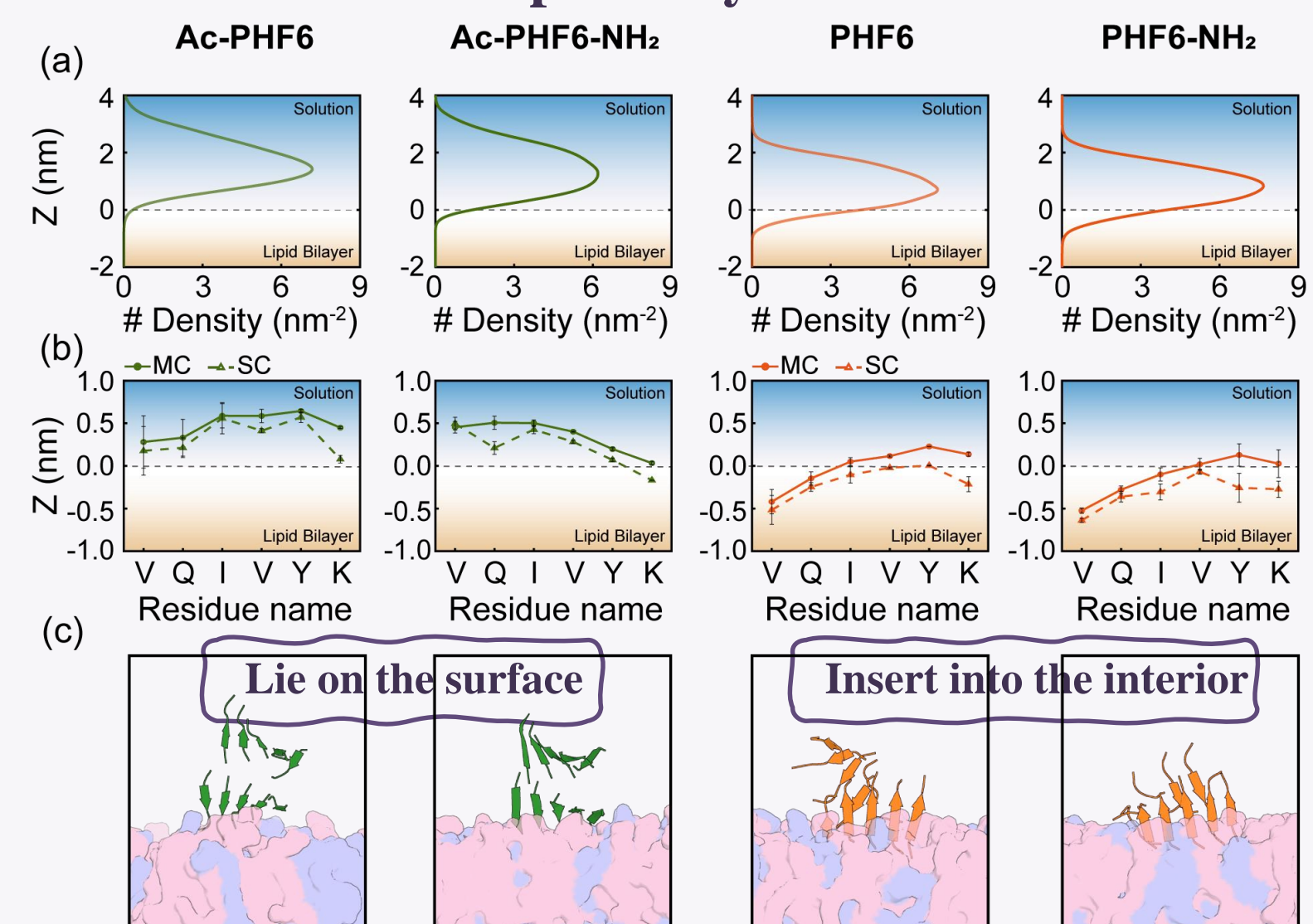


Fig. 4. Binding modes of proteins to membranes in the four systems.

Mechanism: the additional salt-bridges formed between free N-termini and lipid molecules

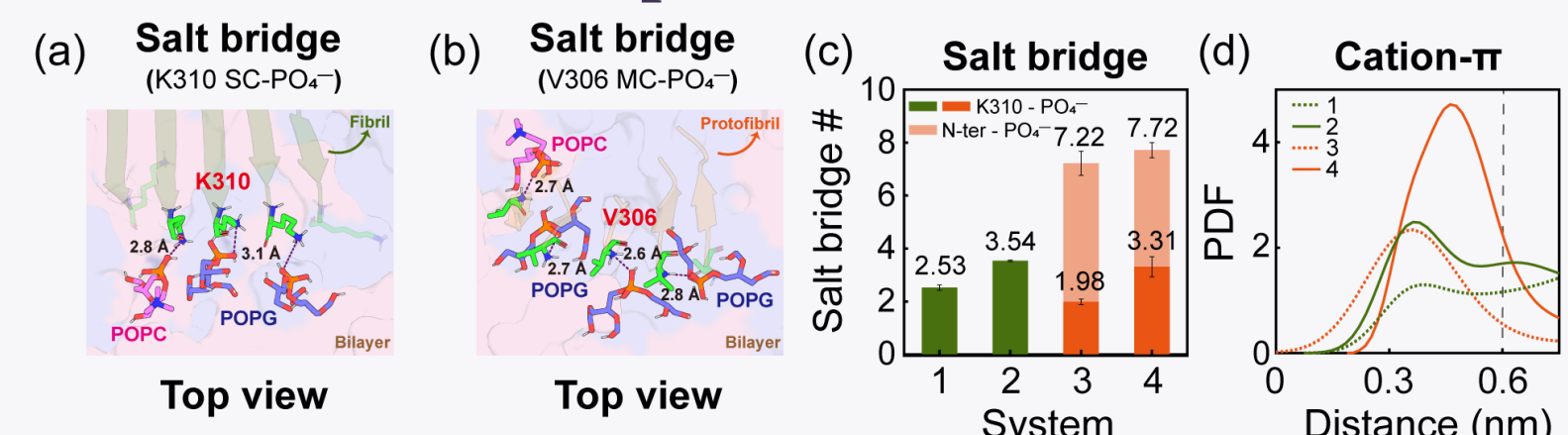


Fig. 5. Analysis of protein-membrane interactions.

Disrupt Membrane

Distinct fibril-membrane interactions result in varying degree of membrane thinning and lipid packing disruption.

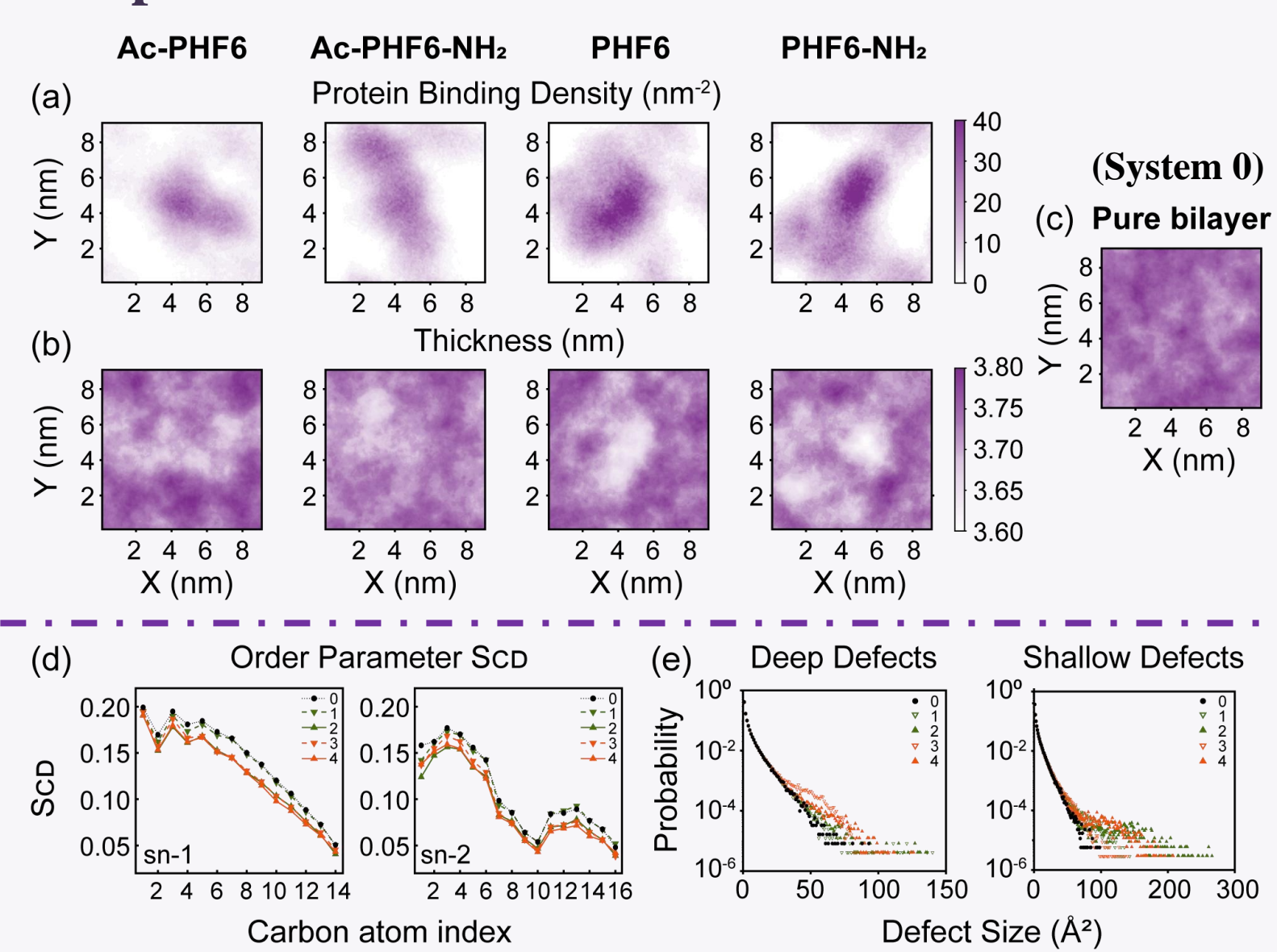


Fig. 6. Influence of protein binding on structural properties of lipid bilayers.

4 | Conclusion

Our simulations emphasize the pivotal role of N-terminal capping in modulating the fibril-membrane binding. N-terminal acetylated fibrils bind on the bilayer surface primarily through lysine-lipid electrostatic attraction, leading to the increased stability of global fibril structures and localized membrane disturbance. Meanwhile, the binding modes of N-terminal free systems, characterized by peptide N-termini inserting into membranes, result in significant stabilization of a single β -sheet layer and more severe membrane disruption.

5 | References

[1] Fitzpatrick, Anthony WP, et al. *Nature* 547.7662 (2017): 185-190.
 [2] Fanni, Adeline M., et al. *Journal of Biological Chemistry* 294.42 (2019): 15304-15317.
 [3] Pretti, Evan, and M. Scott Shell. *Proceedings of the National Academy of Sciences* 120.48 (2023): e2309995120.