

Caveolin Induced Membrane Curvature and Lipid Clustering: Two Sides of the Same Coin?

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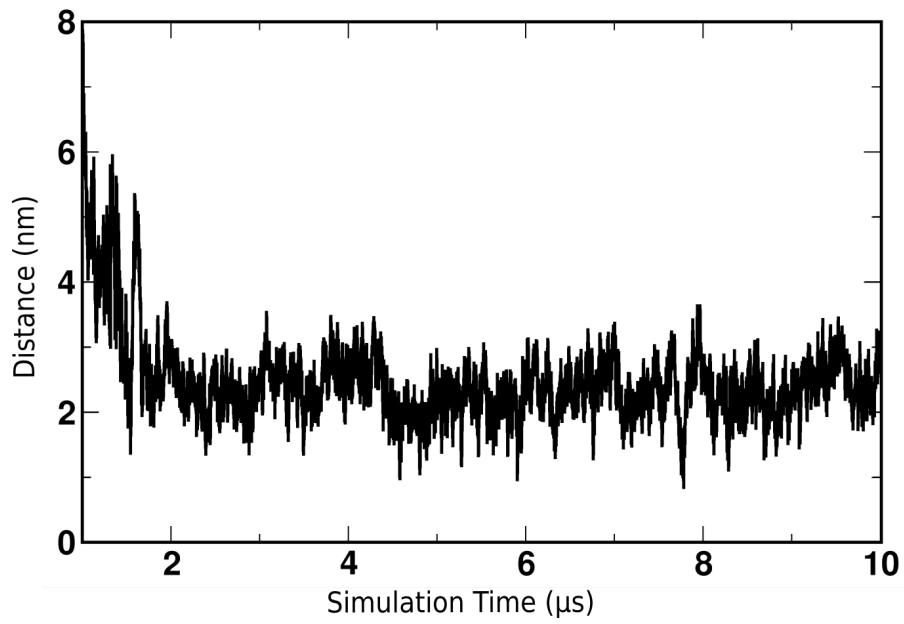


Figure 2: The average depth of insertion and inter-helical angle of the IMD during the course of the simulations.

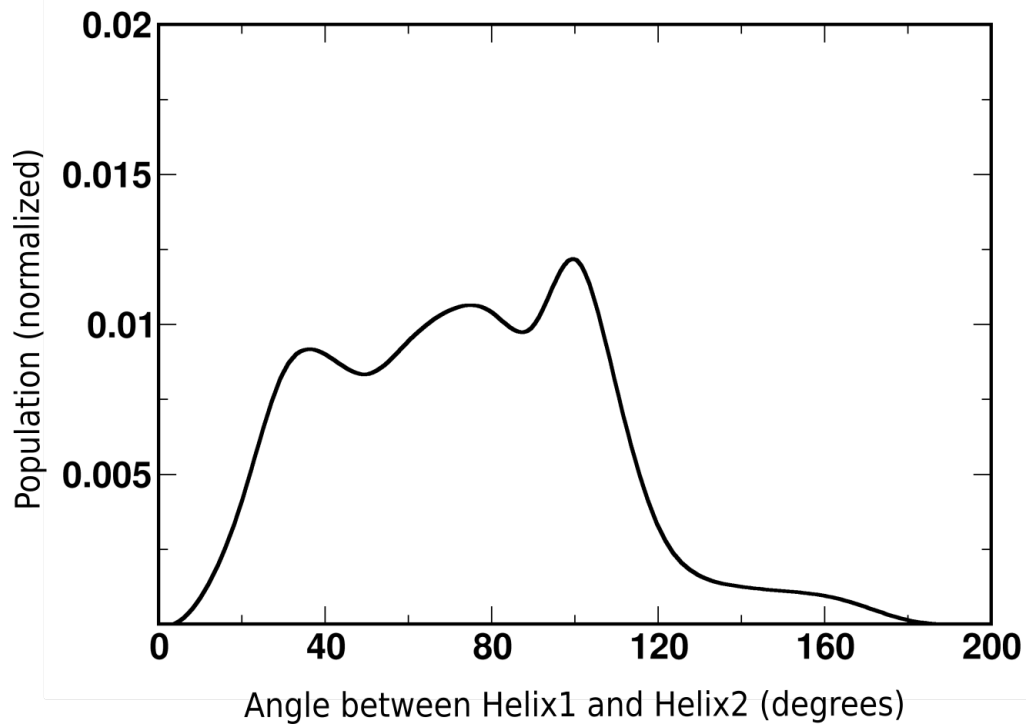


Figure 3: The inter-helical angle between the two helices in the IMD. The normalized population density is calculated from the bound regime in all three simulation sets. The smaller values represent compact conformations and the larger values correspond to open 'banana' shaped conformers.

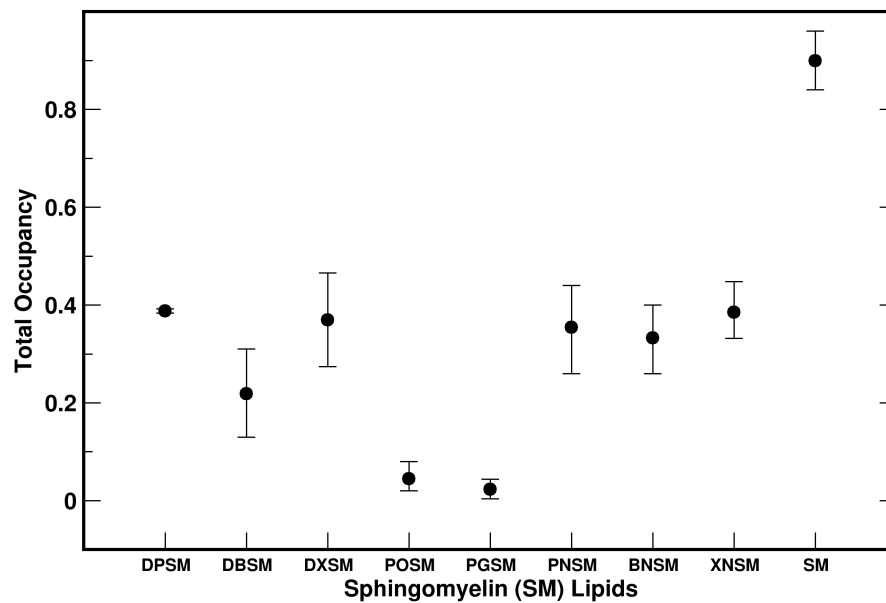


Figure 4: The total occupancy time of cav-1 (as a whole) and different SM lipid types (individually and considered together). The occupancy time is calculated as defined in the Methods section.