

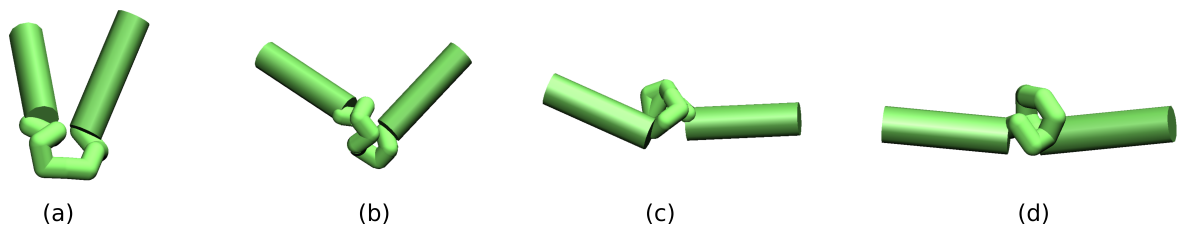
Supporting Information : Differential Membrane Curvature Induced by Distinct Protein Conformers

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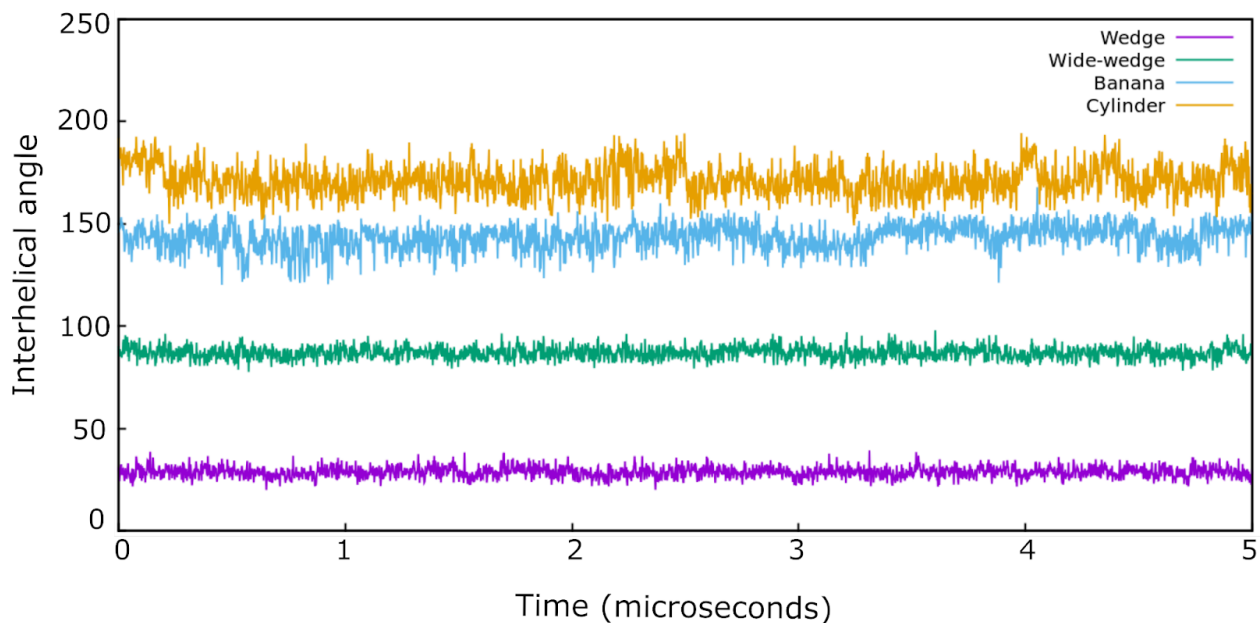
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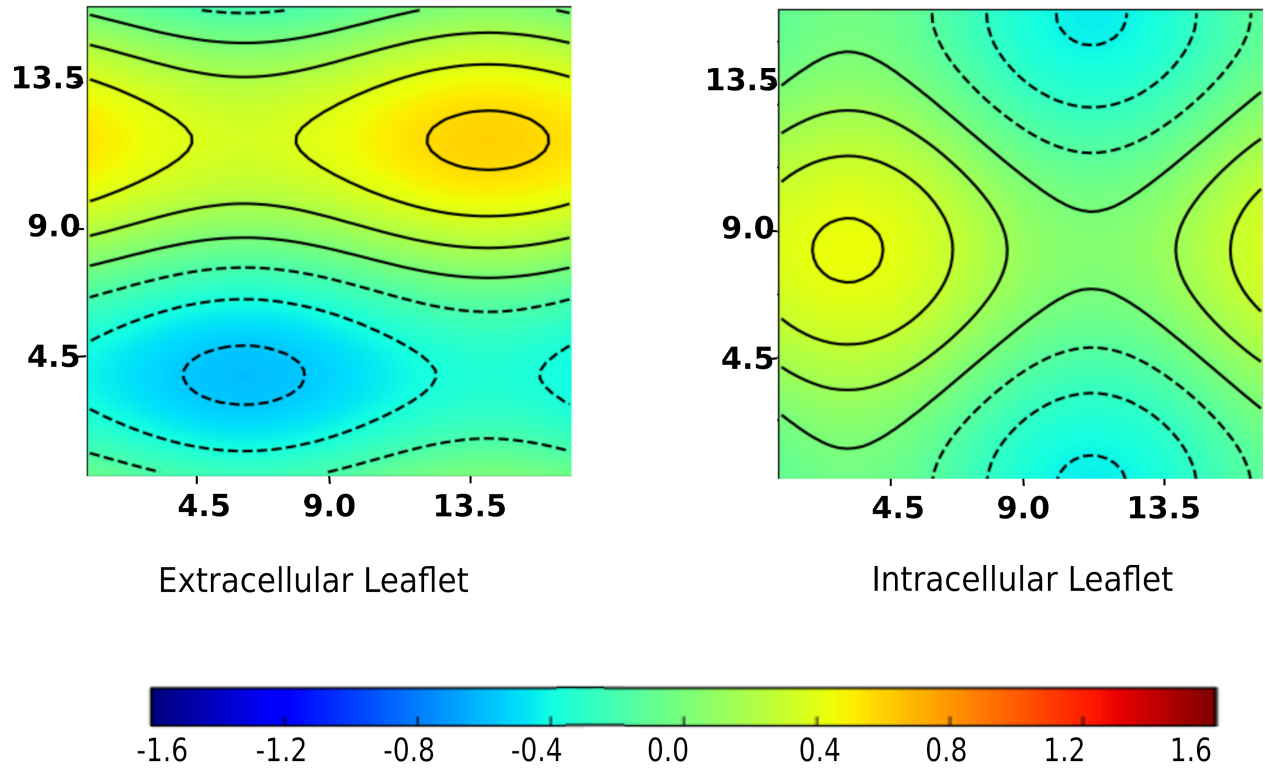
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Supplementary Figure 1: Representative snapshots of the four caveolin-1 conformers considered: (a) wedge, (b) wide-wedge, (c) banana, and (d) cylindrical conformers.

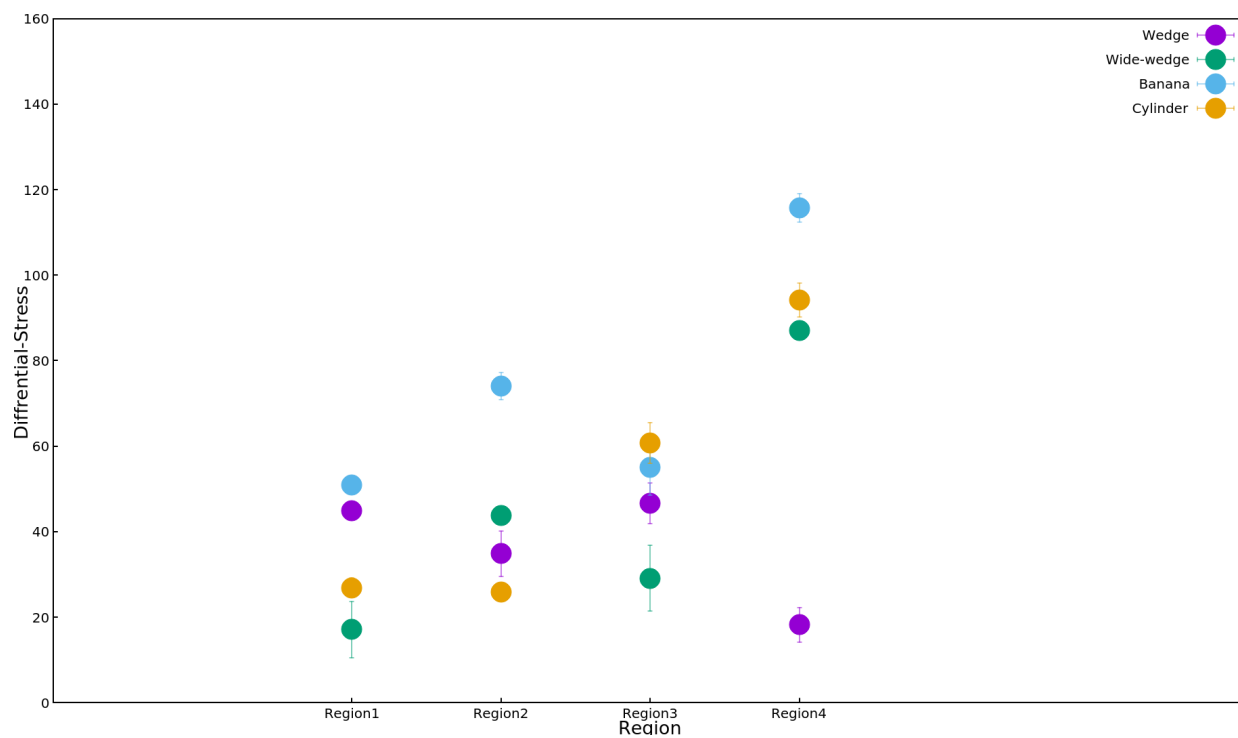


Supplementary Figure 2: Time evolution of the inter-helical angle in caveolin-1. The plots correspond to the four conformers: wedge (purple), wide-wedge (green), banana (blue) and cylindrical (yellow) conformers.

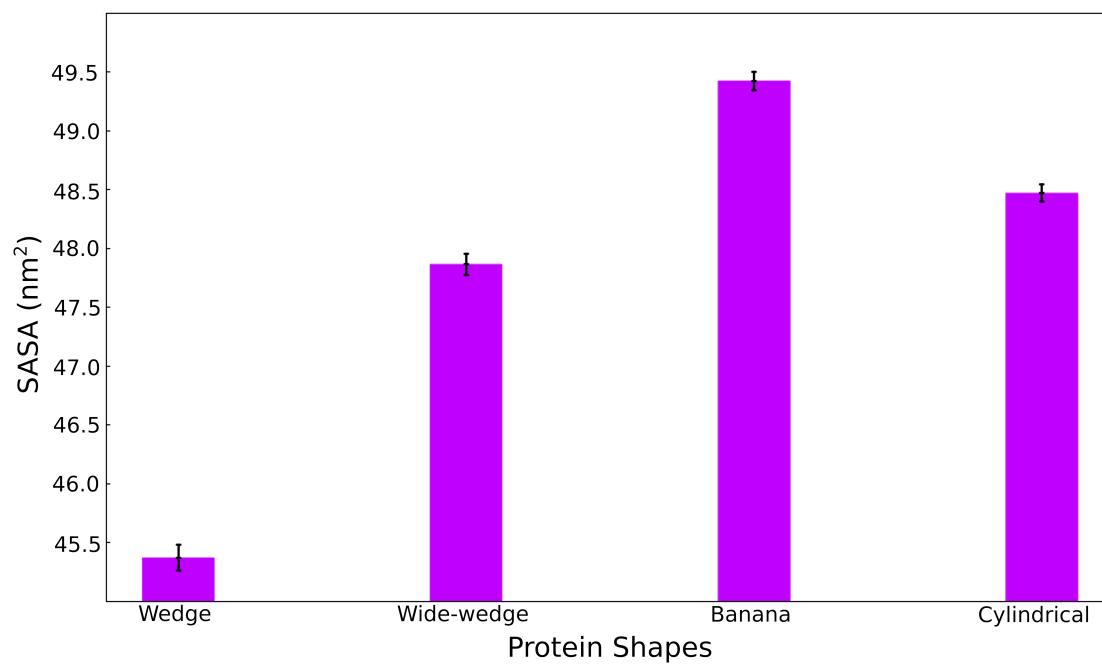


Curvature ($\times 10^{-2} \text{nm}^{-1}$)

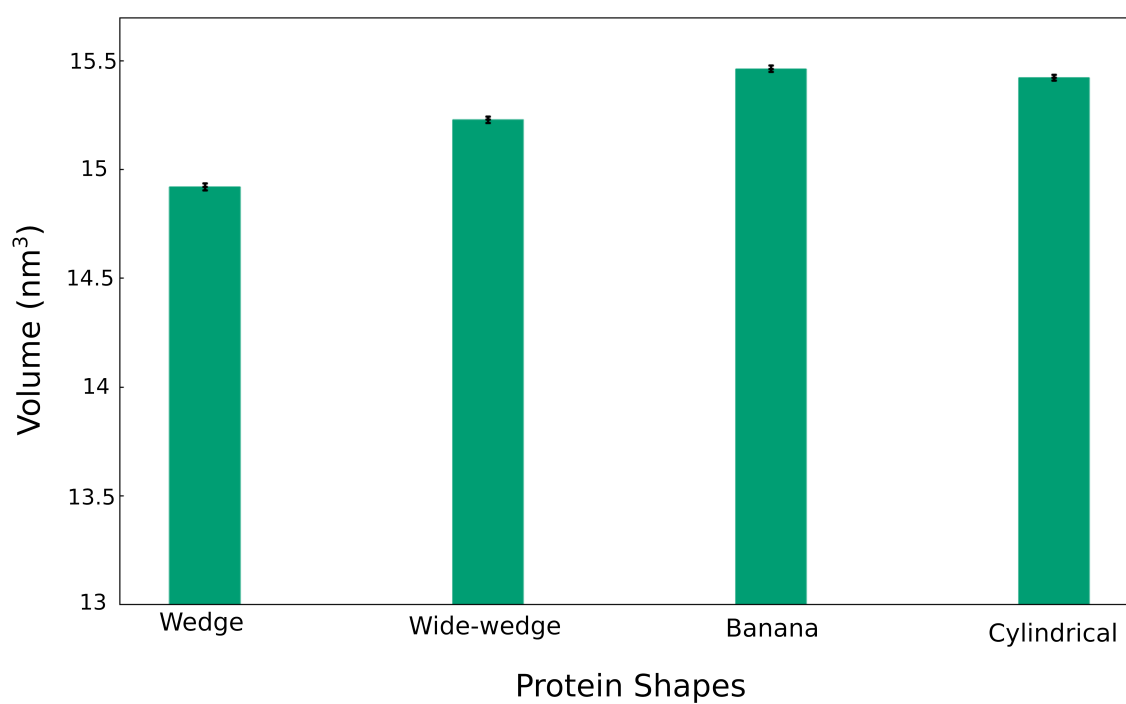
Supplementary Figure 3: The mean curvature of the membrane in the absence of the bound protein. Left panel shows the membrane curvature for the extracellular leaflet and the right panel corresponds to the membrane curvature for the intracellular leaflet.



Supplementary Figure 4: Differential net stress between the leaflets of the membrane. The lipid bilayer is divided into four regions based on the pressure profile of the membrane: (1) chain-termini (or bilayer core), (2) chain-core, (3) glycerol backbone, and (4) lipid head-groups.



Supplementary Figure 5: The solvent accessible surface areas of the protein in the wedge, wide-wedge, banana, cylindrical conformations, averaged over the time course of the simulations.



Supplementary Figure 6: The volume of the protein calculated for wedge, wide-wedge, banana, cylindrical conformations averaged over the time course of the simulations.