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Quantifying membrane perturbation induced by membrane-remodeling proteins

Large-scale membrane remodeling events, such as budding, fusion, fission, and pore formation, help maintain cellular homeostasis. Integral and peripheral membrane proteins play crucial roles in these remodeling events. By using coarse-grained molecular dynamics simulations, we quantify the protein-induced membrane perturbation fields. By employing the continuum Helfrich model and incorporating a protein-induced distance-dependent spontaneous curvature tensor, we capture the intrinsic curvature properties of remodeling proteins and associated emergent effects at the mesoscale.

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