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Curvature Forces in Membrane Lipid-Protein Interactions[1]
MICHAEL F. BROWN, Departments of Chemistry and Biochemistry and Physics, University of Arizona, Tucson AZ 85721 — Membrane protein conformational changes, folding, and stability may all involve elastic deformation of the bilayer. Non-specific properties of the bilayer play a significant role in modulating protein conformational energetics. A flexible-surface model (FSM) describes the balance of curvature and hydrophobic forces in lipid-protein interactions. The FSM describes elastic coupling of membrane lipids to integral membrane proteins. Curvature and hydrophobic matching to the lipid bilayer entails a stress field that explains membrane protein stability. Rhodopsin provides an important example, where solid-state NMR and FTIR spectroscopy characterize the energy landscape of the dynamically activated receptor. Time-resolved UV-visible and FTIR spectroscopic studies show how membrane lipids affect the metarhodopsin equilibrium due to non-specific material properties. Influences of bilayer thickness, nonlamellar-forming lipids, detergents, and osmotic stress on rhodopsin function are all explained by the new biomembrane model. By contrast, the older fluid-mosaic model fails to account for such effects on membrane protein activity. According to the FSM proteins are regulated by membrane lipids whose spontaneous curvature most closely matches the activated state within the lipid membrane.

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