1060-92-231 **Benjamin R Capraro***, Department of Chemistry, University of Pennsylvania, 231 S 34th St, Philadelphia, PA 19104, and **Aiwei Tian**, **Michael C Heinrich** and **Tobias Baumgart**.

Coupling of membrane shape and local protein and lipid composition and its relevance to intracellular trafficking.

The sorting of lipids and proteins in cellular membrane sorting centers, such as the trans-Golgi network and the endocytic recycling compartment, lies at the heart of fundamental biological phenomena such as organelle homeostasis and membrane signaling. We study biophysical contributions to the sorting of membrane components, using experimental lipid model membranes, and analytical thermodynamic and membrane elasticity theory. We will present measurements of thermodynamically reversible membrane curvature sensing for peripherally binding membrane proteins, e.g., showing cholera toxin subunit B to partition away from regions of high positive membrane curvature, and the Epsin N-terminal homology domain to enrich in such regions. While we find that ideally diluted lipids are not significantly sorted in curvature gradients, consistent with theory and simulation, in ternary mixture lipid vesicles, lipid sorting is observed to be amplified by cooperative interactions. Two regimes of amplified curvature demixing are distinguished: the weak segregation limit in compositions near a demixing phase boundary, and the strong segregation limit, deep in the coexistence region. We will describe both regimes by means of thermodynamic models and also discuss dynamic aspects of curvature sorting. (Received March 30, 2010)