

Abstract Submitted
for the MAR11 Meeting of
The American Physical Society

The driving forces of membrane remodeling by non-intrinsically curved proteins CHRISTOPHER J. RYAN, University of California, Berkeley, JEANNE C. STACHOWIAK, Sandia National Laboratories, EVA M. SCHMID, DANIEL A. FLETCHER, PHILLIP L. GEISSLER, University of California, Berkeley — Membranes are dynamically remodeled during numerous processes essential to cells. Among the most well-studied effectors of this remodeling are BAR family proteins, which are small and have a banana-like intrinsic curvature that senses, forms, and stabilizes curved membranes without expending energy as ATP or GTP. Recent experiments in reduced systems have shown, however, that small proteins that feature no such intrinsic curvature can similarly cluster at and dramatically remodel membranes. These proteins have no distinguishing features other than their size and their membrane-binding sites, and the dominant effect that is driving curvature is not well understood. Here, we present a coarse-grained simulation study that captures protein steric and binding effects as well as membrane fluctuations at large scales. We use this model to systematically test for the role that such attributes play in the resulting dynamics and equilibrium structures of remodeling processes that feature this motif.

Christopher J. Ryan
University of California, Berkeley

Date submitted: 19 Nov 2010

Electronic form version 1.4