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Membrane shape instabilities induced by BAR domain proteins[1]

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Membrane curvature has developed into a forefront of membrane biophysics. Numerous proteins involved in membrane curvature sensing and membrane curvature generation have recently been discovered, including proteins containing the crescent-shaped BAR domain as membrane binding and shaping module. Accordingly, the structure determination of these proteins and their multimeric complexes is increasingly well-understood. Substantially less understood, however, are thermodynamic and kinetic aspects and the detailed mechanisms of how these proteins interact with membranes in a curvature-dependent manner. New experimental approaches need to be combined with established techniques to be able to fill in these missing details. Here we use model membrane systems in combination with a variety of biophysical techniques to characterize mechanistic aspects of BAR domain protein function. This includes a characterization of membrane curvature sensing and membrane generation. We also establish kinetic and thermodynamic aspects of BAR protein dimerization in solution, and investigate kinetic aspects of membrane binding. We present two new approaches to investigate membrane shape instabilities and demonstrate that membrane shape instabilities can be controlled by protein binding and lateral membrane tension.

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