Shape deformations of biomembranes are controlled by various proteins. Many of these proteins contain a binding module known as the BAR (Bin-Amphiphysin-Rvs) domain, which consists of a banana-shaped dimer. We have revealed anisotropic spontaneous curvatures of banana-shaped domains induce assembly of the protein rods and change membrane shapes using implicit-solvent meshless membrane simulations. The protein rods cooperatively induce tubulation as well as formation of percolated rod networks, striped bumps, polygonal tubes, and polyhedral vesicles [1-6].

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1/Cside
1/Crod

Tubulation from Flat Membrane [3,6]

Tubulation via percolated network at high rod density $\phi_{\text{rod}} = 0.4$

Percolated networks are transiently formed at $C_{\text{side}} < 0$. Acceleration of tubulation by addition of small inclusions with isotropic spontaneous curvature

Membrane and Protein Models
Membrane particles, which have orientational degrees of freedom, self-assemble to form one-layer membrane. A protein rod is modeled by a linear chain of membrane particles. No direct attractive interactions are taken between the rods. The rods are assembled by membrane-mediated interactions.

Membrane Structures Induced by Two Types of Protein Rods [5]

Tubulation via percolated network at high rod density $\phi_{\text{rod}} = 0.4$

Two types of rods of opposite curvatures form straight and stripe bumps. Positive tension stabilizes stripe assembly.

Rod Self-assembly on Vesicle [1-6]

acceleration of tubulation by addition of small inclusions with isotropic spontaneous curvature