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. A small spontaneous curvature perpendicular to the rod stabilizes a percolated network structure and alters the tubulation dynamics.

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.

Self-Assembly of Protein Rods [1,2] (\(C_{side} = 0\))

Membrane tube
Low rod density \(\phi_{rod} = 0.166\)

The rods assemble via two directional phase separations unlike a conventional 2D phase separation.

High rod density \(\phi_{rod} = 0.5\)

Triangular and buckled discoidal tubes are formed.

Vesicle
\(\phi_{rod} = 0.3\)

Polyhedral vesicles are formed.

\(\phi_{rod} = 0.4\)

Elliptic disk

Triangular hosohedron

Triangular prism

Membrane Rupture [4]
high-genus vesicles resulting from rupture

Vesicles are ruptured for high density of stiff proteins, rapid protein adhesion, and/or low edge tension.

Tubulation from Flat Membrane [3]

Low rod density \(\phi_{rod} = 0.1\)

Tubules are formed via rod assembly. A little dependence on \(C_{side}\).

High rod density \(\phi_{rod} = 0.4\)

Percolated networks are transiently formed at \(C_{side} < 0\). It suppresses tubule protrusion.