



A. The 3D map of the FtsH•HflK/C complex in detergent-free DIBMA polymer, showing two copies of FtsH (pink) surrounded by 12 copies of HflK (blue) and HflC (cyan), resembling a nautilus-like assembly at 12 Å resolution (GSFSC).

B. The 3D structure of two copies of FtsH (pink) insulated by 24 copies of the HflK/C complex in DDM detergent at 4.5 Å resolution (GSFSC). There is an opening that might serve as an entryway for membrane protein degradation.

C. Side view of 2D class averages of the FtsH•HflK/C DIBMA-reconstituted complex, showing the membrane-reshaping effect, with the membrane traveling through the complex and extending beyond with two distinct curvatures.

D. The first structure of adaptor-mediated substrate delivery in the AAA protease family. The structure shows SspB (green) delivering an ssrA-tagged substrate (red) to ClpXP (purple) at 3.7 Å resolution (GSFSC) (Ghanbarpour, A.; et al. *PNAS*, 2021).

E. Overlay of the map and model for ClpXP bound to DHFR.MTX during substrate unfolding. The first structure in the AAA protease family showing how these enzymes unfold their substrate (GSFSC resolution: 2.8 Å) (Ghanbarpour, A.; et al. *Nature Communications*, under revision).