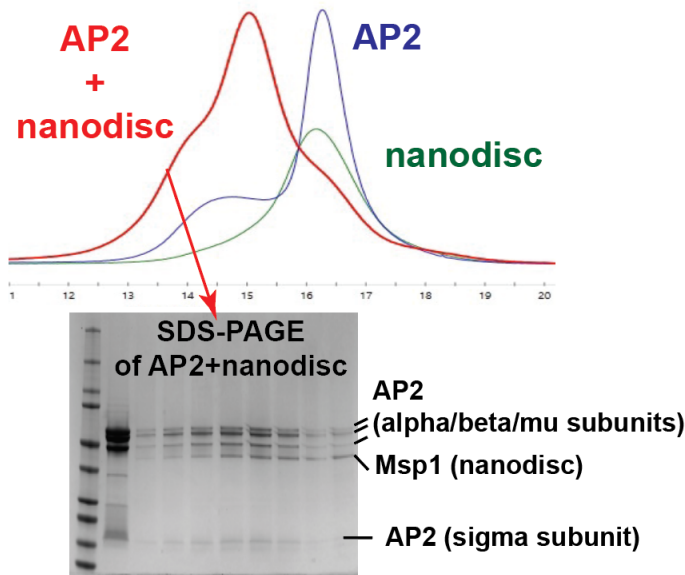


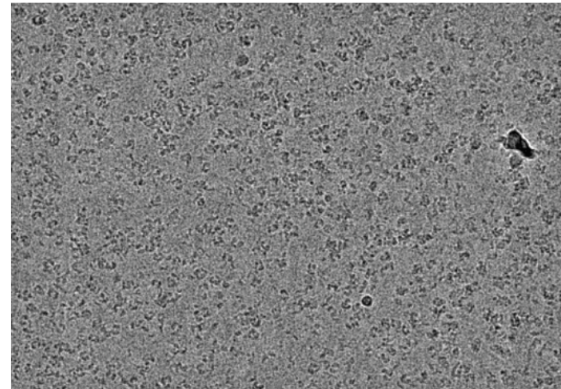
Cryo-EM structures of membrane-engaged protein complexes using lipid nanodiscs

We aim to use nanodiscs as a template to solve high-res structures of peripheral membrane proteins bound to the membrane. We are using the AP2 clathrin-adaptor complex as a test case, as it is known to bind membranes and undergo a large conformational change upon membrane binding. We have purified this complex, collected a test dataset on a 200 keV Talos Arctica, and have used cryoSPARC/ Relion to determine a 3.8 Ang structure. This structure shows AP2 bound to the nanodisc and in the "open", membrane-engaged conformation. However, resolution is still limiting to build an atomic model of the membrane-protein interfaces.

A. Gel filtration Binding Assay

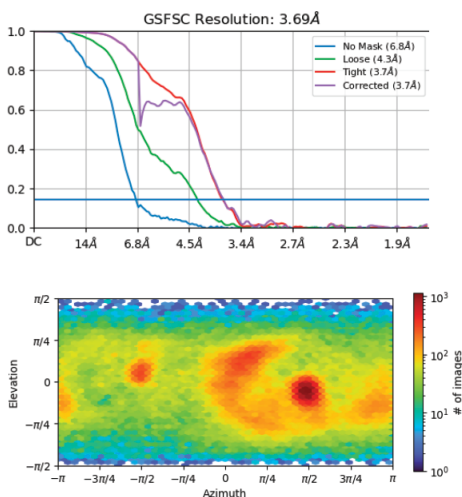


B. Example micrograph



Talos Arctica
K3 DED
45,000x magnification
1.8 um defocus

C. FSC and angular distribution plots



D. cryo-EM map of AP2-nanodisc (note: this is a composite of 3 focused refinements and the nanodisc was filtered separately)

