

Ultrafoil R 1.2/1.3 300 mesh grids with Human ACADL protein were prepared using a Vitrobot instrument at NCCAT using 4.0 blot time. The grid was screened using a 200 kV Glacios with Falcon IV direct detector. Representative low and high resolution images are shown (Figure 1).

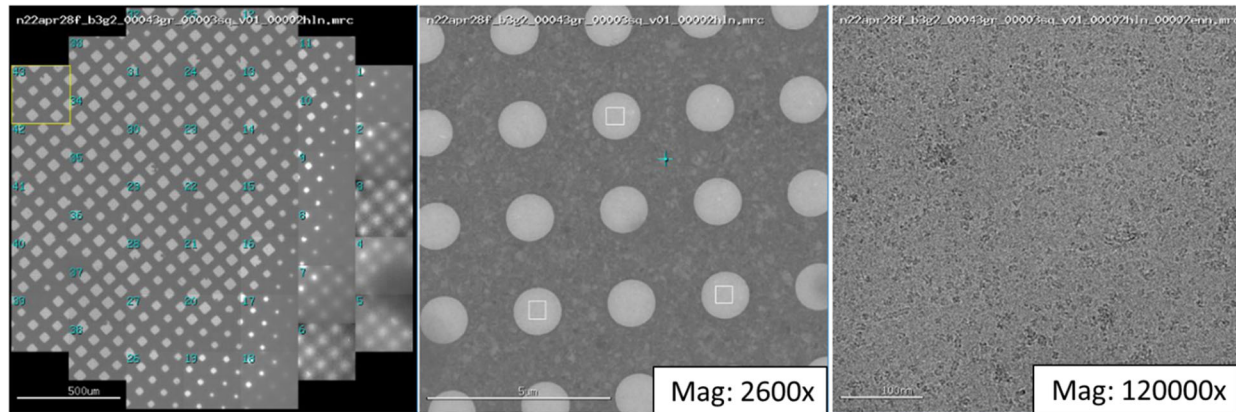


Figure 1. Grid atlas and representative images of the holes (2600x magnification) and high resolution image (120000x magnification) for the grid recorded using Glacios with Falcon IV detector (Alison).

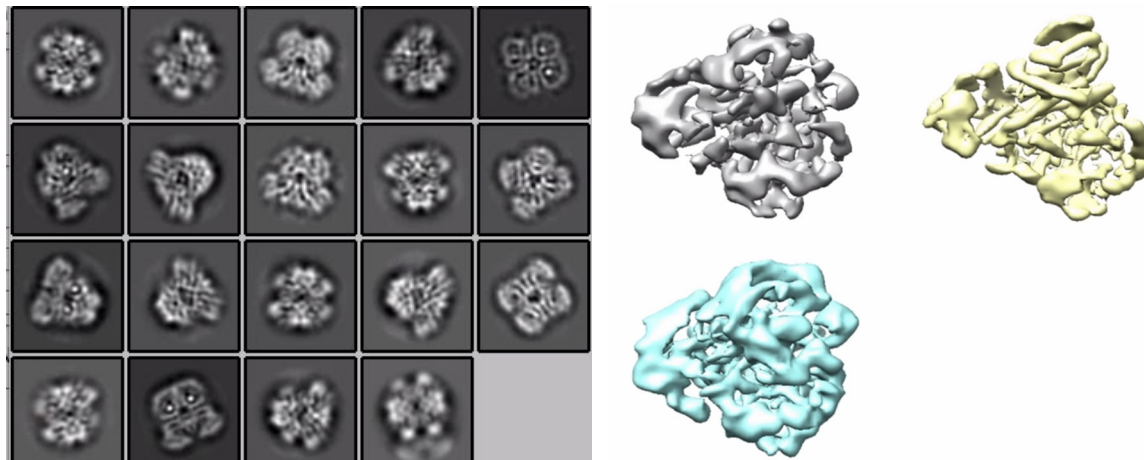


Figure 2. 2D classes and 3D reconstruction. Micrographs were collected on a Titan Krios with Gatan K2 direct electron detector (UT Health) using a different grid prepared using the same protein sample and Vitrobot settings. The data was processed using Relion 4. 232492 particles were picked to determine the 2D classes shown. Multiple 3D reconstructions were generated for distinct conformations of the ACADL homotetramer. The highest resolution reconstruction is 6.5 Angstrom (yellow electron density map) using 70,643 particles.