Ultrafoil R 1.2/1.3 300 mesh grids with Human ACADM protein and S-(+)-3,4-decadienoyl-CoA inhibitor 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 resoution images are shown (Figure 1).

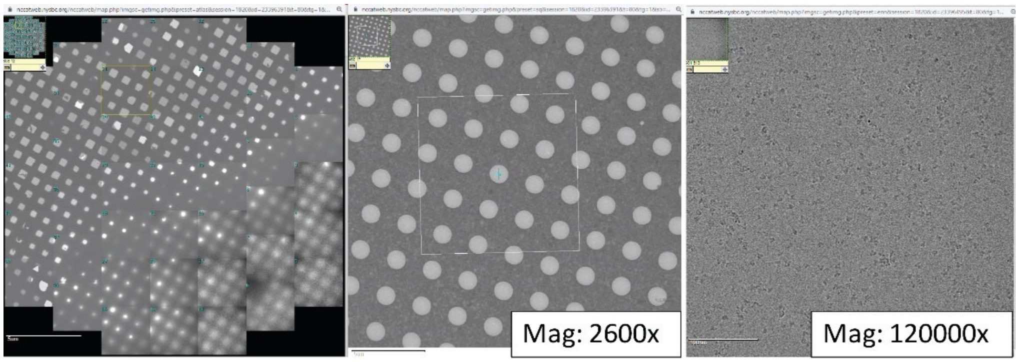

Figure 1. Grid atlas and representative images of the holes (2600x magnification) and high resolution image (120000x magnification) for the grid.

Micrographs were collected on the Glacios overnight using a different grid prepared using the same protein sample and Vitrobot settings. The data was processed using Cryosparc live. 420346 particles were picked and used to generate 2D classes and a 5.62 Å reconstruction (figure 2)

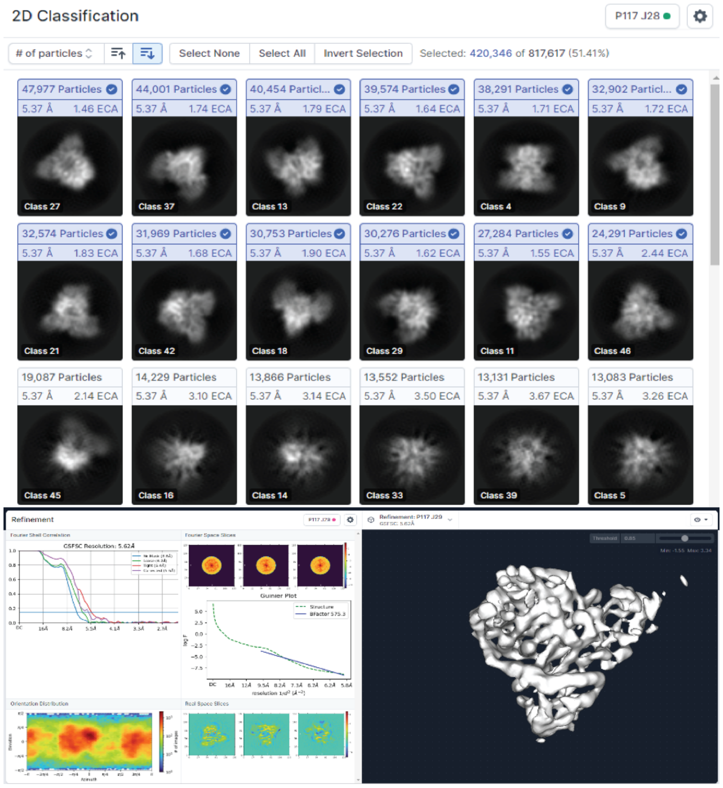

Figure 2. 2D classes and 3D reconstruction determined from 302 micrographs collected on a 200 kEV Glacios with Falcon IV detector.