Preliminary Results

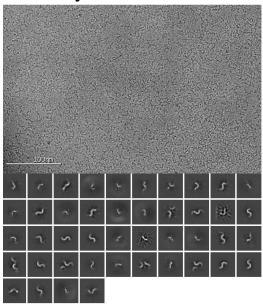


Fig. 1. 2D classes of the minimal Nup358/KLC2 complex. Top: representative cryo-electron micrograph, collected by the PI with the Krios6 cryo-TEM at NYSBC. Bottom: representative 2D classes of 1,355,298 particles from 4188 micrographs.

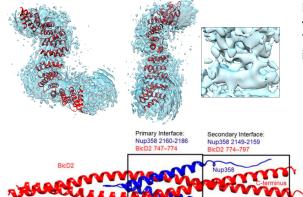
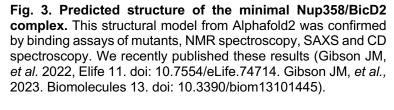
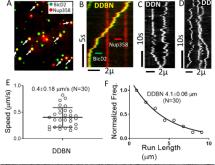


Fig. 2. Cryo-EM map of a minimal KLC2/Nup358 complex which the PI has determined at the NCCAT center; α -helices are visible. The published X-ray structure of KLC2 fused to a short LEWD peptide is docked into the map.





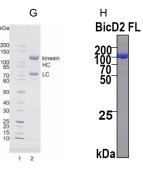


Fig. 4. The dynein/dynactin/BicD2/Nup358 complex (DDBN) moves processively on MT. Top panel: DDBN complex. (A) Yellow dots show that Nup358 (red) binds to BicD2 (green). (B) Kymograph of DDBN. (C,D) Both dynein/dynactin/Nup358 (DDN) and dynein/dynactin (DD) complexes diffuse on MT. (E,F) Speed and run length of the active DDBN complex. (G) SDS-PAGE of Ms kinesin-1 with heavy chains (HC) and light chains (LC).

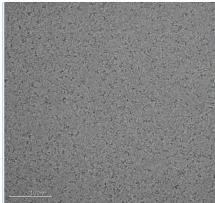


Fig. 5. Representative cryo-electron micrograph of a complex assembled from the full-length kinesin-1 heavy chain and a BicD2 fragment, collected by the PI with the Glacios cryo-TEM at NYSBC.