Preliminary Results

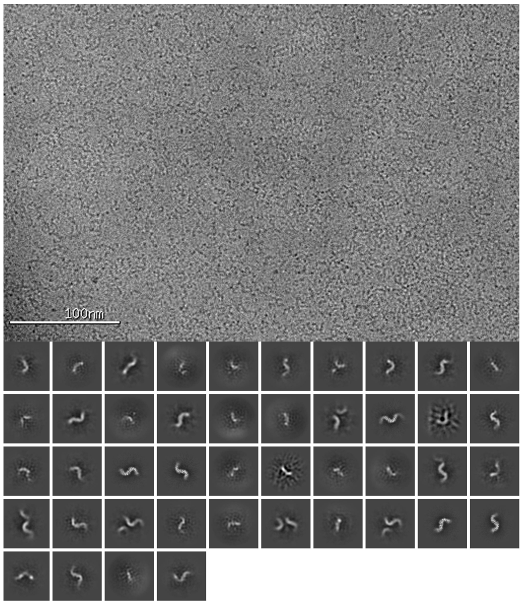

Fig. 1. 2D classes of the minimal Nup358/KLC2 complex. Top: representative cryo-electron micrograph, collected by the PI with the Krios6 cryo-TEM at NYSBC. Bottom: representative 2D classes of 1,355,298 particles from 4188 micrographs.

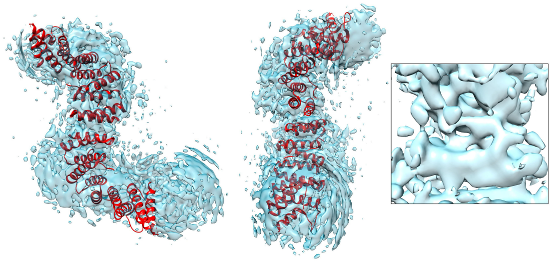

Fig. 2. Cryo-EM map of a minimal KLC2/Nup358 complex which the PI has determined at the NCCAT center; α-helices are visible. The published X-ray structure of KLC2 fused to a short LEWD peptide is docked into the map.

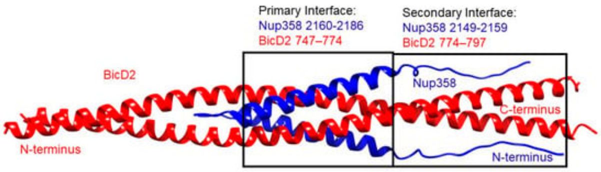

Fig. 3. Predicted structure of the minimal Nup358/BicD2 complex. This structural model from Alphafold2 was confirmed by binding assays of mutants, NMR spectroscopy, SAXS and CD spectroscopy. We recently published these results (Gibson JM, *et al.* 2022, Elife 11. doi: 10.7554/eLife.74714. Gibson JM, *et al.,* 2023. Biomolecules 13. doi: 10.3390/biom13101445).

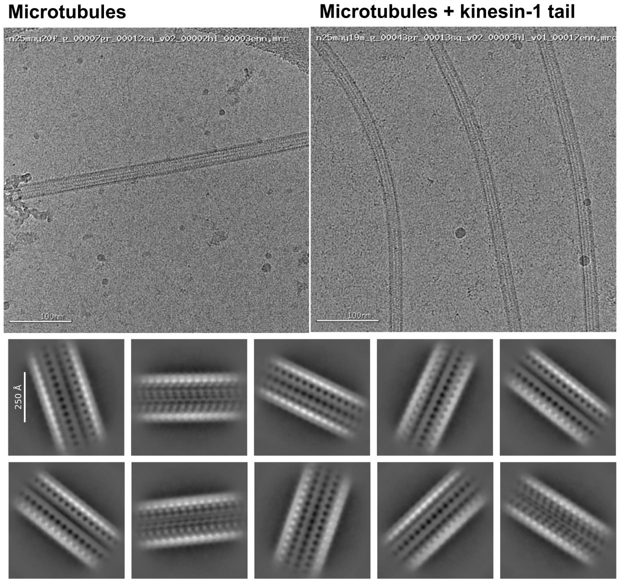

Fig. 4. Representative cryo-electron micrograph and representative 2D classes of microtubules decorated with the kinesin-1 tail, collected by the PI with the Glacios cryo-TEM at NYSBC. A representative micrograph of microtubules without the kinesin-1 tail is shown as a control.