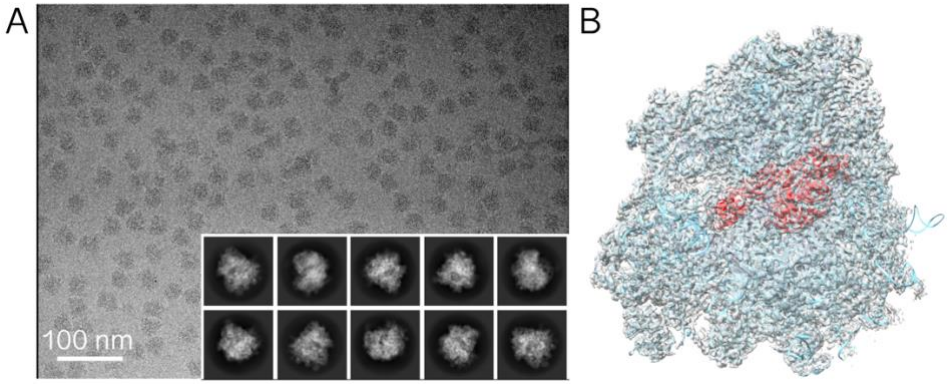

Figure 1. Cryo-EM of translation quality control complexes. (A) Cryo-EM micrograph of purified 80S particles and 2D class averages (inset). (B) Preliminary 2.6 Å reconstruction of 80S ribosome (blue) in complex with eEF2 (red) (unpublished).

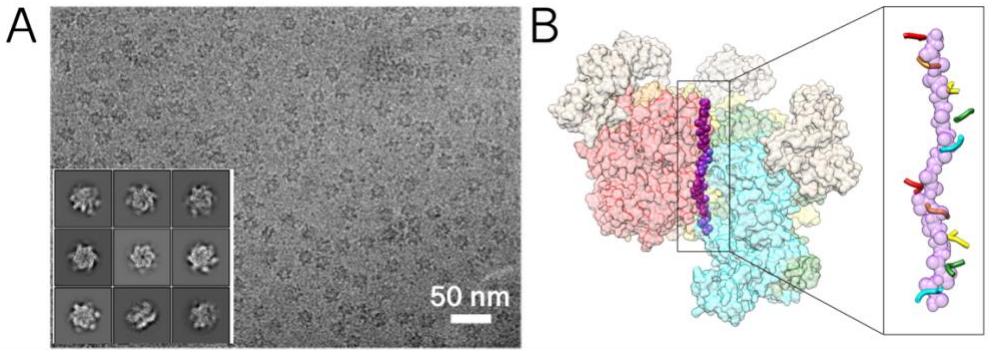

Figure 3. Cryo-EM of Cdc48 protein unfolding complex. (A) Cryo-EM micrograph of Cdc48 isolated from endogenous sources and 2D class averages (inset). (B) Model of unfolded protein threaded through the central pore of Cdc48 derived from cryo-EM density. Adapted from Cooney*, Han* et al. *Science* 2019.

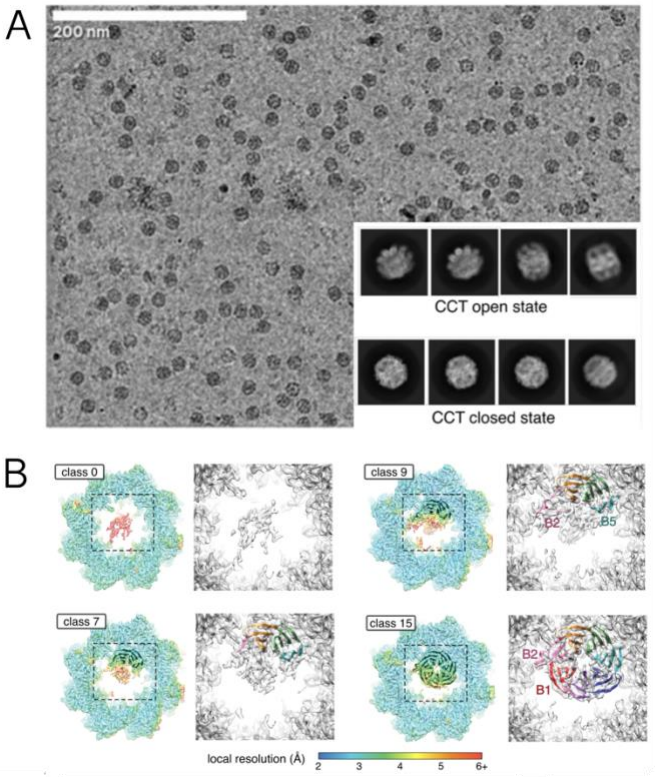

Figure 2. Cryo-EM of substrate-bound CCT complexes. (A) Cryo-EM micrograph of native CCT complexes isolated from HEK293T cells and 2D class averages (inset). (B) Snapshots of CCT-mediated folding reveal the folding trajectory of a beta-propeller protein. 4 out of 16 classes shown; left, color-coded resolution heat map; right, fitted model into 2.8 – 3.0 Å resolution density. Adapted from Wang*, Sass* et al. *Mol. Cell* 2023 (in press).