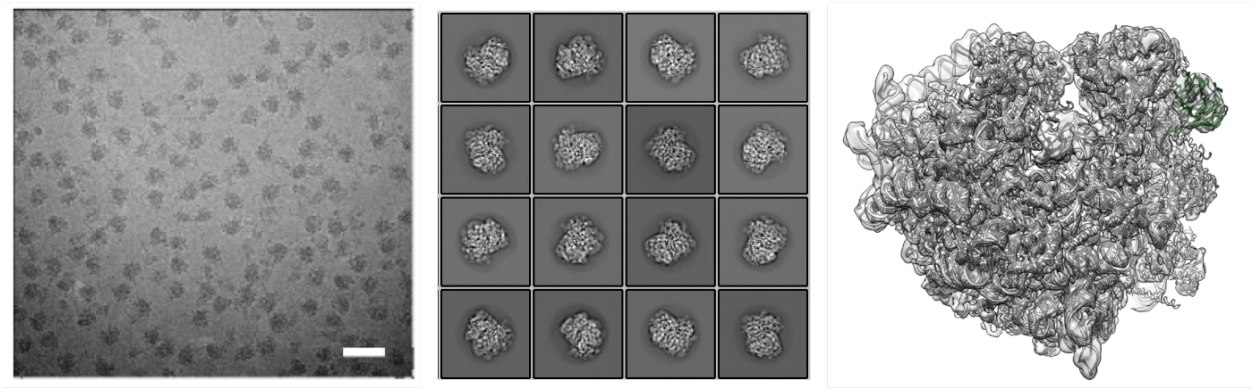

Figure 1. Cryo-EM of translation quality control complexes. Data shown of 80S human ribosome particles prior to splitting. Left, cryo-EM micrograph of purified 80S particles. Middle, reference-free 2D class averages. Right, preliminary 3.4 Å reconstruction of 80S ribosome (unpublished).

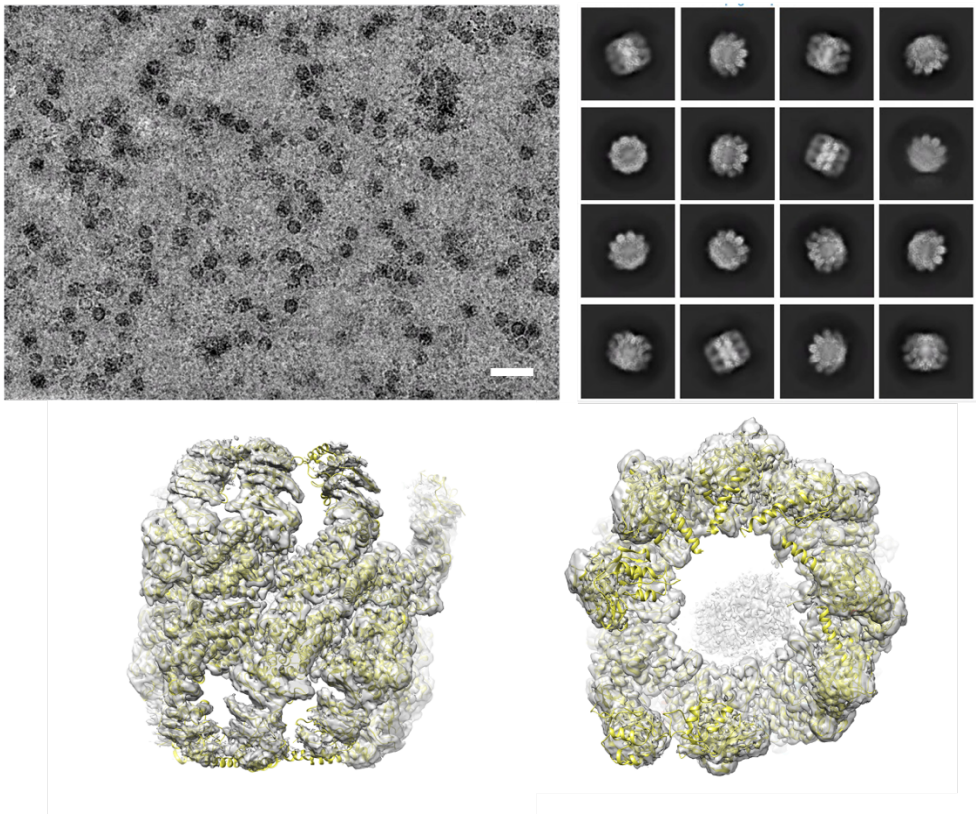

Figure 2. Cryo-EM of substrate-bound CCT complexes. Top left, cryo-EM micrograph of native CCT complexes isolated from HEK293T cells. Top right, reference-free 2D class averages. Bottom row, side and top views respectively of 3.0 Å reconstruction with putative substrate density observed in the central cavity.

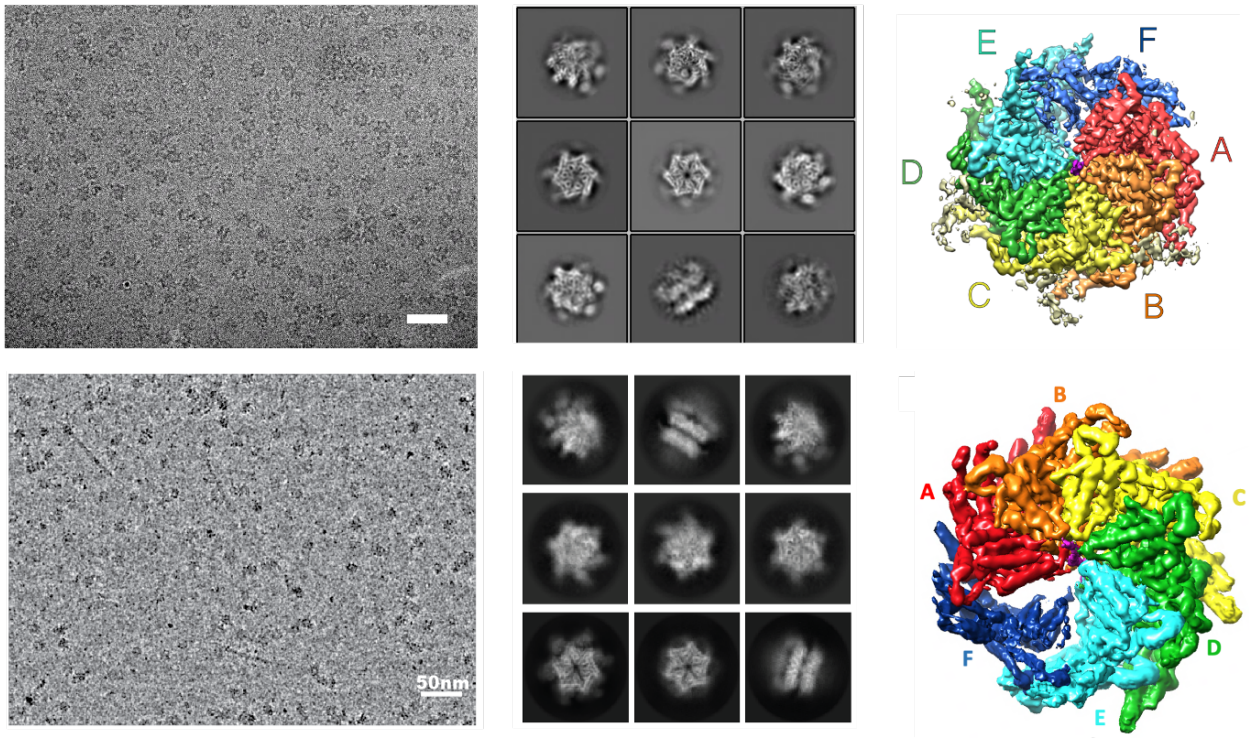

Figure 3. Cryo-EM of yeast Cdc48 (top row) and human p97 (bottom row) complexes. Left, cryo-EM micrographs of Cdc48/p97 isolated from endogenous sources. Middle, reference-free 2D class averages. Right, segmented cryo-EM reconstructions of the substrate-bound hexamers reveal conserved features between yeast and human structures and imply a conserved mechanism of substrate unfolding.