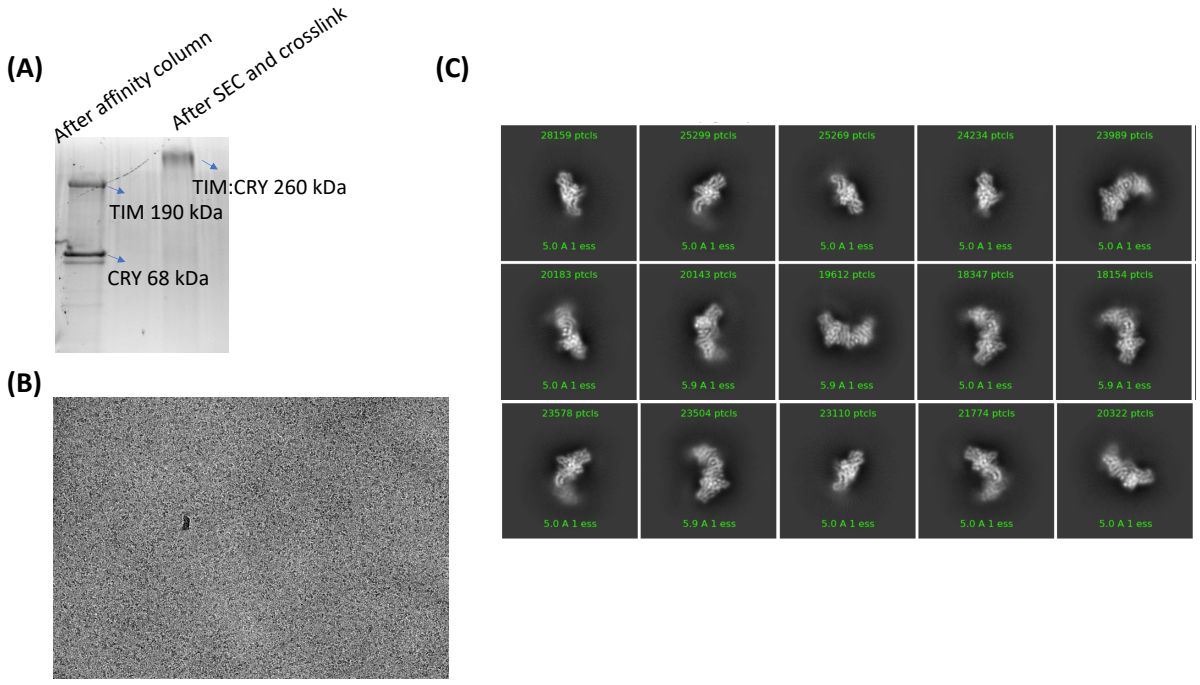

Figure 1: CryoEM of the TIM:CRY complex. (A) Purification of the TIM:CRY complex as shown by SDS-PAGE after affinity purification, chemical cross-linking and size-exclusion chromatography (SEC). (B) A representative micrograph collected on a 200 KeV Arctica Talos with K3 detector at the Cornell Center for Materials Research (CCMR). (C) Representative 2D classification of TIM:CRY complexes from ~1,500 micrographs and ~2 million particles. 2D classes were generated by CryoSPARC followed by the motion correction in RELION and particle picking by Topaz.

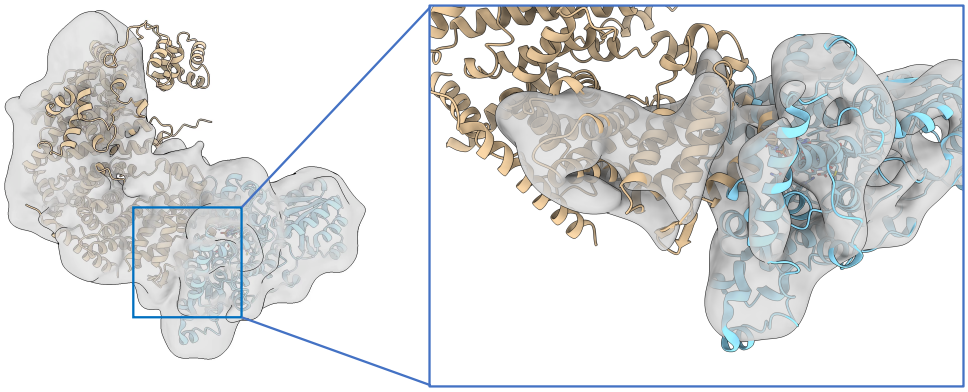

Figure 2: Preliminary 3D reconstruction of TIM:CRY at 7 Å resolution from CryoEM data. The model docked into the density is derived from structures for CRY (blue, PDB ID 4GU5), and TIM (yellow, predicted by alphafold, https://www.alphafold.ebi.ac.uk/entry/P49021). Inset: expanded view of the TIM:CRY interface superimposed on the 3D map that was generated by CryoSPARC. Docking was achieved by UCSF ChimeraX. EM shown at a higher contour level in the inset. Given the high uncertainty in the TIM structure, the relative orientations of the components are tentative.