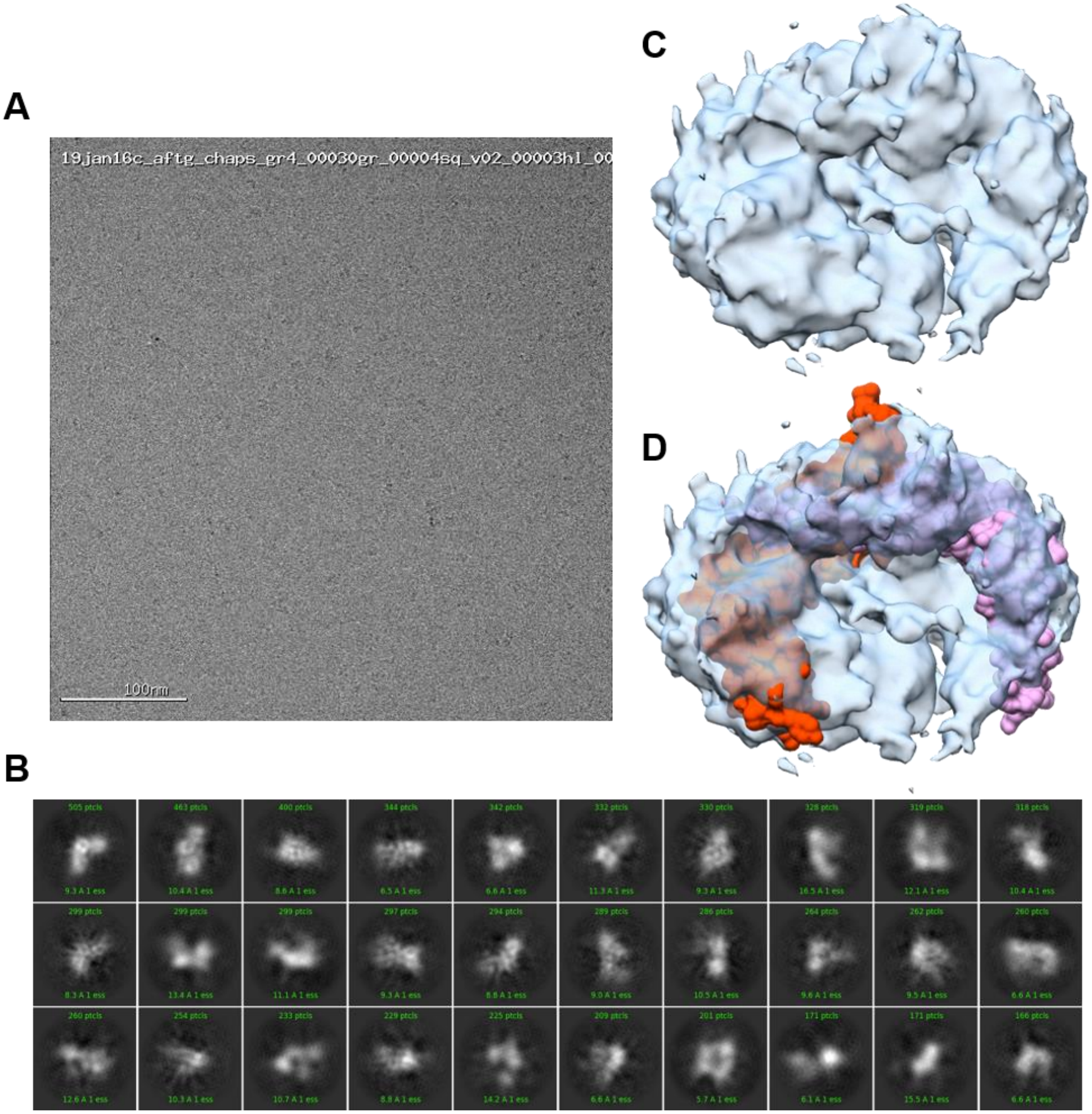

Fig. 1. Screening of the RicAFT complex under cryo conditions. **A.** Representative micrograph collected on a Technai F20 equipped with FEG and K2 detector. **B.** 2D class averages from a clean dataset of 8.5k particles. Box size: 144 pix, pixel size: 1.22 Å/pix. **C.** Ab initio 3D reconstruction from the same particle set used for 2D classification in B, created in Cryosparc2. **D.** Preliminary fitting of the RicAF heterodimer to the ab initio generated 3D volume. The density at the center of the reconstruction likely corresponds to the RicT protein. Fitting performed in Chimera.