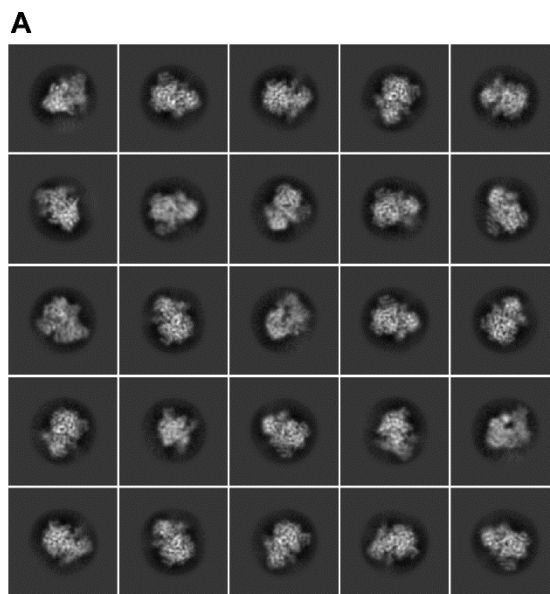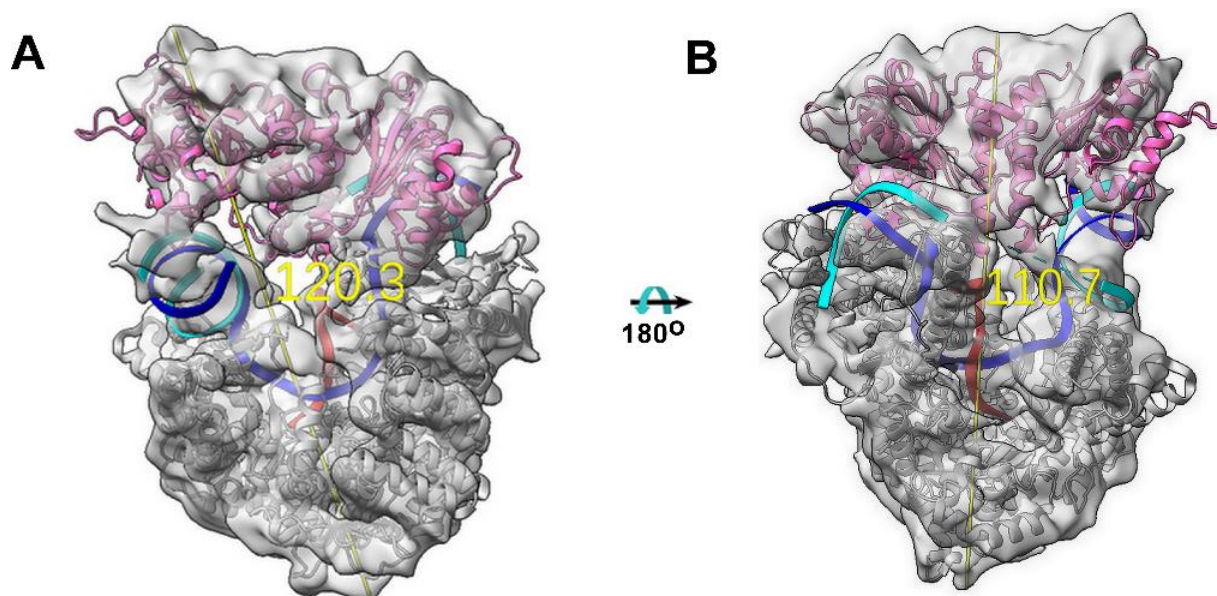**Figure 1.** Cryo-EM grid preparation. Sample images of the assembled EC on UltraAuFoil R1.2/1.3 gold grids using the Atlas (A), Grid Square (B), Foil hole (C) and Data Acquisition (D) presets captured in EPU cryoEM imaging software.



**Figure 2.** The 25 most populated classes from 2D classification of selected particles containing elongation complex used for 3D reconstruction.



**Figure 3.** A high-resolution structure generated from EC particles composed of mtRNAP (grey), TEFM (pink), RNA (red) and scaffold DNA (blue, cyan) superimposed on the published crystal structure of the EC (PDB:5OLA). Non-uniform 3D-refinement in CryoSPARC reported a ~5Å resolution map (A) which shows electron density for TEFM and the PPR domain in slightly different conformations compared to the published crystal structure (B).