

Fig. 1. Representative micrograph (left) and 2-D classes (right).

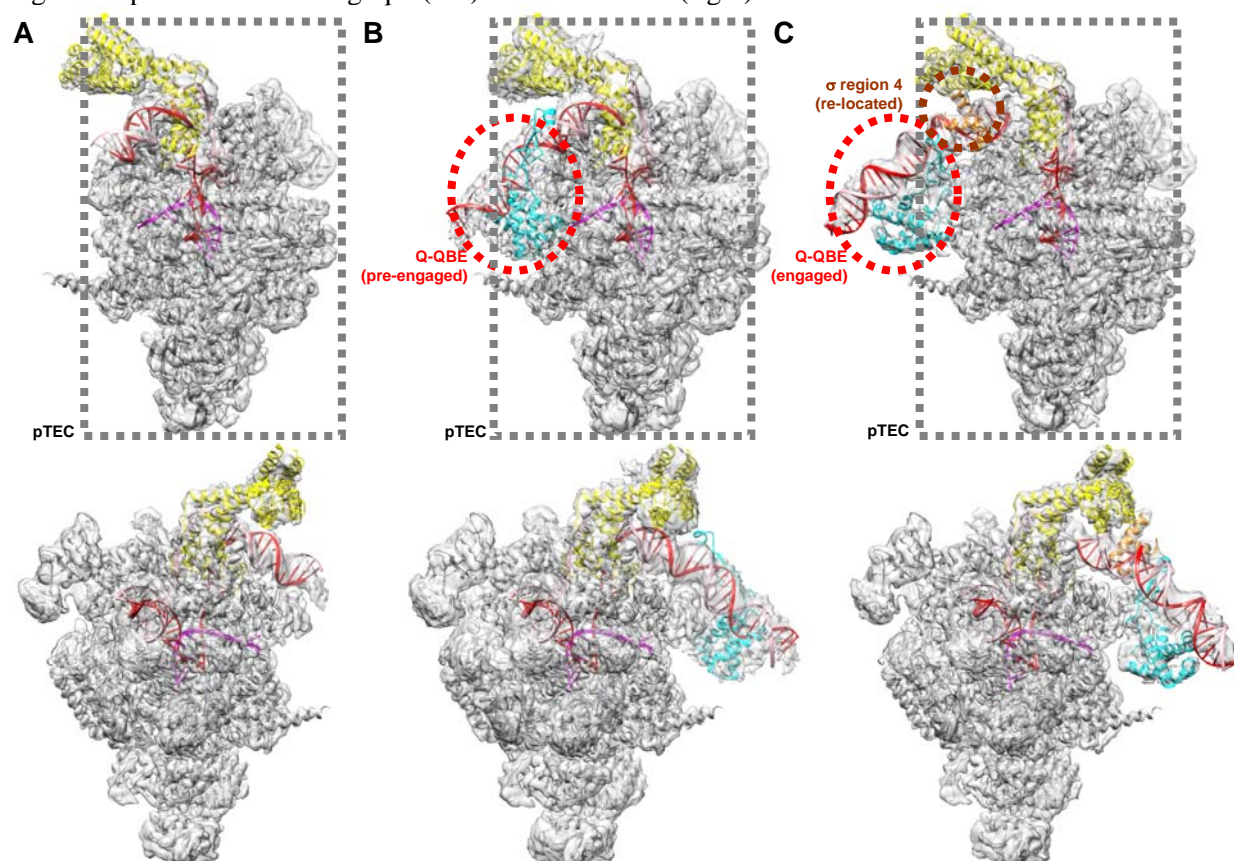


Fig. 2. Fitted maps for the three identified 3D sub-classes (two views of each). **(A)** Target for Qlambda loading (sigma-containing TEC paused at the PR'lambda sigma-dependent pause element; 61,000 particles; 3.4 Å). **(B)** Intermediate in Qlambda loading (partly engaged Qlambda loading complex; 58,000 particles; 3.4 Å). **(C)** Product of Qlambda loading (fully engaged Qlambda loading complex; 50,000 particles; 3.5 Å)

Gray surface, cryo-EM initial reconstruction; gray rectangle labelled "pTEC," fitted structural model of sigma-containing TEC paused at sigma-dependent pause element (RNAP and RNA from PDB 6ALF as gray and magenta ribbons; sigma, DNA template strand, and DNA nontemplate strand from PDB 4YLN as yellow, red, and pink ribbons); red oval labelled "Q-QBE," fitted crystal structure of Qlambda bound to Qlambda binding element (unpublished crystal structure determined as part of this project; Qlambda as cyan ribbon, and DNA template and DNA nontemplate strands as red and pink ribbons); and orange circle labelled "sigmaR4," sigma region 4 (sigma region 4 from PDB 4MEY as orange ribbon).