

Fig. 1. Q 21 loading complex: representative micrograph, 2-D classes, and initial reconstruction (9.5 Å)

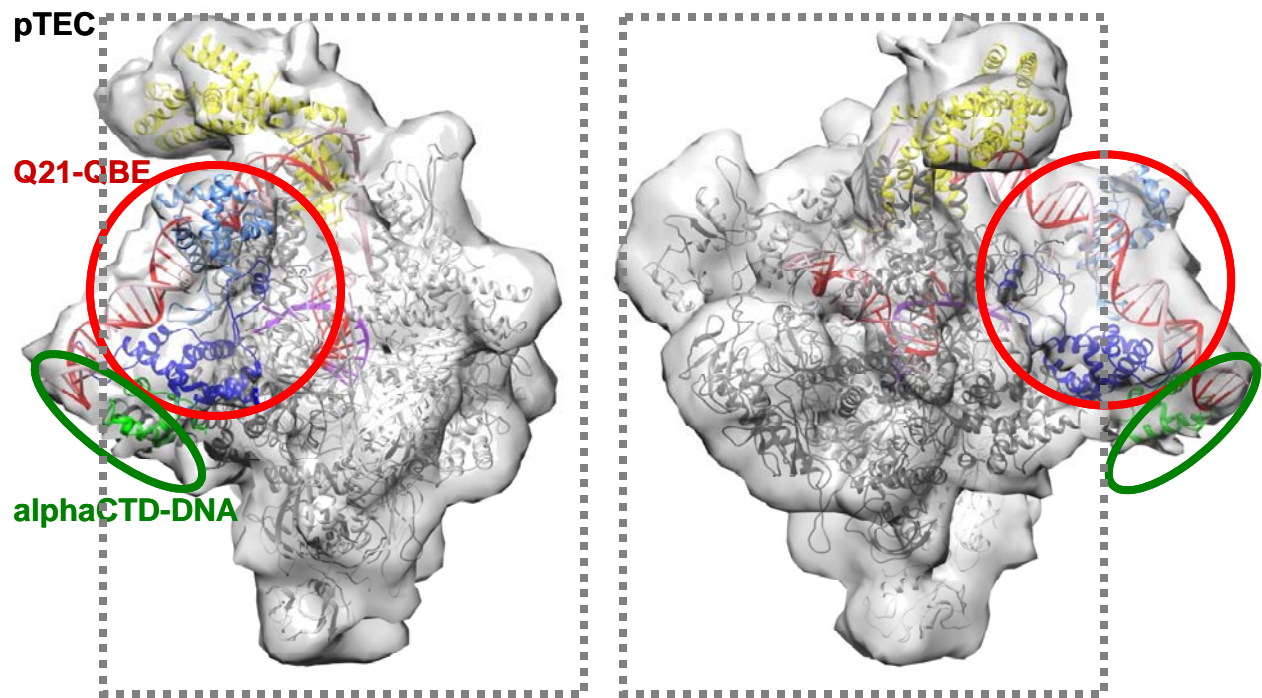


Fig. 2. Q 21 loading complex: fitted map (two orthogonal views). Gray surface, cryo-EM initial reconstruction (9.5 Å); red circle labelled "Q21-QBE," fitted crystal structure of Q21 bound to Q21 binding element (upstream Q21 protomer as blue ribbon, downstream Q21 protomer as cyan ribbon, and DNA template and DNA nontemplate strands as red and pink ribbons); gray rectangle labelled "pTEC," fitted structural model of TEC paused at sigma-dependent pause element (RNAP and RNA from PDB 5UPC as gray and magenta ribbons; sigma region 2, DNA template strand, and DNA nontemplate strand from PDB 4YLN as yellow, red, and pink ribbons); and green oval labelled "alphaCTD-DNA" (alphaCTD, DNA template strand, and DNA nontemplate strand from PDB 1LB2 as green, red, and pink ribbons).