Fig. 1. Representative cryo-EM data and reconstruction for *P. aeruginosa* CSE bound to cofactor PLP. **A**, A micrograph of the complex. Representative cryo-EM image obtained on Titan Krios at NYUSoM. **B**, 2D classification of 1,716,720 particles after initial cleanup. **C**, A graph showing FSC of half-maps after 3D refinement. **D**, Final cryo-EM map of the CSE tetramer with structural model traced in the map. **E**, Fragment of the cryo-EM map zoomed in on the catalytic and drug-binding sites of CSE. Protein is in green. PLP is in magenta. Residues in orange sandwich an aromatic ring of the drugs. Map at 5.0 σ level is in brown color; map for PLP and highlighted residues are at 4.0 σ level.
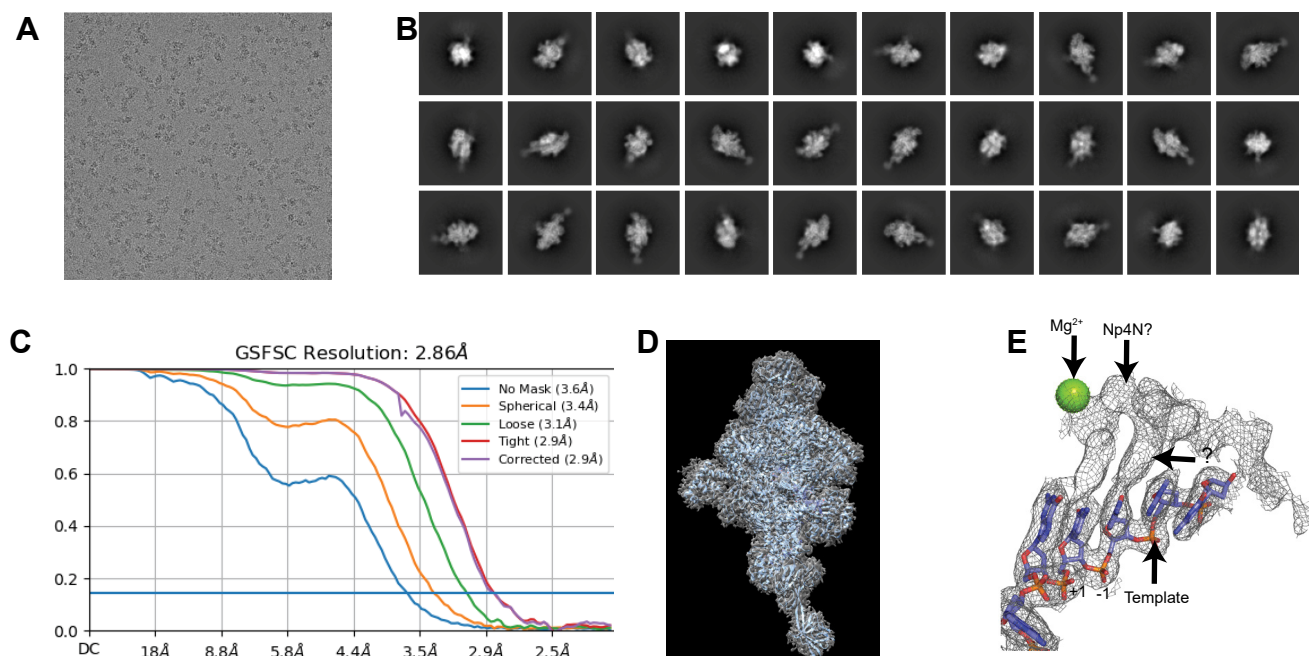

Fig. 2. Representative cryo-EM data and reconstruction for RNAP-Np4N complex. **A**, A micrograph of the complex. Representative cryo-EM image obtained on Arctica at NYUSoM. **B**, 2D classification of 195,730 particles after initial cleanup. **C**, A graph showing FSC of half-maps after 3D refinement. **D**, Final cryo-EM map of the transcription initiation complex. The map shows RNAP bound to the σ70 factor. **E**, Fragment of the cryo-EM map zoomed in on the catalytic site of RNAP bound to Np4N. Cryo-EM map is contoured at 3.0 σ level.