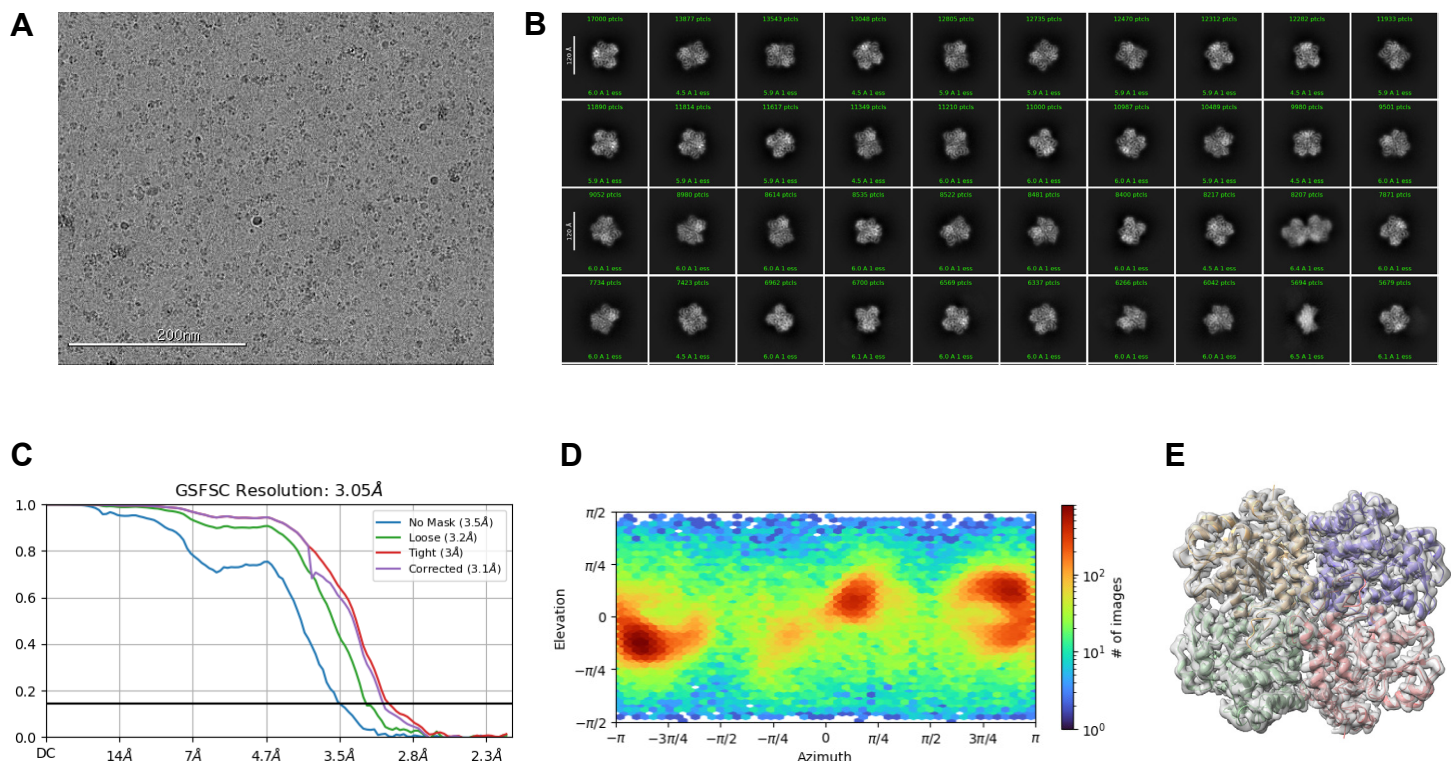**Fig. 1.** Representative cryo-EM data and reconstruction for *P. aeruginosa* CSE bound to cofactor PLP. **A**, A micrograph of the complex. Representative cryo-EM image obtained on Titan Krios at NYUSoM. **B**, 2D classification of 1,716,720 particles after initial cleanup. **C**, A graph showing FSC 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 human CSE. **A**, A micrograph of the protein. Representative cryo-EM image obtained on Arctica at NYUSoM. **B**, Representative 2D classes of 584,000 particles after initial cleanup. **C**, A graph showing FSC of half-maps after 3D refinement. **D**, Viewing direction distribution for a representative 2D class. **E**, Final cryo-EM map of the human CSE tetramer with structural model traced in the map. Each monomer is in a different color.