



Figure 5—figure supplement 1. Cryo-EM data collection, processing, and model building for phosphoAP2-NECAP-DNA ‘clamped’ structure.

A. Representative motion-corrected, dose-weighted cryo-EM micrographs of phosphoAP2-NECAP-DNA complex.

B. Classification and refinement pipeline used for structure determination. Particles were extracted and 2D classified in Relion3. ‘Clean’ particles were re-extracted and used for *ab initio* model generation and refinement in cryoSPARC v2. 2D and 3D FSC plots are shown for the final model.

C. Final cryo-EM structure colored by local resolution.

D. Histogram plot of Ca RMSD of top ten molecular models from Rosetta refinement. Inset shows molecular model colored and scaled by RMSD.