



Figure 1—figure supplement 2. Comparison of NECAP solution structure and phosphoAP2-NECAP cryo-EM structure

A. Cryo-EM map of phosphoAP2-NECAP is shown with a solid surface (left) and with a transparent surface with the closed AP2 crystal structure docked (middle). Masking the region corresponding to AP2 and subtracting this density from the full map gives a psuedo difference density map (right).

B. Solution structure of NECAP_{PHear} (PDB 1TQZ) docked into the difference density from (A). NECAP_{PHear} comprises a single alpha helix and beta sheet, which can be clearly seen in the cryo-EM density. However, the solution structure has some conformational differences compared to the AP2-bound cryo-EM structure.

C. The molecular model for NECAP_{PHear} and AP2 mu (AA 154-158) are shown in the cryo-EM density. PDB 1TQZ was used as a starting model to manually rebuild in Coot and refine using Rosetta.