



Figure 5—figure supplement 2. Structural comparison of 'unclamped' and 'clamped' phosphoAP2-NECAP structures

A. Cartoon diagram of phosphoAP2-NECAP 'unclamped' structure. NECAP is not shown. Top: AP2 subunits are colored as labeled. Bottom: AP2 is colored by per-residue RMSD. Values were calculated in PyMol using whole-molecule alignment of 'unclamped' vs 'clamped' phosphoAP2-NECAP.

B. Cryo-EM maps of 'unclamped' (top) and 'clamped' (bottom) phosphoAP2-NECAP structures. Maps were locally filtered by local resolution to standardize comparison between maps. Cryo-EM density corresponding to beta AA 404-474 is shown (right). Both maps are colored by local resolution using the same color gradient (color key in (C)).

C. The NECAP_{Ex} binding site (beta AA 404-474) is shown for the 'unclamped' phosphoAP2-NECAP (top) and 'clamped' phosphoAP2-NECAP (bottom) structures. A small region of beta partially melts when the Ex domain is bound.