

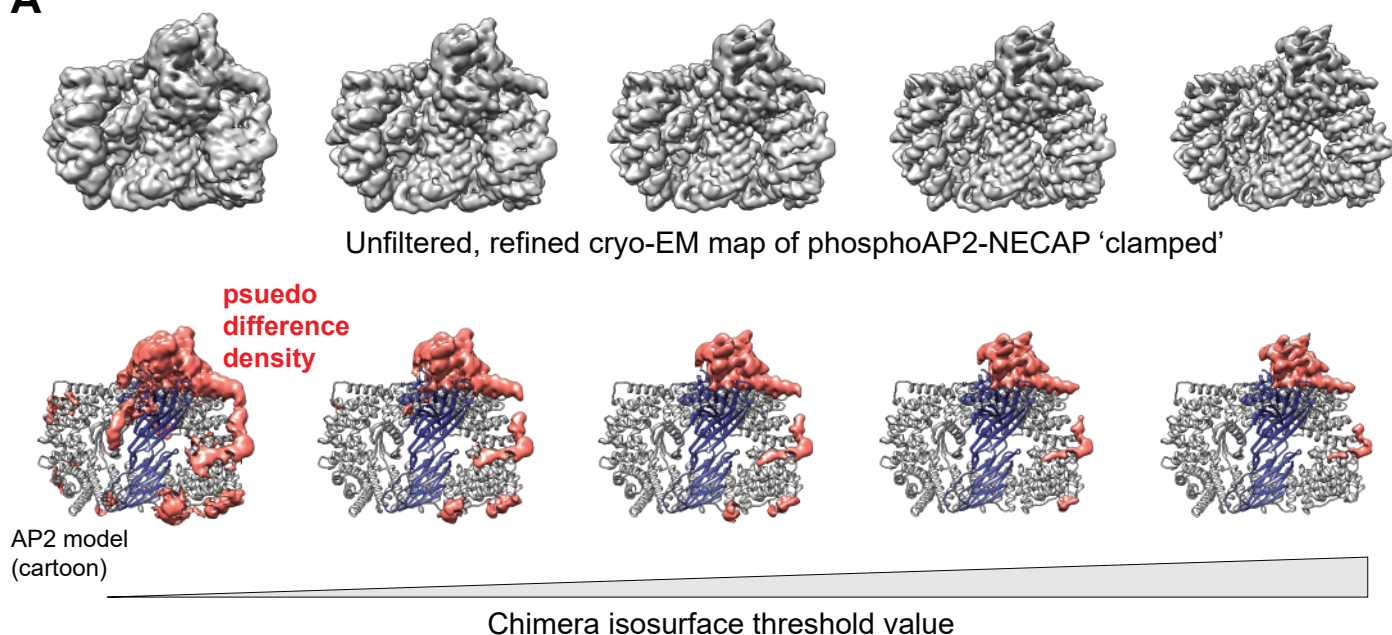
A

Figure 6—figure supplement 1. The NECAP_{Ex} domain binds along the surface of the beta subunit

A. The unfiltered, refined cryo-EM map of 'clamped' phosphoAP2-NECAP is shown at different isosurface threshold levels (top). A psuedo difference density map was made in Chimera by masking the region corresponding to AP2 and subtracting this map from the full map (bottom). The remaining density is shown colored salmon. The same threshold levels are shown top and bottom.

B. The psuedo difference density from (A) is shown at a low threshold level and with a Gaussian filter applied. Regions of the map corresponding to obvious AP2 features, such as loops omitted from our molecular model, were manually removed in Chimera. We hypothesize that a region of NECAP_{Ex} cryo-EM density (boxed in red) corresponds to a conserved region of the sequence called the KEG motif (AA 153-154). This is consistent with structural restraints based on the distance of this motif (16 residues) from the C-terminus of NECAP_{PHear} in our molecular model (AA 8-137).

B