



**Figure 1—figure supplement 3. Model building for mu pT156 linker region**

**A.** Cryo-EM map of phosphoAP2-NECAP is shown with a crystal structure of “closed” AP2 docked (2VGL.pdb)

**B.** The mu linker, which contains the phosphorylated T156 residue, is shown in closer detail. In the crystal structure, T156 is unmodified and the model ends in this region at residue 159.

**C.** The mu linker region (AA 154-168) from the molecular model for pAP2-NECAP is shown overlaid with the same region from the AP2 crystal structure (2VGL.pdb). Our map contains additional density in this linker region, and residues 154-158 were built extending from the N-terminus of the 2VGL model at residue 159. The model was built manually in Coot and refined using Rosetta CM.