

Figure 1: GRK domain structure and function. Top, domain diagram of GRK subfamilies. Green regions are implicated in receptor binding. Bottom: Model of GRK2 activation. In its basal state, the GRK crosslink to Rho*. Only GRK2-S487C formed a crosslink to Rho* using kinase domain is in an open, inactive conformation. Upon BMOE encounter of an activated receptor, the disordered GRK N-terminus forms a helix (α N) that docks into the cytoplasmic cleft of the activated GPCR and also packs against the complex. **Figure 2: Workflows for trapping and imaging GRK-Rho* complexes.** **A)** AlphaFold2 model of GRK2-Rho* and the position of two residues in the implicated in receptor binding. **B)** The Rho*-GRK2 complex only forms in light and with the ligands ATP and ADP, but not with active site inhibitors staurosporine and CCG258208. **C)** Optimization generates higher yields of the Rho*-GRK2 complex. **D)** 2D class average of the Rho*-GRK2-G $\beta\gamma$ complex using a hinge and AST of the kinase domain to trigger domain LMNG micelle to solubilize Rho*. **E)** Auto-phosphorylated GRK5-ADP closure to an active state. GRK1 may need to at least crosslinks using BM(PEG)₃ to Rho* in a light dependent manner (data not shown) and can be separated from unreacted and self-crosslinked GRK5 by nucleotides, and in this state α N and the large lobe could passage through tandem Q and SP Sepharose columns, and then from remain bound to the cytoplasmic cleft and the unreacted Rho* by Ni²⁺-NTA pulldown in the presence of Fab13, which co-phosphorylated tail of the receptor, respectively, to facilitate elutes with the complex. **F)** 2D class average of the Rho*-GRK5-Fab13 complex using an LMNG micelle to solubilize Rho*. Pink circles indicate additional rounds of phosphorylation. Red circles indicate Rho* phosphosites.

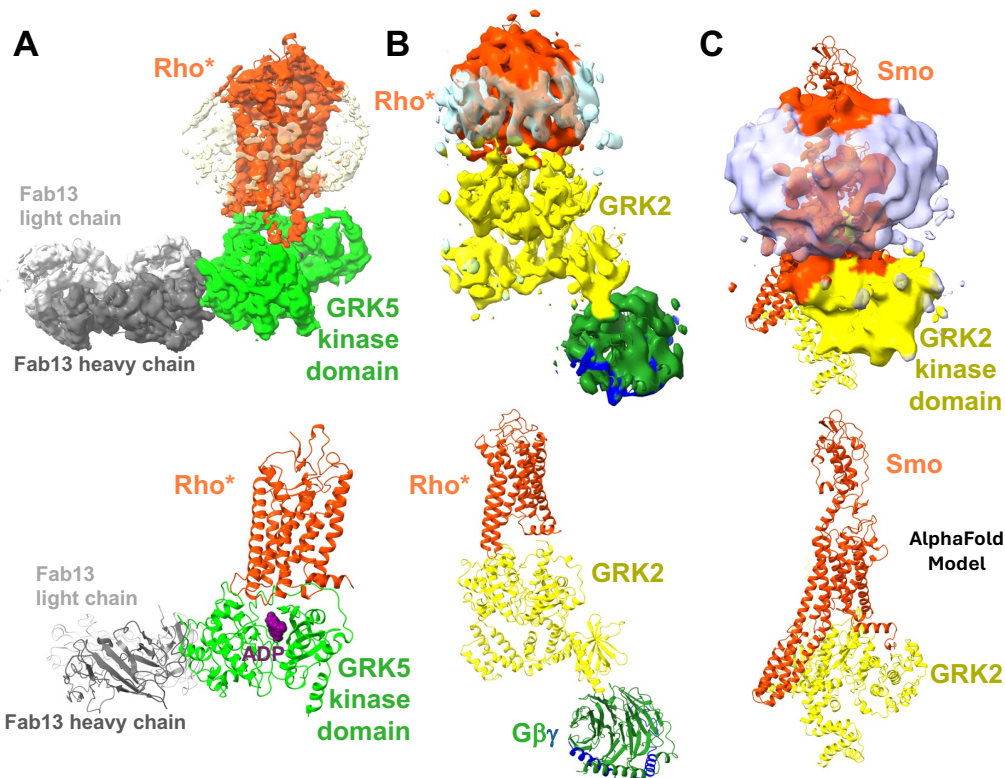


Figure 3: Preliminary reconstructions and models of GRK-GPCR complexes. **A)** Rho*-GRK5-Fab13. **B)** Rho*-GRK2-G $\beta\gamma$. **C)** Smo-GRK2.