

Structural Studies of RGS Proteins

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Beamline: **X25**

Trimeric G proteins function as molecular switches between seven-helix transmembrane (7TM) receptors and intracellular effectors. In the GDP-bound resting state the α subunit is tightly associated with a $\beta\gamma$ dimer. Upon receptor-mediated exchange of GDP for GTP, the α subunit dissociates from the $\beta\gamma$ complex and modulates the function of specific downstream effectors. The activated G proteins, however, are down regulated by regulator of G protein signaling (RGS) proteins. RGS proteins share a common 120-amino acid RGS domain that acts as a GTPase Activating Protein (GAP) by strongly enhancing $G\alpha$'s inherent GTPase activity. We have solved the structure of the RGS domain of the retinal mouse protein RGSr to 1.9 Å by molecular replacement from data collected at X25. In addition, we have crystals of an RGSr•G alpha complex. Data taken at X25 shows that crystals of RGSr•G alpha soaked in lead solutions extend in resolution to at least 2.9 Å.