

# Structure of rhodopsin mutants that constitutively activate the receptor

Prof. Gebhard F. X. Schertler

PSI and ETH Zürich  
gebhard.schertler@psi.ch

G-protein coupled receptors are regulating every aspect of our human existence. They link us with visual perception, smell, taste to our environment and they control our mental state, happiness and consciousness. A drug like LSD will change our mental state and our perception of the world. LSD is acting mainly over G-protein coupled receptors. More than 70 structures of 15 different GPCRs have been determined in complex with ligands of varied pharmacology. From this we are able to extract important molecular signatures of G-protein coupled receptor signaling. We have studied the structure of the  $\beta_1$  adrenergic receptor in several crystal forms and with several ligands. This provides important insights into ligand selectivity based on activation of the receptor and G-protein activation. The third intracellular loop which is important for G-protein activation is now resolved in several of our structures and shows two distinct conformations. We now for the first time have observed a conformation of the fully inactivated receptor. The comparison of different loop conformations is allowing us to give a possible molecular explanation for the phenomenon of basal activity of GPCRs. The new structures also suggest a mechanism for a number of constitutively activating mutants. In addition this is very important for understanding the concept of inverse agonists and partial agonists in a molecular way. We have resolved several structures of constitutively active rhodopsin in an active conformation with its natural agnostic retinal bound to the receptor. These structures give excellent insight into the activation mechanism of GPCRs and can explain some of the complex signaling behavior of G-protein coupled receptors.

## References

1. Deupi X., Edwards P., Singhal A., Nickle B., Oprian D., Schertler GF, Standfuss J: Stabilized G protein binding site in the structure of constitutively active metarhodopsin-II. *Proc Natl Acad Sci U S A* 2012, vol. 109 no. 1 119-124
2. Standfuss J, Edwards PC, D'Antona A, Fransen M, Xie G, Oprian DD, Schertler GF: Crystal structure of constitutively active rhodopsin: How an agonist can activate its GPCR. *Nature* 2011, 471:656-660
3. Moukhametzianov R, Warne T, Edwards PC, Serrano-Vega MJ, Leslie AG, Tate CG, & Schertler GF: Two distinct conformations of helix 6 observed in antagonist-bound structures of a beta1-adrenergic receptor. *Proc Natl Acad Sci U S A* 2011, 108: 8228-8232.
4. Warne T, Moukhametzianov R, Baker JG, Nehme R, Edwards PC, Leslie AG, Schertler GF, & Tate CG: The structural basis for agonist and partial agonist action on a beta 1-adrenergic receptor. *Nature* 2011, 469, 241-244
5. Warne T, Serrano-Vega MJ, Baker JG, Moukhametzianov R, Edwards PC, Henderson R, Leslie AGW, Tate CG: Schertler GF: Structure of a  $\beta_1$ -adrenergic G-protein-coupled receptor. *Nature* 2008, 454:486-491.
6. Ye S, Zaitseva E, Caltabiano G, Schertler GF, Sakmar TP, Deupi X, Vogel R: Tracking G-protein-coupled receptor activation using genetically encoded infrared probes. *Nature* 2010, 464:1386-9.
7. Kobilka B, Schertler GF: New G-protein-coupled receptor crystal structures: insights and limitations. *Trends Pharmacol Sci* 2008, 29:79-83.
8. Rasmussen SGF, Choi H-J, Rosenbaum DM, Kobilka TS, Thian FS, Edwards PC, Burghammer M, Ratnala VRP, Sanishvili R, Fischetti R, Schertler GF, Weis WI, Kobilka B: Crystal structure of the human  $\beta_2$  adrenergic G-protein-coupled receptor. *Nature* 2007, 450:383-387.
9. Standfuss J, Xie G, Edwards P, Burghammer M, Oprian DD, Schertler GF: Crystal structure of a thermally stable rhodopsin mutant. *J Mol Biol* 2007, 372:1179-1188.