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Structures of a Cyanobacterial Photoreceptor and its Soluble Transducer. Hartmut Luecke, Depts. of Biochem., Biophysics & Computer Science, Univ. of California, Irvine, CA 92697, hudel@uci.edu, <http://bass.bio.uci.edu/~hudel/>

The Cubic Lipid Phase (CLP) method for membrane protein crystallization has been refined to allow large-scale screening of various membrane proteins. Various parameters (CLP lipid, water content, bilayer lipid additive, pH, ionic strength, precipitating agent etc.) can be varied. Several distinct seven-transmembrane proteins have been crystallized and their structures determined.

Sensory Rhodopsin (SR): Atomic resolution structures of a phototaxis receptor in haloarchaea, the first sensory member of the widespread microbial rhodopsin family, have yielded insights into spectral tuning and the interaction face with its membrane-embedded transducer. Spectral differences between the sensory rhodopsin and light-driven proton pump bacteriorhodopsin depend largely on the repositioning of a conserved arginine residue in the chromophore-binding pocket. Information from the structures combined with biophysical and biochemical analysis have established a model for receptor activation and signal relay involving light-induced helix tilting in the receptor transmitted to the transducer by lateral transmembrane helix-helix interactions.

Anabaena SR (ASR): Most recently, the structure of a sensory rhodopsin from the cyanobacterium *Anabaena* has been determined to 1.9 Å resolution. This represents the first bacterial rhodopsin structure. In comparison to the archaeal rhodopsins BR and SR there are many striking rearrangements and shifts in hydrogen bonding patterns and hydration on both the extracellular and the cytoplasmic half of the receptor. Also, the cytoplasmic face, which is thought to interact with the soluble transducer, is structurally well-defined and very different from that of the archaeal rhodopsins. The structure of the soluble transducer of this photoreceptor (ASRT) has also been determined - it forms a C4 tetramer with a new fold.