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Editorial

Rhodopsin—Advances and perspectives

Rhodopsin, the best-studied G-protein-coupled receptor (GPCR), was identified as the light-sensitive retinal photoreceptor molecule in the 1870s by Franz Boll (Baumann, 1977; Boll, 1877) and Willy Kuehne (Kuehne, 1878; Kuhne, 1977). Rhodopsin occupies center stage between two important physiological pathways, both carried out by functional modules (Hofmann, Spahn, Heinrich, & Heinemann, 2006): phototransduction as an archetype of a sensory transduction module and the retinoid cycle, in which the retinal chromophore is reisomerized in a long series of reactions. Phototransduction and the retinoid cycle play complementary roles in vertebrate vision. Early research focused on bleaching intermediates of rhodopsin and the identification of its chromophore, vitamin A aldehyde (retinal), by George Wald (Wald, 1968). Determination of the rhodopsin protein sequence (Hargrave, 1982; Ovchinnikov et al., 1982) and identification of its gene (Nathans & Hogness, 1983) in mammalian photoreceptor cells, followed by the cloning of genes encoding the cone and invertebrate (*Drosophila melanogaster*) photopigments (O'Tousa et al., 1985; Zuker, Cowman, & Rubin, 1985), represented major advances in rhodopsin research. Since 1990, rhodopsin research has accelerated dramatically. First, mutations in the human rhodopsin gene were found to be causative for autosomal dominant retinitis pigmentosa (Dryja et al., 1990). Today in excess of 100 mutations in the rhodopsin gene have been associated with dominant and recessive retinal dystrophies, as well as non-progressive stationary nightblindness. Second, the three-dimensional crystal structure of unbleached rhodopsin was determined, and represents the first such structure for any of the large family of heptaspanning membrane receptors (Palczewski et al., 2000). More recently, crystal structures of late photointermediates were reported (Salom et al., 2006). This structure is a first step towards an understanding of how changes on the cytoplasmic surface of rhodopsin enable the coupling to its cognate G protein, transducin. Moreover, several helices are likely involved in the oligomeric state of rhodopsin, including helices I and II, as derived from the crystallographic studies (Fig. 1), consistent with the previous modeling investigations.

The meeting Rhodopsin—Advances and perspectives, held April 27/28 in Ft. Lauderdale, Florida, summarized recent advances in rhodopsin research in eight platform sessions and one poster session (45 presentations). The sessions were designed to provoke in-depth discussions among experimental and theoretical biophysicists, molecular and cellular biologists, and clinician scientists. Questions to be answered or discussed included whether rhodopsin forms induced or constitutive dimers or oligomers, whether such quaternary structure is functionally important and how much it contributes to its performance as a visual amplifier, how exactly rhodopsin releases its chromophore after photobleaching, and what the nature of the interaction between rhodopsin and its binding partners transducin, rhodopsin kinase, and arrestin might be.

This special issue contains 17 articles reviewing recent developments on rhodopsin/GPCR structure, its interactions with downstream components, and biosynthesis and trafficking of rhodopsin in photoreceptors. On day 1 of the meeting, the focus was on coupling of rhodopsin to its G protein, transducin, and arrestin (6 papers), as well as on similarities and differences of rhodopsin and other GPCRs (2 papers). On day 2, the focus was on mechanisms of release of the retinal chromophore from rhodopsin and rhodopsin regeneration (2 papers) and cone opsins (1 paper). The meeting ended with sessions on trafficking through the connecting cilium with emphasis on centrins, components of the basal body and cilium, and a final session on rhodopsin mutations and retina disease (2 papers). The articles in this special issue of *Vision Research* illustrate that in spite of 130 years of rhodopsin research, much remains to be done. We hope this special issue will help update our knowledge on G-protein-coupled receptors, and fertilize a new generation of GPCR enthusiasts.

We thank all speakers and poster presenters for their enthusiastic participation during the meeting, their timely submissions, and their patience during the process of manuscript revision. After months of preparation, the organizers were rewarded by a meeting of high-quality presentations, stimulating and engaging discussions, a strong poster session, and the introduction of numerous students to the field.

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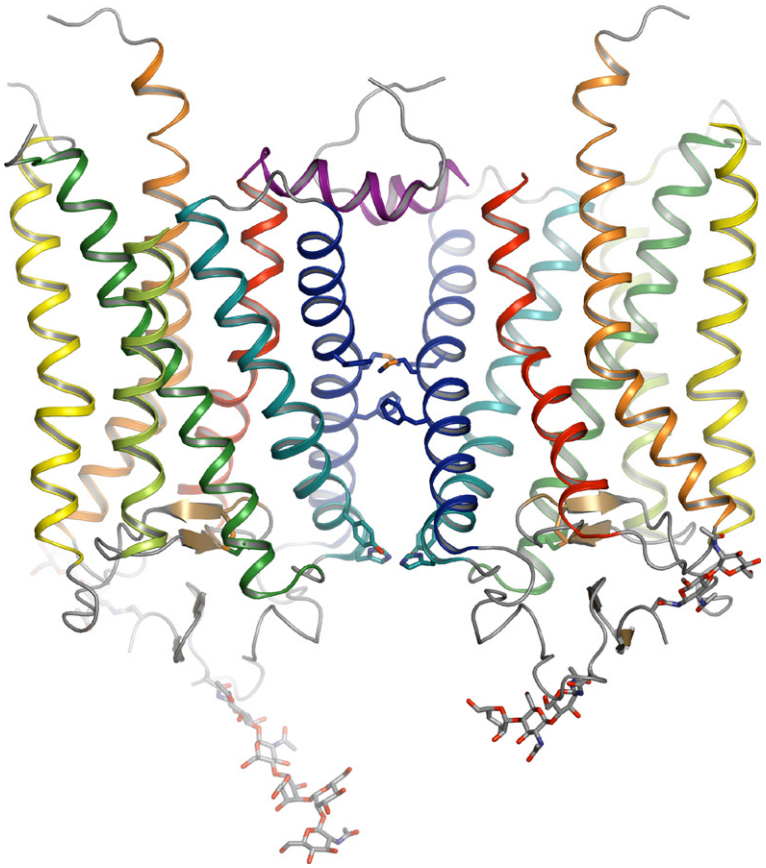

Fig. 1. Rhodopsin dimer as seen in crystals of the illuminated, Schiff base deprotonated state of rhodopsin (PDB ID: 2I37). Transmembrane helices I–VII and helix VIII are colored from blue to purple. Key residues that constitute the dimer interface are shown in stick representation. For details see Salom et al. (2006). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this paper.)

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