The Meta-Transition of the Rhodopsin Photolysis Sequence as Result of Protein-Lipid-Interactions in the Receptor Membrane Surface

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In the photolysis sequence of the visual pigment rhodopsin the formation of the meta II-state received an exceptional position because this step was assumed to represent the trigger for the physiological process of visual excitation. To study this transition step comparitive investigations were performed in the isolated life retina as well as in rhodopsin containing membrane fragments at different steps of desintegration. The results of these measurements lead to the conclusion that the kinetics of the meta-transition does not depend on the properties of the rhodopsin only but much more on its interactions with the lipids in the receptor membrane. For this reason, the models proposed in the literature up to now (e.g. (1),(2)) were not sufficient to explain the dependence of the meta-transition on temperature, pH, ionic strength, alcohol addition etc. With regard to special findings reported in the literature on the influence of differently structured lipids and detergent molecules on the meta-transition (e.g. (3),(4)) a membrane model of rhodopsin is resulting from the comprehensive investigations reported here that has the following features:

1. In the meta I state the rhodopsin is exposed to a strong expansive tension which is counterbalanced by the first layer of surrounding lipids.
2. During the transition into the meta II state the rhodopsin is expanding against the membrane surface tension towards a new equilibrium position.
3. The influence of pH, ionic strength, and alcohol addition is mainly mediated by the surface properties of the membrane lipids.
4. In the expansion model the thermodynamic quantities as activation energy E_A (describing the kinetics of the transition) and the standard enthalpy change ΔH° (determining the equilibrium of meta-states) are given by the dependence of the membrane surface potential on the expansion.

By this membrane model the kinetical and thermodynamical behaviour of the meta-transition of rhodopsin is explained.

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