

Molecular Mechanism for Thermal Stability of Microbial Rhodopsins: A Spectroscopic Study

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Abstract

Rhodopsins, also called retinal proteins are a class of photoreceptor proteins found in almost all domains of life, including, mammals, bacteria and archaea [1]. These proteins consist of an opsin apoprotein and a covalently bound retinal chromophore that absorbs light for conversion of energy in microbial rhodopsins and initiation of intra-/ intercellular signaling in animal rhodopsin. We have studied external stimuli-dependent thermal denaturation of several microbial rhodopsins, including, thermophilic rhodopsin (TR), bacteriorhodopsin (bR), gloebacter rhodopsin (GR) and proteorhodopsin (PR) using different spectroscopic methods. The protein of our primary interest, TR, prepared from the genome of a thermophilic bacterium *Thermus thermophiles* shows resistance to high temperatures. The ultrafast photoisomerization of this protein was found to be independent of temperature to about 70 °C [2]. We have found that the thermal denaturation of microbial rhodopsins can be catalyzed by illumination of the retinal chromophore and the resulting apoprotein is much less stable than the retinal-bound opsin. We propose that the hydrolysis of retinal protonated Schiff base is the rate determining step of the thermal denaturation of the studied proteins [3]. Our studies with artificial TR pigments, derived from synthetic retinal analogs, support this proposal.

References:

1. Ernst, O.P.; Lodowski, D.T. et al., *Chem. Rev.* **2014**, 114, 126.
2. Iyer, E.S.S.; Misra, R. et al., *J. Am. Chem. Soc.* **2016**, 138, 12401.
3. Misra, R.; Sudo, Y.; Sheves, M. (submitted for publication)