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Direct observation of light-induced structural changes in photoreceptors by dynamic crystallography

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Photoreceptors are signaling proteins that convert a light signal into a biological signal. Photoreceptors use chemically distinct chromophores to capture photons from different wavelengths. When primary photo-events originating in the chromophore propagate, they drive further conformational changes, which alter protein-protein interactions and/or enzymatic activities. Establishing such a sequence of structural events at atomic resolution holds the key to full understanding of the light perception and signaling mechanisms in photoreceptors. Dynamic crystallography is a powerful tool that enables direct observations of protein structural dynamics at atomic resolution. In a dynamic crystallography experiment, a biochemical reaction or a signaling process is initiated in the crystalline state. X-ray diffraction datasets collected before and after the reaction initiation are compared via the difference Fourier method for examination of conformational changes along the reaction coordinates. However, how to acquire useful dynamic information by crystallography remains a major challenge for many biological systems. In my talk, I will present how we apply dynamic crystallography to directly observe light-induced structural changes in different photoreceptor systems. I will discuss how to design and perform dynamic crystallography experiments, how to process and analyze a collection of difference maps in order to extract structural changes and to determine light-induced structural intermediates. This method and its applications to light-sensitive systems would broadly interest the structural biology community who wish to study protein structural dynamics at high resolution