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Allosteric Action and Protein Structural Relaxation Studied by Time-Resolved X-ray Crystallography. Vukica Šrajer^a, James Knapp^b, William Royer^b, Reinhard Pahl^a, ^aUniv. of Chicago, Chicago, IL, ^bUniv. of Massachusetts Medical School, Worcester, MA

Time-resolved macromolecular crystallography has successfully completed the phase of feasibility studies with the use of high flux third-generation synchrotron sources, demonstrated ability to detect small structural changes on ns and sub-ns time scale even at relatively low levels of reaction initiation in the crystal of 15-40% (Šrajer et al., 2001; Schotte et al., 2003; Bourgeois et al., 2003; Anderson et al., 2004; Schmidt et al., 2004; Rajagopal et al., 2005) and with significant advances in processing and analysis of time-resolved Laue data (Schmidt et al., 2003, Rajagopal et al., 2004; Rajagopal et al., 2005). The most recent example from the BioCARS 14-ID beamline (Advanced Photon Source) on the use of ns time-resolved X-ray crystallography will be presented: the study of allosteric action in real time in a cooperative dimeric hemoglobin.

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