

Abstract for an Invited Paper
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Watching proteins function with 150-ps time-resolved X-ray crystallography¹

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We have used time-resolved Laue crystallography to characterize ligand migration pathways and dynamics in wild-type and several mutant forms of myoglobin (Mb), a ligand-binding heme protein found in muscle tissue. In these pump-probe experiments, which were conducted on the ID09B time-resolved beamline at the European Synchrotron and Radiation Facility, a laser pulse photodissociates CO from an MbCO crystal and a suitably delayed X-ray pulse probes its structure via Laue diffraction. Single-site mutations in the vicinity of the heme pocket docking site were found to have a dramatic effect on ligand migration. To visualize this process, time-resolved electron density maps were stitched together into movies that unveil with $<2\text{-\AA}$ spatial resolution and 150-ps time-resolution the correlated protein motions that accompany and/or mediate ligand migration. These studies help to illustrate at an atomic level relationships between protein structure, dynamics, and function.

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