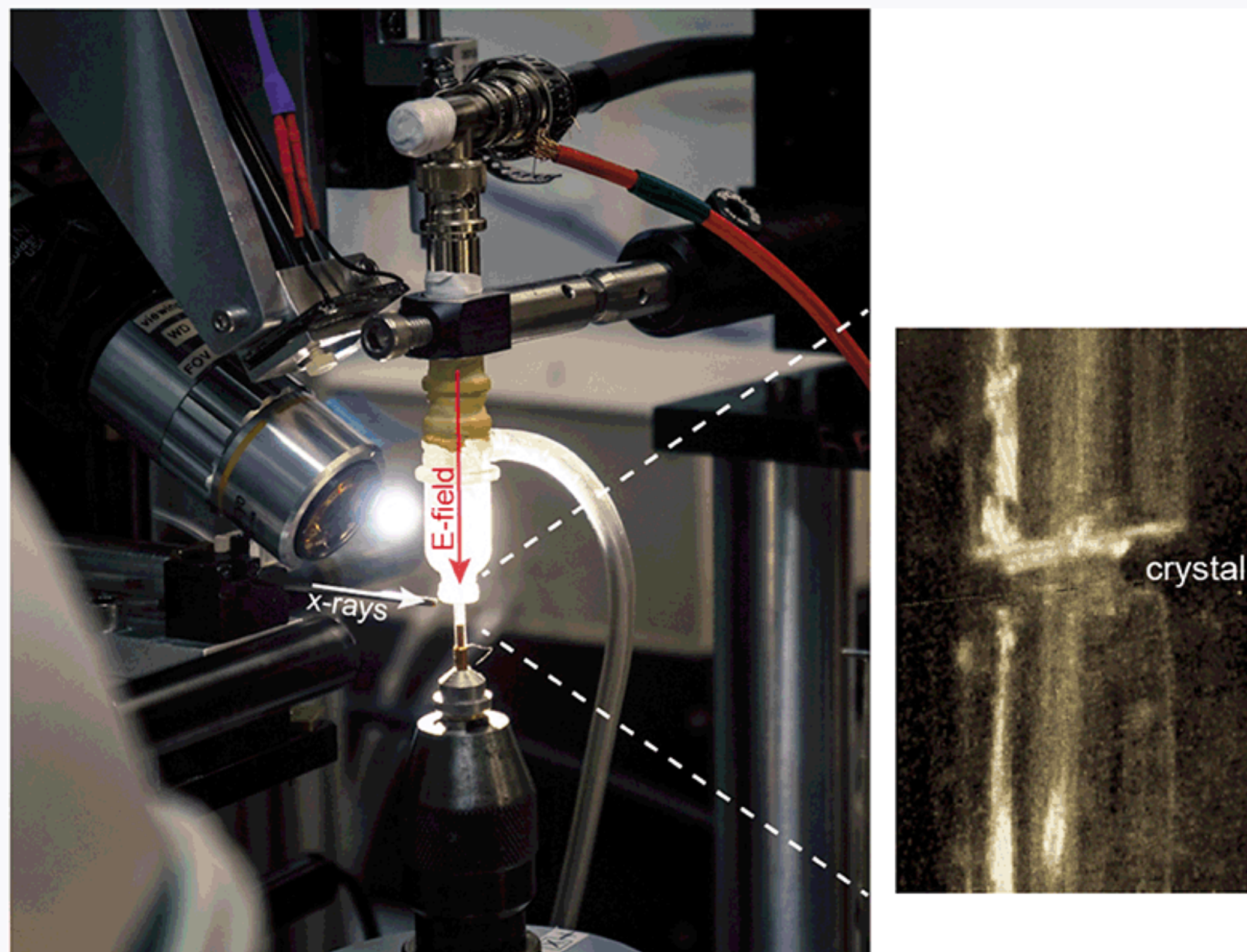


THE ADVANCED PHOTON SOURCE

A NEW WAY TO SEE PROTEINS IN MOTION



A new technique to watch proteins in action involves applying large voltage pulses to protein crystals simultaneously with x-ray pulses, as shown in the photo (at left) of the experimental set-up in the BioCARS beamline at the APS. At right is a close-up view of a crystal sandwiched between electrodes that deliver the voltage.

A team of researchers has developed a new imaging technique that makes x-ray images of proteins as they move in response to electric field pulses. The method could lead to new insights into how proteins work. The technique had its first application in experiments at the U.S. Department of Energy Office of Science's Advanced Photon Source (APS).

The new method, which the researchers call EF-X (electric field-stimulated x-ray crystallography), is aimed at stimulating motions within proteins and visualizing those motions in real time at atomic resolution, he said. This approach makes it possible to create video-like images of proteins in action – a goal of future

research. The method involves subjecting proteins to large electric fields of about 1 million volts per centimeter and simultaneously reading out the effects with x-ray crystallography.

The researchers' EF-X experiments, which utilized the BioCARS 14-ID x-ray beamline at the APS, showed proteins can sustain these intense electric fields, and further that the imaging method can expose the pattern of shape changes associated with a protein's function.

This is not the first report of seeing atomic motions in proteins, but previous reports were specialized for particular proteins and particular kinds of motions, but is the first to open up the investigation to po-

tentially all possible motions, and for any protein that can be crystallized.

Ultimately, this work could explain how proteins work in both normal and disease states, with implications in protein engineering and drug discovery. An immediate goal is to make the method simple enough for other researchers to use.

The group used the technique to study the PDZ domain of the human ubiquitin ligase protein LNX2, and found new information on how the protein actually works.

Contact: rama.ranganathan@utsouthwestern.edu, v-srajer@uchicago.edu

See: Doeke R. Hekstra^{1‡}, K. Ian White¹, Michael A. Socolich¹, Robert W. Henning², Vukica Šrajer², and Rama Ranganathan¹, "Electric-field-stimulated protein Mechanics," *Nature* **540**, 400 (15 December 2016). DOI: 10.1038/nature20571

Author affiliations: ¹UT Southwestern Medical Center, ²The University of Chicago [‡]Present address: Harvard University

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(Adapted from a UT Southwestern Medical Center press release by Deborah Wormser)

CALL FOR APS GENERAL-USER PROPOSALS

The Advanced Photon Source is open to experimenters who can benefit from the facility's high-brightness hard x-ray beams.

General-user proposals for beam time during Run 2018-1 are due by Friday, October 27, 2017.

Information on access to beam time at the APS is at http://www.aps.anl.gov/Users/apply_for_beamtime.html or contact Dr. Dennis Mills, DMM@aps.anl.gov, 630/252-5680.

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www.anl.gov

Advanced Photon Source
Bldg. 401/Rm A415
Argonne National Laboratory
9700 S. Cass Ave.
Argonne, IL 60439 USA
www.aps.anl.gov
apsinfo@aps.anl.gov



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