# **Resource Summary Report**

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# **BioCARS**

RRID:SCR\_001439 Type: Tool

**Proper Citation** 

BioCARS (RRID:SCR\_001439)

#### **Resource Information**

URL: http://cars9.uchicago.edu/biocars/

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**Description:** Biomedical technology research center and training resource that is a state-ofthe art, national user facility for synchrotron-based studies of dynamic and static properties of macromolecules by X-ray scattering techniques such as crystallography (specializing in timeresolved), small- and wide-angle X-ray scattering and fiber diffraction. BioCARS operates two X-ray beamlines, embedded in a Biosafety Level 3 (BSL-3) facility unique in the U.S. that permits safe studies of biohazardous materials such as human pathogens.

Abbreviations: BioCARS

Synonyms: BioCARS: A Synchrotron Structural Biology Resource

**Resource Type:** biomedical technology research center, training resource, service resource, access service resource

Defining Citation: PMID:21685684

**Keywords:** synchrotron, macromolecule, x-ray, crystallography, x-ray scattering, fiber diffraction, biological process, time-resolved crystallography, structural biology technology center

Funding: NIGMS P41GM103543; NCRR P41RR007707

Resource Name: BioCARS

Resource ID: SCR\_001439

Alternate IDs: nlx\_152665

Record Creation Time: 20220129T080207+0000

Record Last Update: 20250508T064705+0000

#### **Ratings and Alerts**

No rating or validation information has been found for BioCARS.

No alerts have been found for BioCARS.

## Data and Source Information

Source: <u>SciCrunch Registry</u>

## **Usage and Citation Metrics**

We found 63 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Zielinski KA, et al. (2024) Scaling and Merging Time-Resolved Laue Data with Variational Inference. bioRxiv : the preprint server for biology.

Kim SO, et al. (2024) Serial X-ray liquidography: multi-dimensional assay framework for exploring biomolecular structural dynamics with microgram quantities. Nature communications, 15(1), 6287.

Greisman JB, et al. (2024) Perturbative diffraction methods resolve a conformational switch that facilitates a two-step enzymatic mechanism. Proceedings of the National Academy of Sciences of the United States of America, 121(9), e2313192121.

Kim C, et al. (2024) Structural dynamics of protein-protein association involved in the lightinduced transition of Avena sativa LOV2 protein. Nature communications, 15(1), 6991.

Hewitt RA, et al. (2024) Laue-DIALS: Open-source software for polychromatic x-ray diffraction data. Structural dynamics (Melville, N.Y.), 11(5), 054701.

Bennett AL, et al. (2024) Microsecond dynamics control the HIV-1 Envelope conformation. Science advances, 10(5), eadj0396.

Zielinski KA, et al. (2024) Resolving DJ-1 Glyoxalase Catalysis Using Mix-and-Inject Serial Crystallography at a Synchrotron. bioRxiv : the preprint server for biology.

Zielinski KA, et al. (2024) Scaling and merging time-resolved pink-beam diffraction with variational inference. Structural dynamics (Melville, N.Y.), 11(6), 064301.

Smith N, et al. (2023) X-ray-driven chemistry and conformational heterogeneity in atomic resolution crystal structures of bacterial dihydrofolate reductases. bioRxiv : the preprint server for biology.

Hekstra DR, et al. (2023) Emerging Time-Resolved X-Ray Diffraction Approaches for Protein Dynamics. Annual review of biophysics, 52, 255.

Greisman JB, et al. (2023) Resolving conformational changes that mediate a two-step catalytic mechanism in a model enzyme. bioRxiv : the preprint server for biology.

Bennett AL, et al. (2023) Microsecond dynamics control the HIV-1 envelope conformation. bioRxiv : the preprint server for biology.

Velazquez-Garcia JJ, et al. (2023) Structural dynamics of a thermally silent triiron(II) spin crossover defect grid complex. Dalton transactions (Cambridge, England : 2003), 52(35), 12224.

Basuroy K, et al. (2023) Axial vs equatorial: Capturing the intramolecular charge transfer state geometry in conformational polymorphic crystals of a donor-bridge-acceptor dyad in nanosecond-time-scale. The Journal of chemical physics, 158(5), 054304.

Wilamowski M, et al. (2022) Time-resolved ?-lactam cleavage by L1 metallo-?-lactamase. Nature communications, 13(1), 7379.

Choi M, et al. (2021) Effect of the abolition of intersubunit salt bridges on allosteric protein structural dynamics. Chemical science, 12(23), 8207.

Bowen CH, et al. (2021) Microbial production of megadalton titin yields fibers with advantageous mechanical properties. Nature communications, 12(1), 5182.

Guo C, et al. (2020) Thermoplastic moulding of regenerated silk. Nature materials, 19(1), 102.

Ren Z, et al. (2020) An automated platform for in situ serial crystallography at room temperature. IUCrJ, 7(Pt 6), 1009.

Henry L, et al. (2020) Real-time tracking of protein unfolding with time-resolved x-ray solution scattering. Structural dynamics (Melville, N.Y.), 7(5), 054702.