

Resource Summary Report

Generated by PRECISE-TBI on Aug 1, 2026

Coherent X-Ray Imaging Data Bank (CXIDB)

RRID:SCR_014722

Type: Tool

Proper Citation

Coherent X-Ray Imaging Data Bank (CXIDB) (RRID:SCR_014722)

Resource Information

URL: <http://cxidb.org>

Proper Citation: Coherent X-Ray Imaging Data Bank (CXIDB) (RRID:SCR_014722)

Description: Database of Coherent X-ray Imaging (CXI) experiments. This data is widely accessible to researchers worldwide.

Abbreviations: CXIDB

Synonyms: Coherent X-ray Imaging Data Bank (CXIDB), CXIDB, Coherent X-ray Imaging Data Bank

Resource Type: data or information resource, data repository, storage service resource, database, service resource

Keywords: coherent xray imaging, cxi, experiment, database, reproducibility

Availability: Available to the research community

Resource Name: Coherent X-Ray Imaging Data Bank (CXIDB)

Resource ID: SCR_014722

Alternate IDs: DOI:10.11577, r3d100011554

Alternate URLs: <https://doi.org/10.11577/>, <https://dx.doi.org/10.11577/>

Record Creation Time: 20220129T080322+0000

Record Last Update: 20260801T190516+0000

Ratings and Alerts

No rating or validation information has been found for Coherent X-Ray Imaging Data Bank (CXIDB).

No alerts have been found for Coherent X-Ray Imaging Data Bank (CXIDB).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Shenoy J, et al. (2025) Scalable 3D reconstruction for X-ray single particle imaging with online machine learning. Nature communications, 16(1), 6812.

Kroon-Batenburg LMJ, et al. (2023) Making your raw data available to the macromolecular crystallography community. Acta crystallographica. Section F, Structural biology communications, 79(Pt 10), 267.

Bhowmick A, et al. (2023) Structural evidence for intermediates during O₂ formation in photosystem II. Nature, 617(7961), 629.

Nass K, et al. (2021) Pink-beam serial femtosecond crystallography for accurate structure-factor determination at an X-ray free-electron laser. IUCrJ, 8(Pt 6), 905.

Im D, et al. (2020) Structure of the dopamine D₂ receptor in complex with the antipsychotic drug spiperone. Nature communications, 11(1), 6442.

Echelmeier A, et al. (2020) Segmented flow generator for serial crystallography at the European X-ray free electron laser. Nature communications, 11(1), 4511.

Morgan AJ, et al. (2020) speckle-tracking: a software suite for ptychographic X-ray speckle tracking. Journal of applied crystallography, 53(Pt 6), 1603.

Shapiro DA, et al. (2020) An ultrahigh-resolution soft x-ray microscope for quantitative analysis of chemically heterogeneous nanomaterials. Science advances, 6(51).

Helliwell JR, et al. (2019) Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. Acta crystallographica. Section D, Structural biology, 75(Pt 5), 455.

Helliwell JR, et al. (2019) Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. Acta crystallographica. Section F, Structural biology communications, 75(Pt 5), 321.

Helliwell JR, et al. (2019) Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. Journal of applied crystallography, 52(Pt 3),

Brändén G, et al. (2019) Coherent diffractive imaging of microtubules using an X-ray laser. *Nature communications*, 10(1), 2589.

Giewekemeyer K, et al. (2019) Experimental 3D coherent diffractive imaging from photon-sparse random projections. *IUCrJ*, 6(Pt 3), 357.

Helliwell JR, et al. (2019) Findable Accessible Interoperable Re-usable (FAIR) diffraction data are coming to protein crystallography. *IUCrJ*, 6(Pt 3), 341.

Helliwell JR, et al. (2019) FACT and FAIR with Big Data allows objectivity in science: The view of crystallography. *Structural dynamics* (Melville, N.Y.), 6(5), 054306.

Tosha T, et al. (2017) Capturing an initial intermediate during the P450_{nor} enzymatic reaction using time-resolved XFEL crystallography and caged-substrate. *Nature communications*, 8(1), 1585.

Hasegawa K, et al. (2017) Development of a dose-limiting data collection strategy for serial synchrotron rotation crystallography. *Journal of synchrotron radiation*, 24(Pt 1), 29.

Daurer BJ, et al. (2017) Experimental strategies for imaging bioparticles with femtosecond hard X-ray pulses. *IUCrJ*, 4(Pt 3), 251.

Sugahara M, et al. (2017) Hydroxyethyl cellulose matrix applied to serial crystallography. *Scientific reports*, 7(1), 703.

Zhou XE, et al. (2017) Identification of Phosphorylation Codes for Arrestin Recruitment by G Protein-Coupled Receptors. *Cell*, 170(3), 457.