Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Mar 31, 2025

Northeastern Collaborative Access Team

RRID:SCR_008999
Type: Tool

Proper Citation

Northeastern Collaborative Access Team (RRID:SCR_008999)

Resource Information

URL: http://necat.chem.cornell.edu/

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Description: Biomedical technology research center for macromolecular crystallography at Sector 24 of the Advanced Photon Source at Argonne National Laboratory. The macromolecules studied by resource users often involve large unit cells, small crystals, weakly diffracting crystals and crystals with weak anomalous scattering. Technological research includes use of silicon monochromators, focusing optics, methods of phase determination, radiation damage, X-ray detectors, automated sample mounting, microdiffraction and crystallographic software.

Abbreviations: NE-CAT, NECAT

Synonyms: Northeastern CAT, Northeastern Collaborative Access Team Undulator Resource for Structural Biology

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

Keywords: synchrotron, x-ray, beamline, structural biology, macromolecular crystallography, macromolecule, crystallography, structural biology technology center

Funding: NIGMS

Resource Name: Northeastern Collaborative Access Team

Resource ID: SCR_008999

Alternate IDs: nlx_152674

Record Creation Time: 20220129T080250+0000

Record Last Update: 20250331T060831+0000

Ratings and Alerts

No rating or validation information has been found for Northeastern Collaborative Access Team.

No alerts have been found for Northeastern Collaborative Access Team.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Rechkoblit O, et al. (2021) Structural basis of DNA synthesis opposite 8-oxoguanine by human PrimPol primase-polymerase. Nature communications, 12(1), 4020.

Joiner AMN, et al. (2021) Structural basis for the initiation of COPII vesicle biogenesis. Structure (London, England : 1993), 29(8), 859.

Rechkoblit O, et al. (2019) Structural insights into mutagenicity of anticancer nucleoside analog cytarabine during replication by DNA polymerase ?. Scientific reports, 9(1), 16400.

Rechkoblit O, et al. (2018) Structural basis for polymerase ?-promoted resistance to the anticancer nucleoside analog cytarabine. Scientific reports, 8(1), 12702.

Wasmuth EV, et al. (2017) Structure and reconstitution of yeast Mpp6-nuclear exosome complexes reveals that Mpp6 stimulates RNA decay and recruits the Mtr4 helicase. eLife, 6.

Shao Y, et al. (2016) A Non-Stem-Loop CRISPR RNA Is Processed by Dual Binding Cas6. Structure (London, England : 1993), 24(4), 547.

Suslov NB, et al. (2015) Crystal structure of the Varkud satellite ribozyme. Nature chemical biology, 11(11), 840.

Pendergast JS, et al. (2014) Wheel-running activity modulates circadian organization and the daily rhythm of eating behavior. Frontiers in psychology, 5, 177.

Shao Y, et al. (2013) Structure of the Cmr2-Cmr3 subcomplex of the Cmr RNA silencing complex. Structure (London, England : 1993), 21(3), 376.

Brockhauser S, et al. (2013) The use of a mini-? goniometer head in macromolecular crystallography diffraction experiments. Acta crystallographica. Section D, Biological crystallography, 69(Pt 7), 1241.

Shao Y, et al. (2013) Recognition and cleavage of a nonstructured CRISPR RNA by its processing endoribonuclease Cas6. Structure (London, England : 1993), 21(3), 385.

Cocozaki AI, et al. (2012) Structure of the Cmr2 subunit of the CRISPR-Cas RNA silencing complex. Structure (London, England : 1993), 20(3), 545.

Wang R, et al. (2011) Interaction of the Cas6 riboendonuclease with CRISPR RNAs: recognition and cleavage. Structure (London, England : 1993), 19(2), 257.

Xue S, et al. (2010) Structural basis for substrate placement by an archaeal box C/D ribonucleoprotein particle. Molecular cell, 39(6), 939.

Mitchell M, et al. (2009) Crystal structure and assembly of the functional Nanoarchaeum equitans tRNA splicing endonuclease. Nucleic acids research, 37(17), 5793.

Rashid R, et al. (2006) Crystal structure of a Cbf5-Nop10-Gar1 complex and implications in RNA-guided pseudouridylation and dyskeratosis congenita. Molecular cell, 21(2), 249.