Resource Summary Report

Generated by T1D on Aug 4, 2026

MacCHESS

RRID:SCR_001443
Type: Tool

Proper Citation

MacCHESS (RRID:SCR_001443)

Resource Information

URL: http://www.macchess.cornell.edu/

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Description: MacCHESS Synchrotron Source for Structural Biology advances structural characterization of proteins and biomolecules critical for understanding key biological processes and properties through leveraging both established and emerging X-ray synchrotron technologies. Used to collect data that comprises all or part of research programs.

Abbreviations: MacCHESS

Synonyms: MacCHESS Synchrotron Source for Structural Biology

Resource Type: access service resource, service resource

Keywords: structure, macromolecule, crystallography, beamlne, x-ray, bending magnet, unit-cell diffraction, ultra-high-resolution diffraction, dispersion phasing, drug design, structural genomics, microdiffraction, cryo-cooling, high pressure cooling, diffraction, software, synchrotron, cryo-crystallography, small-angle x-ray solution scattering, microcrystallography, structural biology, structural biology technology center

Funding: NIGMS GM103485

Availability: Free, Freely Available

Resource Name: MacCHESS

Resource ID: SCR_001443

Alternate IDs: nlx_152668

Record Creation Time: 20220129T080207+0000

Record Last Update: 20260804T043119+0000

Ratings and Alerts

No rating or validation information has been found for MacCHESS.

No alerts have been found for MacCHESS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Rodriguez Carrero RJ, et al. (2025) Genetic and biochemical characterization of a radical SAM enzyme required for post-translational glutamine methylation of methyl-coenzyme M reductase. mBio, 16(2), e0354624.

Florio TJ, et al. (2022) Differential recognition of canonical NF-?B dimers by Importin ?3. Nature communications, 13(1), 1207.

Lisitskaya L, et al. (2022) Programmable RNA targeting by bacterial Argonaute nucleases with unconventional guide binding and cleavage specificity. Nature communications, 13(1), 4624.

Hashimoto H, et al. (2020) Structural Basis of Protein Arginine Methyltransferase Activation by a Catalytically Dead Homolog (Prozyme). Journal of molecular biology, 432(2), 410.

Niazi M, et al. (2020) Biophysical analysis of Pseudomonas-phage PaP3 small terminase suggests a mechanism for sequence-specific DNA-binding by lateral interdigitation. Nucleic acids research, 48(20), 11721.

Sen K, et al. (2017) Active-site protein dynamics and solvent accessibility in native Achromobacter cycloclastes copper nitrite reductase. IUCrJ, 4(Pt 4), 495.

McDermott LA, et al. (2016) Design and evaluation of novel glutaminase inhibitors. Bioorganic & medicinal chemistry, 24(8), 1819.

Moustafa IM, et al. (2015) Structural models of mammalian mitochondrial transcription factor B2. Biochimica et biophysica acta, 1849(8), 987.

Nam KH, et al. (2012) Nucleic acid binding surface and dimer interface revealed by CRISPR-associated CasB protein structures. FEBS letters, 586(22), 3956.