

Resource Summary Report

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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: service resource, access service resource

Keywords: structure, macromolecule, crystallography, beamline, 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: 20260810T040310+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 [ASWG](#) .

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- κ B dimers by Importin β 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.