Resource Summary Report

Generated by RRID on May 25, 2025

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: Biomedical technology research center that is funded for two purposes: for core research as motivated by the important biomedical problems and support to all structural biologists making use of the Cornell High Energy Synchrotron Source (CHESS) facility for crystallographic and small-angle X-ray scattering experiments, as well as for novel experiments requiring special equipment and staff assistance not readily available at other synchrotron sources. MacCHESS provides a facility for developing new technology and for advancing the research goals of structural biologists as well as the broader biological research community. MacCHESS has a strong commitment to training future leaders, who will be able to translate advances in synchrotron science and structural biology into valuable biomedical applications. It operates three insertion-device beamlines (stations A-1, F-1 and F-2) devoted to macromolecular crystallography. The resource also supports additional bending magnet stations for part-time macromolecular X-ray experiments. The resource specializes in large unit-cell diffraction, ultra-high-resolution diffraction, multiple-wavelength anomalous dispersion (MAD) phasing, rapid-throughput crystallography (structure-based drug design and structural genomics), microdiffraction, high-pressure cryo-cooling, multiple-beam diffraction and software development.

Abbreviations: MacCHESS

Synonyms: Macromolecular Diffraction Facility at the CHESS, Macromolecular Diffraction Facility at the Cornell High Energy Synchrotron Source

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

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

Resource Name: MacCHESS

Resource ID: SCR_001443

Alternate IDs: nlx_152668

Record Creation Time: 20220129T080207+0000

Record Last Update: 20250525T032645+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 8 mentions in open access literature.

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

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.

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.

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.

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.