

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

Colorado University at Boulder Macromolecular X-ray Crystallography Core Facility

RRID:SCR_019310

Type: Tool

Proper Citation

Colorado University at Boulder Macromolecular X-ray Crystallography Core Facility
(RRID:SCR_019310)

Resource Information

URL: <https://www.colorado.edu/facility/biomolecular-x-ray-crystallography/>

Proper Citation: Colorado University at Boulder Macromolecular X-ray Crystallography Core Facility (RRID:SCR_019310)

Description: Provides resources for crystallization and structure determination of biological macromolecules and complexes. Supports research in the Department of Biochemistry. We are happy to extend our help to researchers from the broader CU community and to researchers outside the university, if time and availability allow us too.

Synonyms: Macromolecular X-ray Crystallography Core

Resource Type: access service resource, core facility, service resource

Keywords: USEDit, ABRF, ABRF

Availability: open

Resource Name: Colorado University at Boulder Macromolecular X-ray Crystallography Core Facility

Resource ID: SCR_019310

Alternate IDs: ABRF_1122

Alternate URLs: <https://coremarketplace.org/?FacilityID=1122>

Record Creation Time: 20220129T080344+0000

Record Last Update: 20260905T133419+0000

Ratings and Alerts

No rating or validation information has been found for Colorado University at Boulder Macromolecular X-ray Crystallography Core Facility.

No alerts have been found for Colorado University at Boulder Macromolecular X-ray Crystallography Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Siwik SH, et al. (2026) Structure of a dopamine-binding RNA aptamer reveals metal-mediated ligand recognition. bioRxiv : the preprint server for biology.

Olenginski LT, et al. (2025) Designing small molecules targeting a cryptic RNA binding site through base displacement. Nature chemical biology.

Siwik SH, et al. (2025) Structural basis for ring-opening fluorescence by the RhoBAST RNA aptamer. Nucleic acids research, 53(12).

Spradlin SF, et al. (2025) Structural and functional clues challenge the hypothesis that the yjdF riboswitch is natively regulated through broad recognition of azaaromatic compounds. Nucleic acids research, 53(21).

Batey R, et al. (2025) Designing small molecules that target a cryptic RNA binding site via base displacement. Research square.

Spradlin SF, et al. (2025) Structural and functional clues challenge the hypothesis that the yjdF riboswitch is natively regulated through broad recognition of azaaromatic compounds. bioRxiv : the preprint server for biology.

Mitchell ME, et al. (2023) Targeting the Conformational Change in ArnA Dehydrogenase for Selective Inhibition of Polymyxin Resistance. Biochemistry, 62(14), 2216.