

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

Colorado University at Boulder Biochemistry Shared Instruments Pool Core Facility

RRID:SCR_018986

Type: Tool

Proper Citation

Colorado University at Boulder Biochemistry Shared Instruments Pool Core Facility
(RRID:SCR_018986)

Resource Information

URL: <https://www.colorado.edu/lab/biochem-instruments/>

Proper Citation: Colorado University at Boulder Biochemistry Shared Instruments Pool Core Facility (RRID:SCR_018986)

Description: Provides access to multitude of instruments and techniques, including EPR, CD and fluorescence spectroscopy, DLS, Sec-MALS, ITC, MST, stopped-flow spectroscopy, chemical quench-flow, imaging systems, centrifuges, scintillation counters, sonicators and more.

Synonyms: Biochemistry and Shared Instrumentation, Biochemistry Shared Instruments Pool

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

Keywords: USEDit, spectroscopy, fluorescence spectroscopy, stopped flow spectroscopy, imaging, centrifuge, scintillation counter, sonicator, EPR, CD, DLS, ABRF, ABRF

Availability: open

Resource Name: Colorado University at Boulder Biochemistry Shared Instruments Pool Core Facility

Resource ID: SCR_018986

Alternate IDs: ABRF_1038

Alternate URLs: <https://coremarketplace.org/?FacilityID=1038>

Record Creation Time: 20220129T080342+0000

Ratings and Alerts

No rating or validation information has been found for Colorado University at Boulder Biochemistry Shared Instruments Pool Core Facility.

No alerts have been found for Colorado University at Boulder Biochemistry Shared Instruments Pool Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 87 mentions in open access literature.

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

Tian W, et al. (2026) Structure of the human HIRA histone chaperone with a nucleosome suggests a stepwise nucleosome assembly mechanism. bioRxiv : the preprint server for biology.

Matthews AM, et al. (2026) The retroelement-derived human protein PEG10 is a regulator of mRNA splicing in neurons. bioRxiv : the preprint server for biology.

DaPron KE, et al. (2026) A Type III secretion system effector evolved to be mechanically labile and initiate unfolding from the N-terminus. bioRxiv : the preprint server for biology.

Wierzba AJ, et al. (2026) Enhancement of RNA Imaging Platforms by the Use of Peptide Nucleic Acid-Based Linkers. Bio-protocol, 16(12), e5453.

Huffine CA, et al. (2026) [CO₂] Alters Cyanobacterial Carboxysome Encapsulation and Redox State. Research square.

Mead EH, et al. (2026) COSMIC-Linked Ras Mutations at the Interface Between H-Ras and PI3K??RBD Frequently Generate Affinity Increases. bioRxiv : the preprint server for biology.

Martin TG, et al. (2026) Multi-omics Insight into Cardiac Myofibril Remodeling in Post-Prandial Burmese Pythons. bioRxiv : the preprint server for biology.

Whited AM, et al. (2026) Tubulin C-terminal tails are pH sensors that regulate microtubule function. bioRxiv : the preprint server for biology.

Weerawarana SR, et al. (2026) TFAM organizes DNA into compact higher order structures. bioRxiv : the preprint server for biology.

Nagy TA, et al. (2026) A phage protein screen identifies triggers of the bacterial innate immune system. *Nature microbiology*, 11(2), 597.

Huffine CA, et al. (2026) Carbon dioxide concentration alters cyanobacterial carboxysome encapsulation and redox state in *Synechococcus* sp. PCC 7002. *Communications biology*, 9(1).

Olenginski LT, et al. (2026) Cryptic RNA binding sites are energetically accessible and chemically addressable. *bioRxiv : the preprint server for biology*.

Baumer ZT, et al. (2026) Computational redesign of a thermostable T7 RNA polymerase. *Protein engineering, design & selection : PEDS*, 39.

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

Walsh KE, et al. (2026) CPSF73 activation and 3' RNA polymerase II pausing are lost during readthrough transcription after heat shock. *Cell reports*, 45(3), 117039.

Tak U, et al. (2026) Bacterial 2',3'-cGAMP activates a SAVED effector to form membrane-disrupting filaments and restrict phage replication. *Cell host & microbe*, 34(4), 720.

Ugay DA, et al. (2025) A Distinct Mechanism of RNA Recognition by the Transcription Factor GATA1. *Biochemistry*, 64(6), 1193.

Roberts JE, et al. (2025) UBQLN2 is necessary for UBE3A-mediated proteasomal degradation of the domesticated retroelement PEG10. *Journal of cell science*, 138(24).

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

Sullivan AE, et al. (2025) The Panoptes system uses decoy cyclic nucleotides to defend against phage. *Nature*, 647(8091), 988.