

Resource Summary Report

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Max Planck Institute of Biochemistry Cryo-EM Core Facility

RRID:SCR_025744

Type: Tool

Proper Citation

Max Planck Institute of Biochemistry Cryo-EM Core Facility (RRID:SCR_025744)

Resource Information

URL: <https://www.biochem.mpg.de/cryoem>

Proper Citation: Max Planck Institute of Biochemistry Cryo-EM Core Facility (RRID:SCR_025744)

Description: Facility for cryo-electron microscopy. Provides microscope access, training as well as scientific and technical support for MPIB-internal users wishing to perform cryo-EM experiments, from sample preparation to data processing.

Abbreviations: MPIB_CEMF

Synonyms: Max Planck Institute of Biochemistry Cryo-EM Facility, Cryo-EM Facility

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

Keywords: cryo-electron microscopy, sample preparation, data processing

Availability: Restricted

Resource Name: Max Planck Institute of Biochemistry Cryo-EM Core Facility

Resource ID: SCR_025744

Record Creation Time: 20240918T053245+0000

Record Last Update: 20260808T190731+0000

Ratings and Alerts

No rating or validation information has been found for Max Planck Institute of Biochemistry Cryo-EM Core Facility.

No alerts have been found for Max Planck Institute of Biochemistry Cryo-EM Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Kuhn CC, et al. (2026) Direct coupling of the human nuclear exosome adaptors NEXT and PAXT with transcription termination and processing machineries. *Nucleic acids research*, 54(4).

Farnung J, et al. (2026) The E3 ubiquitin ligase mechanism specifying targeted microRNA degradation. *Nature*, 652(8110), 784.

Kobayashi W, et al. (2026) Feed-forward loops by NR5A2 ensure robust gene activation during pre-implantation development. *Development (Cambridge, England)*, 153(1).

Andree GA, et al. (2026) Cysteine availability tunes ubiquitin signaling via inverse stability of LRRC58 E3 ligase and its substrate CDO1. *Nature communications*, 17(1).

Abbas DK, et al. (2026) Evolutionarily conserved spliceosome-exosome pathway in nuclear mRNA surveillance. *Genes & development*, 40(13-14), 1119.

Du J, et al. (2026) E2 variants for probing E3 ubiquitin ligase activities. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2524899122.

Farnung J, et al. (2026) The E3 ubiquitin ligase mechanism specifying target-directed microRNA degradation. *bioRxiv : the preprint server for biology*.

Zhuang Z, et al. (2026) Charged molecular glue discovery enabled by targeted degron display. *Nature chemical biology*.

Yuste-Checa P, et al. (2025) Structural analyses define the molecular basis of clusterin chaperone function. *Nature structural & molecular biology*.

Hermann MD, et al. (2025) Normal macrophage signaling and gene expression in Rosa26 Cas9-expressing mice. *ImmunoHorizons*, 9(11).

Maiwald SA, et al. (2025) TRIP12 structures reveal HECT E3 formation of K29 linkages and branched ubiquitin chains. *Nature structural & molecular biology*, 32(9), 1766.

Iermak I, et al. (2025) Molecular mechanisms governing the formation of distinct Upf1-containing complexes in yeast. *Cell reports*, 44(10), 116415.