

Resource Summary Report

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Max Planck Institute of Biochemistry Mass Spectrometry Core Facility

RRID:SCR_025745

Type: Tool

Proper Citation

Max Planck Institute of Biochemistry Mass Spectrometry Core Facility
(RRID:SCR_025745)

Resource Information

URL: https://www.biochem.mpg.de/mass_spectrometry

Proper Citation: Max Planck Institute of Biochemistry Mass Spectrometry Core Facility
(RRID:SCR_025745)

Description: Mass spectrometry core facility. Facility uses chromatography systems, mass spectrometers and workflows for in-depth analysis of biomolecules.

Abbreviations: MPIB-MS

Synonyms: Mass Spectrometry Facility, Max Planck Institute of Biochemistry Mass Spectrometry Facility

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

Keywords: Mass spectrometry, chromatography systems, mass spectrometers, biomolecules, analysis,

Availability: Restricted

Resource Name: Max Planck Institute of Biochemistry Mass Spectrometry Core Facility

Resource ID: SCR_025745

Record Creation Time: 20240918T053245+0000

Record Last Update: 20260808T190730+0000

Ratings and Alerts

No rating or validation information has been found for Max Planck Institute of Biochemistry Mass Spectrometry Core Facility.

No alerts have been found for Max Planck Institute of Biochemistry Mass Spectrometry Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Kosztik J, et al. (2026) Genomic and proteomic analyses of the maize root isolate *Rhodococcus erythropolis* NI86/21 reveal extensive genome plasticity and parallel evolution of herbicide degradation. *Applied and environmental microbiology*, 92(2), e0240725.

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

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

Li R, et al. (2026) Single-molecule dynamics of the TRiC chaperonin system in vivo. *Nature*, 652(8109), 481.

Andree GA, et al. (2026) Cysteine availability tunes ubiquitin signaling via inverse stability of LRR58 E3 ligase and its substrate CDO1. *Nature communications*, 17(1).

Kurscheidt K, et al. (2026) Composite SMG5-SMG6 PIN domain formation is essential for NMD. *Nature communications*, 17(1).

Guyot C, et al. (2026) IL4i1 activity generates oncometabolites that rescue neuroblastoma cells from oxidative death. *Cell reports*, 45(6), 117441.

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

Sauer J, et al. (2026) Metabolic adaptations of inflammatory macrophages govern ferroptosis susceptibility via the GCH1-BH4-iNOS axis. *Journal of immunology* (Baltimore, Md. : 1950), 215(6).

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

Kiss L, et al. (2025) UbiREAD deciphers proteasomal degradation code of homotypic and branched K48 and K63 ubiquitin chains. *Molecular cell*, 85(7), 1467.

Bauernfried S, et al. (2025) Inflammasome-independent IL-1?? activation via staphopain A protease of *Staphylococcus aureus*. *The Journal of biological chemistry*, 301(10), 110574.

Russier M, et al. (2025) Differential cell survival outcomes in response to diverse amino acid stress. *Life science alliance*, 8(11).

Pravata MV, et al. (2025) DCHS1 Modulates Forebrain Proportions in Modern Humans via a Glycosylation Change. *bioRxiv : the preprint server for biology*.

Rodschinka G, et al. (2025) Comparative CRISPRi screens reveal a human stem cell dependence on mRNA translation-coupled quality control. *Nature structural & molecular biology*, 32(10), 1932.

Lubosch A, et al. (2025) The immune response against cancer is modulated by stromal cell fibronectin. *Neoplasia (New York, N.Y.)*, 67, 101196.

Speidel JD, et al. (2025) Phosphorylation of SNX17 impedes activation of Retriever-mediated sorting. *The Journal of biological chemistry*, 301(6), 110222.

Klose CJ, et al. (2025) The EMC acts as a chaperone for membrane proteins. *Nature communications*, 16(1), 7097.

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