

Resource Summary Report

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Max Planck Institute of Biochemistry Imaging Facility

RRID:SCR_025739

Type: Tool

Proper Citation

Max Planck Institute of Biochemistry Imaging Facility (RRID:SCR_025739)

Resource Information

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

Proper Citation: Max Planck Institute of Biochemistry Imaging Facility (RRID:SCR_025739)

Description: Facility for light microscopy and flow cytometry. Users are instructed by staff in operation of hardware and software and, if necessary, are supported in acquisition, processing and quantitative evaluation of images.

Abbreviations: MPIB-IF

Synonyms: Imaging Facility, Max Planck Institute of Biochemistry Imaging Facility

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

Keywords: light microscopy, flow cytometry, images, acquisition, processing, quantitative evaluation of images,

Availability: Restricted

Resource Name: Max Planck Institute of Biochemistry Imaging Facility

Resource ID: SCR_025739

Record Creation Time: 20240918T053245+0000

Record Last Update: 20260804T043836+0000

Ratings and Alerts

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

No alerts have been found for Max Planck Institute of Biochemistry Imaging Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Bonnet J, et al. (2026) Histone modification cross-talk and protein complex diversification confer plasticity to Polycomb repression. *Genes & development*, 40(1-2), 43.

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

Sitron CS, et al. (2025) ??-Synuclein aggregates inhibit ESCRT-III through sequestration and collateral degradation. *Molecular cell*.

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

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