

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: access service resource, core facility, service resource

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: 20260821T194315+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 11 mentions in open access literature.

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

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

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).

Panevska A, et al. (2026) Optimizing spatial organization of FtsZ rings for large-scale constriction in synthetic cells. *Nature communications*, 17(1).

Steinek C, et al. (2026) Dynamic Binder Exchange Improves Protein Labeling Efficiency in DNA-PAINT up to 15-Fold. *Angewandte Chemie (International ed. in English)*, 65(11), e18685.

Tang X, et al. (2026) Metabolically regulated proteasome supramolecular organization in situ. *Cell*, 189(4), 1153.

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

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.

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

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.