Resource Summary Report

Generated by nidm-terms on Jul 28, 2026

Max Planck Institute of Biochemistry Biochemistry Core Facility

RRID:SCR_025743
Type: Tool

Proper Citation

Max Planck Institute of Biochemistry Biochemistry Core Facility (RRID:SCR_025743)

Resource Information

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

Proper Citation: Max Planck Institute of Biochemistry Biochemistry Core Facility (RRID:SCR_025743)

Description: Facility for bioorganic chemistry and biophysics. Offers services for studying protein structure and folding, protein-protein or protein-ligand interactions and protein complex formation, synthesis, purification and characterization of organic compounds, automated solid phase synthesis of peptides.

Abbreviations: MPIB-BCB

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

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

Keywords: bioorganic chemistry, biophysics, protein structure, protein folding, protein-protein interactions, protein-ligand interactions, protein complex formation, organic compounds, peptides

Availability: Restricted

Resource Name: Max Planck Institute of Biochemistry Biochemistry Core Facility

Resource ID: SCR_025743

Record Creation Time: 20240918T053245+0000

Record Last Update: 20260728T043729+0000

Ratings and Alerts

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

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

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

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.

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.