# Resource Summary Report

Generated by SPARC SAWG on Sep 14, 2026

## Max Planck Institute of Biochemistry; Martinsried; Germany

RRID:SCR_011380
Type: Tool

### Proper Citation

Max Planck Institute of Biochemistry; Martinsried; Germany (RRID:SCR_011380)

### Resource Information

**URL:** http://www.biochem.mpg.de/en/index.html

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**Description:** Proteins are the molecular building blocks and engines of the cell, and are involved in almost all processes of life. The scientists at the Max Planck Institute of Biochemistry (MPIB) investigate the structure of proteins and how they function from individual molecules up to whole organisms. With about 850 employees coming from 45 nations, the MPIB is one of the largest institutes within the Max Planck Society. In currently seven departments and about 25 research groups, scientists contribute to the newest findings in the areas of biochemistry, cell biology, structural biology, biophysics and molecular science. They are supported by several scientific, administrative and technical service facilities.

**Abbreviations:** MPIB

**Synonyms:** Max Planck Institute of Biochemistry, MPI of Biochemistry

**Resource Type:** institution

**Resource Name:** Max Planck Institute of Biochemistry; Martinsried; Germany

**Resource ID:** SCR_011380

**Alternate IDs:** GRID grid.418615.f ISNI 0000 0004 0491 845X Wikidata Q878218, nlx_97833

**Alternate URLs:** https://ror.org/04py35477

**Record Creation Time:** 20220129T080304+0000

**Record Last Update:** 20260912T195733+0000

## Ratings and Alerts

No rating or validation information has been found for Max Planck Institute of Biochemistry; Martinsried; Germany.

No alerts have been found for Max Planck Institute of Biochemistry; Martinsried; Germany.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 8 mentions in open access literature.

**Listed below are recent publications.** The full list is available at SPARC SAWG .


Boondam Y, et al. (2025) Comparative effects of standardized Centella asiatica extract (ECa 233) and its active compound mixture on proteomics and mitochondrial function. Scientific reports, 15(1), 29348.

Chen X, et al. (2023) The FXR1 network acts as signaling scaffold for actomyosin remodeling. bioRxiv : the preprint server for biology.

Shan B, et al. (2023) Protocol for quantitative proteomic analysis of heterogeneous adipose tissue-residing progenitor subpopulations in mice. STAR protocols, 4(4), 102676.

Wang H, et al. (2023) H3K4me3 regulates RNA polymerase II promoter-proximal pause-release. Nature, 615(7951), 339.

Molitor L, et al. (2023) Depletion of the RNA-binding protein PURA triggers changes in posttranscriptional gene regulation and loss of P-bodies. Nucleic acids research, 51(3), 1297.

Gerner MC, et al. (2021) Packed red blood cells inhibit T-cell activation via ROS-dependent signaling pathways. The Journal of biological chemistry, 296, 100487.

Antonyshyn JA, et al. (2019) Limited Endothelial Plasticity of Mesenchymal Stem Cells Revealed by Quantitative Phenotypic Comparisons to Representative Endothelial Cell Controls. Stem cells translational medicine, 8(1), 35.

Mondello P, et al. (2017) Dual inhibition of histone deacetylases and phosphoinositide 3-kinase enhances therapeutic activity against B cell lymphoma. Oncotarget, 8(8), 14017.