

## Details

### Bavarian Center for Biomolecular Mass Spectrometry (BayBioMS)

The Bavarian Center for Biomolecular Mass Spectrometry (BayBioMS) is a state-of-the-art science and technology platform of the TU Munich. It provides access to modern mass spectrometric equipment to research groups from the TU Munich, as well as to external research partners on a national and international level. The BayBioMS supports its partners with optimized methods for proteomic, metabolomic and bioinformatic applications in the diverse field of life sciences, including biomedicine, clinical, microbial, plant or food research.

**Address:** Gregor-Mendel-Strasse 4  
85354 Freising  
Bayern  
Deutschland  
[To website](#)

### Host Institution

**Technische Universität München**  
Arcisstrasse 21  
80333 München  
Bayern  
Deutschland  
<http://www.tum.de>

### Scientific Domain

**Primary Subjects:**

- Biology
- Medicine
- Agriculture, Forestry, Horticulture and Veterinary Medicine
- Chemistry

**Secondary Subjects:**

- Physics
- Mathematics

### Category

Genomic, Transcriptomic, Proteomics and Metabolomics Facilities

### Scientific Services

**Section Proteomics:** The BayBioMS offers the complete methodological spectrum of modern proteomics: - protein identification by LC-MS/MS from all organisms with sequenced genomes; - relative protein quantification using common approaches (SILAC, TMT, label-free); - absolute protein quantification using isotopically labeled reference peptides as well as label-free protein abundance estimations; - analysis of post-translation modifications (phosphorylation, acetylation etc.); - deep fractionations of peptides using different fractionation technologies (e.g. high pH reverse phase); - analysis of protein complexes; - project planning, execution, data analysis and publication

**Section Metabolomics:** The BayBioMS offers the complete methodological spectrum of modern metabolomics: - non-targeted metabolite profiling using TOF-MS in biological samples; - identification of Phase I oder Phase II reaction products or other biotransformations; - quantitative analysis of metabolites for example by means of stable isotope dilution analysis; - project planning, execution, data analysis and publication

## Scientific Equipment

- LC-MS/MS: Orbitrap Fusion Lumos Tribid
- LC-MS/MS: Q Exactive HFX
- LC-MS/MS: Orbitrap Exploris
- MALDI-TOF MS/MS: ultrafleXtreme
- LC-MS/MS: API 5500 QTrap
- LC-MS/MS: Triple TOF 6600
- GC-MS: GCMS-TQ8040

## Keywords

- Proteomics
- Metabolomics
- Bioinformatics

## Networks

**Collaborative Research Center 1371 („Microbiom Signatures“)**

<https://www.sfb1371.tum.de/de/>

**The European Proteomics Infrastructure Consortium providing access (EPIC-XS), Horizon 2020**

<https://epic-xs.eu>

**BMBF - CLINSPECT-M - Clinical Mass Spectrometry Center Munich**

<https://www.gesundheitsforschung-bmbf.de/de/clinspect-m-klinisches-massenspektrometrie-zentrum-munchen-10979.php>

## Users per annum

**Internal Users:** 40

**External Users in total:** 40

**External Users:** 25

**External Users in the EU:** 13

**External Users outside of EU:** 2