

## Details

### Mass Spectrometry of Biomolecules at LMU (MSBioLMU)

The service unit >>Mass Spectrometry of Biomolecules at LMU (MSBioLMU)<< is part of the Department Biology I of the LMU Munich. The service can be used by internal working groups, as well as by external research establishments. A range from small molecules / metabolites (Metabolomics) to large polypeptides (Proteomics) are detected and quantified routinely in different matrices. To this end, the service unit employs several mass spectrometers and chromatographs. Currently we are using a QTOF-MS/MS, a timsTOF-MS/MS and two GC-TOF-MS. Compounds are separated by gas or liquid chromatography (GC, LC, nano-LC). But also an analysis without any separation is possible. The service includes sample measurements, advisory service in experimental design and data exploration. To analyze the data, several software tools and mass spectral libraries are used.

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[To website](#)

### Host Institution

**Ludwig-Maximilians-Universität München**  
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80539 München  
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<http://www.uni-muenchen.de>

### Scientific Domain

**Primary Subjects:**

- Biology
- Chemistry

**Secondary Subjects:**

- Medicine
- Agriculture, Forestry, Horticulture and Veterinary Medicine

### Category

Genomic, Transcriptomic, Proteomics and Metabolomics Facilities

### Scientific Services

The service covers compounds ranging from small molecules (Metabolomics) to large polypeptides (Proteomics). To analyze metabolites the polar fraction of a sample is measured by GC-TOF-MS, fragmented and annotated using databases. Unknown compounds are evaluated as well and can be assigned to substance classes. In addition an identification using standards can be done. The non-polar fraction is analyzed by LC-timsTOF-MS/MS. An structure elucidation of single compounds is possible as well, performing additional fragmentation experiments. Lipid analysis (Lipidomics) is also possible. Large biomolecules / proteins are routinely proteolytic digested to obtain the peptide signature. These are analyzed via nano-LC-QTOF-MS/MS. Software tools like MaxQuant or ProteinScape are used for protein identification. MSBioLMU can analyze several matrices; from single gel bands or spots up to high complex cell extracts.

### Scientific Equipment

- nano-LC-QTOF-MS/MS
- LC-timsTOF-MS/MS
- GC-TOF-MS

- GC-TOF-MS
- HPLC
- nano-UHPLC

## Keywords

- Mass Spectrometry
- Metabolism
- Metabolomics
- Proteomics
- Plant Physiology

## Networks

**SFB TR175**

<https://www.tr175.bio.lmu.de/>

**PhotoRedesign (Redesigning the Photosynthetic Light Reactions)**

<https://cordis.europa.eu/project/id/854126/de>

## Users per annum

**Internal Users:** 15

**External Users in total:** 17

**External Users:** 15

**External Users in the EU:** 2

**External Users outside of EU:** 0