

## Details

### Protein analysis unit (ZfP)

Founded in 2002 as a core facility of four collaborative research centres (SFB413, 594, 596 and Transregio 5) the Protein Analysis Unit (Zentrallabor für Proteinanalytik, ZfP) has matured to become the first core facility of the Biomedical Centre (BMC), which renders services beyond the groups of the founding member laboratories. The ZfP is set up as a recharge facility to cover running costs. Currently (Nov. 2012) the ZfP operates one MALDI-TOF, one Quadrupole-TOF hybrid mass spectrometer and two high-resolution (FWHM > 60.000) mass spectrometers that were installed in April 2008 and in February 2011. The ZfP is furthermore equipped with a capillary electrophoresis system, an off-gel analyser and a stand alone capillary HPLC system that allow an elaborate pre-fractionation of samples to enable the ZfP to get a more thorough analysis of very complex mixtures. All measurements of the core facility are searched against public databases using various search algorithms (MASCOT, SEQUEST, X!Tandem and Andromeda). Quantifications are done using MaxQuant, Xcalibur and various software tools developed in house. Since 2015 the ZfP is located at the Protein Analysis unit of the LMU BioMedical Center in Martinsried-Großhadern.

**Address:** Großhadernerstr. 9  
82152 Planegg-Martinsried  
Bayern  
Deutschland  
[To website](#)

## Host Institution

**Ludwig-Maximilians-University of Munich**  
Geschwister-Scholl-Platz 1  
80539 München  
Bayern  
Deutschland  
<http://www.uni-muenchen.de>

## Scientific Domain

**Primary Subjects:**  
• Biology  
• Medicine

**Secondary Subjects:**  
• Chemistry

## Category

Genomic, Transcriptomic, Proteomics and Metabolomics Facilities

## Scientific Services

Molecular weight analysis by MS-MALDI (MALDI-TOF) Molecular weight analysis by ESI-MS (Q-TOF) Protein Identification by Peptide Mass Fingerprinting Protein Identification by LC-MSMS Off-line peptide separation by Stagetip, HPLC or IEF Characterization of protein post-transcriptional modifications (phosphorylation, acetylation, methylation, ubiquitylation). Characterization of protein-protein interactions Characterization of protein complex stoichiometry Quantitative analysis of label free, metabolic (SILAC) and chemically labeled (reductive dimethylation) proteins Inter- and intraprotein crosslink identification

## Scientific Equipment

- LTQ Orbitrap
- LTQ Orbitrap XL
- HPLC Ultimate 3000
- HPLC Ultimate
- MALDI Voyager STR
- QSTAR QTOF
- OFFGEL 3100 Fractionator
- ETTAN Micro HPLC
- Advion Nanomate
- Advion Nanomate LESA
- CE Electrophoresis System
- Server for Protein ID and Quantification

## Keywords

- Proteomics
- Protein analytics
- LC-MS/MS
- MALDI
- PMF
- SILAC
- Labelfree
- Crosslink
- Mass spectrometry
- Post translational modifications
- Histone modification

## Networks

**CIPSM Center for Integrated Protein Science Munich**

<https://www.cipsm.de/>

**STATegra-Statistical methods and tools for the integrative analysis of diverse -omics data**

<https://bioconductor.org/packages/release/bioc/html/STATegRa.html>

**EpiGenesys-Advancing epigenetics towards systems biology**

<https://www.epigenesys.eu/>

## Users per annum

**Internal Users:** 30

**External Users in total:** 35

**External Users:** 31

**External Users in the EU:** 3

**External Users outside of EU:** 1