

Equipment

- Thermo Scientific Orbitrap Elite mass spectrometer
- Thermo Scientific Q Exactive Plus Orbitrap mass spectrometer
- Thermo Scientific Ultimate 3000 RSLCnano liquid chromatography system (2x)
- Waters Alliance HPLC system for off-line peptide chromatography
- Gel electrophoresis (1D/2D) equipment

Data analysis:

- MaxQuant (peptide/protein identification and quantification)
- Perseus (statistical data analysis)
- Cytoscape (network analysis)







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Core Facilities – Technologies, equipment and expertise for ambitious research goals

The IZKF provides valuable resources for a cost effective and high-quality research environment by operating:

-  Brain Imaging Facility
-  Genomics Facility
-  Immunohistochemistry Facility and Confocal Microscopy Facility
-  Proteomics Facility
-  Transgenic Service
-  Two-Photon Imaging Facility
-  Flow Cytometry Facility

Multiple technologies and state-of-the-art equipment are available for all researchers of the Faculty of Medicine. Experienced technology experts provide services at any stage of the research process, including experimental design, method development, sample work-up and data interpretation on a partial cost recovery basis.

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Proteomics Facility

Qualitative/Quantitative Proteomics

Interactome Analysis

Targeted Protein Analysis

Identification and Quantitation of Post-Translational Modifications

Biomarker Identification

Dr. Christian Preisinger

Proteomics Facility

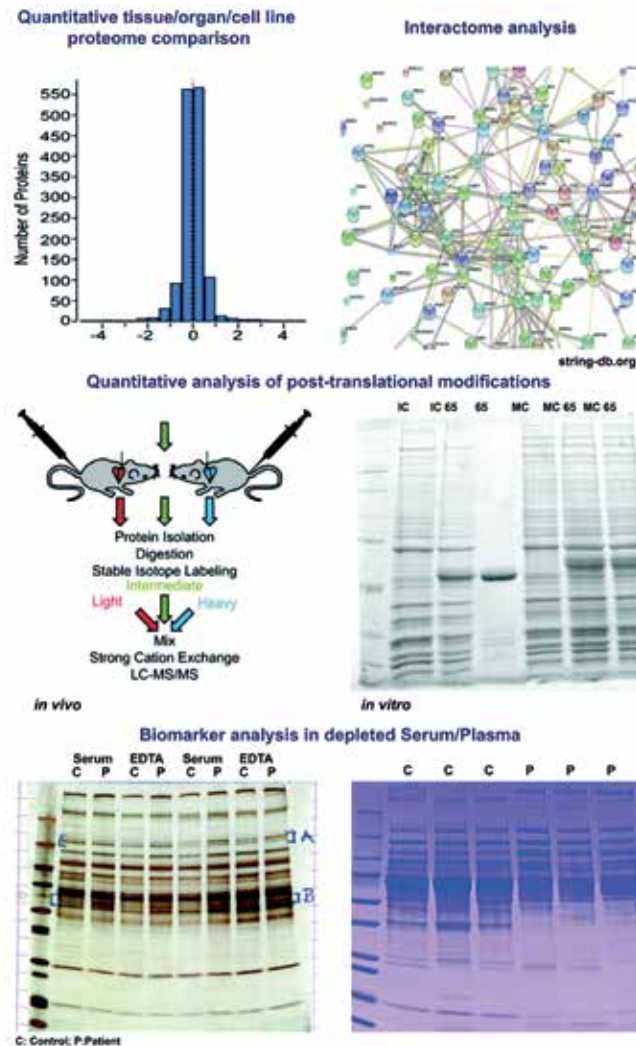
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Why use Proteomics and how to use it to your advantage?

Proteomics is the analysis of all proteins as well as their post translational modifications (PTMs) in cells, tissues, body fluids (such as serum/plasma) or entire organisms expressed by the respective genome at a given time point. This can be extended to in depth quantitative analysis of changes in protein (and PTM) levels in response to defined stimuli or disease states. These goals are usually achieved by a combination of sample separation techniques such as chromatography approaches and ultra high resolution mass spectrometry (nanoLC-MS/MS). Proteomics has become a standard analytical and extremely powerful research technology in essentially all research conducted within the medical faculty (molecular medicine, biochemistry, cell biology and systems biology).

The proteomics facility can aid in answering medically relevant questions, such as differences in tissue proteomes (e.g. liver or kidney samples from transgenic mice vs wt littermates) or changes in the phosphorylation pattern of the cellular proteome inferred by oncogenic signaling processes by using quantitative nanoLC-MS/MS. The proteomics facility provides support for the generation of such experimental setups and workflows based on the individual scientific question of the respective research group. This includes advice and suggestions for the process of appropriate sample generation (including proper controls). The facility also offers experimental support in protein enrichment strategies such as co-IPs and affinity purification as well as PTM-specific protein and peptide enrichment strategies (such as phosphopeptide analysis).



The Team of the Proteomics Facility

What services do we offer?

Pre-experimental consulting

- Sample generation, experimental conditions, biochemical prerequisites

Sample preparation

- Lysis of cells, tissues, organs
- 1D SDS-PAGE
- Sample lysis and proteolytic digestion (Trypsin, LysC, GluC, etc.)
- Peptide fractionation (reversed phase, ion exchange, and affinity chromatography), enrichment of phosphopeptides (pSer, pThr and pTyr) using TiO₂/Ti-IMAC or antibodies
- Mass spectrometry analysis from single proteins up to highly complex protein/peptide mixtures (cell lysates, immunoprecipitated complexes), analysis of modified peptides
- Data analysis (peptide/protein identification and quantification)

Data interpretation and advice on follow-up experiments