

Equipment

- Thermo Scientific Q Exactive Plus mass spectrometer
- Thermo Scientific Exploris 480 mass spectrometer
- Thermo Scientific UltiMate 3000 RSLCnano liquid chromatography system
- Thermo Scientific Vanquish Neo UHPLC liquid chromatography system
- Gel electrophoresis and Western blotting equipment

Data analysis:

- MaxQuant, MSFragger, Proteome Discoverer, DIA-NN (peptide/protein identification and quantification)
- Perseus (statistical data analysis)



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

The Interdisciplinary Center for Clinical Research (IZKF) provides valuable resources for a cost-effective, high-quality research environment.

A wide range of technologies and state-of-the-art equipment are available for all RWTH Aachen University researchers. Experienced technology experts provide services at every stage of the research process, including experimental design, method development, sample work-up, and data interpretation, on a partial cost recovery basis.

BIF Brain Imaging Facility

PF Proteomics Facility

CMF Confocal Microscopy Facility

FCF Flow Cytometry Facility

TF Transgenic Facility

2PIF Two-Photon Imaging Facility

IHF Immunohistochemistry Facility

GF Genomics Facility

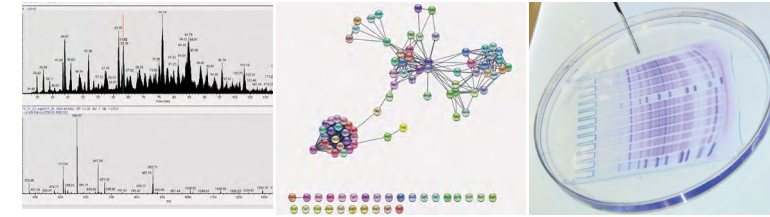


3D SRF Super Resolution Facility



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PF Proteomics Facility

IZKF

Qualitative/quantitative proteomics

Interactome analysis

Targeted protein analysis

Identification and quantitation of post-translational modifications

Biomarker identification

Dr. Christian Preisinger

Proteomics Facility

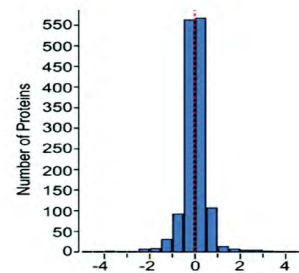
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Why use Proteomics Facility and how to use it to your advantage?

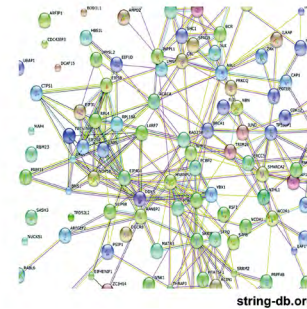
Proteomics is the of all proteins as well as, their post-translational modifications (PTMs) in cells, tissues, body fluids (such as serum/plasma or cerebrospinal fluid) or entire organisms expressed by the respective genome at a given time point. This can be extended to include in-depth quantitative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

The Proteomics Facility can aid in answering medically and biologically relevant questions, such as differences in tissue proteomes (e.g. liver samples from patients vs healthy controls) or changes in the phosphorylation pattern of the intracellular proteome inferred by oncogenic signalling by using quantitative nanoLC-MS/MS. The Proteomic 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 und suggestions relating to the process of appropriate sample generation (including proper controls) and adequate sample size. The Proteomics Facility also offers experimental support on protein enrichment strategies such as co-immunoprecipitations and affinity purification as well as PTM-specific protein and peptide enrichment strategies (e.g. phosphopeptides).

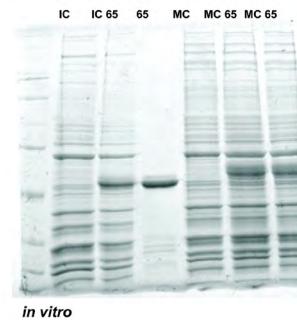
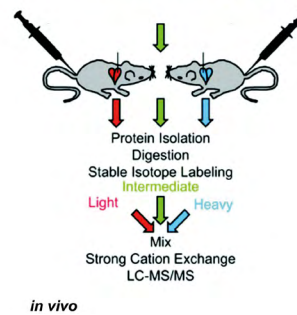
Quantitative tissue/organ/cell line proteome comparison



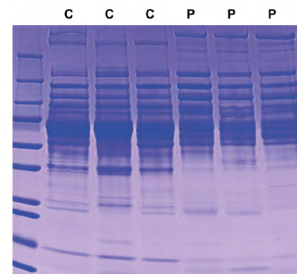
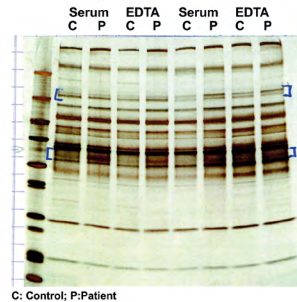
Interactome analysis



Quantitative analysis of post-translational modifications



Biomarker analysis in depleted Serum/Plasma



The Proteomics Facility team

What services do we offer?

Pre-experimental advice and support

- Sample generation, experimental conditions, biochemical prerequisites

Sample preparation

- Lysis of cells, tissues, organs
- Serum/plasma depletion
- 1D SDS-PAGE
- Proteolytic digestion of protein solutions or affinity-purified proteins on-bead (Trypsin, LysC, GluC, etc.)
- Peptide fractionation (high-pH reverse phase, strong anion/cation exchange), enrichment of phosphorylated peptides (pSer, pThr, pTyr) using TiO₂ or antibodies
- Mass spectrometry analysis from single proteins to highly complex protein/peptide mixtures using data-dependent and data-independent acquisition methods
- Data analysis (peptide/protein identification and quantification), bioinformatics