

Details

Proteomic Platform - Core Facility (ProtCF)

The Proteomics Platform Core Facility (ProtCF) is located at the Institute of Surgical Pathology (IKP) in Freiburg and supports mass spectrometry-based proteomics research. ProtCF handles projects from the Faculty of Medicine at the University of Freiburg, other university faculties, and external research collaborations. In addition to offering pure measurement services using state-of-the-art mass spectrometry methods, ProtCF also provides, upon request, support and execution of experimental design, sample preparation, measurement, data analysis, biostatistics, and data interpretation. The standard range of services includes: gel-free proteome analysis using Data Independent Acquisition (DIA) or Data Dependent Acquisition (DDA), co-immunoprecipitation (Co-IP) analyses, quantitative proteome comparisons using both label-free and label-based quantification methods (e.g., TMT), identification of post-translational modifications, identification of protease cleavage sites using N-terminomics, identification of proteins from gel bands, targeted proteomics, and proteomic analysis of a wide variety of sample types including cells from tissue culture, tissue from animal models, patient material (fresh tissue, urine, blood serum, liquor), cryo-conserved tissue, formalin-fixed-paraffin embedded tissue, and more.

Address: Breisacher Strasse 115a 79106 Freiburg Baden-Württemberg Deutschland <u>To website</u>

Host Institution

Universitätsklinikum Freiburg Hugstetter Strasse 55 79106 Freiburg Baden-Württemberg Deutschland https://www.uniklinik-freiburg.de

Scientific Domain

Primary Subjects:

- Biology
- Medicine

Secondary Subjects:

Chemistry

Category

Genomic, Transcriptomic, Proteomics and Metabolomics Facilities

Scientific Services

1) Identification of proteins and peptides with liquid chromatography electrospray tandem mass spectrometry (LC-MS/MS) or MALDI-MS. 2) Comparative quantitation (explorative) with the following techniques: label-free ("LFQ"), metabolic labeling ("SILAC"), or chemical labeling (dimethylation or tandem mass tags). 3) Data-independent acquisition (DIA) proteomics especially for explorative cohort studies. 4) Targeted proteomics (incl. quantitation) of peptide and protein panels with single/multiple reaction monitoring or parallel reaction monitoring. 5) N-terminomics for the investigation of proteases 6) For all aforementioned types of proteomics: sample preparation (gel-based or gel-free), also incl. chromatographic fractionation. 7) Data analysis with MaxQuant, Fragpipe, OpenMS, DIA-NN und Spectronaut for explorative proteomics; Skyline or OpenSwath for targeted proteomics or DIA, respectively. 8) Teaching and training in proteomics, especially for doctoral students in medicine or science or post-graduates.

Scientific Equipment

• timsTOF fleX mass spectrometer

- Q-Exactive+ mass spectrometer
- Evosep One Chromatography System
- 2x nanoflow HPLC
- Nitrogen Generator Genius XE Nitrogen
 Agilent Bravo (automated sample prep)
- Agilent 1100 HPLC (microflow)
- UV/VIS plate reader
- Server for data analysis

Keywords

- Proteomics
- Degradomics
- ٠ mass spectrometry
- MRM/SRM
- Data-independent acquisition (DIA)

Networks

Users per annum

Internal Users: 40 External Users in total: External Users: 4 External Users in the EU: 3 External Users outside of EU: 1

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