

Details

Proteomic Platform - Core Facility (ProtCF)

The proteomics platform ProtCF supports mass spectrometry based proteome research. ProtCF is based on a joint initiative by the Institute of Surgical Pathology and the Institute of Molecular Medicine and Cell Research at the Faculty of Medicine, University of Freiburg. Naturally, ProtCF is also open to users beyond the Faculty of Medicine. ProtCF supports the following areas of proteomics: (1) explorative identification and comparative quantitation of the proteome composition of complex biological systems such as cells, tissues, and bodily fluids. (2) targeted proteomics ("single/multiple reaction monitoring") of pre-selected proteins from complex proteomes together with the possibility of absolute quantitation. (3) spatially resolved proteomics ("Maldi Imaging"). ProtCF services further include project planning as well as sample preparation and data analysis. ProtCF special capabilities include the proteomic analysis of formalin-fixed, paraffin-embedded specimens and so-called "degradomic" techniques to investigate substrates and specificity of proteolytic enzymes. www.uniklinik-freiburg.de/pathologie-en/protcf100.html

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Host Institution

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<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) Spatially resolved, explorative proteomics ("MALDI Imaging"). 6) N-terminomics for the investigation of proteases 7) For all aforementioned types of proteomics: sample preparation (gel-based or gel-free), also incl. chromatographic fractionation. 7) Data analysis with t MaxQuant, Trans Proteomic Pipeline or OpenMS for explorative proteomics; Skyline or OpenSwath for targeted proteomics or DIA, respectively; Cardinal for Maldi imaging. 8) Teaching and training in proteomics, especially for doctoral students in medicine or science or post-graduates.

Scientific Equipment

- Q-Exactive+ mass spectrometer
- Fusion Lumos Tribrid Massenspektrometer
- TSQ Vantage mass spectrometer
- nanoflow HPLC for (1 - 3)
- AB/Sciex 4800 MALDI mass spectrometer
- iMatrix MALDI matrix sprayer
- Agilent 1100 HPLC (microflow)
- UV/VIS plate reader
- Server (24 CPUs) for data analysis

Keywords

- Proteomics
- Degradomics
- MALDI Imaging
- MRM/SRM

Networks

Users per annum

Internal Users: 10 (siehe auch mehrere beiliegende Unterstützungsschreiben)

External Users in total:

External Users: 4

External Users in the EU: 3

External Users outside of EU: 1