

Proteomik Plattform

- Core Facility (ProtCF)

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1. General

- The Proteomics Platform Core Facility (ProtCF) is a research infrastructure of the Medical Faculty of the University of Freiburg. ProtCF is based on a joint initiative of the Institute for Surgical Pathology (IKP) and the Institute for Molecular Medicine and Cell Research (IMMZ) of the Medical Faculty of the University of Freiburg.
- ProtCF is registered with the research infrastructure portal of the German Research Foundation (<u>https://risources.dfg.de/detail/RI_00486_de.html</u>).
- The terms of use are binding for all users of the ProtCF.

2. Management and Contact

- ProtCF is led academically by Professor Oliver Schilling, Institute for Surgical Pathology.
- Contact: <u>proteomics@uniklinik-freiburg.de</u>
- ProtCF is supported by further staff and scientists. ProtCF benefits from the experience, research and development of the supporting institutes (IMMZ, IKP) in the field of mass spectrometric proteomics. Current details can be found on the website (<u>www.uniklinik-freiburg.de/pathologie-en/proteomics-facility.html</u>).

3. Services

• A successful proteomic experiment depends on experimental planning, sample preparation, mass spectrometric measurement and data analysis. ProtCF supports all four aspects.

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- Before starting a proteomics project, a consultation with ProtCF should take place; this
 includes the experimental planning, coordination of cohort size and biostatistics, sample
 preparation, schedule, and possibly inclusion proteomics in an ethics vote
- ProtCF supports a variety of sample types, proteome techniques and proteome projects. Details of the sample hand-over (e.g. type of container, quantity, location) are adapted to project-specific needs in the first project meeting
- Before submitting samples, a form should be completed with project information and agreements. Details will be provided at the first project meeting
- "proteomics@uniklinik-freiburg.de" should be notified at least 24 hours before submission of the sample.
- ProtCF offers proteomic-mass spectrometric bioanalytics with the following available instrumentation (as of spring 2020):
 - Q-Exactive + mass spectrometer, coupled to nanoflow HPLC (at least 30 hours of measurement per week reserved for ProtCF)
 - TSQ Vantage mass spectrometer, coupled to nanoflow HPLC (at least 30 hours of measurement per week reserved for ProtCF)
 - For selected cases: Fusion Lumos Tribrid, coupled with Nanoflow HPLC
 - AB / Sciex 4800 MALDI mass spectrometer (at least 30 hours of measurement per week reserved for ProtCF) o
- The measurement options are currently (as of spring 2020) being expanded and modernized. Current updates are listed on the ProtCF website (<u>https://www.uniklinik-freiburg.de/pathologie-en/proteomics-facility.html</u>)
- ProtCF offers bioinformatic evaluation of the mass spectrometric data with the following available software:
 - Trans Proteomic Pipeline
 - o MaxQuant
 - OpenMS
 - o skyline
 - Cardinal •
- ProtCF supports the following quantification methods of explorative proteomics:
 - o Label-free
 - o SILAC
 - o dimethylation
 - Tandem mass tags
- ProtCF has particular experience in the proteomic analysis of formalin-fixed, paraffinembedded samples and in proteomic techniques for the characterization of proteolytic enzymes.
- Users are responsible for sample preparation.
- Upon request, ProtCF also offers sample preparation, including stable isotope labeling and chromatographic fractionation. The additional consumable costs are borne by the users.

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- ProtCF reserves the right not to measure samples that are visibly contaminated or that damage the device performance.
- ProtCF coordinates and starts the mass spectrometric runs and organizes the data transfer.
- Basic computer skills of the user, also for spreadsheets, are required.
- Training on proteomics is offered; usually once a year; more often if there is a corresponding demand.

4. Access

- The ProtCF user groups include:
 - 1. members of the medical faculty of the University of Freiburg,
 - 2. members of other faculties and institutes of the University of Freiburg,
 - 3. external academic users,
 - 4. non-academic users.
- The user groups can be prioritized in the above order (see also the section on prioritization below).
- Non-academic projects are only accepted if this is in accordance with the relevant regulations of the university or faculty.
- For external and non-academic users, it may be necessary to consult the contracting agency / central office for technology transfer..

5. Cost-contributions (fees)

- ProtCF users should participate in the expenditure.
- The usage costs are based on the recommendations of the DFG for mass spectrometry: "DFG form 55.04 - 06/16: Information on device usage costs and device centers"
- The usage costs are currently 25 EUR / h measurement time.
- Further bioinformatic data analysis (beyond mere "peptide spectrum matching") is 50 EUR / h.
- If the measurement capacities permit (prioritization see below), ProtCF welcomes projects with external users (outside of the University of Freiburg). A surcharge up to full cost recovery can be added. The support of the Technology Transfer Office of the University of Freiburg (ZFT) can be requested to coordinate the details.
- The cost of consumables is borne by users.
- Cost contributions by users may be subject to VAT. ProtCF focuses on research projects of the medical faculty. As of autumn 2019, it is being assumed that no VAT will be charged for transactions within the so-called "Buchungskreis 2".

6. Instrument usage and prioritization

- Projects of the Medical Faculty are prioritized over projects of other faculties or external projects.
- Academic projects have priority over non-academic projects.
 - Samples are usually measured on a "first-come-first-serve" basis
 - Priorities can be granted for projects with very time-critical deadlines (e.g. submission of revision publication, provisional data for an application with submission deadline).
 - Samples with similar mass spectrometric requirements can be bundled.



- For large projects, initial tests can be carried out to ensure the sample quality and the appropriateness of the mass spectrometric approach.
- In case of strong overbooking (more than four weeks waiting time for measurement time), ProtCF can consult external experts in the field of proteomics in order to include the scientific project content in the prioritization.

7. Publications

- For simple measurements, acknowledgment of ProtCF is appropriate.
- ProtCF strives for a collaborative approach to achieve optimal proteome results. For example, this approach can include comprehensive scientific advice on proteomic test planning and interpretation of the results in the context of the scientific question. In this context, the co-authorship of selected ProtCF members should be considered.
- The joint authorship of selected ProtCF members should also be considered if the proteome data (created or analyzed in collaboration with ProtCF) is a central or predominant aspect of a project
- The aspect of co-authorship or acknowledgment should be clarified (as far as possible) in the first project consultation.
- In both cases (co-authorship or acknowledgment), the presentation of the proteomic methodology, data, and results should be coordinated with ProtCF to ensure that the usual standards and requirements are met, e.g. in relation to the storage of raw data or the presentation of methodological details.
- If it is deemed probable that intellectual property will result from a project with ProtCF, the support of the Technology Transfer Office of the University of Freiburg (ZFT) should be used to clarify this topic accordingly.

8. Data storage, ethics, other

- Users are responsible for archiving their proteome data.
- Users are responsible for complying with the rules of data protection and ethical permission, especially for proteomic analysis of human tissue.

9. Signature of the responsible person

Freiburg, January 2020

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