



User Guidelines

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1. Services

The mission of the joint CECAD/CMMC Proteomics Core Facility is to offer mass spectrometry-based proteomics services and to continuously develop and establish new methods to further strengthen the analytical toolbox available to the users.

Services include but are not limited to:

- Identification of gel-separated and Coomassie-stained proteins
- Identification and site-localization of selected post-translational modifications
- Deep quantification of proteomes using data-dependent or data-independent approaches
- Analysis of Co-IPs using label-free or stable isotope labeling approaches (SILAC, TMT, iTRAQ, dimethyl labeling)
- Basic reversed phase and size exclusion fractionation
- Data analysis for all of the services listed above
- Storage of raw and processed MS data in publicly available repositories for publication
- Scientific advise for applications of 3rd party funding

2. Contact

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3. Equipment

- Q-Exactive HF-X coupled to EASY nLC 1200 UPLC
- 2x Q-Exactive Plus coupled to EASY nLC 1000 UPLC
- LTQ Orbitrap Discovery coupled to EASY nLC II
- TripleTOF 6600 coupled to Eksigent nanoLC 2D
- Agilent 1260 HPLC for offline fractionation
- PAL-RTC robotic system

4. Terms of usage

Research groups interested in using the services of the Proteomics Core Facility should make an appointment with the scientific staff of the facility to discuss the scientific background of the respective project, the most appropriate analytical technique as well as time and cost aspects.

All projects and corresponding samples will be registered in an online sample submission portal, accessible from within the university network. In general, the sample preparation is performed by the user. The technical staff of the facility can assist the user at any time during sample preparation.

All analyses are subject to user fees. Graduated prices apply to the different user groups defined in section 5. Please contact the facility for a quote. Bills are sent out quarterly. Charging for services does not preclude authorship on manuscripts. If the scientific staff of the facility have made a substantial intellectual and/or experimental contribution to a publication (e.g. experimental design, method development, data interpretation, figure design, text contributions, manuscript proofreading etc.) they should be treated as any other co-author, as it is stated in the „Good Scientific Practice“ [guidelines](#) of the German Research Foundation (DFG).

The facility reserves the right to reject samples if sample preparation requirements are not fulfilled or if the experimental design of the project was not discussed with the scientific staff of the facility prior sample handover.

5. Analysis priorities

The Proteomics Core Facility is in principle accessible for all researchers from academic research institutions. All samples will be processed and analyzed according to the date of handover to the facility. In case of high amounts of samples priority will be granted in the following order: (I) researchers affiliated to CECAD or CMMC, (II) researchers affiliated to the University of Cologne, the University Hospital of Cologne, or any of the Max-Planck Institutes from Cologne, (III) researchers from other academic research institutions. Exceptions will be made in urgent cases, for example if additional data is required for a manuscript in revision. The head of the facility ultimately takes the decision about the sample priority.

6. Data analysis

The scientific staff of the facility will conduct the data analysis. However, the users are free to choose to analyze the raw data on their own. Users can use the workstation available in the facility for data analysis. Raw data will be stored and archived by the facility on servers of the regional computing center of the University of Cologne (RRZK) and are made available to the user or uploaded to public repositories upon request.

7. Violation of guidelines

By making use of any of the services described above the user accepts the present guidelines. Future samples of a user can be rejected from analysis in case of violation of these guidelines.

Köln, 4-Jan-18



Christian K. Frese



Stefan Müller