

## Service Portfolio Core Facility Proteomics (CF Pro)

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### Our service

The core facility's services comprise mass spectrometric sample preparation including protease digestion, mass spectrometric analysis, and the primary processing and evaluation of data for both qualitative and quantitative purposes. The listed prices are strictly valid for research groups of the University Medical Center Göttingen (UMG), but can be extended to members of other institutions on the Göttingen Campus. For terms and conditions please see the User's Agreement document.

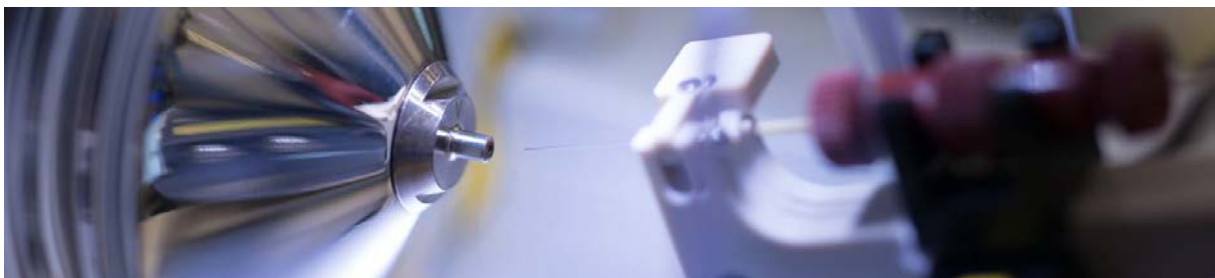
### Equipment

The Core Facility is currently equipped with the following analytical systems:

- Mass spectrometer Thermo Scientific Q Exactive (Hybrid Quadrupole/Orbitrap, QqOT)
- Mass spectrometer Bruker timsTOF Pro 2 (Hybrid Quadrupole/Time-of-flight, QqTOF)
- Pressure Cycler Barocycler 2320 EXT
- Chromatograph GE Äkta Pure 25
- Invitrogen Xcell SureLock™ Mini-Cell System

### Submitting projects and samples

Each set of analyses has to be preceded by a project discussion with a representative of the Core Facility to determine and agree on the goal of the analysis, the required steps, the associated cost, and the communication of data and results. Samples should be submitted directly at our laboratory (UBFT 3.D2 330) after arrangement via phone or mail.



### Contact information

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### Location

UBFT (UMG Main Building)  
Department of Clinical Chemistry  
3.C2 405 (Office) / 3.D2 330 (Lab)  
Robert-Koch-Straße 40  
37075 Göttingen

Service items	Time [h]	Cost/unit [€]
Molecular weight determination by ESI-MS	0.2	12
LC/MS/MS analysis of 2D gel spots after in-gel digestion	0.7	12
LC/MS/MS analysis of SDS-PAGE bands after in-gel digestion	1.0	17
LC/MS/MS analysis of complex samples after solution digestion	1.5/2.0/3.0	26/34/51
Pressure Cycling-based lysis and digestion (Barocycler EXT2320)	6.0	10
Ti-IMAC bead-based phosphopeptide enrichment	1.0	68
High pH RP-C18 fractionation, spin column	2.5	22
Custom data processing and annotation	1.0	48

All prices on display are for internal customers only (UMG, University of Göttingen and Göttingen Campus). External pricing is available on request and may include full cost calculation and V.A.T.

Additional cost might be incurred for the inclusion of blanks and QC experiments as necessary. The cost of analysis is agreed upon and documented using the "Project Agreement" form prior to analysis. Typical analysis packages based on workflow and complexity include:

Whole proteome analysis (incl. SILAC label) per sample	Time	Cost/Sample
SDS-PAGE separation of protein mixtures Fractionation into 23 equidistant slices, in-gel digestion	n/a	included
LC/MS/MS analysis, 23 fractions, 1 technical replicate + Blank + QC (1 h per injection)	25 h	425 €
Protein identification by database searching	n/a	included
(Quantitative evaluation of SILAC data)	1 h	48 €
<b>Complete offer per sample</b>	<b>25 (26) h</b>	<b>425 (473) €</b>

Affinity purification analysis (AP-MS) per sample+control	Time	Cost/Sample
SDS-PAGE separation of protein mixtures, fractionation into 11 equidistant slices, in-gel digestion	n/a	included
LC/MS/MS analysis, 2x11 fractions, 2 technical replicates (1 Sample, 1 Control) + 2Blanks + QC (1 h per injection)	47 h	799 €
Protein ID, quantitation by Spectral Counting and reporting	n/a	included
<b>Complete offer per sample</b>	<b>47 h</b>	<b>799 €</b>

DIA-MS label-free whole proteome profiling per 4 samples	Time	Cost/Sample
SDS-PAGE cleanup + in-gel digestion OR solution digestion	n/a	included
Spectral library generation: High pH RP-C18 12 fractions, LC/MS/MS analysis, 2 technical replicates, 2 h per injection	48 h	864 €
DIA-MS analysis for quantitation, 3 technical replicates, 2 h per injection incl. iRT standards	24 h	424 €
Protein identification by database searching	n/a	included
Quantitative evaluation of DIA-MS data	2 h	96 €
<b>Complete offer e.g. for 4 samples</b>	<b>72 h</b>	<b>1384 €</b>