

Core Facility – Proteomic Mass Spectrometry

MARTIN-LUTHER-UNIVERSITÄT
HALLE-WITTENBERG



Service Capability and Standard Costing 2023

Instrumentation

Peptide work

- ThermoFisher Exploris 480 with Ultimat3000 LC [Intact Proteins](#)
- Waters Synapt G2s Q-TOF with M-Class Acquity UPLC

MRMs

- Waters Xevo TQD with nanoAcquity LC (in cooperation with Department of Enzymology Mike Schutkowski's Lab)

Simple peptide/ small molecule

- Bruker ultrafleXtreme TOF/TOF

Further equipment

- Gel electrophoresis
- BioDrop - Opentrons 2

Software

Mascot Server

- ProteomeDiscoverer (with OpenMS nodes)
- Byonic Search Engine
- PEAKS studio
- PLGS and ISOQuant
- Intact MassTM
- Scaffold Q+S
- MaxQuant
- Perseus
- Skyline (with MSStats)
- R for Proteomics

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Typical Project Workflows

- In-Gel digestion and protein identification
- Intact protein mass measurement
- Protein characterisation (mutants/ domains/ recombinants/ termini etc.)
- Full gel lane analyses
- Small molecule MALDI measurements
- (Post) Affinity purification analyses
- (Post) Co-Immunoprecipitation
- Label and label-free quantitation (TMT tags, Label-free DDA & DIA)
- Single and multiple reaction monitoring (SRM, MRM)
- Large-scale discovery proteomics & validation
- PTM characterisation and localisation

The core facility has the capability to provide a full spectrum analysis from sample clean-ups through to statistical analyses and to contribute sections/materials & methods/figures for publications. It is essential that every user fully discusses their project or analytical aim with a facility representative. A project agreement sheet must be completed and signed before analyses can be performed.

Price List

Task Performed	Unit €
Digest ¹ incl. clean up ²	25
fractionation / enrichment spin columns ³	12
nanoESI (per hour) ⁴	25
MALDI spot (legacy)	15
Protein ID	15
Intact Mass Decovolution	15

¹ In Gel or USP3

² C18 or graphite spin tips

³ TiO₂ / High pH Fraction / SCX

⁴ In addition, we will be adding 20% surcharge for washes and QC samples