Core Facility
Proteomic Mass Spectrometry

MARTIN-LUTHER-UNIVERSITÄT
HALLE-WITTENBERG

Service Capability and Standard Costing

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

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 €
In Gel Digest	7
USP3	10
C18	10
TiO$_2$ spin columns	10
High pH Fraction columns	10
SCX column	10
MALDI spot (legacy)	12
nanoESI (per hour)	25
Protein ID	15
Intact Mass Decovolution	15