



Overview

We provide a full proteomic infrastructure for the identification and characterization of proteins that include various platforms for protein and peptide separation, and state-of-the-art mass spectrometry for MS and LC-MS/MS experiments.

Service

Our activity can be divided into:

- Mass Spectrometry Services
- Proteomics Services
- Data Analysis

All the services include appropriate scientific consultancy, assistance in pre- and post-analysis, data interpretation and a report of the analytical data.

Innovation

We are constantly updating our existing protocols, software and technologies to ensure the quality of our work. We continuously develop and improve new and existing protocols and tools and make them available for collaboration with researchers and customers.

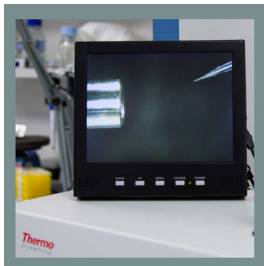
Quality

Our facility keeps updated with and works according to the newest guidelines for quality assessment for proteomics, such as the:

- “Universal Metrics for Quality Assessment of Protein Identifications”. [PMID: 16567383]
- “Recommendations for Mass Spectrometry Data Quality Metrics for Open Access Data”. [PMID: 22213554]

Services

MASS SPECTROMETRY

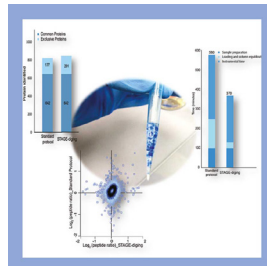


Molecular weight determination of intact proteins by ESI and MALDI mass spectrometry

MS-based determination of N- and C-termini of proteins and products of limited proteolysis

Peptide characterization via MALDI-TOF and MALDI-TOF/TOF

PROTEOMICS



Protein identification from gel or in solution

Targeted analysis (PRM)

Label Free quantification

Protein quantification by stable-isotope labeling (SILAC)

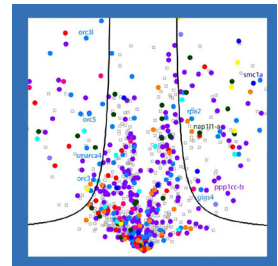
Identification of post-translational modifications

Phosphopeptides Enrichment (TiO2 and IMAC)

Multi-dimensional peptide separation (isoelectric focusing and liquid chromatography)

Proteomic profiling of simple and complex samples (IP, total cell lysate, secretome, isolated organelles)

DATA ANALYSIS



Results report and interpretation are provided with Proteomics state-of-the-art softwares:

Mascot, Sequest and Andromeda for protein identification and PTMs validation

Proteome Discover 1.4 for protein identification and PTMs analysis.

Skyline for targeted quantitation.

MaxQuant-Perseus for identification, quantification and statistical analysis.

Open source software packages (BioGrid, String, Enrich-R) for functional analysis.