



Overview

The **Proteomics** and **Metabolomics** unit provides a full infrastructure for the identification, characterization and quantification of proteins, metabolites and lipids. The unit includes several instrumental platforms for the separation of those molecules starting from simple or complex samples. The proteomics, metabolomics and lipidomics analysis rely on state-of-the-art mass spectrometry coupled with liquid chromatography (LC-MS/MS).

Service

Our activities can be divided into:

- Proteomics services
- Proteomics data analysis
- Metabolomics Services
- Lipidomics Services

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.

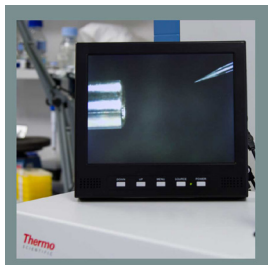
Quality

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

- "Lipid standards initiative guidelines". [lipidomicstandards.org/]
- "Universal Metrics for Quality Assessment of Protein Identifications". [[PMID: 16567383](https://pubmed.ncbi.nlm.nih.gov/16567383/)]
- "Recommendations for Mass Spectrometry Data Quality Metrics for Open Access Data". [[PMID: 22213554](https://pubmed.ncbi.nlm.nih.gov/22213554/)]

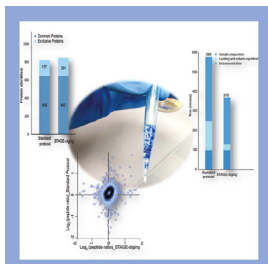
Services

MASS SPECTROMETRY



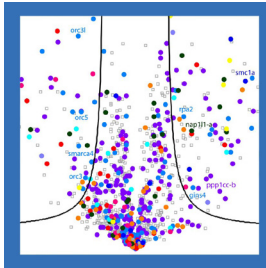
- Molecular weight determination of intact protein by ESI-MS
- Peptide characterization by nano-LC-ESI-MS
- MS data acquisition in DDA and DIA mode

PROTEOMICS



- Protein identification from gel and in solution
- Label Free quantification
- Protein quantification by stable-isotope labeling (SILAC)
- Identification of post-translation modifications
- Phospho-peptides enrichment (TiO₂ and TiIMAC)
- Proteomic profiling of simple and complex samples (IP, total cell lysate, secretome, matrisome, isolated organelles, tissues)

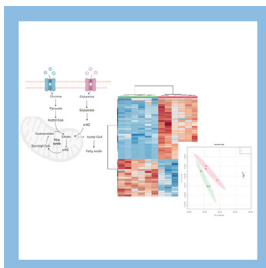
DATA ANALYSIS



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

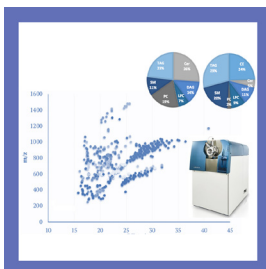
- Mascot, Sequest and Andromeda for protein identification and PTMs validation
- Proteome Discoverer 1.4 and Proteome Discoverer 2.4 with SequestHT for protein identification and PTMs analysis
- MaxQuant and Perseus for identification, quantification and statistical analysis
- Spectronaut 15.7 using a library-free (directDIA) and a library-based (DIA) approach for DIA-MS acquisition
- Open source software packages (BioGrid, String, Enrich-R) for functional analysis

METABOLOMICS



- Targeted metabolomics analysis (HILIC and RP)
- Semi-targeted metabolomics analysis
- Untargeted metabolomics analysis
- Stable isotope tracing
- Analysis of cell, tissues, yeast and other matrixes (intracellular and extracellular)
- Metabolomics data analysis: raw data, normalized data, graphs and statistical analysis (PCA, heatmaps and other) [Xcalibur MultiQuant, Metaboanalyst, R studio]

LIPIDOMICS



- Shotgun Lipidomics Analysis (nanoLC-MS/MS)
- Analysis of cell, tissues, yeast and other matrixes (intracellular and extracellular)
- Folch extraction (polar and apolar phase)
- Lipidomics data analysis (MSdial): raw data, normalization, graphs and statistical analysis (metaboanalyst)
- Lipid classes and unsaturation analysis