

Proteomics Platform

Category:

D. Nanomaterial exposure assesment

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Short technology description/Overview:

The platform is dedicated to various applications such as the analysis of complex protein mixtures, the comparison of proteomes under various conditions or treatments applied to the cell/tissue/organism studied, and the identification of proteins that are differentially expressed.

The electrophoresis facility, part of the proteomic platform, is focused on gel-dependent proteomics and in particular on the 2D-DIGE (difference in gel electrophoresis) technology, relying on a combination of equipments including the IPGPhor, Ettan DALT, a 2D Optimizer for gradients, the Typhoon Confocal scanner and the DeCyder 2D Software (GE-Healthcare). This approach allows to compare quantitatively the proteome of a treated cell or tissue sample versus an untreated sample. Recently we also developped an alternative CyDye labelling method centered on cysteines, intended to resolve the so called redox-proteome, which means the set of oxidized proteins (for example in cells or in body fluids).

The MassSpec facility combines different mass spectrometers.

- An ion trap HCT ultra (Bruker) with the possibility of electron-transfer dissociation (ETD) fragmentation. This MS can be coupled to a Dionex Ultimate 3000 nanoLC system.
- A maXis (Bruker) mass spectrometer. maXis is a high resolution mass spectrometer used for quantitative label free proteomics analysis, small molecules and proteins analysis. This electrospray ionisation MS is coupled to a 2D-LC system for gel free analysis.

A central bioinformatics server for storage and processing of MS data completes the proteomic platform (MASCOT, Matrix Science server integrated in ProteinScape, Bruker).

Up to now the facility has been mainly dedicated to identify proteins separated by 2D-DIGE gels but recently, we have also started gel-independent proteomics only relying on the MassSpec facility.

Our Platform offers various possible applications and services:

- Differential proteomics using the 2D-DIGE approach with a focus on subproteomics.
- Characterization & identification of posttranslational modifications (PTM) (phospho-, sumo-subproteomics, redox-proteomics).
- Quantitative proteomics: label free.
- Whole small protein analysis in complex samples.
- Interactome in the context of DNA-protein interactions.
- Proteomics in the field of eco-toxicology.

Main Features (Equipment Capabilities):

- With its ppm to sub ppm mass accuracy and its high resolution (30000 to 50000 FWHM) in MS and MSMS, the maXis mass spectrometer offers high confidence in protein identification specially in complex mixture analysis and targeted label free protein quantification.

Any further Information:

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