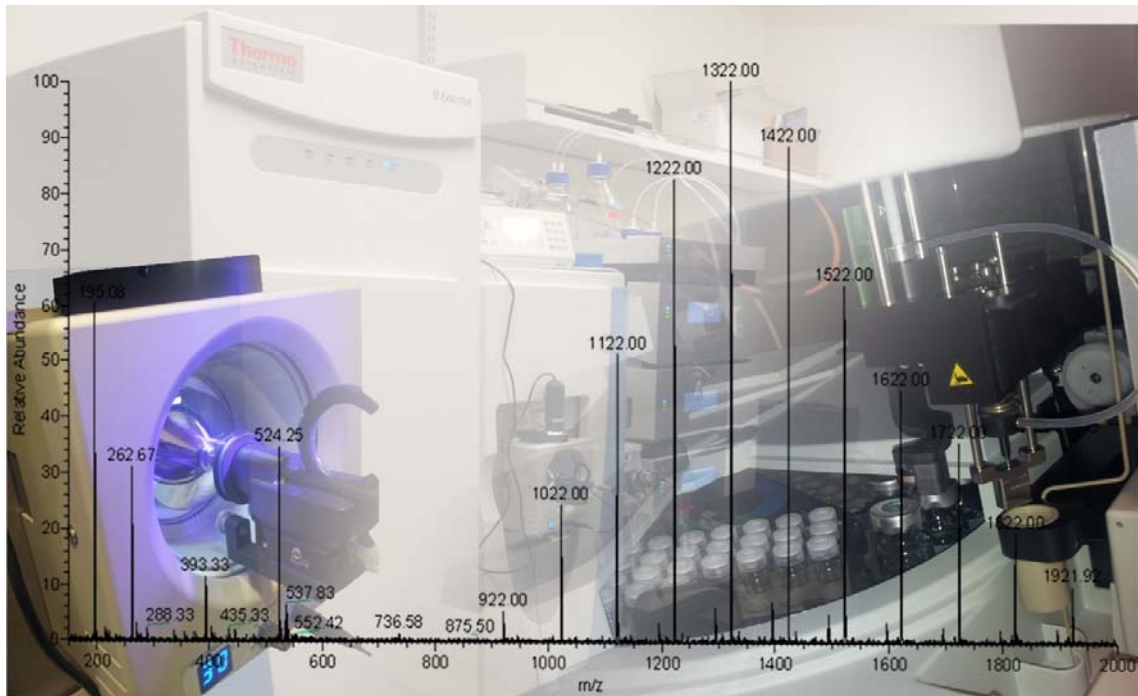


## Proteomics Platform

### Protein identification and quantification by mass spectrometry



The Proteomics Platform at the Université de Sherbrooke offers a wide range of mass spectrometry services for the entire research community. The main applications are the identification of purified proteins, proteins in complex samples and post-translational modifications as well as the use of quantitative proteomics methods (label-free, SILAC, iTRAQ). We offer sample preparation services including in-gel and in-solution tryptic digestion, desalting of samples using ZipTips and the bioinformatics support for the identification and quantification of proteins. It is also possible to obtain the necessary reagents for all stages of the experiments. The staff at the platform make their expertise available directly to the customer for the design, execution and analysis of their experiments.

#### Services

- Sample preparation
  - o Reduction, alkylation and Novex SDS-Page
  - o Tryptic digestion (in-gel and in-solution)
  - o Desalting by ZipTips
- Identification of proteins
  - o Analysis by nanoLC-MS/MS on Orbitrap
  - o Identification by MaxQuant and/or Proteome Discoverer
- Quantitative proteomics
  - o Label-free
  - o SILAC
  - o iTRAQ



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