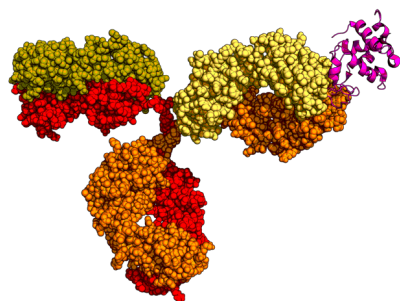




High Resolution Biological and Chemical Mass Spectrometry

The YSciCore Mass Spectrometry Facility supports academic and industrial research and innovation in the Greater Toronto Area. We are located in the Life Sciences Building at York University's Keele Campus. The Facility provides chemical and biological molecular analysis services using state-of-the-art liquid chromatography-mass spectrometry (LC-MS) techniques. We offer a number of workflows to support development in proteomics, metabolomics, small molecule, and high resolution accurate mass determination.



Services

The YSciCore Mass Spectrometry Facility at York University offers a wide range of MS and LC-MS services:

- High Resolution Accurate Mass (HRAM)
- Fragmentation and Structural Analysis (MSⁿ)
- Protein Intact Mass Determination
- Proteome Profiling (nanoLC-MS)
- Peptide Mapping (nanoLC-MS)
- Metabolome Profiling (LC-MS)
- Small Molecule Quantitation (LC-MS)
- Untargeted and Targeted Quantitative Proteomics (nanoLC-MS)

We understand certain workflows come with their unique requirements. The Facility offers flexibility in its service offerings and is happy to accommodate your specific needs.

Contact Us

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Mass Spectrometry Specialist
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Mass.Spec@yorku.ca

or visit
YSciCore.info.yorku.ca



YSciCore



Mass Spectrometry

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Proteomics

Proteomics is the qualitative and quantitative study of the proteome under physiological and pathological conditions. With our high-resolution Orbitrap Elite and Easy nanoLC1000 UPLC system, the facility can support numerous proteomic workflows such as:

- **Stable Isotope Labelling with Amino Acids in Cell Culture (SILAC)**
- **iTRAQ and Tandem Mass Tag (TMT) Labelling**
- **Label Free Quantitation**
- **Shotgun Profiling**

Bioinformatic tools and computers are able to sequence the enormous amount of data into protein quantities, interaction partners, and networks; which ultimately assist in understanding and developing better treatments for a variety of diseases. The Facility has licensed installations with recurring updates for the following software:

- **Proteome Discoverer 1.4**
- **Proteome Discoverer 2.2**
- **MaxQuant 1.6.2.3**

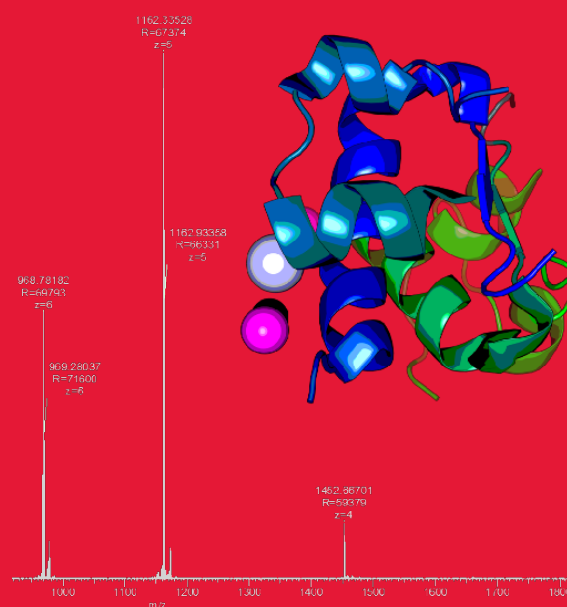


Biological Molecules

Proteins adopt a number of different conformations and modified states that occur both in the cell and during biopharmaceutical manufacturing. Identifying and quantifying these proteoforms is critical for developing a fundamental understanding of their function in health and disease, as well as providing information on their safety, efficacy, and stability as protein-based biotherapeutics.

The Orbitrap Elite is uniquely suited for proteoform discovery-based investigations and can provide multi-attribute methods (MAM) to monitor critical quality attributes including:

- **Post-Translational Modifications (Deamidation, Oxidation, Glycosylation, etc.)**
- **Changes in Protein Mass (Clips, Truncations, Mutations)**
- **Higher Order Structural Changes**



Small-molecule

Small molecule quantitative LC-MS/MS methods are a cornerstone in pharmaceutical ADME/DMPK studies, biomarker validation, clinical research, food safety, forensics, toxicology, and environmental analyses.

The YSciCore Facility houses an Agilent 1260 Infinity II Quaternary HPLC system that is capable of supporting a wide-range of small-molecule workflows in:

- **Metabolomics**
- **Lipidomics**
- **Small and large biological molecule characterization and quantitation**

