



PROTEOMICS AND METABOLOMICS

Mass spectrometry is one of the leading technologies to comprehensively identify and quantify proteins and other biomolecules in virtually every biological sample and environment. Due to its unparalleled sensitivity and accuracy, mass spectrometry is the method of choice for a plethora of applications ranging from biomarker discovery to absolute quantifications of biomolecules. Equipped with the latest mass spectrometric instrumentation, the Monash Proteomics and Metabolomics Platform combines cutting-edge technology with state-of-the-art methodology to provide the best possible results and expertise to customers and collaborators.

KEY INSTRUMENTATION

Mass Spectrometers

- Orbitrap Eclipse Tribrid (Thermo Scientific)
- 3x Orbitrap Exploris 480 (Thermo Scientific)
- Orbitrap Exploris 120 (Thermo Scientific)
- Orbitrap Fusion Tribrid (Thermo Scientific)
- 2x Q-Exactive HF Hybrid Quadrupole-Orbitrap (Thermo Scientific)
- Q-Exactive Plus Hybrid Quadrupole-Orbitrap (Thermo Scientific)
- Impact II (Bruker)
- TSQ Altis Plus (Thermo Scientific)

HPLC Systems

- Vanquish Neo UHPLC System (Thermo Scientific)
- Ultimate 3000 Rapid Separation UHPLC Systems (Thermo Scientific)
- LC1260 Preparative System (Agilent Technologies)
- Elute RSLC System (Bruker)
- Vanquish Flex UHPLC System (Thermo Scientific)

Liquid Handling Solutions, N-terminal Sequencer & Others

- PPSQ-53A Protein Sequencer (Shimadzu)
- Opentrons OT-2 (Opentrons)
- Kingfisher Duo Prime (Thermo Scientific)
- Signature Q100 (OLink)
- cellenONE X1 (Scienion)
- HDX Parallel Extended (Trajan)

WORKING WITH US

Fee for service
Consultancies
Collaborative research
Instrument access

PROTEOMICS SERVICES

Qualitative proteomics/shot-gun proteomics

Identifies as many proteins as possible in a sample.

Single Cell Proteomics

Identifies and quantifies proteins at the single-cell level.

OLink® Technologies

Provides high-quality measurements of protein biomarkers including cytokines and chemokines. We run Target96, Target 48, Flex and Focus assays.

Quantitative proteomics

By using label-based or label-free quantitative approaches such as Tandem Mass Tag (TMT) labelling, shotgun proteomics or data-independent acquisition mass spectrometry (DIA-MS), we can analyse global proteomic changes between any number of biological samples. More targeted methods such as Multiple Reaction Monitoring (MRM) or Parallel Reaction Monitoring (PRM) are also in place to quantify selected proteins with unprecedented sensitivity and accuracy.

Cross-linking mass spectrometry (CX-MS)

Identifies interacting domains and binding interfaces within proteins and protein complexes.

Hydrogen Deuterium Exchange (HDX)

Provides insights into folding, conformational changes, and overall structure of proteins and protein complexes.

Phosphoproteomics and Analysis of post-translational modifications (PTMs)

Provides detailed information on any PTM of interest on a single or global protein level.

Cellular Thermal Shift Assay (CESTA)

Detects changes in a protein's thermal stability upon ligand binding.

Intact Mass Determination/Top-Down Proteomics.

Determines the exact mass of any protein of interest and its top-down fragments.

De-Novo Protein and Antibody Sequencing

Deciphers the complete amino acid sequence of antibodies and proteins.

N-terminal sequencing

Identifies the exact N-terminal amino acid sequence of any protein!

METABOLOMICS & LIPIDOMICS SERVICES

Comparative Metabolomics

Quantifies as many metabolites as possible across samples and experimental conditions.

Targeted Metabolomic Analysis

Provides absolute quantitative measurements of metabolites of interest.

Stable Isotope Labelled Workflows

Enables functional studies of metabolic pathways.

Comparative Lipidomics

Quantifies as many lipids as possible across samples and experimental conditions.

Semi-Targeted Lipidomic Analysis

Provides absolute quantitative measurements of lipids of interest.

EXPERTISE

Our team provides academic and commercial researchers access to state-of-the-art proteomics, metabolomics and lipidomics technologies, as well as expertise to answer questions surrounding the identification, characterisation and quantification of proteins and other biomolecules.

MONASH PROTEOMICS AND METABOLOMICS PLATFORM

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