



Biomedical Proteomics Facility

Summary

Proteomics involves the separation and characterisation of many proteins from complex biological mixtures, to gain an impression of the proteins present in a fluid/tissue cell or the proteome at a particular point in time. Mass spectrometry provides superior information about a protein's characterisation compared with gene expression analysis alone.

The Monash University Biomedical Proteomics Facility has 'best of class' capability co-located and integrated with a wide variety of bioplatfroms such as protein production, x-ray crystallography, the Australian Synchrotron and monoclonal antibody production allowing the seamless conduct of commercial or academic multidisciplinary projects.

- Collaborative research
- Fee for service
- Consultancy or other flexible arrangements

Our expertise

The Monash University Biomedical Proteomics Facility is open to academic investigators from any institution as well as industrial clients. This service is complimented by research personnel with specialised know-how and expertise in the proteomics field as well as state-of-the-art proteomics equipment.

Infrastructure

The proteomics facility contains the following equipment:

Bruker Daltonics HCT Ultra Ion Trap with Electron Transfer Dissociation (ETD)

ETD is a new method of peptide and protein sequencing which allows mapping of the precise sites where proteins are phosphorylated.

The Ultra Trap is an "all rounder" instrument with best sensitivity and accuracy between MALDI and QToF with the following functionality:

- Protein identification with MS/MS sequencing;
- Basic mass analysis of peptides and proteins;
- Post translational modification analysis;
- Quantitation.

Bruker Daltonics Micro Q-ToF

Features

- Accurate mass determination of low mass molecules and peptides with 5ppm (sub Dalton level) accuracy
- Accurate mass determination of proteins (5ppm accuracy)
- Protein quantitation
- De novo sequencing



Bruker HCT Ultra Trap

Nano LC system

Features

- Sensitive separation of sub-picomole amounts of proteins and peptides prior to mass spectrometry analysis

The Multidimensional Nano LC, Bruker micro QToF and Ultra Trap HCT comprise the ARC Centre of Excellence in Structural & Functional Microbial Genomics Automated, Multiplexed, High Resolution Proteins Analysis Facility (AMHRPAF).

Applied Biosystems 4700 MALDI ToF ToF

Features

- Protein identification with peptide mass fingerprinting and ToF-ToF sequencing
- Basic mass analysis with sub 0.1Da accuracy of molecules up to around 5000Da. Using a less accurate mode larger molecules, to an almost limitless size, can be analysed
- Quantitation using isobaric tags such as iTRAQ™



Bruker Micro Q ToF

Procise N-terminal Sequencer

Features

- N-terminal Edman sequencing of proteins in solution or on PVDF membranes down to 12 pmol
- Gel Electrophoresis (PAGE) and imaging with a range of equipment for 1 and 2D electrophoresis and gel scanning including Difference Gel Electrophoresis (DIGE) capability

Services available

1 Protein Characterisation

The MALDI TOF microQToF instruments are used to determine the molecular mass of your protein(s) of interest.

2 Protein Quantification

Protein expression/quantitation at the level of 1D and 2D gels (DIGE), as well as multi dimensional LC technologies incorporating both affinity coded as well as isobaric tag (eg. iTRAQ™, ICAT, SILAC etc.) technologies. The relative abundance of selectively expressed proteins (i.e. in control and experimental extracts) can be ascertained using such isobaric tagging methods.

3 Protein Identification

Peptide mass fingerprint (PMF) analysis can be performed, supported by MS/MS sequence confirmation using the Applied Biosystems 4700 MALDI ToF ToF. This instrument is ideally suited to the high throughput identification of proteins or peptide bands/spots excised from 1D and 2D gels, or LC purified proteins. If difficulty is encountered in the identification of a protein due to low abundance, a sensitive LC MS/MS based protein identification on our Dionex nano LC coupled with the Bruker HCT Ultra Ion Trap can be used.

4 De novo and confirmatory protein sequencing

The Applied Biosystems Procise N-Terminal Sequencer provides the capacity to identify and absolutely confirm protein identity based upon N-Terminal sequence analysis (up to 40 amino acids) using automated Edman degradation chemistry.

5 Post-translational modifications

The Bruker HCT Ultra Trap with ETD capability is an extremely powerful tool for identifying and characterising post-translational modifications, as well as the precise site within a protein where the modification occurs.

Samples are submitted via a service request form which can be downloaded from our website.

For more information contact us or visit us at

www.med.monash.edu.au/biochem/facilities/proteomics/index.html

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Location

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Australian Government
Australian Research Council

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ARC Centre of Excellence in

