

TRI PROTEOMICS CORE

Proteomics is a technique that aims to study all protein components in a system. The TRI Proteomics Core can facilitate identification and quantitation of thousands of proteins in a single analysis. At the basic level, Proteomics can identify changes in proteins present with different treatment conditions. More advanced techniques can assist with characterising alterations of protein structure (modifications) and protein-protein interaction networks to help understand mechanisms of protein action.

The TRI Proteomics Facility provides a comprehensive Proteomics sample analysis service. Core facility staff can assist with all stages of the Proteomics workflow; from extracting proteins from whole cells and proteomics sample preparation, to sample analysis and comprehensive documentation of all work undertaken.

In addition to specialised services, the TRI Proteomics Core enables access to specialised sample preparation and sample analysis instruments.

The TRI Proteomics core is one of only a few Proteomics facilities within Australia where interested users can gain training in the operation of Robotic liquid handlers and high-end Mass Spectrometers. Contact the Proteomics Core for more information on training schedule.

Services

Sample preparation	Digest & clean-up: In-Gel Digest & clean-up: FASP Digest & clean-up: In-Solution Sample precipitation
Additional sample preparation	Detergent Removal with HiPPR™ Column SDS PAGE & colloidal coomassie staining FFPE antigen retrieval Immunoprecipitation C18-Sample Clean-up
Sample Mass Spec and Data Analysis	MS + Data Analysis Data Processing & Analysis Feasibility Testing
Assay Development	Sample Preparation Testing Method Validation

Capabilities

Q Exactive Plus with Ultimate 3000 RSLnano HPLC	Proteomics Data dependent analysis (DIA) Proteomics Data independent analysis (DDA) Proteomics Parallel Reaction Monitoring (PRM)
Q Exactive High Field with Ultimate 3000 RSLnano HPLC	Proteomics Data dependent analysis (DIA) Proteomics Data independent analysis (DDA) Proteomics Parallel Reaction Monitoring (PRM) Quantitative Proteomics (TMT)
Bravo Robot	BCA or Bradford protein assay Protein In-Gel digest Protein In-Solution digest Co-Immunoprecipitation C18 Sample clean-up
Direct Detect Spectrometer OffGel electrophoresis fractionator	Protein, peptide and lipid quantitation Isoelectric point separation of analytes for two-dimensional gel electrophoresis
Bioruptor Pico	Cell and tissue homogenisation DNA fragmentation
Proteome Discoverer	Identification and quantification for DIA and TMT mass spectrum data analysis
Spectrum Mill	Identification and quantification for DIA mass spectrum data analysis
Preview	Quick overview analysis of sample quality: digest efficiency, and modifications
Skyline	MRM, PRM, DIA, DDA mass spectrum analysis software
Panorama AutoQC	LCMS instrument performance evaluation