

WEHI Proteomics Facility

We employ the latest mass spectrometry innovations at the interface between basic and clinical research from experimental design, sample preparation, data acquisition, through advanced biostatistics.



Scan the QR code to see more about WEHI proteomics facility

Global Proteome Profiling
Differential protein expression
Subcellular fractions (e.g. secretome)

XL-MS (Crosslinking MS)
Structural proteomics
Protein dynamics & complexes

Clinical biofluid proteomics
Plasma, EVs, patient biofluids
Paired MS + Olink analyses*

PTM & Phosphoproteomics
PTM analysis (e.g. GlyGly)
Quantitative Phosphoproteomics

Cell surface labelling
Cell surface markers
Cell surface interactions

Immunoprecipitation-MS*
Protein-protein interaction networks
*Includes HA-tagged, FLAG-tagged

Intact 'Top Down' MS
Protein dynamics, Protein complexes
Protein isoforms (PTMs), Protein IDs

Proximity Biotin Labelling
In situ interactomics (TurboID)
Protein-protein interaction networks

Antibody de novo sequencing
Antibody characterisation
Epitope mapping

Low-input/LCM Proteomics
Low-input, high-sensitivity
Laser-capture microscopy samples

timsTOF Pro x2 (Bruker)
DIA
Cell Surface, Clinical Proteomics, Global proteomics

Impact II Q-TOF (Bruker)
DIA
TurboID, IP, HA-tag, FLAG-tag

Native MS Development

Orbitrap Eclipse (Thermo Fisher Scientific)
Intact MS 'top down'

maXis II Q-TOF (Bruker)
DIA
XL-MS, PTMs, Antibody sequencing, Low Input/GPF

Q-Exactive Classic (Thermo Fisher Scientific)
DIA
Low-Input Phosphoproteomics, LCM Proteomics

Orbitrap Astral (Thermo Fisher Scientific)
DIA
Low-Input Phosphoproteomics, LCM Proteomics

Small Molecule Development

Contact WEHI Proteomics



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