

Advanced Technology and Biology Division

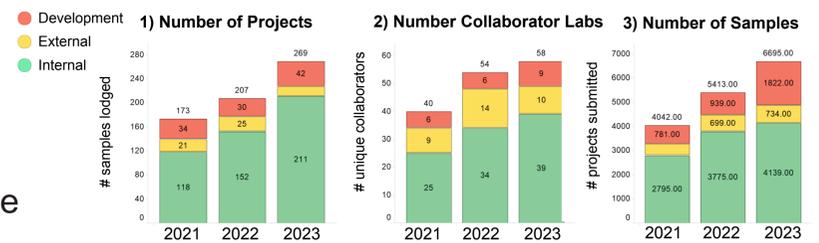
WEHI Proteomics Facility



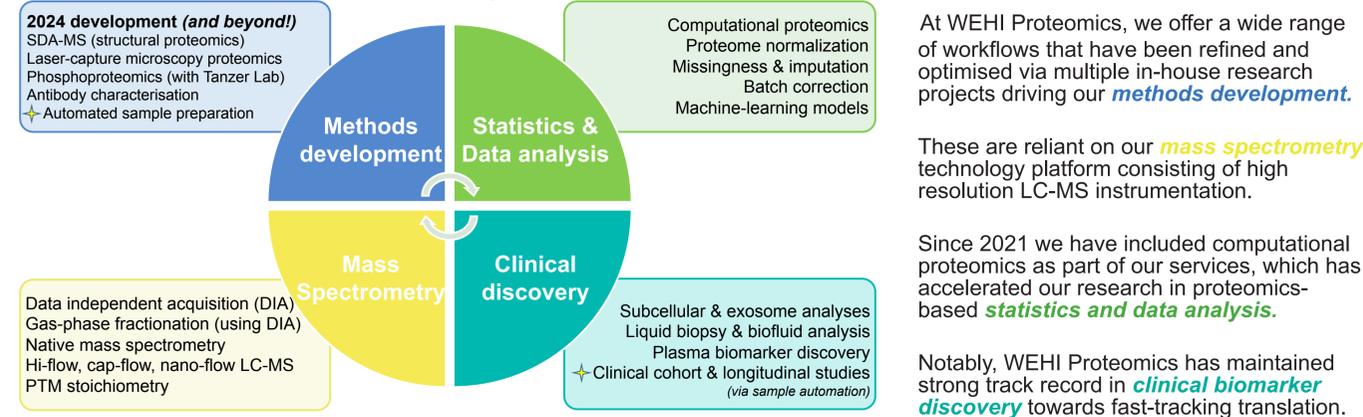
Established in 2021, we provide the latest mass spectrometric instrumentation for researcher-led exploration, identification and quantification of proteins and peptides. We are a team of 6 postdoctoral scientists specialising in mass spectrometry-based proteomics.

From experimental design and sample preparation, to data analysis and statistical evaluation, our staff can undertake a broad range of proteomics experiments on behalf of users which are cost-recovered at a WEHI-subsidised hourly rate.

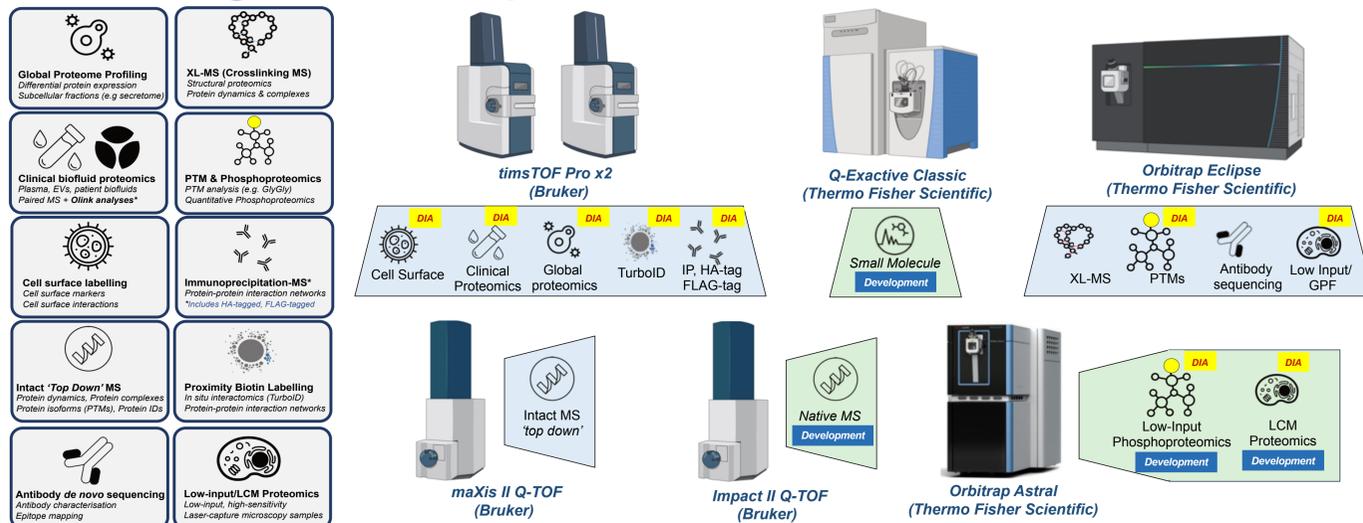
Between 2021-2023, we have processed >12,000 samples that were submitted by 90 collaborating labs (55 internal, 25 external) across 543 projects with an average completion time within 60 days of sample submission. We have overseen 106 development projects towards expanding proteomics workflows, totalling >3500 hours.



Current research projects / research interests



Technologies, techniques, and instrumentation



Recent Top Publications

- Meng, Y., Garnish, S.E., Davies, K.A. et al. *Phosphorylation-dependent pseudokinase domain dimerization drives full-length MLKL oligomerization.* **Nat Commun** 14, 6804 (2023).
- Low, R.R.J., Fung, K.Y., Gao, H. et al. *S100 family proteins are linked to organoid morphology and EMT in pancreatic cancer.* **Cell Death Differ** 30, 1155–1165 (2023).
- Triglia, T., Scally, S.W., Seager, B.A. et al. *Plasmeprin X activates the PCRCR complex of Plasmodium falciparum by processing PfRh5 for erythrocyte invasion.* **Nat Commun** 14, 2219 (2023).
- Roy, M.J., Surudoi, M.G., Kropp, A. et al. *Structural mapping of PEAK pseudokinase interactions identifies 14-3-3 as a molecular switch for PEAK3 signaling.* **Nat Commun** 14, 3542 (2023)

Services offered by WEHI Proteomics

1. MS sample preparation

WEHI Proteomics staff prepare samples for proteomics analysis. Users need only provide cell pellets, biofluids (e.g. plasma/urine), or cell/tissue lysates.

Our services include:
 Protein quantitation (e.g. BCA), sample enrichment (e.g. streptavidin affinity purification, exosome enrichment), C18 cleanup/peptide desalting, phosphopeptide and diGlyc enrichment.

Users can also be trained, or perform sample preparation supervised by facility staff.

2. MS instrument acquisition

Samples are queued, injected and analysed on one of our 7 mass spectrometers via liquid chromatography and MS spectra are acquired.

Our MS instruments include:
 2 x timsTOF Pro MS (Bruker)
 1 x Orbitrap Astral MS (Thermo)
 1 x Orbitrap Eclipse Tribrid MS (Thermo)
 1 x Q-Exactive Classic MS (Thermo)
 1 x maXis II Q-TOF MS (Bruker) (**Native MS**)
 1 x Impact II Q-TOF MS (Bruker) (**Intact MS**)

3. Proteomics data analysis

We have an in-house biostatistician (Dr Jumana Yousef) who assesses all data and undertakes data QC and statistical analyses (e.g. differential expression).

Our routine data analysis includes:
 • R markdown .html document which contains all steps performed in the analysis
 • Interactive Spotfire document of all results

We also undertake additional analyses upon request including time-course analysis, k-means clustering, correlation analysis, GO enrichment and more!

WEHI Proteomics charges an hourly rate for time spent by facility staff on:

- sample preparation
- MS instrument time
- data analysis

Our hourly rate is subsidised by WEHI for all internal researchers.

Note, we don't charge for pre-project meetings, **but we encourage them!**

Users should reach out to discuss future experiments before they begin collecting samples so we can help with experimental design and ensure the best results!

Meet the team

- Dr. Laura Dagley: Facility manager**
BBSMSc (Hons) Melbourne, PhD Melbourne
- Dr. Samantha Emery-Corbin: Deputy facility manager & clinical proteomics**
BSc (Hons), PhD Macquarie University
- Dr. Toby Dite: Structural, Intact and PTM Specialist**
BBSMSc (Hons) Melbourne, PhD Melbourne
- Dr. Dylan Multari: General Proteomics**
MRes, PhD Macquarie University
- Dr. Jumana Yousef: Bioinformatician/Statistician**
Statistics (MSc) NMSU, Bioinformatics (MSc) Melbourne, PhD Monash
- Dr. Vineet Vaibhav: Clinical and Cell Surface proteomics**
BSc BHU, Biotechnology (MSc) IIT Bombay, PhD Macquarie University

Recent achievements

Capacity

Since 2021, we have increased our capacity across the board resulting in an almost doubling of project submissions, collaborators and samples!

| Projects | Collaborators | Samples |
|-----------------|----------------|------------------|
| 2021: 139 | 2021: 34 | 2021: 3261 |
| 2022: 177 ▲ 27% | 2022: 48 ▲ 41% | 2022: 4474 ▲ 37% |
| 2023: 217 ▲ 56% | 2023: 49 ▲ 44% | 2023: 4873 ▲ 49% |

Accessibility

Due to method development improvements, we halved MS instrument times per sample, reducing sample turnaround times and saving \$\$ for users!

| Avg total hrs/sample | Avg MS hrs/sample |
|----------------------|-------------------|
| 2021: 80 | 2021: 40 |
| 2022: 40 | 2022: 20 |
| 2023: 20 | 2023: 10 |

Range

With our staff dedicating 0.2 FTE towards method development and protocol optimisations, we have several new methods available within our facility!

- Clinical biofluid proteomics
Plasma, EVs, patient biofluids
Paired MS = Olink analyses*
- Antibody de novo sequencing
Antibody characterisation
Epitope mapping
- Low-input/LCM Proteomics
Low-input, high-sensitivity
Laser-capture microscopy samples

Contact

Dr Laura Dagley, Proteomics Facility Manager
proteomicsfacility@wehi.edu.au

