# 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



# About WEHI proteomics

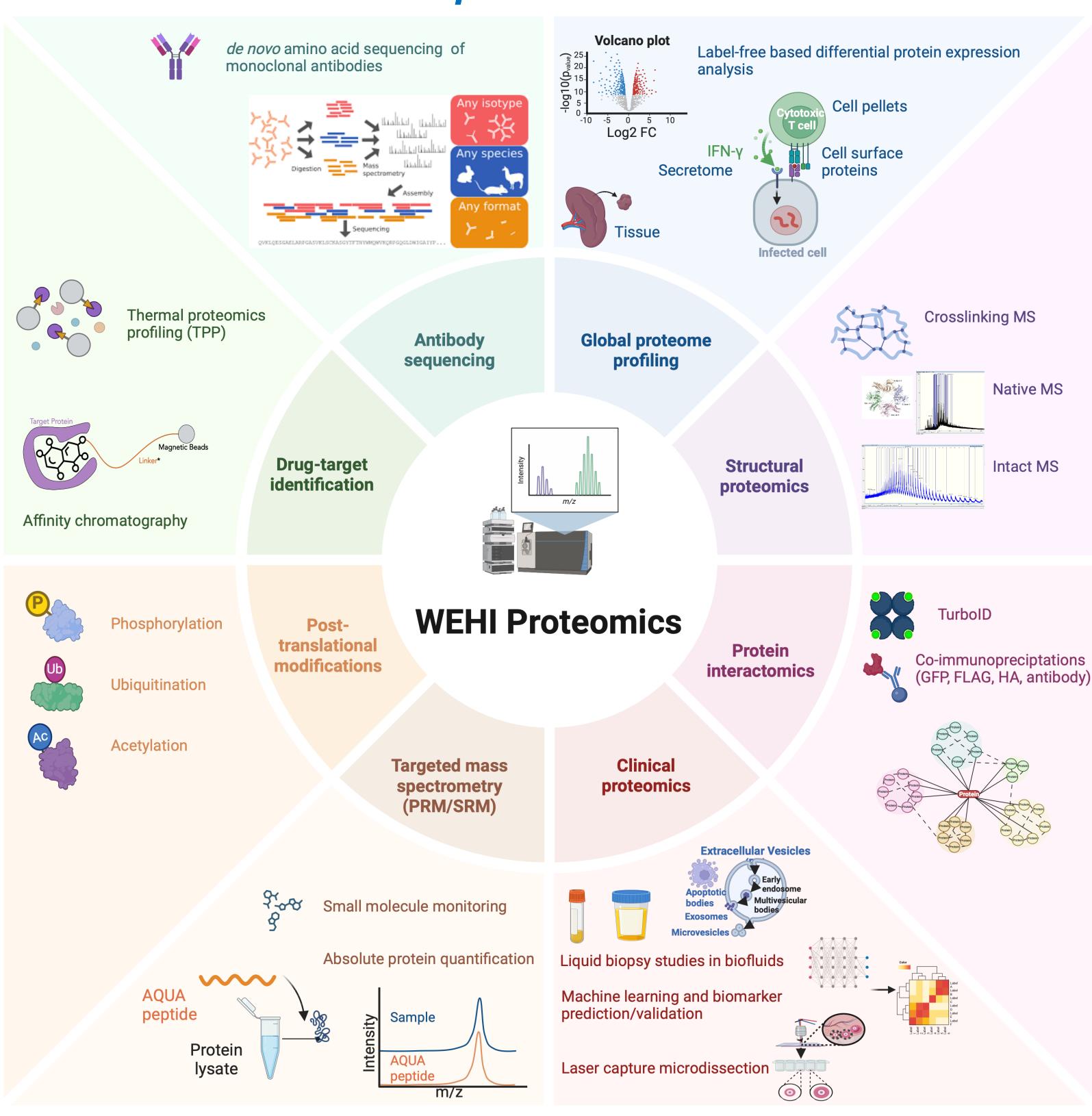
Established in 2021, we provide the latest mass spectrometric instrumentation for researcher-led exploration, identification and quantification of proteins and peptides. We are a multidisciplinary team consisting of research scientists, software engineers and biostatisticians with a common goal of specialising in mass spectrometry-based proteomics.

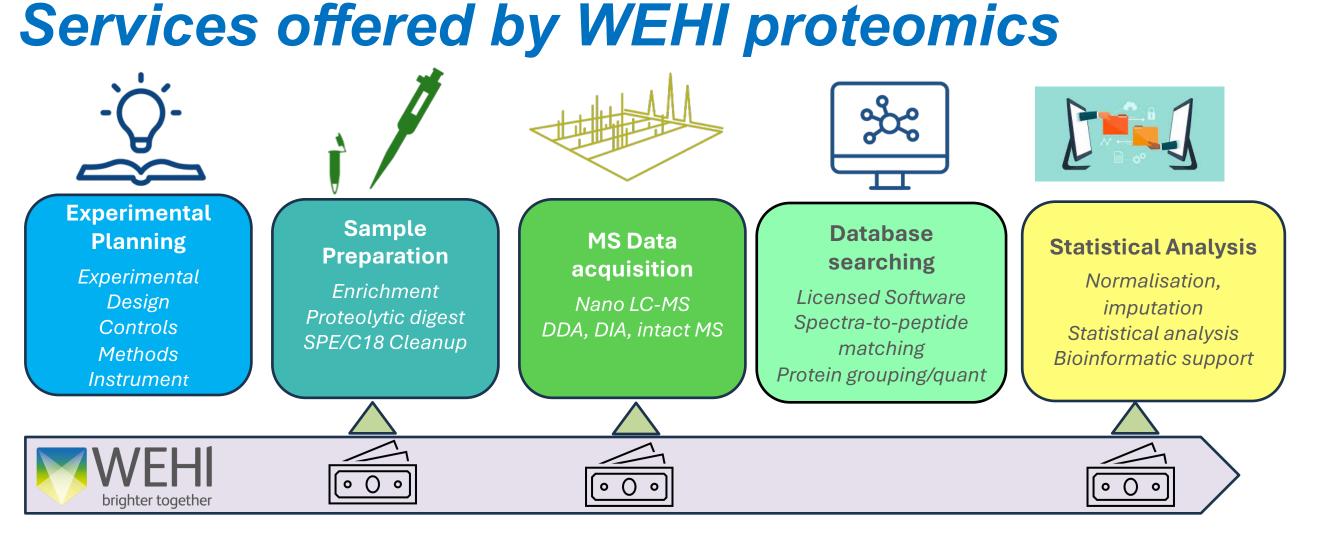
From experimental design and sample preparation, to data analysis and statistical evaluation, our staff can undertake a broad range of mass spectrometry-based proteomics experiments on behalf of users at an hourly rate which is subsidised for WEHI researchers.

While most of our users are from WEHI, we do work with external academics and commercial laboratories in Victoria and throughout Australia.



# Current capabilities and research areas

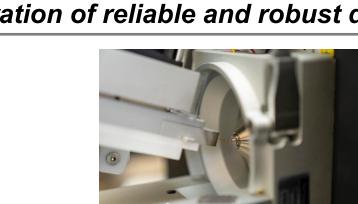




WEHI Proteomics charges an hourly rate for time spent by facility staff on: 1) Sample preparation

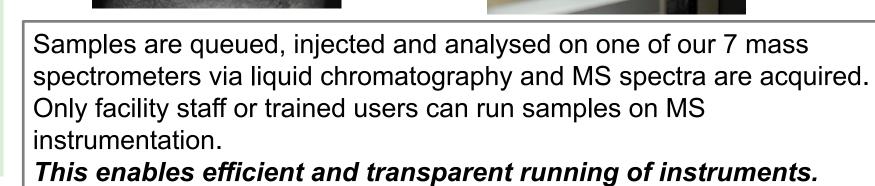


2) MS instrument time



Sample collection is performed by collaborators using recommended reagents/consumables/SOPs. Facility staff prepare samples for proteomics analysis. Users need only provide cell pellets, biofluids (e.g. plasma/urine), or cell/tissue lysates. This step is key to the generation of reliable and robust data.

Serum Plasma
Buffy Coalt
(white blood cells
and platelets)
Red blood cells



3) Statistical analysis



Facility staff set up database searches on raw MS data. Our in-house

biostatistician analyses all datasets and generates a data QC report as a .html (R markdown document). Analysed data is sent to users via Spotfire, an interactive visualisation tool for further interrogation. Users liaise directly with our in-house biostatistician and can request custom analyses.

Our hourly rate is subsidised by WEHI for all internal researchers and is fully cost recovered for external/commercial work.

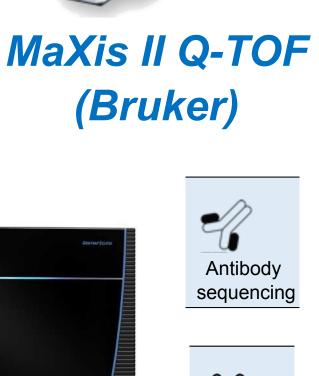
### The facility has 7 mass spectrometers and provides the latest mass spectrometric instrumentation:



Orbitrap Q-Exactive MS (Thermo Fisher)



Impact II Q-TOF (Bruker)



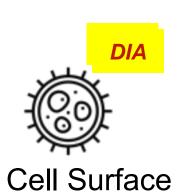
Orbitrap Eclipse Tribrid MS (Thermo Fisher)

(Thermo Fisher)

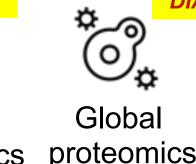


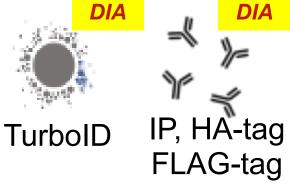
TimsTOF Pro HT (Bruker)

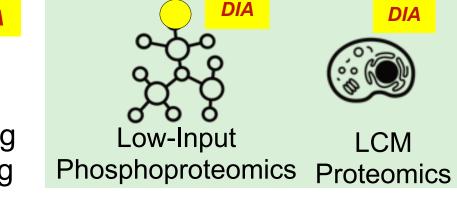
TimsTOF Pro MS (Bruker)









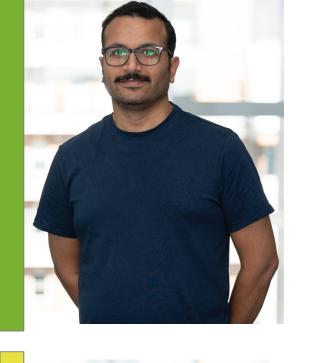


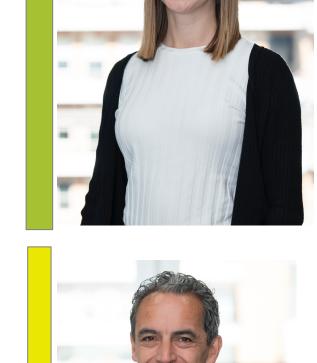


## Meet the team



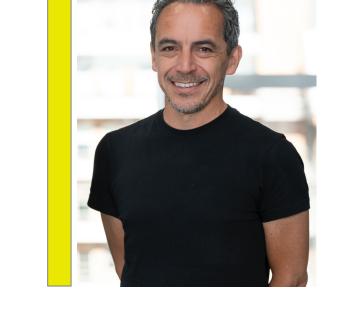












Dr. Jumana Yousef, Biostatistician Statistics (MSc) NMSU, Bioinformatics (MSc) Melbourne, PhD Monash

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Sukhdeep Spall, Lab manager BSc India, MSc (Biochem) India, MSc (Biotech) Melbourne

Dr. Steve Binos, LC-MS specialist BScience Monash, (Hons) Melbourne, PhD Melbourne

Julian Kelabora, Development & integration manager

BApSc (Information Technology), RMIT

# Recent top publications

- Callegari S, Kirk NS, Gan ZY, Dite T, Cobbold SA, Leis A, Dagley LF, Glukhova A, Komander D. Structure of human PINK1 at a mitochondrial TOM-VDAC array. Science. 2025;388(6744):10.1126/science.adu6445.
- Kauppi M, Hyland CD, Viney EM, White CA, de Graaf CA, Welch AE, Yousef J, Dagley LF, Emery-Corbin SJ, Di Rago L, Kueh AJ, Herold MJ, Hilton DJ, Babon JJ, Nicola NA, Behrens K, Alexander WS. Cullin-5 controls the number of megakaryocyte-committed stem cells to prevent thrombocytosis in mice. Blood. 2025;145(10):10.1182/blood.2024025406
- Kuo SF, **Spall S**, Emery-Corbin SI, Mohamed A, Dite T, Chow K, Hughes P, **Dagley LF**#, Webb AI#. Quantitative Proteomic Analysis Unveils Protein Concentration Effects in Neat Urine Compared to Urine Extracellular Vesicles. J Proteome Res. 2025 doi:10.1021/acs.jproteome.5c00060
- Cagigas ML, Masedunskas A, Lin Y, Emery-Corbin SJ, Yousef JM, Dagley LF, Olechnowicz S, Bowden R, Hayward R, Low G, Muirhead R, Brand-Miller J, Fogeltholm M, Raben A, Demaria M, Fuller SJ, Fontana L. Short-Term Severe Energy Restriction Promotes Molecular Health and Reverses Aging Signatures in Adults With Prediabetes in the PREVIEW Study. Aging Cell. 2025 Jun 16:e70123. doi: 10.1111/acel.70123.

