# The WEHI Proteomics facility: tools, techniques and technologies



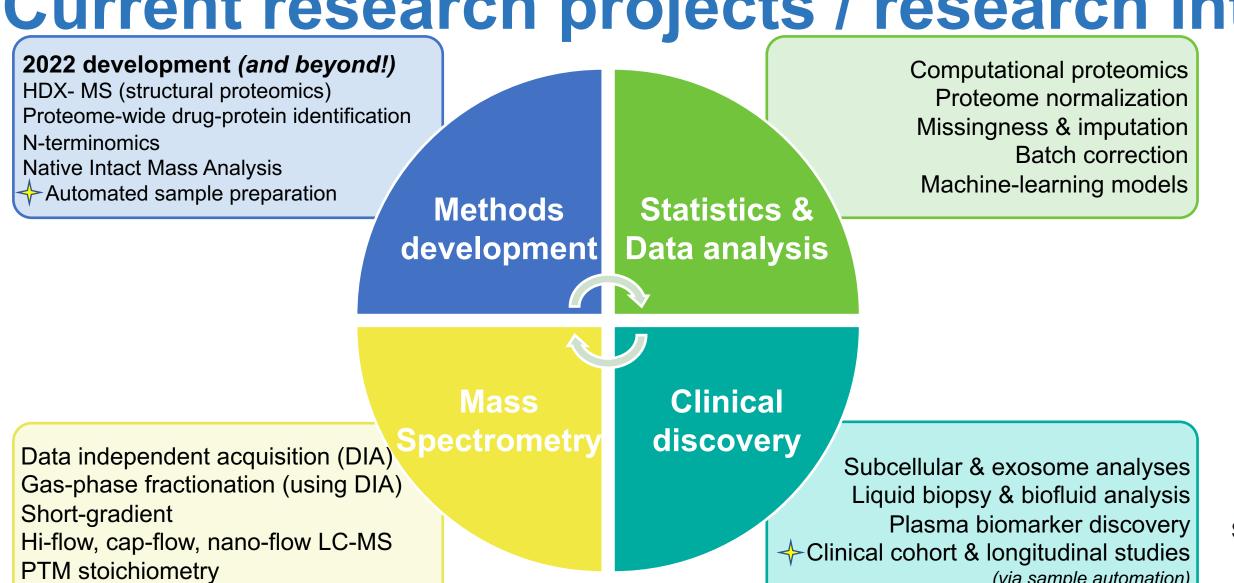
<u>Dagley LF<sup>1,2</sup></u>, Emery-Corbin SJ<sup>1,2</sup>, Dite T<sup>1,2</sup>, Yousef JM<sup>1,2</sup>, Adhikari S<sup>1,2</sup> and Vaibhav V<sup>1,2</sup>

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We provide the latest mass spectrometric instrumentation for researcher-led exploration, identification & quantification of proteins and peptides. Since 2021 we have hired 5 new staff 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 proteomic experiments which are cost-recovered for internal users at a WEHI-subsidised hourly rate and fully cost-recovered for external users. Since implementing these changes we have processed over 9500 samples which have been submitted by 70 collaborating labs (43 internal, 22 external) across 381 projects. We have also overseen 64 developmental projects, which include method development, totalling over 2000 hours towards expanding proteomic workflows at WEHI.

# 1) Number of Samples 2) Number Collaborator Labs 3) Number of Projects

#### Current research projects / research interests



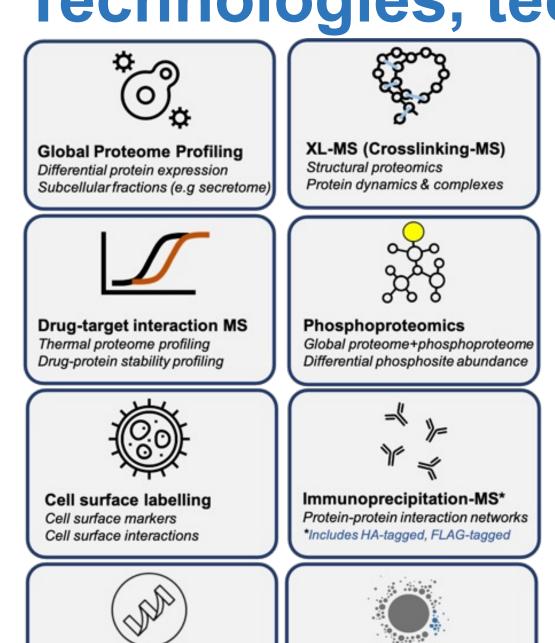
At WEHI Proteomics we offer a wide range of workflows that we are seeking to expand through multiple in-house research projects which drive our *methods development*. These are reliant on what we consider our key research interest, which is our mass spectrometry technologies and platform.

Since 2021 we have included computational proteomics as part of our services, which has accelerated our research in proteomic statatistics and data analysis.

Notably, WEHI Proteomics has maintained a strong track record in contributions for clinical discovery, towards fast-tracking translation.



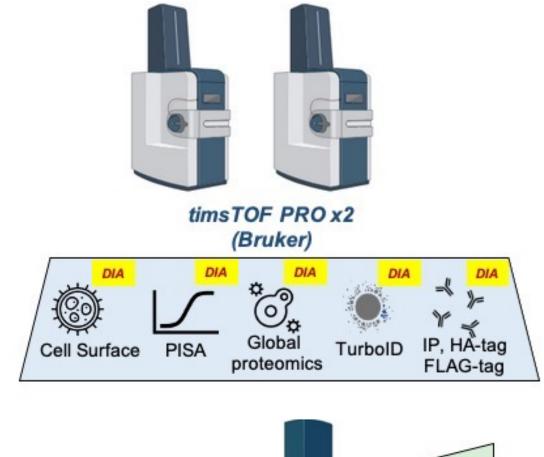
## Technologies, techniques, and instrumentation



Proximity Biotin Labelling

Protein-protein interaction networks

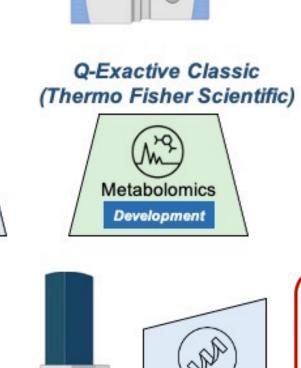
In situ interactomics (TurboID)



(DE)

HDX-MS

maXis II QTOF



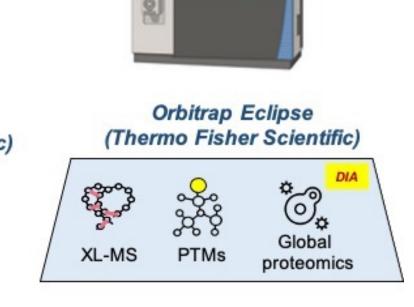
Impact II QTOF

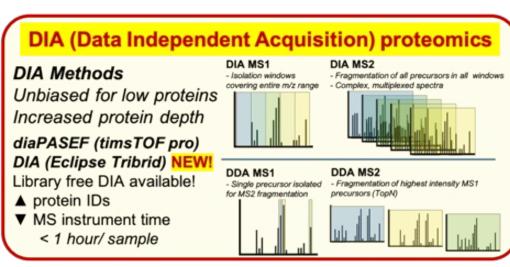
(Bruker)

Intact MS

'top down'

(via sample automation)





#### Centre for Cancer Biology

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research

**Outreach and outputs** 



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WEHI proteomics facility staff have authored over 71 publications with both internal and external collaborators in the last 5 years, including 9 first/co-first author contributions. We predominantly work with academic institutes from across Australia, but also offer fee-for-service research for commercial organisations.

### Services offered by WEHI Proteomics

LEAP HDX Robot

(PAL CTC)



#### 1. MS Sample Preparation

WEHI Proteomics staff prepare sample for proteomic analysis. Users need only provide cell pellets, biofluids (e.g. plasma), or lysates.

#### Our services include:

Intact 'Top Down' MS

Protein isoforms (PTMs), Protein IDs 📗

Protein quantitation (e.g. BCA), sample enrichment (e.g. streptavidin affinity purification, exosome enrichment), TPP (thermal proteome profiling), C18 cleanup/ desalting, phosphopeptide enrichment. Users can also be trained, or perform sample preparation supervised by facility staff.



2. MS Instrument Acquisition

Samples are queued, injected and analyzed on one of our 6 mass spectrometers, and MS spectra are collected for proteome analysis.

- 1 x Eclipse Oribtrap Tribrid (Thermo) 1 x QExactive Classic (Thermo)
- 1 x maXis QTOF (Bruker) (HDX/Intact only) 1 x Impact II QTOF (Bruker) (Intact Only)
- Our Instruments include: 2 x timsTOF pro (Bruker)

# 3. Proteomics Data Analysis

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

#### Our routine data analysis includes: R markdown document of all steps in

analysis Interactive Spotfire document of all results We also undertake additional analyses on request including timecourse analysis, kmeans clustering, correlation analysis, GO enrichment & more!

Since 2021, the Proteomics Facility charges an hourly rate for time spent by facility staff on 1) sample preparation, 2) MS instrument time and 3) data analysis. Our hourly rate is subsidised 40% 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 BBiomedSc (Hons) *Melbourne*, PhD *Melbourne* 

Dr. Samantha Emery-Corbin: Deputy facility manager BSc (Hons), PhD Macquarie University

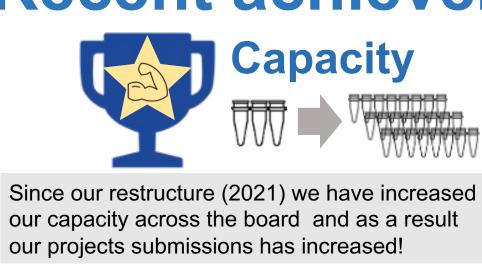
Dr. Toby Dite: Protein PTM specialist BBiomed (Hons) *Melbourne*, PhD *Melbourne* 

Dr. Subash Adhikari: Drug-target identification specialist MolBiotech (MSc) *Uni Bonn,* PhD *Macquarie University* 

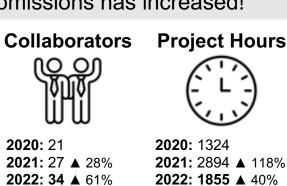
Dr. Jumana Yousef: Bioinformatician/Statistician Statistics (MSc) NMSU, Bioinformatics (MSc) Melbourne, PhD Monash

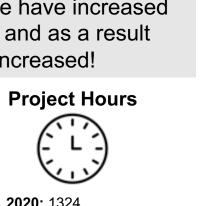
Dr. Vineet Vaibhav: Clinical and general proteomics BSc BHU, Biotechnology (MSc) IIT Bombay, PhD Macquarie University

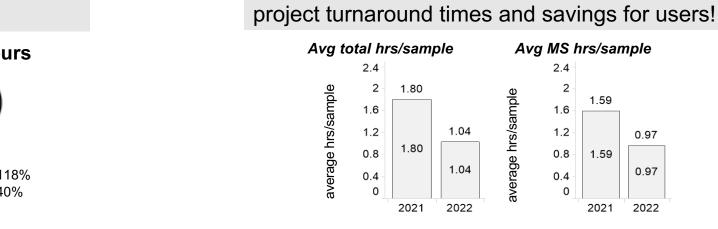
### Recent achievements



\*NB: Submissions shown January - August



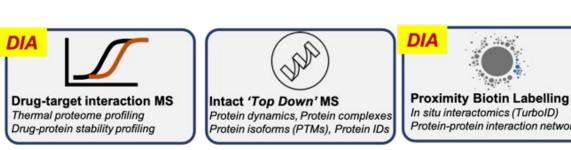








With our new staff expertise combined with our recent methods development we have many new services available at WEHI proteomics!



#### Contact

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



Due to method development in 2021, we halved

MS instrument time in 2022, meaning better

ccessibility