

28TH ANNUAL LORNE PROTEOMICS SYMPOSIUM

2 - 5 FEBRUARY 2023 | MANTRA LORNE

DELEGATE HANDBOOK

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DELEGATE INFORMATION

VENUE

Mantra Lorne

Mountjoy Parade, Lorne VIC 3232, Australia

P: (03) 5228 9777 | F: (03) 5289 1185

www.mantralorne.com.au

CONFERENCE SECRETARIAT

ASN Events Pty Ltd

9/37 Smith Street

Fitzroy, VIC 3065, Australia



Contact person on-site:

Jordyn Trolove | M: +61 (0)488 121 355 | email: jordyn.t@asnevents.net.au

REGISTRATION DESK

The registration desk will be open at the following times:

Thursday 2 nd February	2:00 PM – 7:00 PM
Friday 3 rd February	7:30 AM – 5:45 PM
Saturday 4 th February	7:30 AM – 6:00 PM
Sunday 5 th February	8:15 AM – 1:30 PM

EXHIBITOR PRIZE DRAW

You will receive a small card in the back of your name badge which is to be used to enter the prize draw. The prize draw will be completed in the last session on Sunday 5th February. To collect the stickers, please visit the exhibitors during Morning Tea, Lunch and Poster Sessions. Once you have received all starts fill out your details on the card and hand it into the registration desk.

For every prize draw card completed, Proteomics 2023 are donating \$5 to the Lorne CFA.


SPEAKER PRESENTATION INSTRUCTIONS

All conference sessions take place in the Convention Room 1. Audio-visual equipment will be supplied and there will be a technician on site to assist with any enquires. Mantra Lorne has a 16:9 screen. **Please make sure your presentation is in 16:9 format** to get the best image. It is the conference preference that ALL presentations be pre-loaded onto the laptop in the session room. Please bring your presentation to the meeting on a USB drive and give this to the technician in advance of the session you are participating in to allow for timely loading and testing. A remote mouse/laser pointer will be provided at the lectern. Please use the pointer to ensure delegates in the overflow rooms can follow as you present.

LIGHTNING TALK INSTRUCTIONS

Prior to each poster session there will be a “Lightning Talk” session. Authors of the selected lightning talks are requested to bring their presentation on a USB Flash drive and load it onto the computer within the lecture room by the morning tea prior to their Lightning Talk session, at the latest. **Presentations are limited to 2 minutes** (maximum 3 slides including any title slides).

POSTER PRESENTATION INSTRUCTIONS

Posters should be size A0 portrait orientation and can be attached to the poster boards with Velcro. Additional Velcro supplies can be obtained from the registration desk. The poster boards are located in the Exhibition Hall and numbered according to your numbers in the program (please refer to the poster listing on page 19 - 23) 

There will be 3 dedicated poster sessions:

- **Poster Session One:** Thursday 2nd February 2023, from 7:00pm – 10:00pm
- **Poster Session Two:** Friday 3rd February 2023, from 1:00pm – 3:15pm
- **Poster Session Three:** Saturday 4th February 2023, from 1:05pm – 3:15pm

You will be required to stand at your poster during your sessions for discussion.

POSTER SET-UP AND REMOVAL

- **Poster Session One:** Posters will be displayed from the start of the symposium on Thursday, 2 February and must be removed before the morning tea on Friday, 3 February.
- **Poster Session Two:** Posters will be displayed from the lunch session on Friday, 3 February and must be removed before the morning tea on Saturday, 4 February.
- **Poster Session Three:** Posters will be displayed from the lunch session on Saturday, 4 February and must be removed before morning tea on Sunday, 5 February.

SOCIAL PROGRAM

Welcome Reception (includes drinks & canapes)

Date: Thursday 2nd February
Time: 7:00 pm – 10:00pm
Location: Exhibition Hall

APS Annual General Meeting

Date: Friday 3rd February
Time: 4:45pm – 5:45pm
Location: Convention Centre
**for members only*

SoAPS Dinner with Invited Speakers (includes bbq & drinks)

Date: Friday 3rd February
Time: 5:45pm – 8:30pm
Location: Croquet Lawn, Mantra

APS Conference Dinner (includes food, drinks & music)

Date: Saturday 4th February
Time: 7:30 pm – 11:00pm
Location: Lorne Football Club



All delegates are invited to attend the social functions. The Welcome reception is included in your registration; however the APS Conference Dinner is an additional cost. If your name badge does not include a ticket and/or you haven't purchased a ticket for this event or would like to purchase an additional ticket for partners, friends, and children, please see the ASN staff at the registration desk.

BUS TRANSFERS

If you purchased a bus transfer departing TO Lorne from **Royal Parade (WEHI) at 12PM on Thursday 2nd February 2023**, the bus will be located outside or as close to The Walter & Eliza Hall Institute (1G Royal Parade, Parkville, VIC). This location is right next to Royal Melbourne Hospital. The bus will arrive approximately 15 minutes before the scheduled departure time and will depart at 12:00pm sharp for Lorne via Tullamarine (Melbourne) Airport.

If you purchased a bus transfer departing TO Lorne from **Tullamarine (Melbourne) Airport at 12:30PM on Thursday 2nd February 2023**, passengers should be in the blue Groups and Charters Bus (the L) zone, opposite the International Terminal (T2), ensuring they have boarded the bus no later than 12:30pm. The bus will have conference signage “LORNE PROTEOMICS 2023” on the front window.

If you purchased a bus transfer departing FROM Lorne on **Sunday 5th February 2023**, the bus will depart at 2:45pm sharp and return to Tullamarine (Melbourne) Airport (arrival time approximately 5:15pm) and then onto WEHI/University of Melbourne, Royal Parade (arrival time approximately 5:45pm)

IMPORTANT:

- *Please ensure you have checked out of your hotel and wait within Mantra Lorne Resort Foyer at least 10 minutes prior to the scheduled departure time*
- *Please allow for **2.5 hours to travel from Lorne** for flight bookings*

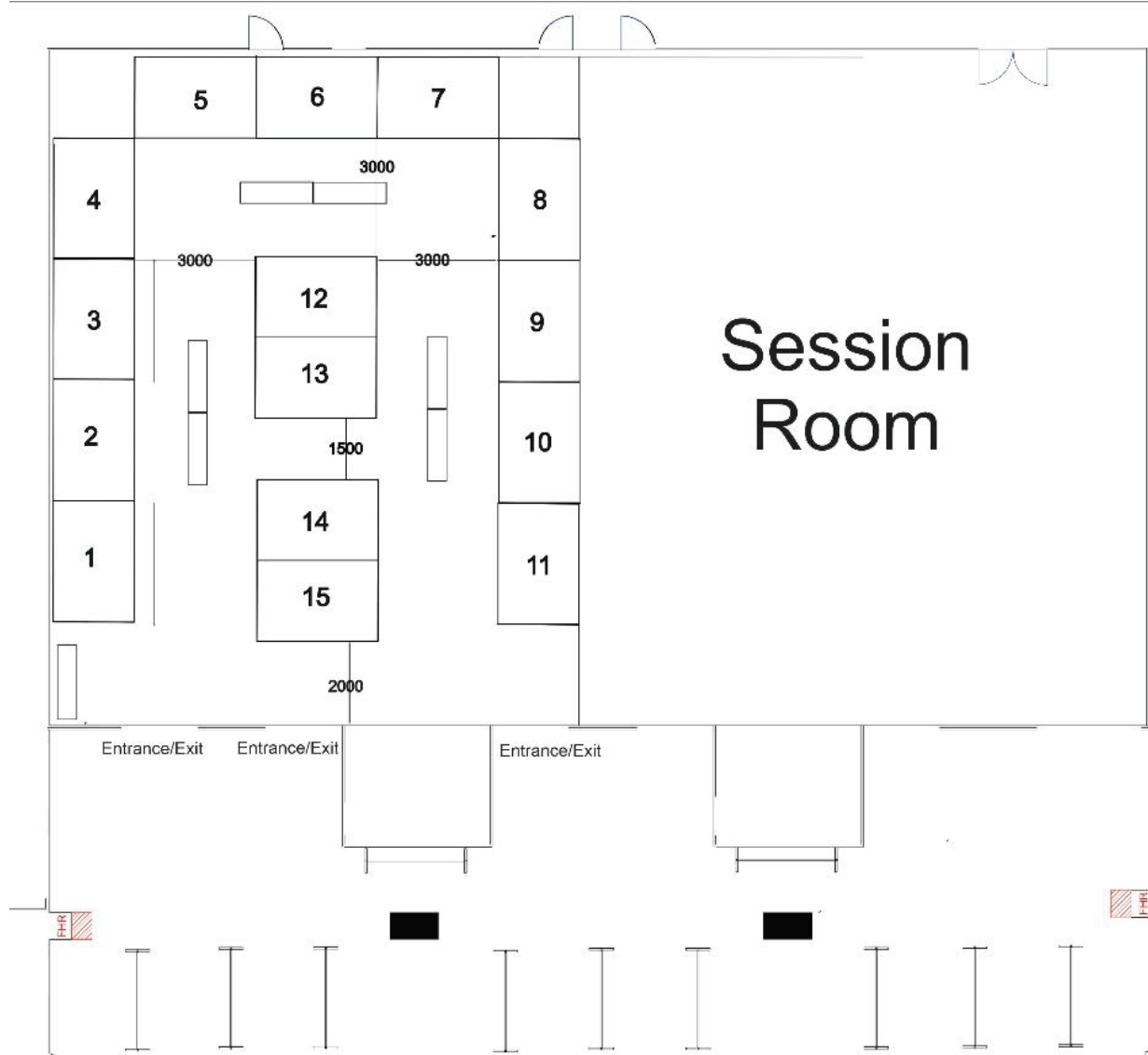
PARENT'S ROOM

The Walter and Eliza Hall Institute of Medical Research will be supporting parents with young children attending the Lorne Symposium in 2023. The room will have space for activities and play for children while parents will be able to listen to the presentations with the AV projection. The APS Committee once again applauds this initiative. We are grateful to the WEHI for their continued support of this initiative to enhance the accessibility of this conference to parents.

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EXHIBITORS



EXHIBITOR LISTING

Booth 1 – Shimadzu
Booth 2 – IonOpticks
Booth 3 – Accurate Mass Scientific
Booth 4 – Mimotopes
Booth 5 & 6 – Thermo Fisher Scientific

Booth 8 – Trajan
Booth 9 – Proteomics International
Booth 11 – Agilent
Booth 12 & 13 – Bruker
Booth 14 & 15 – SCIEX

INVITED SPEAKERS

INTERNATIONAL SPEAKERS



HYUN JOO AN
CHUNGNAM NATIONAL UNIVERSITY

Dr. Hyun Joo An is a professor at Chungnam National University (CNU) in the Graduate School of Analytical and Science and Technology. She is also director of the Asia-Pacific Glycomics Reference Site (AGRS), which develops and validates new analytical platforms for glycomic and glycoproteomic analysis in collaboration with government agencies and regional industry. She received her PhD from the University of California at Davis (United States) in 2003 and worked as an associate specialist and postdoctoral researcher at UC Davis. Dr. An returned to Korea and has been at CNU since 2011. Dr. An was also the co-founder of Glycometrix, Inc, an ovarian cancer diagnostic company based on the first glycomics patent for cancer. She is the editorial advisory board of *Mass Spectrometry Reviews*, *Scientific Reports*, *Bioanalysis*, *International Journal of Molecular Science*, and *Journal of Analytical Science and Technology*.

Dr. An's research focuses on bioanalytical mass spectrometry, with applications to glycomics, glycolipidomics, and glycoproteomics. She is developing mass spectrometry-based tools for biopharmaceutical characterization, cancer biomarker discovery, xenotransplantation, and brain glycome. She has authored and co-authored more than 150 peer-reviewed publications on these subjects and holds 30 related patents.



ERIN BAKER
UNIVERSITY OF NORTH CAROLINA

Erin S. Baker is an Associate Professor at the University of North Carolina in Chapel Hill, NC. To date, she has published over 150 peer-reviewed papers utilizing different analytical chemistry techniques to study both environmental and biological systems. Erin is currently serving as the Vice President of Education for the International Lipidomics Society, Events Committee Chair for Females in Mass Spectrometry (FeMS) and as an Associate Editor for the *Journal of the American Society for Mass Spectrometry*. She has received seven US patents, two R&D 100 Awards, and was a recipient of the 2016 ACS Rising Star Award for Top Midcareer Women Chemists, 2022 ASMS Biemann Medal, and 2022 IMSF Curt Brunnée Award. Currently, her research group utilizes advanced separations and novel software capabilities to examine how the environment affects human health.



SHEENA D'ARCY
THE UNIVERSITY OF TEXAS AT DALLAS

Sheena D'Arcy is an Associate Professor in the Department of Chemistry and Biochemistry at The University of Texas at Dallas. She received her Ph.D. in structural biology at the University of Cambridge under the tutelage of Sir Professor Tom Blundell. She trained in the HHMI laboratory of Professor Karolin Luger at Colorado State University. Her research is currently funded by grants from the National Institute of General Medical Sciences, NIH, the Welch Foundation, and the Wellcome Trust. She has served as a Board Member for the UT System Proteomics Network, and the International Society of Hydrogen-Deuterium Exchange. The D'Arcy laboratory employs an integrated structural approach to understand the regulation and dynamics of chromatin and works to expand the application of hydrogen-deuterium exchange coupled to mass spectrometry to challenging and important biological systems including enzyme engineering and drug discovery pipelines, protein-nucleic acid complexes, and large multi-protein machines.



KATHERINE DONOVAN
DANA-FARBER CANCER INSTITUTE/HARVARD MEDICAL SCHOOL

Katherine Donovan is a Lead Scientist in the Fischer Lab at Dana-Farber Cancer Institute/Harvard Medical School where she works on the development of molecular-glues and PROTAC molecules for targeted protein degradation. She completed her PhD training in protein biochemistry and structural biology at the University of Canterbury, New Zealand. After joining the Fischer Lab as a Postdoc she developed an interest in proteomics as a specialized technology for quantifying protein-level expression changes in response to various perturbations. Katherine set up and led proteomics teams focused on degrader screening and target identification in the Fischer Lab as well as in the Center for Protein Degradation. She has used proteomics technology to identify the degradation targets of many molecules including the identification of SALL4 as the protein likely underlying the teratogenicity of thalidomide. Katherine led a large effort to map the degradable kinome and now to aid her quest to map the degradable proteome she has recently started a public degradation proteomics initiative which provides free target mapping of degraders. Katherine continues to work on several projects related to ligase biology and protein degradation and also oversees the TPD proteomics operation in the Fischer Lab and Center for Protein Degradation.



BEN GARCIA
WASHINGTON UNIVERSITY SCHOOL OF MEDICINE

Benjamin A. Garcia obtained his BS in Chemistry at UC Davis in 2000, where he worked as an undergraduate researcher in Prof. Carlito Lebrilla's laboratory. He received his PhD in Chemistry in 2005 at the University of Virginia under Prof. Donald Hunt and then was an NIH NRSA Postdoctoral Fellow at the University of Illinois under Prof. Neil Kelleher from 2005-2008. From there Ben was appointed as an Assistant Professor in the Molecular Biology Department at Princeton University from 2008-2012, until his recruitment as the Presidential Associate Professor of Biochemistry and Biophysics at the University of Pennsylvania Perelman School of Medicine in 2012, promoted to full Professor in 2016, and named the John McCrea Dickson M.D. Presidential Professor in 2017. Ben moved in the summer of 2021 to the Washington University School of Medicine in St. Louis to become the Head of the Department of Biochemistry and Molecular Biophysics. The Garcia lab has been developing and applying novel proteomic approaches and bioinformatics for interrogating protein modifications, especially those involved in epigenetic mechanisms such as histones during human disease, publishing over 375 publications. He is presently an Associate Editor of the Analytical Chemistry, and Mass Spectrometry Reviews journals; and serves on the editorial boards for the Molecular Omics, the Journal of Proteome Research and the Molecular and Cellular Proteomics journals. He also serves on the Board of Directors for the U.S. Human Proteome Organization (HUPO), the HUPO Governing Council/Executive Committee and the Executive Committee of the American Chemical Society (ACS) Analytical Chemistry Division. Ben has been recognized with many honors and awards for his mass spectrometry research including the American Society for Mass Spectrometry (ASMS) Research Award, a National Science Foundation CAREER award, an NIH Director's New Innovator Award, the Presidential Early Career Award for Scientists and Engineers (PECASE), an Alfred P. Sloan Fellowship, the PITTCON Achievement Award, the Ken Standing Award, the ACS Arthur F. Findeis Award, The Protein Society Young Investigator Award, the ASMS Biemann Medal, the HUPO Discovery in Proteomic Sciences Award, and was named a Fellow of the Royal Society of Chemistry.



JENNIE LILL
GENENTECH

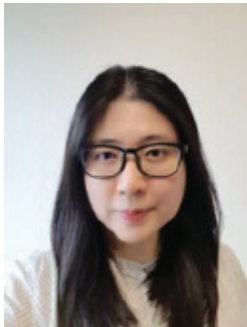
Jennie Lill is the Executive Director of the Proteomics and Next Generation Sequencing Department at Genentech. She has worked on numerous drug discovery efforts over the past 20 years in addition to previously leading the Engineered T cell program in immune-oncology for Research at Genentech in addition to being heavily involved in other cancer immunology modalities such as the development of cancer vaccines. Her research focuses on using proteomics to study cell death mechanisms and associated proteolysis events, post translational modification mediated intracellular biological pathway modulation as well as the MHC Ligandome in the context of disease.

Jennie received her Bachelors in Science in Molecular Biology from the University of Warwick, her Masters in Biotechnology and her Ph.D. in Mass Spectrometry and Cancer Immunology from the University of Nottingham Trent, UK. She then continued her work on Immuno-peptidomics at Zycos in Massachusetts before moving to Activx Biosciences in La Jolla. Since 2004 she has been at Genentech where she is also passionate about mentorship, diversity & teambuilding.



NICOLA TERNETTE
UNIVERSITY OF OXFORD

Nicola is leading the Antigen Discovery Group at the University of Oxford. Her team specializes in sequencing of HLA-associated peptidomes using nanoflow ultra-performance liquid chromatography tandem mass spectrometry (LC-MS) in pathogen infection, solid tumours, haematological cancers and autoimmune diseases. Her team is interested in understanding disease and treatment outcome association with the HLA gene locus, and the mechanisms associated. The group further investigates the consequences of interference with the antigen presentation machinery on HLA presentation in cancer and is developing novel bioinformatics approaches to MS spectral interpretation for HLA cancer antigen discovery and prediction.



WEI WU
A*STAR SINGAPORE IMMUNOLOGY NETWORK (SigN)

Wei Wu received her PhD from the National University of Singapore in 2014 with dual-training in cancer biology and mass spectrometry. In this period, she was supported by the President's Graduate Fellowship and was the recipient of three international Young Investigator Awards in Berlin, Yokohama and Beijing, each time showcasing her ability to combine MS technologies with the pursuit of mechanisms in cancer biology. During her postdoc in the Netherlands with world renowned protein scientist Albert Heck, Wei developed diverse and sensitive affinity tools to measure signalling in the tumor micro-environment (TME), and became interested in antigen presentation. In 2017, she started her group in Utrecht University with a niche in cancer antigen discovery and TME crosstalk, focusing on the extracellular factors needed for immunosurveillance and T cell function. In this period, her extensive collaborations with Dutch scientists in tumor immunology only intensified her interest, in providing mechanistic resolution and technological solutions, towards better immunotherapy and pre-emptive intervention. Since 2021, Wei served as a nominated representative from central Europe in the world Human Proteome Organisation (HUPO) council, and was appointed to the international executive committee of the HUPO Human Immuno-Peptidome Project (HUPO-HIPP). In 2022, she moved back to Singapore to join A*STAR Singapore Immunology Network (SigN), and became jointly appointed as Associate Professor in the Department of Pharmacy at the National University of Singapore.

NATIONAL SPEAKERS



DARREN CREEK
MONASH INSTITUTE OF PHARMACEUTICAL SCIENCES

Associate Professor Darren Creek leads the Malaria Metabolomics and Proteomics group at the Monash Institute of Pharmaceutical Sciences (MIPS), is Director of the Monash Proteomics and Metabolomics Facility (Parkville Node) and coordinator of the MIPS Global Health Therapeutic Program Area. He completed his PhD at Monash University in 2007, and has worked in Uganda, Scotland and Australia on malaria drug discovery, clinical trials, and parasite metabolism. He developed new analytical tools for metabolomics, and has used metabolomics and proteomics to discover new metabolic pathways and drug mechanisms, as described in over 130 publications. He served on the Boards of National and International Metabolomics Societies and was awarded the Inaugural Metabolomics Society Medal in 2019.



SIMON COBBOLD
WALTER AND ELIZA HALL INSTITUTE (WEHI)

Simon Cobbold is a senior post-doctoral researcher in the Komander Lab using mass spectrometry to explore ubiquitin signalling. Located within the Ubiquitin Signalling Division at WEHI, he works across five different labs to apply mass spectrometry to understand the ubiquitin machinery which drives disease. This includes defining the substrate repertoire of E3 ligases and deubiquitinases via remnant ubiquitin-site profiling and deciphering the polyubiquitin architecture which underpins innate immune signalling and PROTAC efficacy.

Completing a PhD at the Australian National University, he then developed mass spectrometry-based metabolomics approaches to understand drug resistance and identify drug targets in the malaria parasite while doing a post-doc at Princeton University and later at University of Melbourne. Currently at WEHI his research interests focus on developing mass spectrometry techniques to capture non-canonical ubiquitination and defining the deubiquitinase inhibition profile of small molecules.



BRETT HAMILTON
UNIVERSITY OF QUEENSLAND

Dr Brett Hamilton manages the Mass Spectrometry Imaging (MSI) facility within The Centre for Microscopy and Microanalysis (CMM) at The University of Queensland. He completed his PhD on ciguatoxins at the University of Queensland in 2003, before moving to Ireland to work on a range of phycotoxins and mycotoxins at Cork Institute of Technology. He returned to Australia to QIMR in 2006, before moving the Mater Hospital Pathology to set up the Mass Spectrometry Imaging facility in 2008. In 2017, he returned to UQ to establish the MSI facility at CMM. A great deal of the MSI he has been involved with has been in collaboration with Dr Eivind Undheim imaging venoms of a wide range of venomous creatures.



JASON LOW
UNIVERSITY OF SYDNEY

Dr Jason Low is a molecular biologist working in the field of gene regulation with a special interest in protein structure, function and engineering.

Jason was under the tutelage of Prof. Marc Wilkins at the University of New South Wales and was awarded his PhD in 2012. During his time with Prof. Wilkins, he studied arginine methylation as a form of post-translational modification, using experimental approaches that included the use of whole proteome microarray technology and peptide mass spectrometry. Since 2013, he has been working within the Structural Biology Group at the University of Sydney and has expanded his research to include the use of structural biology techniques. He pioneered the use of protein crosslinking mass spectrometry in the Group and has been using it extensively to support protein structure determination and analyses in his research. In particular, he uses protein crosslinking mass spectrometry to study complexes that are not easily amenable to established structural biology techniques, such as X-ray crystallography, protein NMR spectroscopy or Cryo-electron microscopy.

Since 2015, Dr. Low has been the Secretary for the Sydney Protein Group (SPG). The SPG is a Special Interest Group of the Australian Society for Biochemistry and Molecular Biology (ASBMB) that focuses on supporting the protein science community in the Greater Sydney region.



GIUSEPPE PALMISANO
MACQUARIE UNIVERSITY

I am a chemist by training with great interest and passion for biochemistry. I obtained my master's and Ph.D. at the University of Bari (Italy) with an exchange period at the University of Southern Denmark (DK). I have >18 years' of experience applying mass spectrometry-based proteomics to understand the intra and extracellular signaling in different biological systems, from plants to humans. I am currently A/Prof. at the University of Sao Paulo (Bra) and Macquarie University (AU). My research focuses on developing novel analytical methods to characterize post-translational modifications (PTMs) from sample preparation, mass spectrometry, and data analysis. Many of these methods are used worldwide and have generated patents and products. Moreover, I have applied these methods to study viral and parasitic diseases such as COVID-19, congenital Zika virus syndrome, and Chagas disease.



BEN PARKER
UNIVERSITY OF MELBOURNE

Associate Professor Benjamin Parker completed his PhD at the University of Southern Denmark and University of Sydney where he developed assays to quantify protein modifications by mass spectrometry to study signalling in cardiovascular disease. He performed post-doctoral research in the Diabetes Program at the Garvan Institute of Medical Research and then obtained an NHMRC Early Career Fellowship in the Metabolic Systems Biology Program at the Charles Perkins Centre. He is currently an NHMRC Investigator Fellow and group leader in the Department of Anatomy & Physiology at The University of Melbourne in the Driving Research Momentum program. His research team is focused on understanding how genetic variants and signal transduction regulate metabolism with the goal of identifying new therapeutic targets to treat metabolic disease.



MARIA TANZER
WALTER AND ELIZA HALL INSTITUTE (WEHI)

Maria is a group leader at the Walter and Eliza Hall Institute in Melbourne, where she also undertook her PhD. During the four years of her PhD, she investigated cell death, cytokine signalling and their roles in inflammation. She moved to Munich, Germany, for her postdoctoral studies. As a Marie-Curie fellow, she learned and applied state-of-the-art mass spectrometry to investigate cytokine signalling and cytokine-induced cell death in the lab of Prof. Matthias Mann, one of the worldwide leading proteomics laboratories. She primarily investigated changes in the global phosphoproteome, ubiquitinome and secretome upon TNF stimulation and TNF-induced cell death.

Maria has just started her independent research group, which will apply high-sensitivity proteomics to investigate signalling that regulates the removal of dead cells and increased cell death during inflammation in vivo and in vitro.



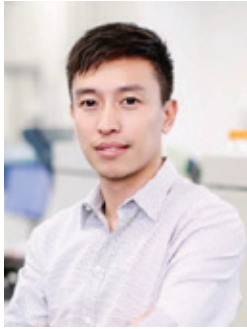
ROGER REDDEL
CHILDREN'S MEDICAL RESEARCH INSTITUTE (CMRI)

Roger Reddel is the Director of Children's Medical Research Institute (CMRI) and the Lorimer Dods Professor, University of Sydney. His training included medical oncology, and laboratory-based molecular cancer research. His research has mostly focussed on cancer cell immortalization. Roger is a co-founder of ProCan®, an internationally collaborative program that aims to develop proteomic techniques and a knowledge base that will enable routine use of proteomics in clinical oncology.



MELANIE WHITE
UNIVERSITY OF SYDNEY

Melanie is leading the Cardiometabolic Proteomics group at the Charles Perkins Centre at the University of Sydney. Currently supported by a Heart Foundation (Australia) Future Leader Fellowship, her research focused on understanding molecular changes in the heart in response to acute and chronic disease states, including ischemia/reperfusion injury and type 2 diabetes. She specializes in the application of mass spectrometry to investigate changes in protein, metabolite, and lipid profiles in rodent models of disease. Given the nature of these pathologies, her group develops and employs enrichment techniques to identify post-translational modifications important in the adaptation process, with a focus on phosphorylation, acetylation, and redox modifications. Melanie and her group also specialize in the development of small animal models of disease, small animal imaging, *ex-vivo* Langendorff perfusion and histology. Melanie has been successful with fellowships from the National Health and Medical Research Council (NHMRC; CJ Martin Overseas Fellowship) Australian Research Council (ARC; DECRA fellowship) and the Heart Foundation (NHF; Future Leader Fellowship), in addition to project funding from the NHMRC and NSW state government. She is the current Secretary for the Australasian Proteomics Society (APS), the APS representative for 2024 25th International Mass Spectrometry Conference (IMSC) and an Australasian representative for the Human Proteome Organisation (HUPO) awards council. In 2022 Melanie was nominated as a Fellow of the American Heart Association (AHA), with awards including the Thomas and Ethel Mary Ewing Scholarship (2005), the APS Early Career Award (2011), and the AHA Paul Dudley White International Scholar Award (2022).



QING ZHONG
UNIVERSITY OF SYDNEY

Dr Zhong is a data scientist with background in computer science, applied statistics and cancer research. He completed his undergraduate study in computer science and obtained a Doctor of Sciences degree in biochemistry and computer science at the ETHZ (Swiss Federal Institute of Technology Zurich) in Switzerland. In 2017, he was recruited as the group leader for Cancer Data Science at Children's Medical Research Institute and was subsequently appointed as a senior lecturer at the University of Sydney.

His group aims to collate and mine big biomedical data to achieve the goals of personalised medicine with a focus of developing data-driven computational tools and sophisticated machine learning algorithms to predict the most effective cancer treatments for individual patients. Related major research areas include computational proteomics, genome-proteome association analysis and multi-omics data integration for large-scale cancer cohorts.

PROGRAM

THURSDAY, 2 FEBRUARY 2023

Welcome to Country and Welcome Address

Chair: Peter Hoffmann

4:00 PM – 4:10 PM

Convention Room 1

The Simpson Lecture

Chair: Marc Wilkins

4:10 PM – 5:00 PM

Convention Room 1

4:10PM

Benjamin Garcia

Quantitative Proteomics for Understanding Histone Mutations in Human Disease

abs# 1

Ken Mitchell Young Investigator Award Lecture

Chair: Sri Ramarathinam

5:00 PM – 5:30 PM

Convention Room 1

5:00PM

David Skerrett-Byrne

The epididymis: a window for relaying stress signals to the male germline and potential offspring

abs# 2

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Vendor Talks

Chair: Peter Hoffmann

5:30 PM – 5:45 PM

Convention Room 1

Symposium One: Students of the APS (SoAPS)

Chairs: Samantha Emery-Corbin & Joel Steele

5:45 PM – 7:00 PM

Convention Room 1

5:45PM

Shawn Goh

Two cysteines are better than one - T cell recognition of peptides bearing penicillin-modified cysteinylated cysteine residues

abs# 3

6:00PM

Julian van Gerwen

The genetic and dietary landscape of muscle insulin signalling and resistance

abs# 4

6:15PM

Molly Talbot

Acute treatment with antioxidant *N*-propionylglycine attenuates mitochondrial cysteine redox post-translational modifications and restores endogenous antioxidants in the diabetic heart, identified using quantitative mass spectrometry.

abs# 5

6:30PM

Yaan Ng

C18ORF25 is a novel exercise-regulated AMPK substrate mediating skeletal muscle function

abs# 6

6:45PM

Erin Humphries

High-throughput proteomics and phosphoproteomics of rat tissue using microflow Zenon SWATH.

abs# 7

Welcome Reception and Poster Session One

7:00 PM – 10:00 PM

Convention Room 2 & 3

FRIDAY, 3 FEBRUARY 2023

Symposium Two: Disease Proteomics I

Chair: Patricia Illing & Dylan Harney

8:50 AM - 10:25 AM

Convention Room 1

- | | | |
|----------------|---|----------------|
| 8:50AM | Nicola Tennette
 | |
| 9:20AM | Roger Reddel
Steps towards utilisation of proteomic data in the cancer clinic | <i>abs# 9</i> |
| 9:45AM | Melanie White
Cardiac adaptations to metabolic disease: Integrating the lipidome, proteome and metabolome
 | |
| 10:10AM | Daniella Hock
Utility of quantitative proteomics in solving rare disease diagnosis | <i>abs# 11</i> |

Vendor Talks

Chair: Patricia Illing

10:25 AM – 10:35 AM

Convention Room 1

Morning Tea and Networking

10:35 AM – 11:00 AM

Convention Room 2 & 3

Symposium Three: Environmental, Microbial & Food Proteomics

Chairs: James Broadbent & Delphine Vincent

11:00 AM - 12:30 PM

Convention Room 1

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- | | | |
|----------------|--|----------------|
| 11:00AM | Darren Creek
Combining Proteomics and Metabolomics Approaches to Discover the Targets of Antimalarial Drugs | <i>abs# 12</i> |
| 11:30AM | Arineh Tahmasian
Targeted proteome measurement of seed storage proteins across genetically diverse lupin varieties for identification of hypoallergenic varieties | <i>abs# 14</i> |
| 11:45AM | Rohan Lowe
Disruption of fungal cell wall carbohydrates modulates EV protein load in a pathway specific manner | <i>abs# 15</i> |
| 12:00PM | Alex Lam
Chemoproteomic Target Deconvolution Approaches in <i>Giardia duodenalis</i> Using Kinase Inhibitors | <i>abs# 16</i> |
| 12:15PM | Evelyne Maes
Proteomic profiling of small extracellular vesicles isolated from an <i>in vitro</i> cell culture bioreactor simulating <i>Mycoplasma bovis</i> infection | <i>abs# 17</i> |

Lightning Talks One

Chair: Ben Crossett

12:30 PM – 12:45 PM

Convention Room 1

- | | | |
|----------------|--|----------------|
| 12:30PM | Mriga Dutt
Functional phosphoproteomic analysis of insulin signalling in ageing bone | <i>abs# 18</i> |
|----------------|--|----------------|

12:32PM	Samantha Emery-Corbin Unbiased plasma proteomics of a large type 1 diabetes cohort in a mass spectrometry facility – potential, perspectives and pitfalls <i>abs# 19</i>
12:34PM	Ronnie Blazev A novel platform integrating single cell muscle physiology with single cell proteomics <i>abs# 20</i>
12:36PM	Kirti Pandey Exploring the phospho-immunopeptidome in haematological malignancy and their specific T cell receptors in cancer precision medicine <i>abs# 22</i>
12:38PM	Mark Larance Defining the Structures and Interactions of the Human Platelet Secretome using Chemical Crosslinking <i>abs# 23</i>
12:40PM	Utpal Bose How do Greater wax moth larvae survive on a plastic diet? <i>abs# 24</i>

Lunch and Poster Session Two

12:45 PM – 3:15 PM

Convention Room 2 & 3

SCIEX Lunch Workshop – The paradigm shifts caused by ultra-fast proteomic analysis

1:00 PM – 2:00 PM

Convention Room 1

Sponsored by



Symposium Four: Bioinformatics, Data Science and Machine Learning

Chairs: Ignatius Pang & Michael Leeming

3:15 PM - 4:30 PM

Convention Room 1

3:15PM	Qing Zhong Machine learning of cancer type and tissue of origin from proteomes of 1,277 human tissue samples and 975 cancer cell lines <i>abs# 25</i>
3:45PM	Subash Adhikari The application of DIA-MS coupled with PISA TPP for drug-target deconvolution <i>abs# 26</i>
4:00PM	Joshua Fehring Characterising the glycosylated immunopeptidome by leveraging diagnostic fragment ions using a novel spectral analysis program <i>abs# 28</i>
4:15PM	Ahmed Mohamed Scaling proteomics to population size cohorts: Early insights and opportunities from ASPREE proteomics <i>abs# 29</i>

APS Annual General Meeting

4:45 PM – 5:45 PM

Convention Room 1

Free Evening or Students of the APS (SoAPS) Event

5:45 PM – 8:30 PM

Croquet Lawn

SATURDAY, 4 FEBRUARY 2023

Bruker Breakfast Workshop – High sensitivity proteomics workflows on the timsTOF SCP Single Cell analysis, Immunopeptidomics, PTM analysis

Streamlined & automated sample processing for in-depth proteomic analyses (video) & Pepsep chromatography update (video)

7:45 AM – 8:45 AM

Convention Room 1

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Symposium Five: Spatial Proteomics

Chair: Peter Hoffmann & Harley Robinson

9:00 AM - 10:10 AM

Convention Room 1

Sponsored by



- 9:00AM** **Per Andren**
Mass spectrometry imaging of brain signalling systems reveals abnormal alterations induced by parkinsonism and L-Dopa therapy *abs# 30*
- 9:30AM** **Brett Hamilton**
Using Mass Spectrometry Imaging (MSI) to answer biological and environmental question *abs# 31*
- 9:55AM** **Matthew Briggs**
Painting a Picture of the Gynaecological Cancer N-Glycome and Proteome *abs# 32*

Lightning Talks Two

Chair: Gavin Reid

10:10 AM – 10:24 AM

Convention Room 1

- 10:10AM** **Sarah Hamzelou**
Nutrition and allergenicity of food-grade protein extracts in novel food *Nannochloropsis oculata* *abs# 33*
- 10:12AM** **Toan Phung**
C3, a collection of data management, visualization and exploration web applications for proteomics data analysis *abs# 34*
- 10:14AM** **Ove Gustafsson**
Ensuring a suitable slice of the computational pie for Australian proteomics *abs# 35*
- 10:16AM** **Natasha Lucas**
The ProtoemeRiver pipeline facilitates reproducible and sharable differential abundance and pathways analyses of proteomics and phosphoproteomics datasets *abs# 36*
- 10:18AM** **Ignatius Pang**
The ProtoemeRiver pipeline facilitates reproducible and sharable differential abundance and pathways analyses of proteomics and phosphoproteomics datasets *abs# 37*
- 10:20AM** **Mengbo Li**
Linear models and empirical Bayes methods for proteome-wide label-free quantification and differential expression in mass spectrometry-based proteomics experiments *abs# 38*

Morning Tea and Networking

10:25 AM – 11:00 AM

Convention Room 2 & 3

Symposium Six: Disease Proteomics II

Chair: Laura Dagley & Pouya Faridi

11:00 AM - 1:05 PM

Convention Room 1

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- | | |
|----------------|---|
| 11:00AM | Wei Wu
Less is more: Prioritising cancer antigen discovery by understanding intracellular antigen processing
<i>abs# 40</i> |
| 11:30AM | Maria Tanzer
A proteomic perspective on the removal of dying cells
<i>abs# 41</i> |
| 11:55AM | Giuseppe Palmisano
Protein arginylation is regulated during SARS-CoV-2 infection
<i>abs# 42</i> |
| 12:20PM | Jerzy Dziekan
Mapping the druggable landscape of malaria parasite through thermal proteome profiling
<i>abs# 43</i> |
| 12:35PM | Scott Bringans
Development of a lectin bead-based diagnostic test for oesophageal cancer
<i>abs# 44</i> |
| 12:50PM | Christopher Overall
PICS and TAILS N-Terminomics Characterization of Monkeypox and SARS-CoV-2 protease active sites and identification of novel Anti-viral Neanderthal Gene Products that are inactivated by SARS-CoV-2 Proteases to Circumvent Host Protection to COVID-19
<i>abs# 45</i> |

Lunch and Poster Session Three

1:05 PM – 3:15 PM

Convention Room 1

Thermo Fisher Lunch Workshop – Mainstreaming Proteomics into rare diagnostics, followed by Multiplexed single cell proteomics for investigating cellular heterogeneity during hypoxi and Scale up your Science of discovery – Orbitrap Ascend Tribrid a new mass spectrometer

1:20 PM – 2:20 PM

Convention Room 1

Sponsored by



Symposium Seven: Glycoscience and Lipids

Chairs: Stuart Cordwell & Cassandra Pegg

3:15 PM – 4:45 PM

Convention Room 1

- | | |
|---------------|--|
| 3:15PM | Hyun Joo An
A Comprehensive Study on Aberrant Glycosylation in the Brain of a Depression Mouse Model
<i>abs# 46</i> |
| 3:45PM | Erin Baker
A Multi-Omic Investigation into the Role of the APOE Genotype in Alzheimer's Disease
<i>abs# 47</i> |
| 4:15PM | Nichollas Scott
<i>Burkholderia</i> O-linked glycosylation systems possess buffering capacity limiting the impact of perturbations in oligosaccharyltransferase levels on the glycoproteome and proteome
<i>abs# 48</i> |
| 4:30PM | Cassandra Pegg
Glycosylation of the SARS-CoV-2 Gamma spike protein
<i>abs# 49</i> |

Symposium Eight: New Technologies

Chairs: Mark Molloy & Andrew Webb

4:45PM – 6:15 PM		Convention Room 2 & 3
4:45PM	Katherine Donovan Chemoproteomic profiling surveys the degradable proteome	<i>abs# 50</i>
5:15PM	Stephen Tate ZenoSWATH an improved performance data-independent acquisition (DIA) on low-level proteomic samples	<i>abs# 51</i>
5:30PM	Daniel Hermanson Increasing the depth of single shot proteomics with enhanced data acquisition and processing strategies	<i>abs# 52</i>
5:45PM	Christoph Krisp Analysis of cellenONE sorted and prepared single cells in a label-free nano-flow LC-MSMS proteomics approach using a nanoElute 2 and an Evosep One system and a timsTOF SCP	<i>abs# 53</i>
6:00PM	Benjamin Herbert Non-small cell lung cancer biomarker discovery from un-fractionated blood cell pellets	<i>abs# 54</i>

APS Conference Dinner
7:30 PM – 11:00 PM

Lorne Football Club

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SUNDAY, 5 FEBRUARY 2023

Symposium Nine: Structural Proteomics and Interactomics

Chairs: Marc Wilkins & Ashleigh Dale

9:00 AM - 10:40 AM

Convention Room 1

9:00AM	Jason Low Cross-linking mass spectrometry discovers, evaluates, and validates the experimental and predicted structural proteome	<i>abs# 55</i>
9:30AM	Sheena D’Arcy Hydrogen-Deuterium Exchange: Beyond the Integrated Structural Approach	<i>abs# 56</i>
9:55AM	Christopher MacRaid Integrating Protein Correlation Profiling with Cross-Linking Mass Spectrometry to build a comprehensive map of protein-protein interactions in the malaria parasite	<i>abs# 57</i>
10:10AM	Annalisa Carli Identification of the Doublecortin like kinase 1 (DCLK1) interactome reveals novel kinase dependent processes involved in gastric cancer progression	<i>abs# 58</i>
10:25AM	Muhammad Zenaidee Enhanced proteoform characterisation using an integrated top-down and bottom-up mass spectrometry approach	<i>abs# 59</i>

Morning Tea and Networking

10:40 AM – 11:10 AM

Convention Room 2 & 3

Symposium Ten: Post-translational Modifications and Signalling

Chair: Melanie White & Mark Larance

11:10 AM - 12:30 PM

Convention Room 1

- | | | |
|----------------|--|----------------|
| 11:10AM | Benjamin Parker
Proteome-wide systems genetics identifies UFMylation as a regulator of muscle function
<i>abs# 60</i> | |
| 11:35AM | Simon Cobbold
Deciphering the ubiquitin code | <i>abs# 61</i> |
| 12:00PM | Ashleigh Dale
A role for protein lysine acetylation in bile resistance in <i>Campylobacter jejuni</i> | <i>abs# 62</i> |
| 12:15PM | Joshua Hamey
Systematic analysis of post-translational modifications in the yeast ribosome reveals extensive heterogeneity | <i>abs# 63</i> |

Closing Plenary Session

Chair: Anthony Purcell

12:30 PM - 1:00 PM

Convention Room 1

- | | | |
|----------------|---|----------------|
| 12:30PM | Jennie Lill
The future of proteomics in Biotechnology | <i>abs# 64</i> |
|----------------|---|----------------|

Closing Ceremony and Award Presentation

Chair: Peter Hoffmann & Anthony Purcell

1:00 PM - 1:30 PM

Convention Room 1

POSTER LISTING

POSTER SESSION ONE – THURSDAY, 2 FEBRUARY 2023

Ritchlynn Aranha Determining the antigen processing requirements for spliced peptide presentation	<i>abs# 101</i>
Craig P Barry Multiplexed single cell proteomics for investigating cellular heterogeneity during hypoxia	<i>abs# 102</i>
Angelo R Bautista Identification of oxidatively modified proteins to utilise as biomarkers of immune cell activation	<i>abs# 103</i>
Alessandra Bicego An Untargeted Method for the Detection of Post Translational Modifications	<i>abs# 104</i>
Todd Blackburn Quantitative targeted and global proteomics reveal novel biomarkers of disease in mouse models of a rare-genetic epilepsy disorder	<i>abs# 105</i>
Lana Brockbals Postmortem interval estimation using an untargeted LC-MS/MS-based proteomics approach	<i>abs# 106</i>
Daniel Bucio Noble DIA-based in silico spectral reference libraries, an improved alternative for peptide quantification in clinical samples via DIA-NN	<i>abs# 107</i>
Tengyi Cai The characterisation of protein binding from in vivo paediatric ECMO circuits	<i>abs# 108</i>
Luke Carroll Characterisation of peptide and protein post-translational modification by cyclic ion mobility	<i>abs# 109</i>
Laura F Dagley The WEHI Proteomics Facility: tools, techniques and technologies	<i>abs# 110</i>
Sarah J Dilmetz Monitoring toxicokinetic properties of PFAS in rat models by targeted mass spectrometry	<i>abs# 111</i>
Toby Dite Enhanced phosphoproteome coverage with gas phase fractionation combined with data independent acquisition (GPF-DIA)	<i>abs# 112</i>
Hao Dong Characterisation of branched ubiquitin architecture using Lb ^{PRO} and intact mass spectrometry	<i>abs# 113</i>
Leigh Donnellan Differentiation of lactyllysine and carboxyethyllysine modified peptides	<i>abs# 114</i>
Mohammadreza Dorvash Pancreatic Cancer HLA-peptidomics: An Unbiased Pursuit of Potential Targets for Immunotherapy	<i>abs# 115</i>
Daniel J. Ellis A multi-omics approach to characterising beer flavour	<i>abs# 116</i>

- Joanne Ford**
High Resolution DIA: A Workflow for Highly Accurate Relative Label-Free Quantification of Microbial Proteins in Complex Cell Lysates *abs# 118*
- Neus Gomila Pelegri**
Adipose derived stem cells spontaneously express neural markers when grown in a PEG-based 3D matrix *abs# 120*
- Gabriel Goncalves**
IFN γ Modulates the Immunopeptidome of Triple Negative Breast Cancer Cells by Enhancing and Diversifying Classical and Non-Classical HLA Presentation *abs# 121*
- Thomas Goulden**
Investigating the structure-activity relationship of concentrated ionic liquids for their capacity to dissolve proteins for proteomic analysis *abs# 122*
- Sabrina Grizzi de Oliveira**
Assessing the impacts of Snomax, an ice-nucleating bacterium for creating artificial snow, on the Australian alpine environment *abs# 123*
- Joel P.A. Gummer**
Quantitation of the Iron Regulatory Hormone Hepcidin in Mammals *abs# 124*
- Dylan Harney**
Towards the next generation in blood plasma analysis: improving analytical speed without compromising performance using improved databases, scanningSWATH and zenoSWATH *abs# 125*

POSTER SESSION TWO – FRIDAY, 3 FEBRUARY 2023

- Paul A. Haynes**
Proteomic analysis of different varieties and species of rice under a range of abiotic stress conditions *abs# 126*
- Enzo Huang**
Are You Ready for High-throughput Single Cell Proteomics with Great Depth of Coverage *abs# 127*
- Joshua JH Hutchings**
An investigation of the physiochemical changes in field pea flour after heat treatment *abs# 128*
- Tasha Lumbantobing**
A proteomics based predictive assay for diabetic retinopathy *abs# 129*
- Jason Ito**
Development of a diagnostic test for defining obstructive airway diseases *abs# 130*
- Nicola M Karakatsanis**
The phospho-regulation of histone demethylases in *Saccharomyces cerevisiae* *abs# 132*
- Manuela Klingler-Hoffmann**
Chemoresistant Cancer Cell Lines Are Characterized by Migratory, Amino Acid Metabolism, Protein Catabolism and IFN1 Signalling Perturbations *abs# 133*
- Jennifer M. S. Koh**
Use of DIA-MS to determine the effects of storage temperature and time on FFPE tissue sections *abs# 134*
- Han Lee**
A complete pipeline for human gut microbiome meta-proteomics study *abs# 135*

Yea Rin Olivia Lee Development of a Novel Trabecular Bone Tissue Microarray for 20µm Resolution N-Glycan MALDI Mass Spectrometry Imaging	<i>abs# 136</i>
Michael G Leeming Simulation of DIA mass spectrometry proteomics data with Synthedia	<i>abs# 137</i>
Terry Lim Kam Sian Supercharge Your Immunopeptidomics	<i>abs# 138</i>
Lawrence Luo Comparative Glycoproteomics Analysis of Different Treatments to Induce Yeast Autolysis in Sparkling Wines	<i>abs# 140</i>
Kyle Macauslane The unfolded protein response and dynamic host subcellular proteome in response to H1N1 and H3N2 influenza virus infection	<i>abs# 141</i>
Bruno Madio Glycoprotein characterization combining native, PTCR and Direct Mass Technology mode mass spectrometry	<i>abs# 142</i>
Rosalee McMahon Stability of cytokines in dried blood spots collected using volumetric absorptive microsampling (VAMS) and stored at various temperatures	<i>abs# 143</i>
Nicole A Mifsud ATLANTIS – ATLAS of peptide ANTigens in Transplantable tISsues	<i>abs# 144</i>
Jeffrey Molendijk Proteome-wide systems genetics identifies UFMylation as a regulator of skeletal muscle function	<i>abs# 146</i>
Mark P Molloy Proteomic Landscape of Human Colorectal Liver Metastasis	<i>abs# 147</i>
Mohadeseh Montazeri Shatouri Application of shotgun proteomics techniques for characterization of proteins and peptides of tuna waste	<i>abs# 148</i>
Dylan H. Multari Species identification of a collection of worked bone artefacts from Pymont, Australia using mass spectrometry of bone collagen	<i>abs# 150</i>
AKM AKMM Muraduzzaman Conserved T cell epitopes offer protection against highly pathogenic avian influenza A/H5N1 in South Asian populations	<i>abs# 151</i>
Yuen Tung Ngai Optimisation of multi-omics MALDI-MSI of lung tissue from mucopolysaccharidosis (MPS) disease murine models	<i>abs# 153</i>
Krishnatej Nishtala Balancing the fine act of single cell proteomics	<i>abs# 154</i>
Myung Jin Oh Dissection of glyco-type and protein changes following differentiation of human induced pluripotent stem cells to cardiomyocytes	<i>abs# 155</i>
Jessica Oliver Investigating the Effect of Radiotherapy on the Immunopeptidome in Colorectal Cancer	<i>abs# 156</i>

Wayne Paes

Inhibition of ERAP1 in cancer unmasks an alternative subset of tumour epitopes recognised by cytotoxic human CD8⁺ T cells *abs# 158*

POSTER SESSION THREE – SATURDAY, 4 FEBRUARY 2023**Robert Parker**

High sensitivity immunopeptidomics on the timsTOF SCP mass spectrometer *abs# 159*

Nicole R Pardini

How to make green, sustainable and on-demand Nitrogen for your Mass Spectrometer and Proteomics research from Air *abs# 160*

Jeremy Potriquet

Accelerating DIA studies with fast microflow LC and Zeno SWATH acquisition *abs# 161*

Jeremy Potriquet

A novel fragmentation technology allows for in-depth glycopeptide characterization in glycoproteins *abs# 162*

Adam Rainczuk

Single cell in multiple cell types using a CellenOne and dia-PASEF combined with PaSER identifies thousands of proteins at scale *abs# 164*

Harley Robinson

Modified mRNA encoding Myc and Cyclin T1 induces cardiac regeneration following myocardial infarction *abs# 166*

Frank Rooney

Quantitative Multiplexed Analysis of Cancer Cell Lines Using Automated Sample Preparation with Increased Speed and Sensitivity *abs# 168*

Thusi Rupasinghe

Utilizing CID and EAD fragmentation for global lipid profiling of human and rat plasma *abs# 169*

Ralf B Schittenhelm

An ACF Multicentre Testing Initiative: Exposing the Limitations of Shotgun Proteomics *abs# 171*

Ben L Schulz

Capturing and Characterising Wild Yeast for Beer Brewing *abs# 172*

Janik Seidel

Mass spectrometry method development and evaluation for host cell protein characterization from clarified cell culture fluid of biopharmaceutical processes *abs# 173*

Joy Seitanidou

Unravelling the glycosylation profile of the oseltamivir-resistant NA protein in the A(H1N1)pdm09 strain *abs# 174*

Nari Seo

Insights into the Biological Function of Algae using Glycomic and Proteomic Approaches *abs# 175*

Adnan AS Shafiq

Shed microvesicles-derived from MDCK cells following oncogenic H-Ras transformed MDCK cells induce EMT in parental MDCK cells and elicit invasive properties to fibroblast *abs# 176*

Mohammad Shahbazy

Mass spectrometry-based thermostability measurements of virus-derived MHC peptides correlate with immunogenicity *abs# 177*

Fatemeh shamekhi

Proinflammatory cytokines improve the HLA ligandome landscape of Diffuse Midline Glioma *abs# 178*

Chloe Shepherd	Differential enhancement of antigen presentation by interferons in lung epithelia	<i>abs# 179</i>
Joel Steele	Monash Proteomics & Metabolomics Facility: Offering analytical solutions to biological questions	<i>abs# 181</i>
Dylan Xavier	A mass spectrometry quality control pipeline to enable clinical proteomics	<i>abs# 182</i>
Erwin Tanuwidjaya	An ACF multicentre testing initiative: exposing the limitations of shotgun proteomics	<i>abs# 183</i>
Hossein HK Valipour Kahrood	<i>Pathway-Analyst: one-click proteomic knowledge generation</i>	<i>abs# 184</i>
Delphine Vincent	Finding the LMA needle in the wheat proteome haystack.	<i>abs# 185</i>
Esther Willems	Unravelling the mechanism-of-action of an inflammatory dampening whey extract through data-independent intracellular proteome analysis	<i>abs# 186</i>
Yue Xuan	Simultaneous targeted and discovery phosphoproteomics of cell signaling pathways using novel hybrid-DIA acquisition strategy	<i>abs# 187</i>
Jumana M Yousef	Minimising intra- and inter-batch variation in large clinical proteomics cohort studies	<i>abs# 188</i>
Jiahui Yu	An investigation into the neoantigenic landscape of microsatellite instability colorectal cancer using immunopeptidomics	<i>abs# 189</i>
Haijian Zhang	Phospho-Analyst visualising and analysing phosphoproteomics data with one click	<i>abs# 191</i>

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