

# DELEGATE HANDBOOK



## The 25th Annual Lorne Proteomics Symposium 2020

6 - 9 February 2020

Cumberland Lorne Resort  
Lorne, Victoria



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# WELCOME

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"Celebrating the silver jubilee of Proteomics in Australia"

It's been 25 years since the beachside town of Lorne first became the home of Proteomics. We are so glad you could join us in 2020 to celebrate the silver jubilee of Proteomics in Australia.

Every year, the Lorne Proteomics Symposium offers a platform to discuss, engage and learn the latest technological developments to facilitate research across multiple disciplines. The program has been designed to celebrate how the field has progressed and highlight key achievements for state-of-the-art research. We will showcase proteomics approaches being applied by the next generation of researchers to address challenges facing clinical and translational medicine, plant, veterinary, and environmental research.

Thanks for joining us at the 25th Annual Lorne Proteomics Symposium!

James Broadbent  
Chair for the 2020 Proteomics Organising Committee

## COMMITTEE

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### PROTEOMICS 2020 ECR COMMITTEE

The ECR committee comprises ECR and MCR researchers from across Australia, all with a keen interest in "omics" workflows to address current and future research challenges. The committee's mission for 2020 is to deliver a symposium that offers enhanced opportunity for ECR/MCRs to present their research and engage with leading experts, discuss and help shape the future of proteomics by reflecting on, and celebrating, the progress of the field over the last 25 years.

**James Broadbent**

CSIRO, Brisbane

**Laura Dagley**

The Walter and Eliza Hall Institute of Medical Research, Melbourne

**Nathan Croft**

Monash University, Melbourne

**Nichollas Scott**

Peter Doherty Institute, Melbourne

**Melanie White**

The University of Sydney, Sydney

**Jarrold Sandow**

The Walter and Eliza Hall Institute of Medical Research, Melbourne

**Patricia Illing**

Monash University, Melbourne

**Mark Condina**

Future Industries Institute, The University of South Australia

**Benjamin Parker**

The University of Melbourne, Melbourne

**Ralf Schittenhelm**

Monash University, Melbourne

**Rommel Mathias**

Monash University, Melbourne

## SPONSORS

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APS would like to thank the following sponsors and supporters of Lorne Proteomics 2020:

### DIAMOND SPONSOR

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S C I E N T I F I C

### PLATINUM PLUS SPONSOR



### PLATINUM SPONSOR



### SILVER SPONSOR



### SUPPORTING SPONSORS



## EXHIBITORS



## SPECIAL THANKS TO



# DELEGATE INFORMATION

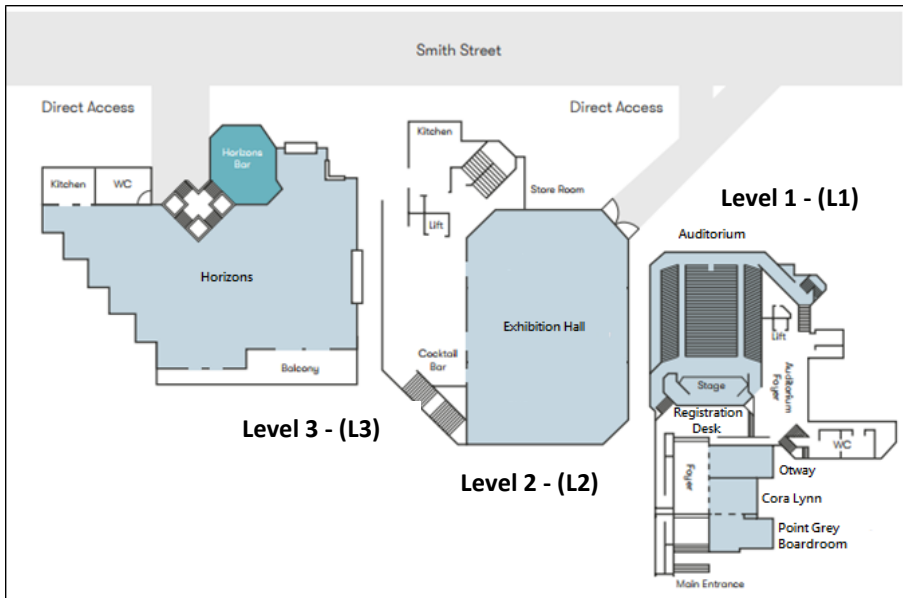
## VENUE

### Cumberland Lorne

150 Mountjoy Parade, Lorne, VIC 3232, Australia

P: +61 3 5289 4444 | F: +61 3 5289 2256

[www.cumberland.com.au](http://www.cumberland.com.au)



## REGISTRATION DESK

The registration desk is in the Auditorium Foyer (L1). Any enquiries regarding your participation in the meeting can be directed to the ASN staff onsite. The registration desk opening hours are as follows:

Thursday 6 <sup>th</sup> February:	2:00 pm – 7:00 pm
Friday 7 <sup>th</sup> February:	7:15 am – 5:00 pm
Saturday 8 <sup>th</sup> February:	8:00 am – 5:30 pm
Sunday 9 <sup>th</sup> February:	8:30 am – 1:30 pm

## REGISTRATION INCLUSIONS

Full delegate registrations include:

- Access to the sessions of your choice
- Printed pocket program
- Coffee keep cup
- All catered sessions (morning teas and lunches)
- Ticket to the social functions (pre-reservation required)
- Access to the conference app (incl. the conference program, speaker profiles and abstracts)
- Access to the ADVBS Symposium (Friday)
- Wireless internet during the conference

## CONFERENCE SECRETARIAT



**ASN Events Pty Ltd**  
9/397 Smith Street  
Fitzroy, VIC 3065, Australia

### Contact person on-site:

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

## SPEAKER PRESENTATION INSTRUCTIONS

All conference sessions take place in the Auditorium (L1). Audio-visual equipment will be supplied and there will be a technician on site to assist with any enquiries. Cumberland 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 well in advance of the session you are participating to allow for timely loading and testing. You will be able to use your own MAC to present, if preferred. However, please remember to bring necessary adapters and inform the technician well in advance of your session for testing. A remote mouse/laser pointer will be provided at the lectern. Please use the pointer to ensure delegates in the overflow rooms are able to 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 in onto the computer within the lecture room (Auditorium) by the morning tea prior to their Lightning Talk session, at the latest. **Presentations are limited to 3 minutes** (max 3 slides incl. any title slides). Movies are not permitted in the presentation.

**Lightning Talks One/Poster Session One:** Posters will be displayed from Friday morning tea and must be removed before the morning tea on Saturday, 8 February 2020.

**Lightning Talks Two/ Poster Session Two:** Posters will be displayed from Saturday morning tea and must be removed before the morning tea on Sunday, 9 February 2020.

## 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 (L2) and numbered according to your poster numbers in the program (please refer to the poster listing on page 34).

There will be 2 dedicated poster sessions:

- **Poster Session One:** Friday, 7 February 2020, from 1:10 pm - 3:10 pm
- **Poster Session Two:** Saturday, 8 February 2020, from 1:30 pm - 2:45 pm

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 morning tea on Friday, 7 February and must be removed before the morning tea on Saturday, 8 February.

**Poster Session Two:** Posters will be displayed from morning tea on Saturday, 8 February and must be removed before the morning tea on Sunday, 9 February 2020.

## INTERNET ACCESS

Free Wi-Fi is available to conference delegates. Simply select the network **Cumberland Conference Centre** and enter the password **lorne3232** on your mobile device and connect. Please note: Access is restricted to one device per person. If you wish to use Wi-Fi on an additional device, you must disconnect on the original device first before logging onto the second device.

## CONFERENCE APP

The official Lorne Proteomics Symposium mobile App is brought to you by  **SHIMADZU** Excellence in Science and will keep you organised during the meeting. Download the official Proteomics 2020 App to access the latest information. You can flag sessions of interest, view floor plans, read abstracts and search for speakers by name.

To download the Proteomics 2020 App onto your smartphone or tablet device follow these instructions:

**Search for 'Currinda' via the App Store from the following platforms**

- Android Products: Google Play
- Apple Products: iTunes

Once you have downloaded the App, you will be prompted to log in

**First you must click on the 'Client' box and search for 'ASN'**

**Select 'ASN' from the list provided below and then you can log in with your email address and password you used to register for the conference**

The Smartphone 'App' will allow you to:

- View the full conference program
- Save your favourite sessions and plan your day
- View and search for speaker bios and abstracts
- Take notes which will then be saved and downloaded from your registration profile
- View Sponsors and Exhibitors

You will be prompted to login each day. For further assistance please see ASN staff at the Registration Desk.



## SOCIAL PROGRAM

### WELCOME RECEPTION

Date: Thursday, 6 February 2020

Time: 7:00 pm – 10:00 pm

Room: Exhibition Hall (L2)

Includes: Drinks & substantial canapes

### APS CONFERENCE DINNER/FESTIVAL OF FOOD

Date: Saturday, 8 February 2020

Time: 7:30 pm – 10:30 pm

Room: Umisango, Jashn, Lorne Central

Includes: Food, drinks & music


### SoAPS DINNER WITH INVITED SPEAKERS

Date: Friday, 7 February 2020

Time: 5:30 pm – 7:30 pm

Location: Lorne Bowls Club

Includes: Dinner & Drinks

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SCIENTIFIC

All delegates are invited to attend the social functions. The costs are included in the full conference registration. However, **pre-reservation is required**. If your name badge does not include a ticket to the social functions and/or you wish to purchase additional tickets for partners, friends and children, please see the ASN staff at the registration desk

## FAMILY ROOM

The Walter and Eliza Hall Institute of Medical Research will again be supporting parents with young children attending the Lorne Conferences in 2020. An overflow room (Otway Room – L1) is available as a viewing room for parents with children. The room will have space for activities and play for children while parents will be able to listen to the presentations with the same AV projection. The APS Committee once again applauds this initiative. We are grateful to the Walter and Eliza Hall Institute of Medical Research for their continued support of this initiative to enhance the accessibility of this conference to parents.



## CERTIFICATE OF ATTENDANCE

On conclusion of the Symposium your certificate of attendance will be emailed to you. This can also be downloaded from your registration profile via the link

<https://members.asnevents.com.au/register/event/1670>.

Simply login by entering your email and password, scroll down to the section “Download Registration Documents” and click on the button “Certificate of attendance”.

## HOTEL CHECK-OUT

Individuals are required to settle their room accounts with Cumberland Lorne by 10am on the morning of your checkout. Please note that the key cards at Cumberland Lorne will expire at 10am and you will no longer have access to your room after that time. Baggage will be left together for the buses if required.

## BUS TRANSFER HOME

Bus will depart from the Cumberland Lorne on **Sunday 9 February @ 2:45pm sharp** and return to Melbourne Tullamarine Airport (arrival time approx. 5:15pm), and then onto WEHI/University of Melbourne, Royal Parade (arrival time approx. 5:45pm).

### **IMPORTANT:**

- Please ensure you have checked out of your hotel and wait within the Cumberland 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.

## USEFUL PHONE NUMBER

Gull Airport Service	+61 3 5222 4966
VLine Bus Service	1800 800 007
Qantas	13 13 13
Jetstar Airways	131 538
Virgin Australia	136 789

## AWARD WINNERS

### The Ken Mitchelhill Award

**Dr Rebecca Poulos, CMRI Sydney** – *Strategies to improve reproducibility of large-scale and longitudinal proteomics abs# 2*

### Early Career Award

**Dr. Rebeca Kawahara, Macquarie University** - *Deciphering the stage-specific glycoprotein signatures of colorectal cancer using integrated mass spectrometry-based omics abs# 45*

**Dr. Keshava Datta, QIMR Berghofer** - *Global proteomic and phosphoproteomic profiling to identify proteins and pathways that regulate cell survival in hypoxic conditions abs# 54*

## 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 9<sup>th</sup> February. To collect the stickers please visit the exhibitors during Morning Tea, Lunch and Poster Sessions. Once you have received all stars fill out your details on the card and hand into the registration desk.

**For every prize draw card completed, Proteomics 2020 are donating \$5 for the bushfire fundraiser. For more details on the initiative please see below.**

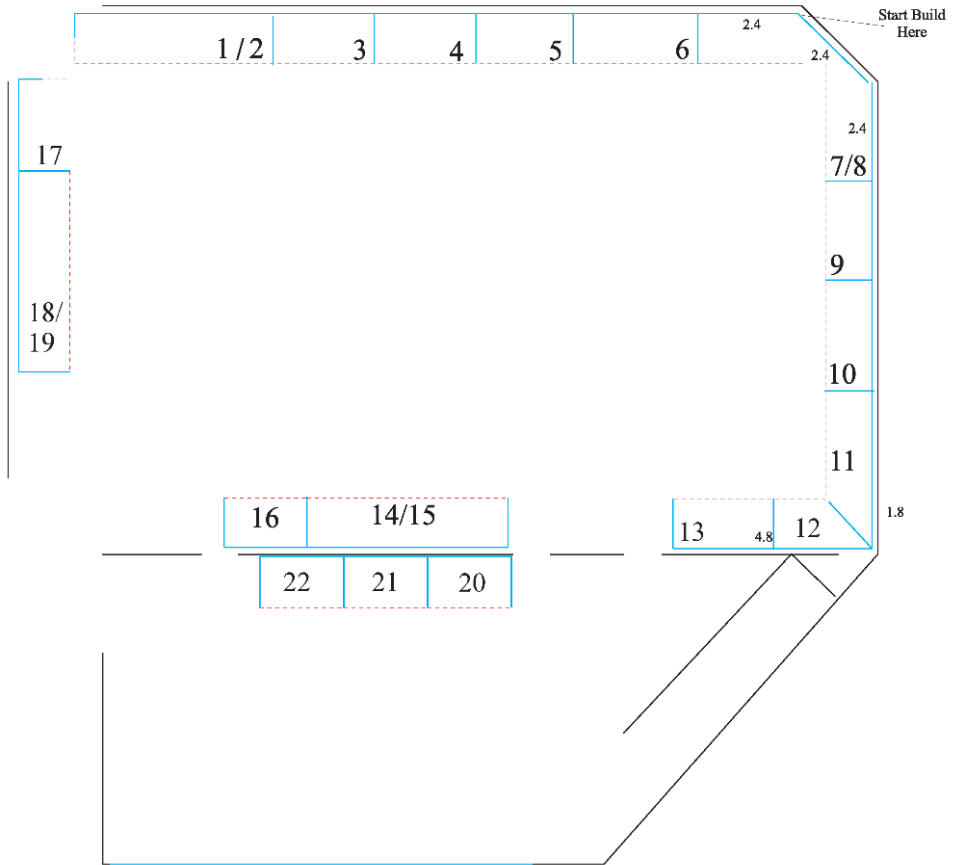
## BUSHFIRE FUNDRAISER

Proteomics 2020 are proud to have partnered with ASN Events and The Cumberland Hotel Lorne on the \$1 per delegate campaign to raise money for the bushfires. In addition, we are also donating an additional \$5 per delegate that completes the prize draw card by Sunday. Our aim is to raise \$5,000 for Lorne CFA across all 5 Lorne Conferences.



**CUMBERLAND**  
LORNE

## EXHIBITORS



SCIEX	14 & 15	Novachem	16
Accurate Mass Scientific	17	Peak Scientific	3
Agilent	20	Proteomics International	22
Bruker	10 & 11	Shimadzu	1 & 2
GE Healthcare	18 & 19	Tecan	5
Genesearch	9	Thermo Fisher	7 & 8
Metabolomics Australia	21	Trajan	4
Mimotopes	6	Waters	13

# INVITED SPEAKERS

## INTERNATIONAL SPEAKERS

### DR BEN COLLINS



#### **School of Biological Sciences, Queen's University of Belfast**

Since August 2019 Ben is a Reader in the School of Biological Sciences, Queen's University of Belfast, UK. His research focuses on broadly on 3 topics: (i) method development and applications in data independent acquisition mass spectrometry; (ii) method development and applications in the analysis of protein interaction networks and protein complexes; and host-pathogen biology with a focus on *Mycobacterium tuberculosis*. Ben is a native of Ireland where he studied chemistry and applied chemistry at the National University of Ireland, Galway. After working as an analytical chemist in Schering-Plough, Ireland, he undertook an MSc in Molecular Medicine at Trinity College Dublin. Ben's PhD was completed at University College Dublin in 2009 where he remained for 1 year as the Agilent Technologies Newman Fellow (postdoctoral) in Quantitative Proteomics. Ben moved to the Institute of Molecular Systems Biology at ETH Zurich in Autumn 2010 as postdoctoral researcher under the supervision of Prof. Ruedi Aebersold, where his research focused on the application of quantitative interaction proteomics in signaling and the development of DIA/SWATH mass spectrometry. Following this Ben was a Group Leader and SNF Ambizione Fellow at IMSB, ETH Zurich with a focus on applying methods developed as a postdoc to relevant problems in host-pathogen biology.

### DR PHILIPP EMANUEL GEYER



#### **Max-Planck Institute of Biochemistry**

Philipp Emanuel Geyer dedicated himself to the vision that mass spectrometry-based blood plasma proteomics will change diagnostics and clinical decision making in a way that will substantially increase our life expectations and the quality of how we live. The overall aim of his PhD thesis in Matthias Mann's laboratories was to pave the way for biomarker discovery and clinical applications of proteomics by precision characterization of the human blood plasma proteome. He attempted this aim by streamlining the standard time-consuming and labor intensive proteomic workflow, resulting in a rapid, robust and highly reproducible robotic platform. After his PhD, he took the opportunity to continue his research with great support from Matthias Mann in his laboratories at the Max-Planck Institute of Biochemistry in Munich and the Center for Protein Research in Copenhagen, where he is heading the plasma proteomics efforts by supporting a team of several very dedicated students focusing on new technology developments and biomarker discovery.

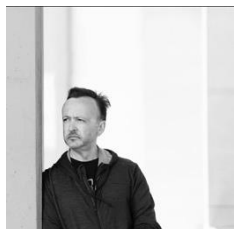
## PROF ANNE-CLAUDE GINGRAS



### *Lunenfeld-Tanenbaum Research Institute and University of Toronto*

Anne-Claude Gingras is a Canada Research Chair in Functional Proteomics, a Senior Investigator in the Lunenfeld-Tanenbaum Research Institute and a Professor of Molecular Genetics at the University of Toronto. She is also Deputy Editor for Molecular and Cellular Proteomics. Dr. Gingras specializes in the study of protein complexes and subcellular proteome organization, combining cutting edge mass spectrometry-based approaches with modern cell and molecular biology techniques. She has developed multiple experimental and computational approaches (many through collaborative efforts) to confidently identify and quantify interaction partners for proteins of interest, and has co-developed a number of widely used software tools to assist in this process. She has applied these powerful systematic approaches to a number of protein classes (e.g. phosphatases, bromodomain-containing proteins, RNA-binding proteins) to accelerate discovery, and is ultimately interested in gaining deep biological insight into the mechanisms of disease. Her work is extremely collaborative, and she continues to be a strong advocate for data transparency and data sharing.

## MR MARTIN KRZYWINSKI



### *Canada's Michael Smith Genome Sciences Centre*

Martin Krzywinski is known for his work in bioinformatics, data visualization and the interface of science and art. He applies design, both data and artistic, to assist discovery, explanation and engagement with scientific data and concepts. His information graphics have appeared in the New York Times, Wired, Scientific American and covers of numerous books and scientific journals such as Nature and Genome Research. He is a contributing author to the Points of View and Points of Significance columns in Nature Methods and the former owner of the world's most popular rat.

## DR STACY MALAKER



### *Stanford University Department of Chemistry*

Dr. Malaker obtained her bachelor's degree from the University of Michigan in Biochemistry and Anthropology-Zoology. During this time, she worked at the Protein Structure Facility, performing peptide synthesis and using mass spectrometry for quality control. She then went on to receive her PhD in Chemistry from the University of Virginia in the laboratory of Professor Donald Hunt. There, her thesis work focused on enrichment and mass spectrometric identification of glycopeptides presented by the MHC class I and II processing pathways. Dr. Malaker has continued to investigate the role of aberrant glycosylation in cancer as an NIH postdoctoral fellow in Professor Carolyn Bertozzi's laboratory at Stanford University. Here, she is using mass spectrometry and glycobiology to investigate mucinase activity on glycoproteins, with the ultimate goal of characterizing cancer-derived mucins.

## DR ROBERT MORITZ



### *Institute for Systems Biology, Seattle*

Dr. Robert Moritz is Faculty member, Professor, and Head of Proteomics Research at the Institute for Systems Biology (ISB) in Seattle, Washington, USA. He began his full-time career at the Ludwig Institute for Cancer Research, Melbourne, Australia from 1983 to 2008 and received his PhD from the University of Melbourne in Biochemistry during that time. He moved to the ISB as faculty member in 2008. The Moritz group develops and applies cutting edge proteomics technologies to biomarker analysis of wellness and aging, disease biomarkers for early detection of cancer and a number of infectious disease pathogens including malaria, tuberculosis and Lyme disease. The Moritz group is the primary developer of the world renowned Trans-Proteomic Pipeline proteomics software tools for statistical validation of proteome identifications, protein crosslinking analysis with Kojak and many online resources for quantitative proteomics. His group developed the complete Human PeptideAtlas, SRMATlas, SWATHAtlas and related software routines to provide quantitative resources and repositories of mass spectrometric assays to all proteins. Dr. Moritz has published more than 260 research articles, a number of book chapters, and holds multiple patents. Dr. Moritz is currently the Vice-President of the Human Proteome Organization (HUPO) and plays a large role in growing the society. He guides several scientific journals as part of the Journals boards and is a member of a number of scientific advisory boards to life-science companies. Dr. Moritz is active in teaching and dissemination of proteomics technologies, fosters education exchanges and create forums for collaborative relationships centered on the proteome.

## PROF MATTHIAS TROST



### *Newcastle University*

Matthias Trost is a proteomics expert with interests in innate immunity and drug discovery. He studied chemistry in Freiburg, Germany and Manchester, UK. He has a PhD in Cellular Microbiology & Proteomics from the Helmholtz Centre for Infection Research, Braunschweig, Germany and was a postdoctoral fellow with Michel Desjardins at the University of Montreal, Canada and with Pierre Thibault, Institute for Research in Immunology and Cancer, Montreal, Canada. In 2010, he became Programme Leader and Head of Proteomics at the MRC Protein Phosphorylation & Ubiquitylation Unit at the University of Dundee, UK. Since 2017, he is Professor of Proteomics at Newcastle University. Matthias's research utilises proteomics to understand innate immunity in macrophages. In 2019, he was given a Wellcome Investigator award to study how ubiquitylation regulates phagosome functions. He also has a strong interest in drug discovery for which his lab pioneered high-throughput MALDI TOF mass spectrometry

## PROF JUDIT VILLEN



### *University of Washington*

Judit Villen is an Associate Professor in the Department of Genome Sciences at the University of Washington. She earned a PhD in Chemistry from the University of Barcelona (Spain) working on peptide vaccines. In 2004, she joined the laboratory of Steve Gygi at Harvard Medical School to work on mass spectrometry based proteomics. During that time, she was involved in several technology developments that propelled phosphoproteomics into mainstream applications in biomedical research, including biochemical methods, mass spectrometry acquisition strategies, and computational approaches for phosphoproteomics data analysis. Research in her laboratory has a dual focus on the global analysis of signaling networks and in developing proteomics methods to study how genetic and posttranslational modifications to protein sequences impact protein structure and function. Her work has been recognized through the ASMS Research award in 2011 and the US HUPO Robert Cotter award in 2014.

## NATIONAL SPEAKERS

## A/PROF MELISSA DAVIS



### *Walter and Eliza Hall Institute of Medical Research*

Associate Professor Melissa Davis is a computational biologist and group leader at the Walter and Eliza Hall Institute, where she leads a highly multidisciplinary research group focused on computational research in cancer progression and plasticity. She is also Joint Head of the WEHI Bioinformatics Division, which employs >60 bioinformaticians, biostatisticians and computational scientists. In 2014, Melissa was awarded a four year National Breast Cancer Foundation Career Development Fellowship, and took up a position as Senior Research Fellow in Computational Systems Biology at the University of Melbourne. Also in 2014 she co-founded the Australian Bioinformatics and Computational Biology Society (ABACBS), serving as Treasurer on the national executive from 2014-2017, and co-convenor of the ABACBS national conference in 2018. Melissa is recognised both nationally and internationally for her work in computational cancer biology.

## PROF ALEKSANDRA FILIPOVSKA



### *The University of Western Australia*

Aleksandra Filipovska received her PhD in 2002 from the University of Otago, New Zealand. From 2003-2005 she was a NZ Foundation for Research, Science and Technology Fellow at the MRC Mitochondrial Biology Unit in Cambridge, the United Kingdom. In 2006 she relocated to Australia as a NHMRC Howard Florey Fellow and established her research group at the Perkins Institute of Medical Research at the University of Western Australia. She was an Australian Research Council Future Fellow until 2014 and since 2014 she has been a NHMRC Senior Research Fellow and Professor at UWA and

the Harry Perkins Institute of Medical Research. She is also a Deputy Director of the ARC Centre of Excellence in Synthetic Biology. Her research interests are in the regulation of gene expression by RNA-binding proteins and the use of multi-omic technologies to elucidate their molecular functions in health and disease. Her research group uses genomic technologies and synthetic biology to design new models of cancer, metabolic and cardiovascular diseases and develop treatments for these disorders.

#### **A/PROF ETHAN GODDARD-BORGER**



##### ***Walter and Eliza Hall Institute of Medical Research***

Ethan Goddard-Borger is an Associate Professor at the Walter and Eliza Hall Institute of Medical Research in Melbourne, Australia. He obtained his PhD in chemistry at the University of Western Australia in 2008. During this time, he developed an inexpensive and shelf-stable diazotransfer reagent, which is now an item of commerce and is routinely used in chemical synthesis, materials science and chemical biology. His postdoctoral studies in glycobiology were conducted with Prof. Stephen Withers at the University of British Columbia (2009-2013), where he studied the enzymology of carbohydrate active enzymes. It was here that he developed novel pharmacological chaperones for the treatment of lysosomal storage disorders. Ethan began his independent research career at the Walter and Eliza Hall Institute of Medical Research in 2013. His laboratory examines how the proteins that build, break and bind glycans impact human disease using a combination of chemical, molecular and structural biology techniques. He is actively involved in drug discovery efforts based on the new targets identified by his research programme.

#### **A/PROF MICHELLE HILL**



##### ***QIMR Berghofer Medical Research Institute***

Michelle Hill obtained PhD in biochemistry at The University of Queensland, Australia. She currently leads the Precision and Systems Biomedicine Laboratory at QIMR Berghofer Medical Research Institute, Brisbane, Australia, which aims to improve health outcomes by harnessing the power of omics and computational systems biology. Michelle has been leading her team in innovative use of mass spectrometry-based omics technologies, including the development of novel biomarker pipelines and subcellular profiling methods. Application of these methods has enabled discovery of blood biomarkers for early detection of oesophageal adenocarcinoma, and discovery of novel lipid-mediated mechanisms for extracellular vesicle cargo loading.



## DR JAMES HUDSON



### ***QIMR Berghofer Medical Research Institute***

Dr James Hudson is the Group Leader for the Organoid Research Lab at QIMR Berghofer. He completed a double major in Chemical and Biological Engineering and subsequently completed his PhD on cardiac tissue engineering at The University of Queensland in 2011. He was then awarded a German Cardiology Society postdoctoral fellowship with Prof Wolfram-Hubertus Zimmermann in Germany. In 2013 Dr Hudson returned to Australia on a NHMRC ECF and is currently an NHMRC CDF and National Heart Foundation Future Leaders Fellow. Over his career Dr Hudson's work has focused on the use of stem cell-derived heart cells for tissue engineering applications and is now working together with academic and industry partners discover new therapeutic targets for heart disease. For this work he has won a number of prestigious awards including the Paul Korner award and QLD Cardiovascular Researcher of the year and also the Centenary Institute Innovation Award.

## DR ANGELA JUHASZ



### ***Edith Cowan University***

Angela Juhasz is an internationally recognized researcher working in cereal grain genomics and grain allergy. She received her PhD in Cereal chemistry from the Budapest University of Technology and Economics in 2002. Before moving to Murdoch University, Australia in 2016, Angela held a Head of Department position at the Applied Genomics Department, Centre of Agricultural Research of the Hungarian Academy of Sciences. In 2019 she joined to the Proteomics group of Professor Michelle Colgrave at the School of Science, Edith Cowan University. During the last ten years her research focus is on the use of proteogenomic tools and 'big data' to understand genetic and environmental impacts on cereal grain development programs, grain allergy and quality. She is actively involved in the gene annotation works of the bread wheat reference genome, and related cereal species, and published a major paper in Science Advances in 2018 on the genome mapping of seed allergens and immune-responsive proteins in wheat.

## PROF DAVID KOMANDER



### ***The Walter and Eliza Hall Institute of Medical Research***

David Komander studied in Germany and Scotland, working on protein kinase structures during his PhD in Dundee. As a postdoc in London, he initiated work on tumour suppressor deubiquitinases, leading to the first structures on CYLD and A20. Focussing on E3 ligases, ubiquitin binding domains and deubiquitinases, he went on to set up his own highly successful research group at the MRC Laboratory of Molecular Biology in Cambridge, UK. He was the recipient of the Lister prize in 2012 and became an EMBO member in 2014. At the end of 2018 David Komander moved to Australia to become head of the newly founded Ubiquitin Signalling Division at the Water and Eliza Hall Institute in Parkville.

## DR TARA PUKALA



### *The University of Adelaide*

Tara Pukala obtained a PhD from the University of Adelaide in 2006, under the supervision of Prof John Bowie. This was followed by a postdoctoral position at the University of Cambridge, UK, working with Prof Dame Carol Robinson in the field of native mass spectrometry. Tara returned to Australia to her current role as lecturer in the Discipline of Chemistry at the University of Adelaide in 2008. Here she leads a multidisciplinary research group focused on developing new approaches, primarily utilising mass spectrometry, to investigate the structure, function and interactions of macromolecules important in biology. Tara is a past recipient of the Australian and New Zealand Society for Mass Spectrometry Bowie Medal, and since 2017 has had the role of Scientific Director of the Adelaide Proteomics Centre.

## DR PENGYI YANG

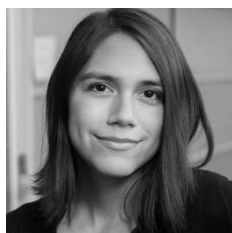


### *The University of Sydney*

Pengyi Yang is senior lecturer at the School of Mathematics and Statistics, The University of Sydney, and an ARC DECRA Fellow and a NHMRC Investigator. He heads the Computational Systems Biology group at Children's Medical Research Institute, and also heads the Computational Trans-Regulatory Biology group at Charles Perkins Centre. As a systems biologist cross-trained in computational and biological sciences, Pengyi combines machine learning and statistical methods to model trans-omic networks that cut across cell signalling, transcriptional, and epigenetic regulations.

## 2020 ADVBS SPEAKERS

## KYLIE BEMIS



### *Northeastern University*

Kylie Bemis is a faculty in the Khoury College of Computer Sciences at Northeastern University. She holds a B.S. degree in Statistics and Mathematics, a M.S. degree in Applied Statistics, and a Ph.D. in Statistics from Purdue University. In 2013, she interned at the Canary Center at Stanford for Cancer Early Detection, where she developed the Cardinal software package for statistical analysis of mass spectrometry imaging experiments. In 2015, she was awarded the John M. Chambers Statistical Software Award by the American Statistical Association for her work on Cardinal. In 2016, she joined the Olga Vitek lab for Statistical Methods for Studies of Biomolecular Systems at Northeastern University as a postdoctoral fellow. In 2019, she joined Northeastern as faculty, where she now teaches data science and develops curriculum for the MS in Data Science program. Her research interests include machine learning and large-scale statistical computing for bioinformatics.

## DR IGNATIUS PANG



### *University of New South Wales*

Ignatius is a postdoctoral research associate at the Systems Biology Initiative at UNSW, under the supervision of Prof. Marc Wilkins. His research focus is on the integrative analysis of 'omics' datasets (e.g. transcriptomics, proteomics, interactomics etc.) to understand how cellular functions are regulated. For example, the Proteomic-Genomics Nexus (PG Nexus) tool enabled the co-visualization of peptides in the context of genomes or contigs, along with RNA-Seq reads, to facilitate the validation of genes and splice or alternatively spliced junctions in mRNA transcripts. The PTMOracle is a Cytoscape app for co-analyzing post-translational modifications (PTMs) in the context of protein interaction networks. He is currently involved in several collaborative projects. These include using multi-omics data to identify biological pathways important for bacterial strains that causes sepsis and using virome-capture sequencing to study the relationships between the virome and the onset of type 1 diabetes in children that are genetically at risk.

## A/PROF DAVID POWELL



### *Monash University*

A/Prof David Powell is a computational biology researcher and the Director of the Monash Bioinformatics Platform. David has a PhD in Computer Science and a background in algorithm development for bioinformatics, and has also worked professionally as a software developer and lead two start up companies in a CTO role. David's recent research has been in visualisation for biological data with an interest in building interactive tools to make analysis and data more accessible for both experts and novice users. His tools have been used by thousands of researchers around the world to visualise and analyse their biological data.

## WORKSHOPS

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### Pre-Lorne Workshop - 1st Australasian Data Visualisation and Bioinformatics Workshop

**Time and date:** Tuesday 4th and Wednesday 5th February 2020, 9:00 am- 5:30 pm

**Location:** University of Melbourne, Australia

Prior to the 1st ADVBS, we will also be hosting a two-day Data Visualisation and Bioinformatics Workshop to provide an exciting hands-on opportunity for the wider-omics community. Through knowledge and experience in how to use, explore, interpret and visualize data in a meaningful way, research can be communicated more effectively. Combined, the ADVBS and Workshop will host an outstanding line-up of international speakers (see below) and showcase talent in the region by covering a variety of engaging topics.

On behalf of the Organising Committee,  
Dr Melanie White (Symposium Chair), University of Sydney

1st ADVBS Organising Committee:

Dr Melanie White (Symposium Chair)  
A/Prof David Powell  
Dr Ignatius Pang  
Dr Deanna Deveson  
Dr Anup Shah

Dr Laura Dagley  
Dr Ralf Schittenhelm  
Dr Ben Parker  
Dr James Broadbent

International Advisory Committee:

Dr Kylie Bemis – USA  
Martin Krzywinski – Canada

### 1st Australasian Data Visualisation and Bioinformatics Symposium (ADVBS)

**Time and date:** Friday 7th February 2020

**Location:** Horizons Room, Cumberland Lorne Resort, Lorne, Victoria, Australia

The ADVBS will focus on integrating computational and statistical approaches to interrogate mass spectrometry-based data, producing visually compelling biological narratives. Running concurrently with the annual meeting of the Australasian Proteomics Society (APS) provides an opportunity for researchers to become data fluent by way of exposure to the latest approaches in data visualization and analysis.

### The Second Australasian Core Facilities Meeting

**Date:** Thursday 6th February 2020

**Time:** 12noon to 3:30pm.

Building on the success of the inaugural meeting at HUPO 2019, co-chairs Ben Crossett and Ralf Schittenhelm aim to bring together the leaders in core facility management for an afternoon of insightful analysis, debate and sharing of best practice. The meeting is ideally suited to those working in or with core facilities or aspiring to move into core facility management.

# PROGRAM

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**THURSDAY, 6 FEBRUARY 2020**

**The Second Australasian Core Facilities Meeting Program**

**Welcome Address**

12:00 PM – 12:05 PM

Horizons Room

**Session 1: David vs Goliath**

12:05 PM – 1:05 PM

Horizons Room

**Richard Wilson**

One man and mass spec, a review of the Utas operating model

**Nicholas Williamson**

The benefits of a subscription model

**Lunch**

1:05 PM – 1:45 PM

Horizons Room

**Session 2: You can't ask that!**

1:45 PM – 2:30 PM

Horizons Room

A team based challenge to design the perfect survey

**Session 3: Delivering Metabolomics**

2:30 PM – 3:30 PM

Horizons Room

**Zofia Felton/Dedreia Tull**

Metabolomics Australia's roadmap into the future

**Esteban Marcellin**

Challenges and merits of running a metabolomics core

**PROTEOMICS 2020 CONFERENCE PROGRAM**

**Registration**

2:00 PM - 7:00 PM

Auditorium Foyer

**Welcome Address**

4:00 PM - 4:10 PM

Auditorium

Chair: James Broadbent

**The Simpson Lecture**

4:10 PM - 5:00 PM

Auditorium

Chair: James Broadbent

4:10PM

**Anne-Claude Gingras**


A proximity map of a human cell *abs# 1*

**Ken Mitchelhill Young Investigator Award Lecture**

5:00 PM - 5:30 PM

Auditorium

Chair: Sean Humphrey

Session sponsored by  **SHIMADZU**  
Excellence in Science

5:00 PM

**Rebecca C Poulos**

Strategies to improve reproducibility of large-scale and longitudinal proteomics  
*abs# 2*

**Vendor Talks**

5:30 PM - 5:45 PM

Auditorium

Chair: James Broadbent

**Symposium One: Students of the APS (SoAPS)**

5:45 PM - 7:00 PM

Auditorium

Chairs: Ashleigh Dale & Shuai Nie

Session sponsored by



5:45 PM

**Yi-Hsuan Tu**

The use of natural products in the leather industry: Depilation without damage  
*abs# 3*

6:00 PM

**Elizabeta Madzharova**

Functional modification of matrix metalloproteinase 9 by substrate glycosylation *abs# 4*

6:15 PM

**Louise Uoselis**

The mitochondrial unfolded protein response: a global translational program that repairs local mitochondrial damage *abs# 5*

6:30 PM

**Alexander W. Rookyard**

Quantitative proteomics of irreversible cysteine post translational modifications in myocardial ischemia / reperfusion (I/R) injury *abs# 6*

6:45 PM

**Chun Zhou**

Glycopeptide variable window SWATH for improved Data Independent Acquisition glycoproteomics *abs# 7*

**Welcome Reception**

7:00 PM - 10:00M

Exhibition Hall

**Registration**

7:15 AM - 5:00 PM

Auditorium Foyer

**Shimadzu Breakfast Workshop - Benefits of targeted omics workflows and beyond**

7:45 AM - 8:40 AM

Auditorium



Breaking the sensitivity barrier to unravelling the novel roles of lipid mediators in pathophysiology  
**Atsuhiko 'Ash' Toyama, Shimadzu Corporation, Singapore/Japan**

The Q-TOF technologies to reproduce the benefits of targeted workflows in high-resolution analyses

**Chris Bowen, Shimadzu Scientific Instruments, Australia**

**Symposium Two: Disease Proteomics I**

8:50 AM - 10:20 AM

Chairs: Patricia Illing & Desmond Li

Auditorium

*Session sponsored by*



8:50 AM

**Philipp E Geyer**

Plasma proteome profiling to assess human health and disease *abs# 8*

9:20 AM

**Anthony Purcell**

Precision cancer immunotherapy - can proteomics rise to the challenge? *abs# 9*

9:35 AM

**Harley Robinson**

Caveolae formation alters intracellular organelle composition and function *abs# 10*

9:50 AM

**Stephanie L Rayner**

Rapid, unbiased identification of protein inclusion components from patient post-mortem brain tissue using Biotinylation by Antibody Recognition (BAR) *abs# 11*

10:05 AM

**Mark A Baker**

Splicing up your sex life *abs# 12*

**Vendor Talks**

10:20 AM - 10:30 AM

Auditorium

Chairs: Patricia Illing & Desmond Li

**Morning Tea**

10:30 AM - 11:00 AM

Exhibition Hall

*Session sponsored by*



**Symposium Three: Environmental, Microbial, Plant Proteomics**

11:00 AM - 12:50 PM

Chairs: Mark Condina & Balu Balan

Auditorium

Session sponsored by



- 11:00 AM **Matthias Trost**  
The role of ubiquitylation on the phagosome: a tale of inflammatory responses and vesicle trafficking *abs# 13*
- 11:30 AM **Angela Juhasz**  
Proteogenomic characterization of einkorn wheat cultivars with low celiac disease response *abs# 14*
- 11:50 AM **Lok Man**  
Multi-omic analysis and functional validation of *Campylobacter jejuni* grown with intestinal bile salts *abs# 15*
- 12:05 PM **Delphine Vincent**  
Proteomics tools for medicinal cannabis *abs# 16*
- 12:20 PM **Sophia Escobar-Correas**  
Digestive physiology and proteomics for controlling an invasive pest *abs# 17*
- 12:35 PM **Tao Wang**  
LC-MS/MS-based multi-omics approach to elucidate developmental adaptations in the parasitic nematode *Haemonchus* *abs# 18*

**Lightning Talks One**

12:50 PM - 1:10 PM

Chair: Ben Crossett

Auditorium

**Cassandra Pegg**

Cellular glycoproteome and proteome during influenza infection *abs# 19*

**Balu Balan**

"RNA regulons" as potential drivers of *Giardia duodenalis* stage transition *abs# 20*

**Joel Cain**

Identification of novel *N*-glycosylation sites from the bacterium *Campylobacter jejuni* *abs# 21*

**Robert JA Goode**

Understanding glycopeptide antibiotic synthesis by mass spectrometric analysis of polycyclic peptides *abs# 22*



**Hannah McKerchar**

Characterising insult-induced protein-protein crosslinks formed during food processing *abs# 23*

**Gabriel Goncalves**

Multi-omic analysis reveals the pro-inflammatory cytokine IFN $\gamma$  modulates the immunopeptidome of triple negative breast cancer cells *abs# 24*

**Lunch and Poster Session One**

1:10 PM - 3:10 PM

Exhibition Hall

**ThermoFisher Workshop**

2:10 PM - 3:10 PM

Auditorium



Dissecting the roles of glycosylation on bacterial proteins within the Burkholderia genus

***Dr Nichollas Scott, Department of Microbiology and Immunology, The University of Melbourne***

Direct measurement of protein translation and degradation rates In vivo at proteomic scales in the clinic and beyond; new approaches to stable isotope metabolic labelling and analysis

***Dr Owen Duncan, School of Molecular Sciences, The University of Western Australia***

**Symposium Four: Post-Translational Modifications and Signalling**

3:15 PM - 4:50 PM

Auditorium

Chair: Samantha Emery-Corbin and Ben Parker

3:15 PM **Judit Villen**

Not provided at time of publishing *abs# 25*

3:45 PM **David Komander**

New tools to study protein ubiquitination *abs# 26*

4:05 PM **Stuart Cordwell**

Deciphering irreversible cysteine redox post-translational modifications in myocardial ischemia / reperfusion injury *abs# 27*

4:20 PM **Dylan J Harney**

HNFAA sumoylation is regulated by fasting. *abs# 28*

4:35 PM **Chris Overall**

Protein TAILS tell remarkable tales: Positional proteomics reveals diverse N-Terminomes and proteolytic landscapes in disease *abs# 29*

**APS Annual General Meeting**

5:00 PM - 5:45 PM

Auditorium

**Students of the APS (SoAPS) Event with Invited Speakers**

5:30 PM - 7:30 PM

Session sponsored by **ThermoFisher**  
SCIENTIFIC

\*If you are not attending the SoAPS function the evening is free for your leisure

**1<sup>st</sup> Australasian Data Visualisation and Bioinformatics Symposium (ADVBS) Program**

**Satellite Symposium – Welcome**

8:55 AM - 9:00 AM

Horizons Room

Chair: Melanie White

**Satellite Symposium – Opening Plenary**

9:00 AM - 9:30 AM

Horizons Room

Chair: Melanie White

9:00 AM **Kylie Bemis**

Challenges in Visualization and Analysis of Mass Spectrometry Imaging  
Experiments *abs# 30*

**Satellite Symposium - Session One: Software Tools**

9:30 AM - 10:30 AM

Horizons Room

Chair: Melanie White

9:30 AM **George Guo**

MassOmics: An R package of a cross-platform data processing pipeline for large-scale  
GC-MS untargeted metabolomics datasets *abs# 31*

9:45 AM **Mohammad Shahbazy**

MHCpLogics: a machine learning-based tool for unsupervised data visualisation and  
cluster analysis of immunopeptidomes *abs# 32*

10:00 AM **Hartmut Schlüter**

OmixLitMiner - Tool for fast evaluation of knowledge and importance of regulated  
individual proteins derived from differential proteomics *abs# 33*

10:15 AM **Hani Jieun Kim**

CiteFuse enables multi-modal analysis of CITE-seq data *abs# 34*

**Satellite Symposium - Session Two: Representing Function**

11:00 AM - 12:15 PM

Horizons Room

Chair: Laura Dagley

## 1<sup>st</sup> Australasian Data Visualisation and Bioinformatics Symposium (ADVBS) Program

- 11:00 AM **Sean J Humphrey**  
*Stimulomics: large-scale mapping of signalling networks downstream of major cell surface receptors abs# 35*
- 11:30 AM **Elise J. Needham**  
Precision phosphoproteomics reveals kinase targets enhancing muscle insulin sensitivity *abs# 36*
- 11:45 AM **Gene Hart-Smith**  
Analytical guidelines for co-fractionation mass spectrometry obtained through global profiling of gold standard *Saccharomyces cerevisiae* protein complexes *abs# 37*
- 12:00 PM **Anjaneyaswamy Ravipati**  
Lipidomic Mapping, Localization and Characterization in Tissues by MALDI- Imaging Mass Spectrometry *abs# 38*

### Satellite Symposium - Session Three: Integrating Multiple Technologies

12:15 PM - 1:05 PM Horizons Room  
Chairs: Anup Shah & Andrew Webb

- 12:15 PM **Mark Larence**  
Multi-Omics Analysis of the Intermittent Fasting Response *abs# 39*
- 12:35 PM **Stephanie E L Town**  
Using genomics and proteomics to understand the antibiotic resistance capabilities of a bacterial pathogen *abs# 40*
- 12:50 PM **Hitesh Kore**  
Protein coding potential of annotated non-coding RNAs encoded by the human genome *abs# 41*

### Satellite Symposium - Lunch and Poster Session One

1:05 PM - 3:15 PM Exhibition Hall

### Satellite Symposium - Session Four: Interpreting Multiple Technologies

3:15 PM - 4:30 PM Horizons Room  
Chair: Nicholas Williamson

- 3:15 PM **Ignatius Pang**  
The Hitchhiker's Guide to the Yeast Interactome *abs# 42*
- 3:40 PM **Thomas Kislinger**  
Identification of aggressive prostate cancer through in-depth proteomics of tissues and urines *abs# 43*
- 4:00 PM **Ralf Schittenhelm**  
LFQ-Analyst, an interactive web-platform to analyse quantitative proteomics data *abs# 44*

## 1<sup>st</sup> Australasian Data Visualisation and Bioinformatics Symposium (ADVBS) Program

4:15 PM **Rebeca Kawahara Sakuma**  
Deciphering the stage-specific glycoprotein signatures of colorectal cancer using integrated mass spectrometry-based omics *abs# 45*

### Satellite Symposium - Closing Plenary

4:30 PM - 5:00 PM Horizons Room  
Chair: Ralf Schittenhelm

4:30 PM **David Powell**  
Interactive visualisation, and reproducibility in bioinformatics *abs# 46*

### Satellite Symposium – Closing Ceremony and Award Presentation

5:00 PM - 5:10 PM Horizons Room  
Chair: Melanie White

## SATURDAY, 8 FEBRUARY 2020

### SCIEX Breakfast Workshop

7:00 AM - 8:30 AM Horizons Room

Enabling ultra-fast proteomics with deep sample coverage  
**Steve Tate, PhD – Manager Software Applications Research Group**



Evaluation of the use of in silico libraries in DIA experiments  
**Jérémy Potriquet, PhD – Field Application Scientist & OMICS Market Development**

### Registration

8:00 AM - 5:30 PM Auditorium Foyer

### Symposium Five: Statistics, Data Science and Machine Learning

9:00 AM - 10:35 M Auditorium

Chairs: Melanie White & Robert Goode

9:00 AM **Martin Krzywinski**  
Fitting big science on a small page *abs# 47*

9:30 AM **Pengyi Yang**  
Trans-omic characterisation of stem cell networks *abs# 48*

9:50 AM **Cecilia Lindskog**  
The Human Protein Atlas - Implications for Human Biology and Precision Medicine *abs# 49*

10:05 AM **Michael G Leeming**  
Phosphomatics: A knowledge-based approach to investigating high-throughput phosphoproteomics data *abs# 50*

## SATURDAY, 8 FEBRUARY 2020

10:20 AM **Daryl Wilding-McBride**  
Delving deeper into the proteome with an improved and highly parallelised feature detection pipeline for the Bruker timsTOF Pro *abs# 51*

### Morning Tea

10:35 AM - 11:00 AM

Exhibition Hall

Session sponsored by 

### Symposium Six: Disease Proteomics II + KHUPO

11:00 AM - 1:05 PM

Auditorium

Chairs: Rommel Mathias & Harley Robinson

- 11:00 AM **Aleksandra Filipovska**  
Fidelity of protein synthesis is required for energy production *abs# 52*
- 11:30 AM **Michelle M Hill**  
Addressing unmet clinical diagnostic needs with proteomics *abs# 53*
- 11:50 AM **Keshava K. Datta**  
Global proteomic and phosphoproteomic profiling to identify proteins and pathways that regulate cell survival in hypoxic conditions *abs# 54*
- 12:05 PM **Lauren A Thurgood**  
Analysis of FFPE tissues to investigate lymph node protein expression in patients with leukemia *abs# 55*
- 12:20 PM **Per E. Andren**  
Simultaneous mass spectrometry imaging of multiple neuropeptides in the brain and alterations induced by experimental Parkinsonism and L-DOPA therapy *abs# 56*
- 12:35 PM **J. Eugene Lee**  
Reference proteome-based subtyping of liver cancer *abs# 57*
- 12:50 PM **Taejoon Kwon**  
Ciliary proteome from motility-defective multiciliated cells *abs# 58*

### Lightning Talks Two

1:05 PM - 1:30 PM

Auditorium

Chair: Nathan Croft

**Christopher H Caboche**  
Mini-malting and mini-mashing methods for early stage validation of new barley varieties and malt accreditation and quality control of beer brewing *abs# 59*

**Ryan Separovich**

The role of upstream phosphorylation in the regulation of histone methylation  
*abs# 60*

**Natasha Vassileff**

Revealing the proteome of brain derived exosomes isolated from human  
amyotrophic lateral sclerosis post-mortem tissues *abs# 61*

**Rune H Larsen**

Development of a primary cell proficient phosphoproteomic workflow *abs# 62*

**Elena Smertina**


Studying uncharacterised non-structural proteins of Rabbit haemorrhagic disease  
virus *abs# 63*

**Amy BP Ribet**

Mapping the lysosomal transporter proteome of osteoclasts uncovers new  
regulators of bone homeostasis *abs# 64*

**Lunch and Poster Session Two**

1:30 PM - 2:45 PM

Exhibition Hall  
Session sponsored by  **Agilent**

**Bruker Workshop**

2:30 PM - 3:30 PM

Auditorium

Using the timsTOF Pro to study ubiquitylation in innate immunity

**Prof. Matthias Trost - Professor of Proteomics Institute for Cell and Molecular  
Biosciences, Faculty of Medical Sciences, Newcastle University, UK**



Data-independent acquisition combined with parallel accumulation – serial fragmentation  
combined (diaPASEF): Bottom-up proteomics with increased ion usage

**Dr. Ben Collins - School of Biological Sciences, Queens University, Belfast, UK**

**Symposium Seven: Glycoscience**

4:00 PM - 5:20 PM

Auditorium

Chairs: Nichollas Scott & Matthew Briggs

## SATURDAY, 8 FEBRUARY 2020

- 4:00 PM **Stacy Malaker**  
Defining the "mucinome": enzyme toolkit for enrichment and analysis of mucin-domain glycoproteins *abs# 65*
- 4:30 PM **Ethan Goddard-Borger**  
Tools and methods for probing the biology of tryptophan C-mannosylation *abs# 66*
- 4:50 PM **Morten Thaysen-Andersen**  
Granule-Specific *N*-Glycosylation and Chlorination Activity of Neutrophil Myeloperoxidase *abs# 67*
- 5:05 PM **Shutao Mei**  
Immuno-peptidomic analysis reveals that deamidated HLA-bound peptides arise predominantly from deglycosylated precursors *abs# 68*
- 5:20 PM **Kathirvel Alagesan**  
Synthetic Glycopeptides assisted large scale glycoproteomics from sample preparation to data analysis *abs# 69*

### Symposium Eight: New Technologies I

5:20 PM - 6:40 PM

Auditorium

Chair: Jarrod Sandow

- 5:20 PM **James Hudson**  
Proteomics Combined with Human Cardiac Organoids to Find New Mechanisms Driving Maturation and Regeneration *abs# 70*
- 5:40 PM **Mark Larance**  
Characterisation of a putative new metabolic hormone in human plasma *abs# 71*
- 5:55 PM **Parthiban Periasamy**  
Strategies to enrich low-molecular weight proteins for proteomic analysis *abs# 72*
- 6:10 PM **Brooke A Dilmetz**  
Rapid separation and identification of beer spoilage bacteria by inertial microfluidics and MALDI-TOF mass spectrometry *abs# 73*
- 6:25 PM **Paul D Veith**  
Deglycosylation of glycoproteins with trifluoromethanesulfonic acid (TFMS): unravelling the chemistry allows extension of the protocol to the analysis of released glycan chains using standard proteomics methods *abs# 74*

### APS Conference Dinner (Festival of Food)

7:30 PM - 11:00 PM

Umisango, Jashn & Lorne Central

The dinner is a celebration of the 25<sup>th</sup> anniversary of Lorne Proteomics. The evening will include short presentations, interviews, and dancing! Food and drinks also provided.

**Registration**

8:30 AM - 1:30 PM

Auditorium Foyer

**Symposium Nine: New Technologies II**

9:00 AM - 10:40 AM

Auditorium

Chair: Ralf Schittenhelm

9:00 AM

**Tara L Pukala**

An integrated mass spectrometry approach towards characterisation of snake venom proteins *abs# 75*

9:20 AM

**Nicola Beckett**

*Detection of intact insulin analogues in post-mortem vitreous humour using forensic toxicology and proteomic tools – application to overdose casework abs# 76*

9:35 AM

**Brett Hamilton**

Functional-Mass Spectrometry Imaging - mapping the location of enzymes by their function *abs# 77*

9:50 AM

**Scott Bringans**

PromarkerD as an immunoaffinity mass spectrometry assay for diabetic kidney disease *abs# 78*

10:05 AM

**Emmanuelle Claude**

Metabolomic/lipidomic DESI imaging of different cell cultures. *abs# 79*

10:20 AM

**Stephan Klatt**

Quantitative, targeted and high-throughput metabolomics workflow of small-volume plasma samples via blood cards. *abs# 80*

**Morning Tea**

10:40 AM - 11:10 AM

Exhibition Hall

**Symposium Ten: Interactomics**

11:10 AM - 12:20 PM

Auditorium

Chairs: Mark Larance & Naomi Koh Belic

11:10 AM

**Ben Collins**

Complex-centric proteome profiling in one day with SEC-SWATH-MS *abs# 81*

11:40 AM

**Melissa Davis**

What are we missing? The hidden impact of missing values in proteomics analysis and results *abs# 82*

12:00 PM

**Jeffrey Smith**

Global and sequence-targeted purification of intact RBP-RNA complexes *abs# 83*



## SUNDAY, 9 FEBRUARY 2020

12:15 PM **Ashleigh L Dale**  
Defining the *Campylobacter jejuni* interactome by cross-linking mass spectrometry (XL-MS) *abs# 84*

### Closing Keynote Lecture

12:30 PM - 1:00 PM Auditorium  
Chair: Nichollas Scott

12:30 PM **Robert L Moritz**  
Comprehensive Quantitative Stability Assay (CQSA) system for defining the molecular resolution of protein-compound interactions in *Mycobacterium tuberculosis* *abs# 85*

### Closing Ceremony and Award Presentation

1:00 PM - 1:30 PM Auditorium  
Chair: James Broadbent

### Bus Transfer to Melbourne Airport & City

2:45 PM sharp Departing from the Cumberland Lorne.

The bus will travel first to Tullamarine (Melbourne) Airport (arrival time approx. 5:15pm), then into Melbourne city, dropping passengers at WEHI/University of Melbourne, Royal Parade (arrival time approx. 5:45pm).

# POSTER LISTING

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## LIGHTNING POSTER SESSION ONE - FRIDAY, 7 FEBRUARY 2020

### **Cassandra Pegg**

Cellular glycoproteome and proteome during influenza infection abs# 19

### **Balu Balan**

“RNA regulons” as potential drivers of *Giardia duodenalis* stage transition abs# 20

### **Joel Cain**

Identification of novel *N*-glycosylation sites from the bacterium *Campylobacter jejuni* abs# 21

### **Robert JA Goode**

Understanding glycopeptide antibiotic synthesis by mass spectrometric analysis of polycyclic peptides abs# 22

### **Hannah McKerchar**

Characterising insult-induced protein-protein crosslinks formed during food processing abs# 23

### **Gabriel Goncalves**

Multi-omic analysis reveals the pro-inflammatory cytokine IFN $\gamma$  modulates the immunopeptidome of triple negative breast cancer cells abs# 24

## POSTER SESSION ONE - FRIDAY, 7 FEBRUARY 2020

### **Christina Andronis**

Towards the generation of a comprehensive proteome map for *Phytophthora cinnamomi*, the causal agent of native dieback abs# 91

### **Ching-Seng Ang**

Interaction of Common Antibiotics with Human Serum Albumin as Determined by Hydrogen Deuterium Exchange and Chemical Cross Linking Mass Spectrometry abs# 92

### **Ali Azimi**

Investigating proteome changes between primary and metastatic cutaneous squamous cell carcinoma using SWATH mass spectrometry abs# 93

### **Todd Blackburn**

Expression of *SCN2A* protein in different mouse models of *SCN2A* encephalopathy and after antisense oligonucleotide treatment abs# 94

### **Utpal Bose**

SWATH-MS proteomics reveals time-dependent acid stress response in *Campylobacter jejuni* abs# 95

### **Kirstyn Carey**

A High Throughput approach to identifying compound inhibitors of mRNA processing and export abs# 96

**Flora Cheng**

The E3 ubiquitin ligase SCF<sup>(cyclin-F)</sup> complex regulates caspase-3, a key executor of the apoptotic cell death program

abs# 97

**Emmanuelle Claude**

Mass Spectrometry Imaging study of Lipid Metabolites in the adult mouse testis

abs# 98

**Penelope V Dalla**

Chronic obstructive pulmonary disease: is autoimmunity a contributing factor?

abs# 99

**Chris Desire**

Measurement of protein losses during sample preparation

abs# 100

**Samantha J Emery-Corbin**

High-confidence identification of protein methylation in *Giardia duodenalis*, a neglected gastrointestinal parasite

abs# 101

**Lee A Gethings**

OMIC Investigation of Chondrocytes' Response to varying mechanical load – Assessment of aging and impact stress

abs# 102

**Fatemeh Habibpourmehraban**

Insights into the proteomics of abiotic stresses in rice

abs# 103

**Joshua Hamey**

Crosstalk between protein methylation and phosphorylation in yeast and human

abs# 104

**Sara Hamzelou**

Proteome response to drought stress of three species of rice from different geographic regions

abs# 105

**Karthik Kamath**

A draft map of the Rice plant proteome

abs# 106

**Jian Kang**

Quantitative proteomic analyses of molecular response to the RNA polymerase I transcription inhibitor CX-5461 in olaparib-resistant ID8 mouse ovarian cancer cells

abs# 107

**Edward EDK Kerr**

Cell wall and whole cell proteomes define flocculation and fermentation behaviour of yeast

abs# 108

**Naomi Koh Belic**

New Stemsation: Proteomic Characterisation of Human Adipose Stem Cells

abs# 109

**Desmond K Li**

Redox modifications of cysteine in the liver of type 2 diabetes mellitus

abs# 110

**Shivanjali J. Lingam**

Association of post-translational modifications in the evolution of diabetic nephropathy in a rodent model of type 2 diabetes mellitus

abs# 111

**Richard Lipscombe**

PromarkerD: A novel test for predicting rapid decline in renal function in type 2 diabetes

*abs# 112*

**Evelyne Maes**

Molecular profiling of fermented dairy products using mass spectral fingerprinting technologies

*abs# 113*

**Federico Martinez-Seidel**

Kinetic mass spectrometry imaging to study cytosolic ribosomes remodeling in plants

*abs# 114*

**Matthew J McKay**

Cotton reproduction: SWATH-MS reveals stage-specific proteins involved in cotton pollen development

*abs# 115*

**Pippa E Mckinstry**

Prevalence and mechanisms of diastaticus-like phenotypes and genotypes in *Saccharomyces cerevisiae* brewing strains

*abs# 116*

**LIGHTNING POSTER SESSION TWO - SATURDAY, 8 FEBRUARY 2020****Christopher H Caboche**

Mini-malting and mini-mashing methods for early stage validation of new barley varieties and malt accreditation and quality control of beer brewing

*abs# 59*

**Ryan Separovich**

The role of upstream phosphorylation in the regulation of histone methylation

*abs# 60*

**Natasha Vassileff**

Revealing the proteome of brain derived exosomes isolated from human amyotrophic lateral sclerosis post-mortem tissues

*abs# 61*

**Rune H Larsen**

Development of a primary cell proficient phosphoproteomic workflow

*abs# 62*

**Elena Smertina**

Studying uncharacterised non-structural proteins of Rabbit haemorrhagic disease virus

*abs# 63*

**Amy BP Ribet**

Mapping the lysosomal transporter proteome of osteoclasts uncovers new regulators of bone homeostasis

*abs# 64*

**Jacob Netherton**

Proteomic Characterisation of poor sperm chromatin compaction suggests nuclear retention

*abs# 131*

**Shuai Nie**

Bacterial death phase initiation by targeted membrane lipid modification

*abs# 132*

**Gillian E Norris**

Defining the interactome of the immunity protein Gcch - what can it tell us about glycocin F induced bacteriostasis?

*abs# 133*

**Matthew O'Rourke**

Using open source data for peptide spectral library generation with data independent analysis label free quantification (DIA-LFQ) for plasma biomarker discovery

*abs# 134*

**Tiago Oliveira**

Unravelling the biological mechanisms of Acute Lymphoblastic Leukemia (ALL) drug-resistance with integrated multi-glycoconjugate analysis

*abs# 135*

**Heather Patsiouras**

Tandem Ion Mobility coupled with Mass Spectrometry for Gas Phase Unfolding studies

*abs# 136*

**Robert S Plumb**

Technical Reproducibility and Analytical Precision for a Multi-omic Study utilising Data Independent Strategies with CCS libraries

*abs# 137*

**Adam Rainczuk**

Turnover optimized short nanoLC gradients on a tims equipped QTOF for high throughput and deep proteome measurements

*abs# 138*

**Rashmi Rana**

Identification of Epidermal Growth Factor Receptor Variant III (EGFR VIII) Expression in Meningioma Indian Patients

*abs# 139*

**Anup D Shah**

A statistical approach to rank differentially expressed proteins using confidence bound on effect size

*abs# 141*

**Pascal Steffen**

Molecular signature associated with lymph node metastasis identified from minimally invasive FFPE colon cancer

*abs# 142*

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DISCOVERIES FOR HUMANITY

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