



# Congress Handbook



**HU**  **O** **ADELAIDE**

18TH HUMAN PROTEOME ORGANIZATION WORLD CONGRESS

AUSTRALIA  
SEPTEMBER 15-19 2019



# Be surprised!



The Human Proteome Organization (HUPO) is an international scientific organization representing and promoting proteomics through international cooperation and collaborations by fostering the development of new technologies, techniques and training.

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# About HUPO

## HUPO Mission Statement

To define and promote proteomics through international cooperation and collaborations by fostering the development of new technologies, techniques and training to better understand human disease.

## Objectives

- Foster global collaboration in major proteomics projects by gathering leading international laboratories in life sciences, bioinformatics, mass spectrometry, systems biology, pathology, and medicine;
- Become the point of contact for proteomics research and commercialization activities worldwide;
- Support large-scale proteomics projects that are aimed at:
  - A mechanistic understanding of fundamental biological processes (often using model organisms and non human species);
  - Directly studying human disease through proteomics techniques and technologies;
  - Coordinate and enable the fostering of communication among funding agencies and industry partners with the proteomics community and coordinate the activities of groups and organisations interested in HUPO's Scientific Initiatives
- Coordinate the development of standard operating procedures related to:
  - Sample preparation, analysis, and repetitions;
  - Data collection, analysis, storage, and sharing;

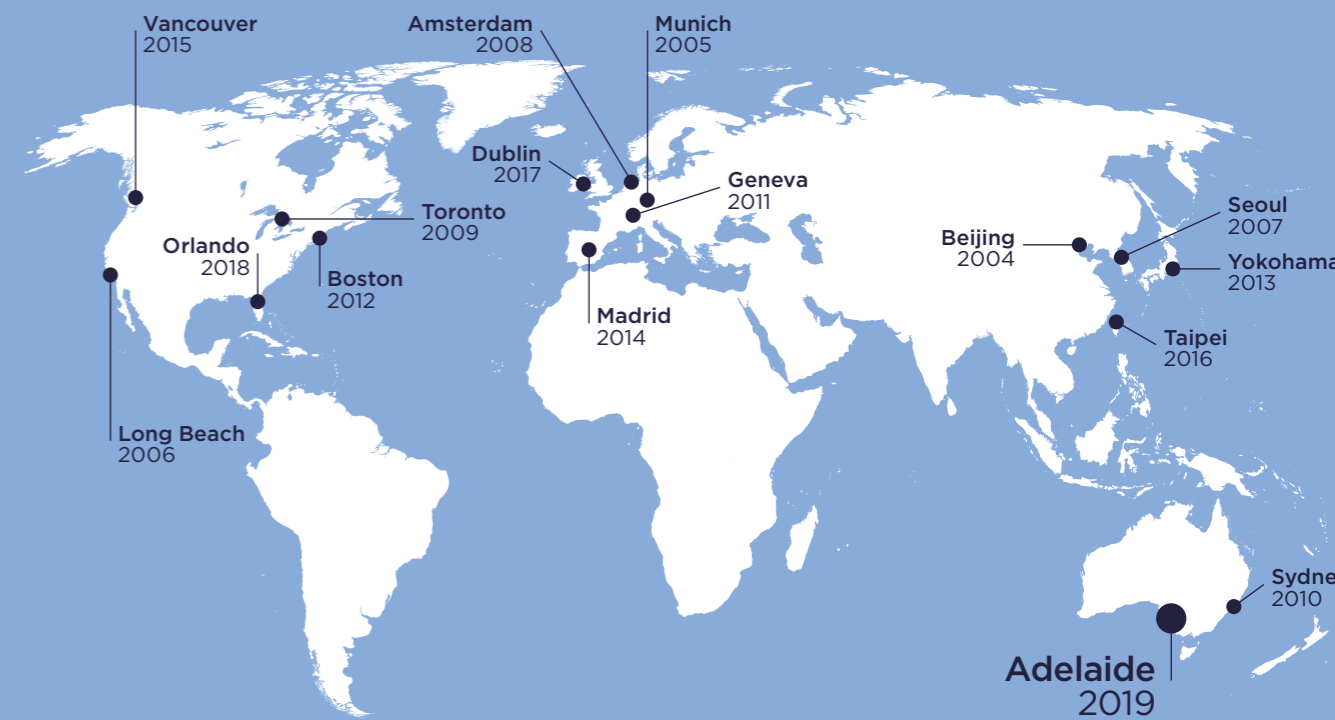
- Play a leading role in:
  - Defining the location and functions of proteins in human health and disease by supporting the definition of common and specific standards for peptide and protein characterization from human and model organism specimen selection and phenotypic evaluation to data collection, storage and analysis allowing free and rapid exchange of data;
  - The creation of country-based ethical and legal policy surrounding the handling, banking and use of human tissue specimens for large-scale proteomics projects.

## How did HUPO Evolve?

HUPO was launched on February 9, 2001. On that date, a global advisory council was officially formed that included leading global experts in the field of proteomics from the academic, government, and commercial sectors. Over the next 12 months, the council, in consultation with industry, identified major proteomics issues and initiatives that needed to be addressed by HUPO. Since its inception, HUPO has received substantial financial assistance from Genome Quebec, Montreal International, McGill University, the National Institutes of Health, and pharmaceutical companies, among others. In addition, it has benefited from considerable in-kind contributions of time and energy from HUPO Council members, research institutes, and pharmaceutical company partners around the world.

The HUPO Office Headquarters are located in Vancouver, BC, Canada.

HUPO Initiatives are prominently showcased at each Annual HUPO World Congress, which are held as per a three year rotation in the Americas, Asia/Oceania and Europe. The number of participants and exhibitors has significantly increased over the years and the Congresses are a must attend for anyone involved in proteomics.



## Annual HUPO World Congresses

### What is Proteomics?

Proteomics has evolved from genomics and the successful sequencing and mapping of the genomes of a wide variety of organisms, including humans.

Genomics involves using reagents, tools and technologies for the high throughput sequencing of DNA and the subsequent storage and annotation of the data. This process is complex and focuses on the information of one target molecule, DNA, in the nucleus of cells. Consequently, there is one genome for each organism.

In contrast, proteomics focuses on the identification, localization, and functional analysis of the protein make-up of the cell. The proteins present in a cell, together with their function, sub-cellular location, and perhaps even structure, change dramatically with the organism, and the conditions faced by their host cells including: age, checkpoint in the cell cycle, and external or internal signaling events.

Thus, there are many proteomes for each organism and consequently, the quantity and complexity of the data derived from the sequencing and mapping of the human proteome are estimated to be at least three times greater than that involved in the human genome project. Acquiring, analyzing, and interpreting these vast data sets requires a series of well-integrated, high-throughput technologies to lead the researcher from experimental design to biological insight.

The field of proteomics is particularly important because most diseases are manifested at the level of protein activity. Consequently, proteomics seeks to correlate directly the involvement of specific proteins, protein complexes and their modification status in a given disease state. Such knowledge will provide a fast track to commercialization and will speed up the identification of new drug targets that can be used to diagnose and treat diseases.

## About HUPO 2019 Congress

In 2019, the 'proteome' will celebrate its 25th birthday by returning home to Australia for the 18th Human Proteome Organization World Congress. The Congress will be hosted by the Australasian Proteomics Society (APS) and held in the beautiful 'City of Churches', Adelaide. HUPO 2019 will focus on "Advancing Global Health Through Proteome Innovation" and will bring together world-leading experts and the next generation of early career scientists to promote how proteomics is advancing our knowledge of human and planetary health. HUPO 2019 will both celebrate what has been achieved and look forward to future advances and discoveries that will revolutionize global health. This will be achieved by a balanced scientific program that will have clearly defined biological and technical streams that focusses on state-of-the-art methodological developments and their applications in human health.

The social program will focus on facilitating collegial interactions in both informal and formal settings, including a major focus on students and early career researchers and our Industry partners.

The scientific program will include 6 major thematic streams, including the Human Proteome Project (HPP); Health and Disease; The Environment; Biological Applications of the Proteome; Enabling Technologies; and 'Beyond the Proteome'. These streams will allow delegates to focus on an area of their interest or to expose themselves to a wider variety of new topics. The program will also include Keynote/Plenary sessions with speakers of the highest international standing, examining topics of widespread interest to HUPO 2019 attendees.

### Objectives of HUPO 2019

- Provide an unsurpassed, **world-class scientific program** of both broad impact and specific interest to HUPO members, delegates and Industry partners;
- Deliver a **collegial social atmosphere** to facilitate interactions amongst researchers, and between researchers and Industry;
- Maximize delegate **interactions with industry** via the scientific and social programs;
- Support an inclusive environment that provides **equal opportunity** for all delegates;
- **Build networks** between researchers, industry and clinicians.

## Welcome

On behalf of the HUPO 2019 Organizing Committee and the Australasian Proteomics Society (APS), we are delighted to welcome you to the 18th World Congress of the Human Proteome Organization (HUPO) in the beautiful City of Churches, Adelaide. We are honored to host your visit to the capital city of South Australia. The HUPO 2019 World Congress will be held in our new state-of-the-art Adelaide Convention Centre. We hope that you enjoy an exciting and productive meeting and a comfortable stay in Adelaide.

The APS is the oldest proteomics-focused society in the world, having been formed in the mid-1990s and has held the annual Lorne Proteomics Symposium for the last 24 years. Lorne will celebrate its silver anniversary in February 2020 with the 25th meeting of the APS. Australia has made a strong contribution to the history of Proteomics and within the HUPO community, indeed the term itself was coined by Marc Wilkins in 1994 and Sydney hosted an outstanding HUPO World Congress in 2010. Since the beginning of HUPO, the Australian proteomics community has been involved in all aspects of running the organization, including holding almost every position on the HUPO Executive Committee.

We hope you will agree that HUPO 2019 is providing an unsurpassed scientific program including more than 80 outstanding invited international speakers who are at the very forefront of proteomics and associated fields, alongside an exceptional spotlight for students and early career researchers. HUPO 2019, the APS and several collaborating proteomics societies from around the world have come together to fund more than 150 young researchers to assist their travel to this World Congress. The scientific program includes 10 Plenary and 36 Keynote sessions, that are divided into 6 Themes - Health and Disease, Biological Applications of the Proteome, Our Human Environment, Beyond the Proteome, the Human Proteome Project and Enabling Technologies. Two 'Special Sessions' have been included - a session devoted to the International Cancer Proteogenome Consortium Project, and a session on 'Biomarkers, Assays and Diagnostics', a strong focus area for proteomics research. The HUPO 2019 World

Congress also thanks its partner organizations, the Australasian Glycoscience Symposium (which holds its 2nd meeting alongside the World Congress) and the Asia-Oceania Agricultural Proteomics Organization (AOAPO), as well as all our sponsors, exhibitors and vendors, particularly our Principal Sponsors, Thermo Fisher Scientific and Bruker. Please visit all our commercial partners in the Exhibition Hall. They make hosting the HUPO World Congress possible.

Adelaide has been consistently listed as one of the ten most liveable cities in the world. Everything you need will be within walking distance in this charming city, including the Adelaide Convention Centre, Conference Hotels, Adelaide BioMed City and Rundle Mall, Adelaide's Shopping and Meeting Centre. Enjoy the fine dining the city has to offer and sample some of the city's small bars and wonderful coffee. Australians believe the best environment for science is one of collegiality. The social program will thus provide unique opportunities for engaging with your colleagues in a relaxed and friendly environment.

Please enjoy Adelaide and the 18th HUPO World Congress.

**Stuart J. Cordwell**

**(Co-Chair, President APS)**

**Peter Hoffmann**

**(Co-Chair, Vice-President APS)**



# HUPO Governance

## HUPO Executive Committee 2019

### President

Stephen Pennington

### Immediate Past-President Elect

Michael Snyder

### Vice President

Robert Moritz

### Treasurer

Christopher Overall

### Secretary General

Michelle Hill

### Member-at-Large

Jennifer Van Eyk

### Member-at-Large

Lydie Lane

## HUPO Office



### Association Manager

Chelsea Prangnell



### Association Coordinator

Amanda Oliveira

## HUPO Council

Ruth Birner-Grünberger

Odile Burlet-Schiltz

Subhra Chakraborty

Yu-Ju Chen

Je-Yoel Cho

Anne Claude Gingras

Ben Collins

Ileana Cristea

Gilberto Domont

Vitor Faça

Daniel Figeys

Benjamin Garcia

Concha Gil

Fabio Gozzo

Rebekah Gundry

Fuchu He

Henning Hermjakob

Michelle Hill

Peter Hoffmann

Vera Ignjatovic

Yasushi Ishihama

Martin Larsen

Emma Lundberg

Lennart Martens

Robert Moritz

Aleksandra Nita-Lazar

Ole Nørregaard Jensen

Christopher Overall

Stephen Pennington

Terence Poon

Anthony Purcell

Jun Qin

Katharina Riedel

Henry Rodriguez

Paola Roncada

Michael Snyder

Sanjeeva Srivastava

Pierre Thibault

Andrea Urbani

Ana Varela Coelho

Olga Vitek

Susan Weintraub

Marc Wilkins

Bernd Wollscheid

Tesshi Yamada

Jong Shin Yoo

## Accelerate Your Proteomics Research



Agilent 1290 Infinity II LC System  
Agilent 6495C Triple Quadrupole  
LC/MS

Get higher throughput, greater robustness and better ease-of-use with the Agilent Jet Stream Proteomics solution which provides near-nanoflow analytical sensitivity using standard-flow chromatography.

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# EVUSEP

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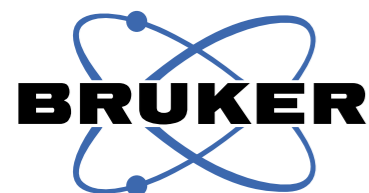
## Congress Sponsors

The 2019 HUPO World Congress acknowledges the support of the following organisations:

### Destination Support



### Principal Partners



### Supporting Partner



thermo scientific



Go beyond today's discovery

Today's cutting-edge research pushes LC-MS to its limits. Obtaining high confidence insight about very complex molecules and biological systems is needed faster than ever before. The Thermo Scientific™ Orbitrap Eclipse™ Tribrid™ mass spectrometer surpasses these limits with new innovations that deliver the ultimate flexibility to expand experimental scope, with built-in intelligence to ensure highest data quality and confidence. One system provides maximum insights so you productively go beyond today's discovery.

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# Delegate Information

## Admission

Congress name badges are required for access to all scientific sessions, including admission to the Exhibition Hall and all social events.

Please note the following access per badge type:

- Full Attendee Badge: All Sessions throughout the Congress
- One Day Badge: All Sessions on the specified day
- Attendees not wearing a badge will be denied admission to the Congress activities
- Pre and Post Congress Workshops and the Congress Dinner are not included in registration cost and are an additional cost

## Venue

Adelaide Convention Centre (ACC)  
North Terrace, Adelaide,  
South Australia 5000,  
Australia  
www.adelaidecc.com.au

## Parking

If you are driving to the Centre, they offer two undercover car parking options with the North Terrace and the Riverbank car parks. Both are located directly under the Centre and are open 24 hours a day, 7 days a week. Clearance is 2.0 metres and automated payment stations accept credit/debit cards (1.5% surcharge applicable). Both car parks are fitted with video surveillance camera systems and security patrols these areas. More details on parking rates [www.adelaidecc.com.au/visiting/the-centre/](http://www.adelaidecc.com.au/visiting/the-centre/)

## Certificate Of Attendance

A personalized Certificate of Attendance will be sent electronically on Friday 20 September 2019.

## Exhibition & Catering

Educational and informational exhibits will be available in the Exhibition Hall, located in Hall H during the Congress. Exhibiting company representatives will be available to answer your questions about their products and services. Please visit the exhibits and thank the representatives for their support. The complete list of exhibits can be found on page 88-91.

Exhibition Hall Hours are as follows:

Monday, 16 September	8:00am - 7:30pm
Tuesday, 17 September	8:00am - 6:30pm
Wednesday, 18 September	8:00am - 4:00pm

## Insurance

The Congress organizers cannot accept liability for personal injuries sustained, or for loss of, or damage to, property belonging to Congress attendees, either during or as a result of the Congress. Please check the validity and coverage of your own insurance.

## Language

English is the official language of the Congress. No translation arrangements have been made.

## Photography

Any photography, filming, taping, recording or reproduction in any medium including via the use of tripod-based equipment of any of the programs and/or posters presented at the 18th Annual World Congress of Human Proteome Organization without the express written consent of the Human Proteome Organization is strictly prohibited. Exceptions to this policy include non-flash photography and audiotape recording using hand-help equipment for strictly personal use, which are permitted if not disruptive.

## Mobile Devices

As a courtesy to the speakers and your fellow attendees, please switch your mobile device(s) to silent while attending the sessions. If using a mobile device (phone, tablet, or camera) to take non-flash photography during Congress sessions, please be courteous to fellow attendees and refrain from blocking the view of those seated behind you.

## Congress Mobile App

Download the HUPO 2019 Congress App to access the latest information on the 18th Annual World Congress of Human Proteome Organization! You can flag sessions of interest, view floorplans, read abstracts and search for speakers by name.

To download the HUPO 2019 Congress App onto your smart phone or tablet device follow these instructions:

1. Search for 'Currinda' via the App Store or Google Play or scan the below QR code.
2. Once you have downloaded the App, you will be prompted to log in.
3. First you must click on the 'Client' box and search for 'ASN'.
4. Select 'ASN' and then you can log in with your email address and password you used to register for the Congress.

If you have any questions please ask the staff at the Registration Desk.



## Wifi

Complimentary ACC Wi-Fi is available to conference delegates. There is no password required.

## Poster Sessions

There will be two poster sessions during the Congress, located in the exhibition hall. Posters will be on display the full day of their assigned session, however presenting authors will only be in attendance during the Poster Sessions on Monday and Tuesday Evening depending on their allocated day.

### Poster Session 1

Poster numbers 401 to 700 are to be displayed from Sunday Evening until the close of the Poster Session on Monday Evening. You must take your poster down following the poster session conclusion on Monday.

- Monday 16th September, 10:00am - 10:40am
- Monday 16th September, 6:00pm - 7:15pm

### Poster Session 2

Poster numbers 701 to 1000 are to be displayed from Tuesday Lunch until Wednesday Morning Tea. You must take your poster down following the conclusion of Morning Tea on Wednesday.

- Tuesday 17th September, 5:15pm - 6:30pm
- Wednesday 18th September, 9:15am - 10:00am

Please Note if posters are not taken down during the advised times, they are likely to be disposed of.

A complete list of posters is located on 66-86.

## Registration Hours

The Congress Registration desk is located in Foyer H.

The open hours are:

Sunday 15th September	2:00pm - 8:30pm
Monday 16th September	6:30am - 5:30pm
Tuesday 17th September	6:30am - 5:30pm
Wednesday 18th September	8:00am - 5:00pm

## Speaker Preparation Room

The Speaker Preparation Room is in the Central Office located next to the Registration Desk.

The open hours are:

Sunday 15th September	12:00pm - 6:00pm
Monday 16th September	7:00am - 5:30pm
Tuesday 17th September	7:30am - 5:30pm
Wednesday 18th September	7:30am - 1:30pm

All presenters are asked to load their presentations at least one full session prior to their session commencing to allow for timely loading and testing of their presentation.

Standard equipment for presentation is a PC based computer running MS PowerPoint, please set documents in widescreen (16:9), a lectern with microphone, and laser pointer will be available for you to utilize in the room.

## Social Media

We invite all HUPO 2019 Congress attendees to use the official conference hashtag #HUPO2019 when posting about the Congress on social media. Adding #HUPO2019 to your post can help connect you with other Congress attendees. Search for #HUPO2019 on Facebook and Twitter throughout the program to share and engage with highlights from colleagues. Be sure to follow HUPO on Twitter, Facebook, and LinkedIn to stay connected during the Congress and throughout the year.



# International Information

## Time Zones

Australia is divided in three separate time zones: Australian Eastern Standard Time (AEST), Australian Central Standard Time (ACST), and Australian Western Standard Time (AWST).

- AEST is equal to Coordinated Universal Time plus 10 hours (UTC +10). This covers the following states; Queensland, New South Wales, Victoria, Tasmania and the Australian Capital Territory.
- ACST is equal to Coordinated Universal Time plus 9.5 hours (UTC +9.5). This covers the following states (which includes Adelaide); South Australia and The Northern Territory.
- AWST is equal to Coordinated Universal Time plus 8 hours (UTC +8). This covers the state of Western Australia.

## Electrical Plugs

You may need an adapter in order to plug your appliances into the power sockets: the adapted required for Australia is Type 1 Australia plug. The plugs in Australia have two flat metal pins, forming an inverted 'V' shape, and occasionally a third pin in the centre. The electrical current in Australia is 220-240 volts, AC 50Hz.

## Left-Hand Traffic

In Australia cars, trams, bikes and other vehicles travel on the left-hand side of the road of a bi-directional traffic. Pedestrians also walk on the left-hand side of a path or a corridor in general. Look to your RIGHT first then left to check oncoming traffic when crossing a street or a road. Same rules apply when you are making turns when driving. The steering wheel of an Australian car is on the right-hand side.

## Currency

Australia's national currency is Australian Dollars (AUD), which comes in denominations of \$5, \$10, \$20, \$50 and \$100 notes. Coins come in 5, 10, 20 and 50 cent and one- & two-dollar denominations.

Credit cards such as American Express, Bankcard, Diners Club, MasterCard, Visa, UnionPay and JCB are accepted in Australia. VISA or MasterCard can be used everywhere credit cards are accepted. American Express and Diners Club are accepted at major supermarket and department store chains and many tourist destinations. A good tip is to carry multiple credit cards and a little cash. Merchants may impose credit card surcharges in some places.

Traveler's cheques are not widely accepted in Australia. If you do purchase traveler's cheques, it is best to buy them in Australian dollars as smaller

shops, restaurants and other businesses are unlikely to know what the exchange rate is if you present a cheque in a different currency such as US dollars or British pounds.

Australia has a Goods and Services Tax (GST) of 10 percent. You may be able to claim a refund for the GST paid on goods if you have spent AUD \$300 or more with a single business, no more than 60 days before departing Australia. Tourist Refund Scheme facilities are located in the departure area of international terminals.

## Weather

Australia's seasons are at opposite times to those in the Northern Hemisphere. September to November is spring, and during September Adelaide experiences average maximum temperatures of around 18 degrees Celsius (or 64.4 degrees Fahrenheit) and average minimum temperatures of 10 degrees Celsius (or 50 degrees Fahrenheit). Adelaide typically experiences around 51.9 mm average of rainfall in September.

## Tipping

Hotels and restaurants do not add service charges to your bill, and tipping is always your choice. In upmarket restaurants, it is common to leave a tip to waiters of 10 percent of the bill for good service.

Some restaurants and cafes will add a 10 percent surcharge to prices on weekends and bank holidays. This is supposed to cover a slightly higher minimum wage for working these days. Some will also charge an extra 1.5 to 3% for card payments. These extra charges will be clearly stated on the menu or at the cash register.

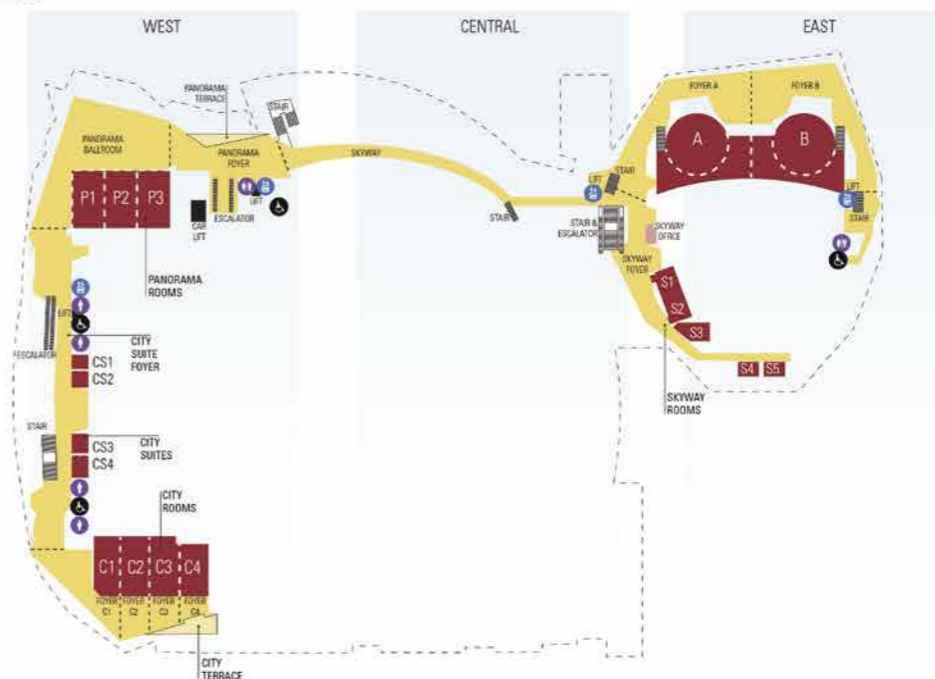
## International Dialling Codes

The international dialling code for Australia is 61. Each region also has an area code, including Central East (New South Wales, Australia Capital Territory) with area code 02; South East (Victoria, Tasmania) with area code 03; Mobile telephones (Australia-wide) with area code 04; North East (Queensland) with area code 07; and Central and West (Western Australia, South Australia and Northern Territory) with area code 08. When calling from outside Australia, leave out the leading '0' from the area code or mobile phone number.

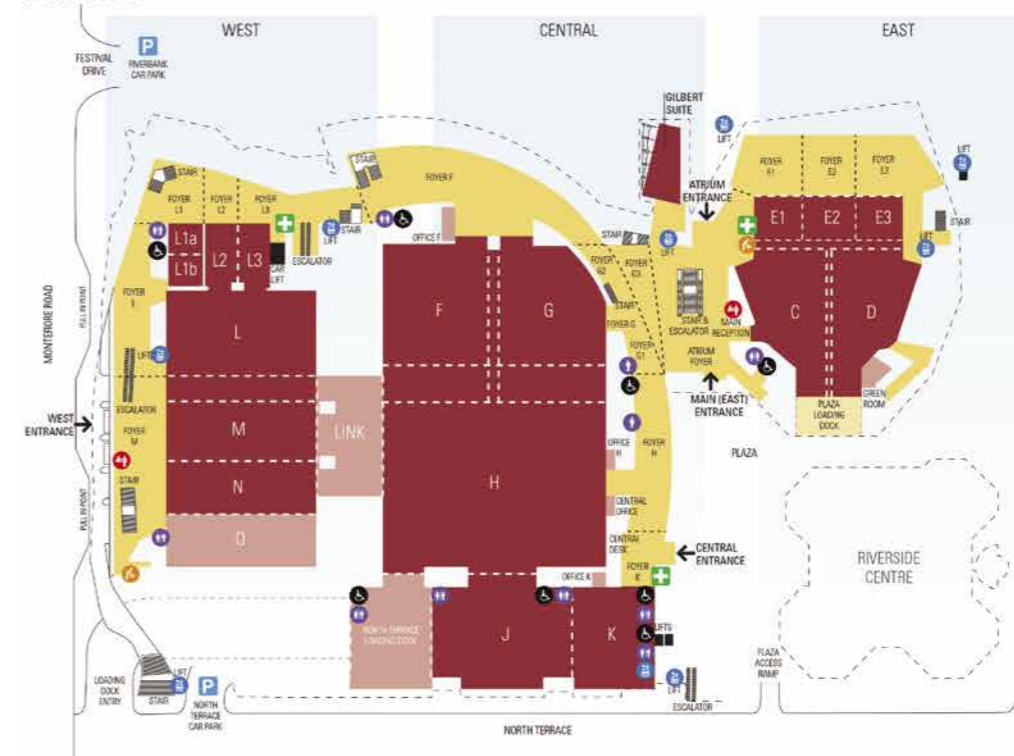
- The outgoing IDD (international direct dialling) code from within Australia is 0011.
- Mobile phone network coverage is available across Australia; however, coverage may be limited in some remote areas.
- Internet access and free WiFi is widely available at internet cafes, accommodation and libraries.
- The emergency number in Australia is 000

# Meeting Room Maps

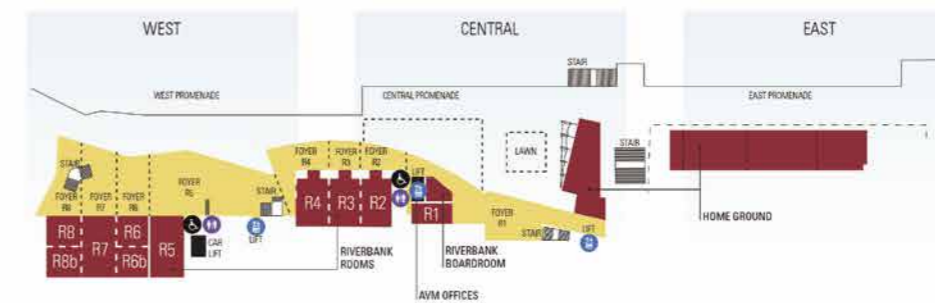
UPPER LEVEL



GROUND LEVEL



LOWER LEVEL



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- TOILET
- ACCESS TOILET
- PARKING
- FIRST AID ROOM
- PARENT ROOM
- STAIRS & ESCALATORS
- FOYER
- FUNCTION AREA



0 5 10 20 30 40 50  
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Aug 2018





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## Plenary Speakers



**Ruedi Aebersold**

ETH Zurich and the University of Zurich, Zurich, Switzerland



**Yu-Ju Chen**

Institute of Chemistry, Academia Sinica, Taipei, Taiwan



**Fuchu He**

National Center for Protein Sciences and Beijing Proteome Research Center, Beijing, China



**Albert Heck**

Utrecht University, Utrecht, The Netherlands



**Glenn F. King**

The University of Queensland, Queensland, Australia



**Kathryn Lilley**

University of Cambridge, Cambridge, United Kingdom



**Nicolle (Nicki) Packer**

Macquarie University, New South Wales, Australia



**James C. Paulson**

The Scripps Research Institute, California, USA



**Michael Snyder**

Stanford University, California, USA



**Mathias Uhlen**

KTH Royal Institute of Technology, Stockholm, Sweden





The journal Molecular & Cellular Proteomics (MCP) fosters the development and applications of proteomics in both basic and translational research. It showcases cutting-edge advances in proteomics, metabolomics and informatics. The American Society for Biochemistry and Molecular Biology publishes MCP. The artwork above is from the MCP Special Collection: Multi-Omics Data Integration.

## Keynote Speakers



**Nathalie  
Y.R. Agar**

Harvard Medical  
School, Brigham and  
Womens' Hospital,  
Boston, USA



**Paul Alewood**

Institute for Molecular  
Bioscience UQ,  
Queensland, Australia



**Hyun Joo An**

Chungnam National  
University, Daejeon,  
South Korea



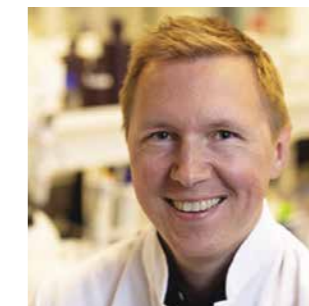
**Erin Baker**

North Carolina  
State University,  
North Carolina, USA



**Emøke  
Bendixen**

Aarhus University,  
Aarhus, Denmark



**Petter Brodin**

Science for Life  
Laboratory, Karolinska  
Institute, Solna,  
Sweden



**Subhra  
Chakraborty**

National Institute  
of Plant Genome  
Research, New Delhi,  
India



**Je-Yoel Cho**

Seoul National  
University, Seoul,  
South Korea



**Chuna  
Choudhary**

University of  
Copenhagen,  
Copenhagen,  
Denmark



**Stephanie M.  
Cologna**

University of Illinois at  
Chicago, Chicago, USA



## Keynote Speakers



**Juergen Cox**

Max Planck Institute of Biochemistry, Martinsried, Germany



**Ileana Cristea**

Princeton University, New Jersey, USA



**Neil Kelleher**

Northwestern University, Illinois, USA



**Jeroen Krijgsveld**

German Cancer Research Center, Heidelberg, Germany



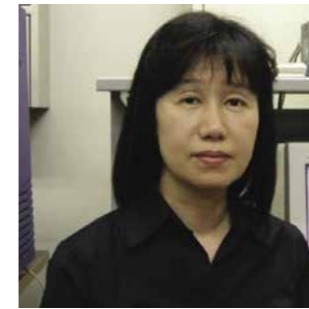
**Meng-Qiu Dong**

National Institute of Biological Sciences, Beijing, China



**Daniel Figeys**

University of Ottawa, Ottawa, Canada



**Setsuko Komatsu**

Fukui University of Technology, Fukui, Japan



**Ho Jeong Kwon**

Yonsei University, Seoul, South Korea



**Melanie Föcking**

Royal College of Surgeons in Ireland, Dublin, Ireland



**Ying Ge**

UW-Madison, Madison, USA



**Lydie Lane**

SIB Swiss Institute of Bioinformatics, Geneva, Switzerland



**Martin R. Larsen**

University of Southern Denmark, Denmark



**Anne-Claude Gingras**

Mount Sinai Hospital, Toronto, Canada



**Rebekah L. Gundry**

Medical College of Wisconsin, Milwaukee, USA



**Janne Lehtiö**

Karolinska Institutet, Solna, Sweden



**Simone Lemeer**

Utrecht University, Utrecht, The Netherlands



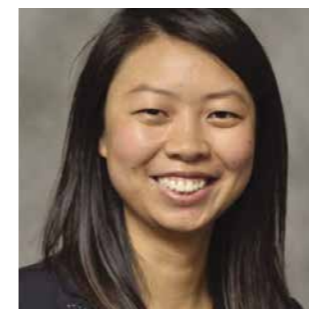
**Leslie Hicks**

University of North Carolina Chapel Hill, Chapel Hill, USA



**David James**

University of Sydney, New South Wales, Australia



**Danni Li**

University of Minnesota, Minnesota, USA



**Lingjun Li**

University of Wisconsin - Madison, Wisconsin, USA



## Keynote Speakers



**Merry L. Lindsey**

University of Nebraska Medical Center, Nebraska, USA



**Emma Lundberg**

SciLifeLab Stockholm and School of Biotechnology, Stockholm, Sweden



**Stephen Pennington**

University College Dublin, Dublin, Ireland



**Brigitte Picard**

Inra, Saint-Genès-Champanelle, France



**Michael MacCoss**

University of Washington, Washington, USA



**Robert Moritz**

Institute For Systems Biology, Washington, USA



**Juri Rappsilber**

TU Berlin, Deutschland, Germany



**Phil Robinson**

Children's Medical Research Institute, New South Wales, Australia



**Hirofumi Nakagami**

Max Planck Institute for Plant Breeding Research, Cologne, Germany



**Peter Nilsson**

KTH & SciLifeLab, Stockholm, Sweden



**Henry Rodriguez**

National Cancer Institute, National Institutes of Health, Maryland, USA



**Michael Roehrl**

Memorial Sloan Kettering Cancer Center, New York, USA



**Aleksandra Nita-Lazar**

National Institute of Allergy and Infectious Diseases, Maryland, USA



**Jesper V. Olsen**

University of Copenhagen, Zealand, Denmark



**Ute Roessner**

University of Melbourne, Victoria, Australia



**Paola Roncada**

University Magna Græcia of Catanzaro, Catanzaro, Italy



**Christopher Overall**

University of British Columbia, Vancouver, Canada



**Akhilesh Pandey**

Mayo Clinic, Minnesota, USA



**Ghasem Hosseini Salekdeh**

Agricultural Biotechnology Research Institute of Iran, Tehran, Iran



**Birgit Schilling**

Buck Institute for Research on Aging, California, USA



## Keynote Speakers



**Jonathan V. Sweedler**  
University of Illinois at Urbana Champaign, Illinois, USA



**Marius Ueffing**  
University of Tübingen, Tübingen, Germany



**Bernd Wollscheid**  
ETH Zurich, Zurich, Switzerland



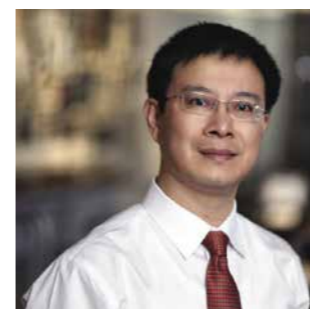
**Pengyuan Yang**  
Fudan University, Shanghai, China



**Zhixin Tian**  
Tongji University, Shanghai, China



**Jennifer Van Eyk**  
Cedars-Sinai Medical Center, California, USA



**Bing Zhang**  
Baylor College of Medicine, Texas, USA



**Qibin Zhang**  
University of North Carolina at Greensboro, North Carolina, USA



**Pengcheng Wang**  
Shanghai Center for Plant Stress Biology, Chinese Academy of Sciences, Shanghai, China



**Melanie White**  
University of Sydney New South Wales, Australia



**Nicola Maria Nathalie Ternette**  
University of Oxford, Oxfordshire, United Kingdom

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**Robert Moritz** Institute for Systems Biology, Seattle, USA

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## Glycoscience Symposium Speakers



**Henrik Clausen**

University of Copenhagen, Copenhagen, Denmark



**Joshua Heazlewood**

University of Melbourne, Victoria, Australia



**Mark Von Itzstein**

Griffith University, Queensland, Australia



**Kay-Hooi Khoo**

Academia Sinica, Taipei, Taiwan



**Lara K. Mahal**

University of Alberta, Alberta, Canada



**Katalin F. Medzihradsky**

Biological Research Centre of the Hungarian Academy of Sciences, Szeged, Hungary



**Giuseppe Palmisano**

University of São Paulo, São Paulo, Brazil



**Katharina Paschinger**

Universität für Bodenkultur, Wein, Austria



**Tadashi Suzuki**

RIKEN, Saitama, Japan



**Hans H. Wandall**

University of Copenhagen, Copenhagen, Denmark



# Clinical Proteomics

Published by BMC, and affiliated with the Human Proteome Organization (HUPO), *Clinical Proteomics* provides a scholarly forum for novel scientific research across the broad spectrum of clinical and translational proteomics.

Placing an emphasis on the application of proteomic technology to all aspects of clinical research and molecular medicine, the journal is committed to rapid scientific review and timely publication of manuscripts.

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## HUPO Awards

### Distinguished Achievement in Proteomic Sciences

The Distinguished Achievement in Proteomic Sciences Award recognizes a scientist for distinguished scientific achievements in the field of proteomic science.

Sponsored by the Journal of Proteome Research (ACS Publications)



**Jennifer Van Eyk**  
Cedars-Sinai  
Medical Center,  
USA

Dr. Van Eyk is an extraordinary scientist and a world leader in the area of clinical proteomics. She has a longstanding record of excellence in applying cutting-edge analytical technologies to address clinically relevant biological hypotheses and in translation into clinical therapies or diagnostics. Dr. Van Eyk has pioneered research focusing on understanding the molecular mechanism underlying acute and chronic cardiac disease and the development of clinically robust circulating biomarkers for personalization of medical care. Particularly, she is well-known for working on cardiac troponin I and its functionally and clinically important phosphorylation and selective proteolysis that is differentially induced with myocardial ischemia, hemodynamics stress and heart failure.

Dr. Van Eyk is a selfless mentor and a role model especially for women scientists and made tremendous impact in their career development. She has trained 17 MSc/PhD students, 24 post-doctoral fellows and 4 MD's. Her strengths in leadership, innovation and ability to move discoveries toward the clinic makes Dr. Van Eyk a worthy winner for the HUPO 2019 Distinguished Achievement in Proteomics Science Award.

## Clinical and Translational Proteomics

This award recognizes a scientist in the field of clinical and translational proteomics.

Sponsored by Clinical Proteomics (BioMed Central)



**Marius Ueffing**  
University of Tübingen, Institute  
for Ophthalmic Research Centre  
for Ophthalmology, Germany

Dr. Ueffing has developed research strategies to combine bioanalytic, proteomic, functional genomics and computational research towards investigation of disease mechanisms and markers. His efforts impact clinical proteomics towards understanding and targeting mechanisms of a number of debilitating diseases. Dr. Ueffing has recently co-discovered 3 new rare diseases as ciliopathies using proteomic methods, and he has applied translational bioanalytical and computational approaches towards better diagnostics and therapies for oncological, neurological and neurosensory diseases with a strong focus on uncovering molecular mechanism. In addition, Dr. Ueffing has discovered that the mutant Parkinson disease associated LRRK2 acts as a protein kinase perturbing vesicular trafficking in CNS neurons that has exploited by initiating pharmacological strategies to target LRRK2. Mapping and functionally characterizing large protein networks associated with Parkinson's disease, syndromic ciliopathies and retinal degeneration, Dr. Ueffing and coworkers have contributed to understand disease on a molecular level and have enabled development of differential clinical diagnosis based on understanding of the impact of mutations and risk variants associated with these diseases discovering new targets for intervention. These achievements allow improved risk prediction and patient stratification according to molecular constraints and rational strategies for therapy development accompanied, and supported, by protein based biosignatures. Dr. Ueffing's significant contributions to clinical translational efforts utilizing proteomics makes him a most worthy winner of the 2019 HUPO Clinical and Translational Proteomics award.



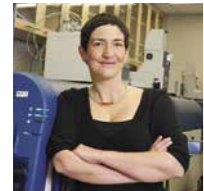
## HUPO Awards

### Discovery in Proteomic Sciences

The Discovery in Proteomic Sciences Award recognizes a scientist for a single discovery in the field of proteomics.

Sponsored by Journal of Proteomics (Elsevier BV)

(Shared by two recipients)



**Anne-Claude Gingras**

**Lunenfeld-Tanenbaum  
Research Institute at Mount  
Sinai Hospital in Toronto,  
Canada**

Dr. Gingras is a tenacious scientist with a research focus on protein-protein interactions. Since protein-protein interactions and protein complexes underpin nearly all cellular functions, proteomics must move beyond the description of overall protein identities and abundances to provide a clearer picture of biology. Protein-protein interactions are also often dysregulated in disease such as cancer, and can often be targeted by pharmacological compounds, making them attractive drug targets. Dr. Gingras has contributed to the development of interaction proteomics methods that discriminate between true interactors of a protein and background contaminants. Some of these achievements include detailed experimental protocols and development or co-development of bioinformatics tools that enable improved analysis of protein-protein interactions by the research community. These tools extend her impact to reach beyond her work in unravelling key interaction changes that occur through the activation of signaling pathways in health and disease. Dr. Gingras has published landmark papers that defined the organization of the yeast kinase-phosphatase network, the human HSP90 co-chaperone machinery and the RNA-associated stress granules and P-bodies, to name but a few. For her contribution to the development of multiple methods to study interactomes, HUPO is proud to bestow the 2019 Discovery in Proteomics award to Dr. Gingras.



**John R. Yates III**

**Scripps Research Institute,  
USA**

Professor Yates has significantly contributed to advances in proteomics and protein biochemistry throughout a career spanning more than 35 years which is supported by his outstanding publication record (>123,000 citations, h-index 174). Dr. Yates research spans molecular measurements using mass spectrometry, the earliest bioinformatic tools to interpret this mass spectrometry data, and chemical methods to enhance the coverage and quantification of proteins by mass spectrometry. His latest research is focused on the development and application of mass spectrometry-based proteomic advancements to answer important questions related to cystic fibrosis, Alzheimer's, schizophrenia and depression. This includes a recent study where he and his team provide comprehensive insights into the molecular disease mechanisms of cystic fibrosis, one of the most common inherited childhood diseases caused by deletion of a single codon for F508 in the cystic fibrosis transmembrane conductance regulator (CFTR) gene, causing loss of function of CFTR, the major cause of cystic fibrosis. These studies also have led to the identification of processes and proteins capable of restoring function to mutated and unfolded proteins in the disease. This discovery has impacted the field of cystic fibrosis and in proteomics by providing a novel approach for the comprehensive identification and analysis of membrane protein interactomes and their dynamics that can be applied to a variety of other studies and potentially help to discover similar disease mechanisms, and it demonstrates the power of intelligent proteomic approaches to answer fundamental questions in biology and medicine. Prof. Yates is an innovative and thought-provoking researcher that has contributed numerous methods to comprehensively study proteomes to highlight the biological context in question in quantitative approaches. We applaud the many achievements to date by Prof John R. Yates III with recognition by the 2019 HUPO Discovery in Proteomics award.

### Science and Technology Award

The Science and Technology Award recognizes an individual or team in private industry who played a key role in commercialization of a proteomics technology, product, or procedure. The emphasis for the award is on making the technology, product, or procedure widely available, which is different from the basic scientific invention.

Sponsored by the HUPO Industrial Advisory Board.



**Scott Tanner, Vladimir Baranov,  
Olga Ornatsky and Dmitry Bandura**

**Fluidigm, USA**

This team, comprising Dr. Scott Tanner, Dr. Vladimir Baranov, Dr. Olga Ornatsky and Dr. Dmitry Bandura, set out in 2005 to apply ICP-MS (TOF) technology in pursuit of high-parameter single cell proteomics. As previous colleagues at MDS Sciex and MDS Proteomics, the four MS technology pioneers set up a lab at the University of Toronto to develop a unique high-parameter mass cytometry. Technology that brings unprecedented understanding of single cell proteomics. The technology was originally conceived by the team while working at PerkinElmer-Sciex and at the University of Toronto, and was spun out into a company by the four colleagues, founders of DVS (now part of Fluidigm Inc), that ultimately commercialized the MS-based system called CyTOF and has been described in more than 40 scientific papers related to mass cytometry. The team are the inventors of 44 issued patents and more than 70 pending patent applications.

Over 250 CyTOF systems are in use daily across 4 continents in driving critical biological discoveries. Fluidigm employs nearly 500 people throughout the world supporting the use of Mass Cytometry in the work of some of the leading academic and pharmaceutical organizations globally. The CyTOF technology now drives many applications both in research and Clinical analysis in single cell proteomics including the most groundbreaking work in Immune Oncology, the subject of the 2018 Nobel Prize for Medicine. The ability to monitor biological systems with highly specific prescribed protein markers through the use of metal conjugated antibodies has resulted in incredibly important discoveries that impact cancer, stem cell research, neurology and immunology. In its endeavors to promote Industrial orientated Proteomics based research, HUPO awards the 2019 Science and Technology Award to the worthy winners, Dr's Tanner, Baranov, Ornatsky and Bandura.

### Distinguished Service Award

The Distinguished Service Award recognizes an exemplary member of the proteomic research community whose dedicated service has made indispensable contributions to the organization and mission of HUPO. This award is presented every other year (2013, 2015, 2017, 2019).



**Robert Moritz**

**Institute for Systems  
Biology, USA**

Dr. Moritz is a world leader in proteomics methods development with a focus on mass-spectrometry applications to comprehensive proteomic quantification and software development for the analysis of Big Data from these comprehensive resources. His group has developed both comprehensive targeted proteomics and methods for whole proteome quantitative measurements using SWATH type approaches. His group develops world-leading pipelines in mass spectrometry data analysis, statistical validation and visualization. His group underpins the MS pillar of HUPO and provides the portal for MS identification data for the Human Proteome Project with PeptideAtlas, and in conjunction with neXtProt. Encompassed in these developments are world-wide accessible web-based resources, and all data and software development tools are both open access and open source for wide dissemination.

Dr. Moritz has served in HUPO as a Council member, Treasurer, Vice President (twice), HUPO IAB Co-chair (twice) as well as the Executive Committee of HUPO. He was co-chair of the 2018 HUPO Congress in Orlando, Florida and assists the many congresses run by HUPO to ensure resources are provided and support is applied when needed. Of particular interest to Dr. Moritz has been his drive to achieve equality in HUPO's efforts with attention to global inclusion, gender equality and broad and transparent distribution of voting powers amongst its members. Dr. Moritz negotiated with several companies to provide resources to enable HUPO members to freely participate in the HPP Phosphopeptide Challenge. He has also been instrumental in shaping HUPO's future financial status with initiatives in "Development", strengthening industrial contacts, and in strategic planning to make HUPO a highly successful organization. Based on his scientific credentials and extensive contributions to HUPO and its members over the past several years in a selfless manner, HUPO is proud to award Dr. Moritz with the 2019 Distinguished Service Award.



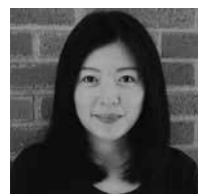
## HUPO Awards

### HUPO 2019 – ECR Manuscript Competition: “Proteomics Highlight of the Year”

The Early Career Researcher Initiative of the Human Proteome Organization is pleased to announce the fifth ECR Manuscript Competition to take place at HUPO 2019 in Adelaide, Australia!

The ECR Manuscript Competition was initiated at HUPO 2015 in Vancouver and has been successfully repeated at all following HUPO world congresses. The competition is a unique opportunity to make early-career researchers more visible to the proteomics community. It serves as a platform to highlight the important contributions that postdoctoral fellows, young clinicians and junior faculty members make to the proteomics field. At HUPO 2019 in Adelaide, Australia September 15-19, 2019 we will repeat this successful event.

Three finalists have been selected to present their publications in a related parallel session at HUPO 2019 in Adelaide, where an expert committee will evaluate their oral presentations. Awards (first place USD \$1,000 and two runners-up each USD \$500) will be presented to the finalists during the Closing Ceremony & Awards Session on September 18, 2019. In addition, the three finalists will receive complimentary registration for HUPO 2019 (registration will be refunded post congress). See who the finalists are on the following pages.



#### Maggie Lam

Dr. Maggie Lam is an assistant professor in Medicine/Cardiology and Biochemistry at the University of Colorado Denver, Anschutz Medical Campus. Her research develops quantitative proteomics and informatics methods to investigate the mechanisms of heart diseases including cardiac aging, fibrosis, and hypertrophy. In previous work she has published methods to assess the in vivo half-life of mammalian hearts at a proteome scale and developed targeted proteomics workflows to quantify mitochondrial protein phosphorylation events. An ongoing project in her lab aims to identify protein alternative isoform expression in the human heart using a combined transcriptomics and proteomics approach. In parallel, her lab actively works with HUPO to develop algorithms that predict gene-disease relationships and track the research trends of different B/D-HPP topics.



#### Ankit Sinha

Dr. Ankit Sinha received his Ph.D in cancer proteomics in December 2018 under the supervision of Dr. Thomas Kislinger at the University of Toronto. Dr. Sinha's doctoral research focused on three key scientific themes with an application of proteomics. Firstly, omics-based technologies are ultra competent for studying longitudinal changes in biological systems<sup>1</sup>. Secondly, proteomics has the advantage of assaying secreted proteins in an accurate and unsupervised manner<sup>2</sup>. Lastly, the flow of information in the dogma of biology can differ as genomic clusters converge to different proteomic clusters<sup>3</sup>. Additionally, during his doctorate, he has contributed to over 20 scientific publications including five publications as the first author. He has received 13 awards throughout his graduate career and recently received the EMBO Long-Term fellowship for post-doctoral training.

To further pursue research training, Dr. Sinha is currently investigating how cancer cells modulate the tumour micro environment and this interdisciplinary research is being conducted with Dr. Felix Meissner (MPI Biochemistry, Munich) and Dr. Dieter Saur (DKFZ/TUM, Munich). The key focus of the investigation is to identify and functionally validate protein markers involved in the development of immune-tolerance of the cancer cells, and the relationship between identified molecular programmes and activated oncogenes. His future career inspiration is to lead a research group as a principal investigator in an academic setting. Dr. Sinha's career vision is based on the postulation that integration of multi-omic analysis will provide a compendium of data which can provide more accurate biomarker and functionally accurate insights into the flow of biological information in cancer. Ultimately, the systematic integration of various dogma of biology will show that the whole is greater than the sum of its individual parts.



#### Eneko Villanueva

Dr. Eneko Villanueva studied Biology at the Pompeu Fabra University, Barcelona, and later obtained a PhD in Biomedical Research at the University of Barcelona. He spent his PhD studying both the basic way in which viruses evolve to optimise their protein synthesis; as well as learning how to engineer them to constrain their protein synthesis to tumours and develop oncolytic viruses. This combination of basic and applied science resulted in several publications as well as a patent.

At his current position as a Wellcome Trust Postdoctoral Fellow in the Cambridge Center for Proteomics in the University of Cambridge, Eneko is trying to follow the “Keep It Simple” paradigm to develop new technologies combining transcriptomics and proteomics to understand the crosstalk between the RNA and the protein worlds. Originally developed as a side project, he recently published OOPS (Orthogonal Organic Phase Separation) method has proved to be of great interest for the cell biology community. By allowing to study RNA-protein interactions in previously inaccessible systems, OOPS is currently used by collaborators in molecular biology, translational medicine and industry, and has also represented a starting point for his current research studying subcellular organisation at spatial and temporal level.

## HUPO PhD Poster Competition

We are delighted to announce that eight finalists have been selected to give a short oral poster presentation at the HUPO 2019 PhD Poster Competition in Adelaide. From these eight presentations, three presenting authors will be identified and awarded (USD \$200 for the winner and USD \$150 for the two runners-up) plus have their congress registration reimbursed.

Tara K. Bartolec, Australia  
Sayantani Chatterjee, Australia  
Mohamed Elzek, United Kingdom  
Komal K. Mandal, Denmark  
Maik Mueller, Denmark  
Ruzanna Mnatsakanyan, Canada  
Tomoya Niinae, Japan  
Tim Van Den Bossche, Belgium

## 2019 Recipient of the MCP Lectureship



#### Mathias Uhlen

Mathias Uhlen has been selected for the MCP Lectureship Award. Molecular & Cellular Proteomics, an official publication of the American Society for Biochemistry and Molecular Biology, introduced its sponsored lectureship series as part of its 10th anniversary celebration in 2011. Each lecturer is a leader in the field of proteomics who presents his or her particular research and interests, with the intent to expand on proteomics' potential to ask (and answer) increasingly complex questions associated with health, energy, food supply and the environment. The lectureships are given at germane meetings and symposia throughout the year, and the lecturers are chosen by the organizers of those meetings. Each lecturer is presented with a crystal plaque to commemorate the occasion.



## HUPO Awards

### HPP Clinical Scientist Travel Grants

The Human Proteome Project (HPP) was established by the Human Proteome Organization (HUPO) to explore the human proteome and to enable the routine, reliable and broad application of state-of-the-art measurements of proteins and proteomes by life scientists and clinicians studying the molecular mechanisms of biological processes and human disease<sup>1</sup>. This will be accomplished through the generation of laboratory and informational resources that support both research and routine measurement of biological process- and/or disease-relevant proteins<sup>2</sup>.

To accomplish these goals, the HPP is reaching out again to clinical scientists or clinicians who are using or are considering using proteomics technologies for their research projects. The HPP is supporting five (5) clinician-scientists with a travel grant to attend the 2019 HUPO World Congress in Adelaide, Australia that will take place from September 15-19, 2019.

We are pleased to congratulate the 2019 HPP Clinical Scientist Travel Grant recipients:

Qing Kay Li  
Rei Noguchi  
Iris Kassem  
Tu Ngoc Nguyen  
Soren Naaby-Hansen

### HUPO 2019 Student/Early Career Researcher Travel Awards

The HUPO 2019 Organizing Committee is delighted to announce that 157 young researchers from 25 countries have been provided HUPO 2019 Student / ECR Travel Awards to support their participation at this years' World Congress to be held in Adelaide, Australia from 15-19th September, 2019. We wholeheartedly congratulate these worthy recipients and look forward to welcoming you all to Adelaide!

We also wish to acknowledge our co-funding partners: Australasian Proteomics Society (APS), German Society for Proteome Research (DGPF), Japanese Proteomics Society (JPrOS), Korea HUPO (KHUPO), Proteomics Society of India (PSI), Singapore Society of Mass Spectrometry (SSMS), Swiss Proteomics Society and US-HUPO.

### Co-Funded HUPO 2019 Student/ECR Travel Award Winners

#### German Society for Proteome Research (DGPF) and HUPO 2019

Sascha Blankenburg  
Christian Hentschker  
Antonia Pries  
Nadine Prust (Netherlands)  
Louise Schelletter  
Jan Stöckl  
Julian Uszkoreit  
Julia Voß

#### Japanese Proteomics Society (JPrOS) and HUPO 2019

Yuma Inamori  
Kaori Konno  
Tomoya Niinae

#### KHUPO and HUPO 2019

Hwangkyo Jeong  
Hyeryeon Jung  
Chae-Yeon Kim  
HanByeol Kim  
Dabin Lee  
Jua Lee  
Nari Seo  
Seojin Yang  
Jeonghun Yeom  
Jiyoung Yu

#### Proteomics Society of India (PSI) and HUPO 2019

Javed Akhtar  
Arunima Sinha  
Boomathi Pandi  
Rahul Chakraborty  
Pragya Barua

#### Singapore Society for Mass Spectrometry and HUPO 2019

Ian Loke  
Wint Wint Phoo

#### Swiss Proteomics Society and HUPO 2019

Maik Müller  
Kathrin Nowak  
Fabian Wendt

#### US-HUPO and HUPO 2019

Natan Basisty  
Hiromi Koh  
Xueshu Xi  
Matthew Waas

### HUPO 2019 Student/ECR Travel Award Winners

Anna Andrejeva (UK)  
Sandra Anjo (Portugal)  
Christopher Ashwood (USA)  
GL Balasubramani (India)  
Ieva Bagdonaite (Denmark)  
Kevin Erzo Castillo (USA)  
Josie Christopher (UK)  
David Clark (USA)  
Alana Costa (Brazil)  
Simon Davis (UK)  
Benedict Dinberger (UK)  
Penchatr Diskul-Na-Ayudthaya (Thailand)  
Mohamed Elzek (UK)  
Sofie Farkona (Canada)  
Andrea Fossati (Switzerland)  
Anders Garlid (USA)  
Ana Gil de Bona (USA)  
Tianqi Gong (China)  
Andreas Hober (Sweden)  
Yajun Hu (China)  
John Janetzko (USA)  
Helena Joaquim (Brazil)  
Ling Lin (China)  
Md Zubair Malik (India)  
Komal K Mandal (Denmark)  
Claudia Martelli (Switzerland)  
Mukul Midha (USA)  
Ruzanna Mnatsakanyan (Germany)  
Varshasnata Mohanty (India)  
Marika Mokou (Greece)  
Muhammad Naadir Ganief (South Africa)  
Kanika Narula (India)  
Jessica Nickerson (Canada)  
Aya Osama (Egypt)  
Matthys Potgieter (South Africa)  
Rashmi Rana (India)  
Divya Rathi (India)  
Sushant Sadotra (Taiwan)  
Cátia Santa (Portugal)  
Darien Schell (South Africa)  
Wenguang Shao (Switzerland)  
Ankit Sinha (Germany)  
Sedigheh Shokri (Iran)  
Margaret Simonian (USA)  
Elizaveta Solovyeva (Russia)  
Arun Tailor (UK)  
Denise Utami Putri (Taiwan)  
Tim Van Den Bossche (Belgium)  
Valerija Vezočnik (Slovenia)  
James Waddington (UK)  
Ke Wang (China)  
Churat Weeraphan (Thailand)  
Mengxi Wu (China)  
Juanjuan Xie (China)  
Yueting Xiong (China)  
Junyu Xu (China)  
Hailun Yang (China)  
Yi Yang (China)  
Yameng Zhang (China)

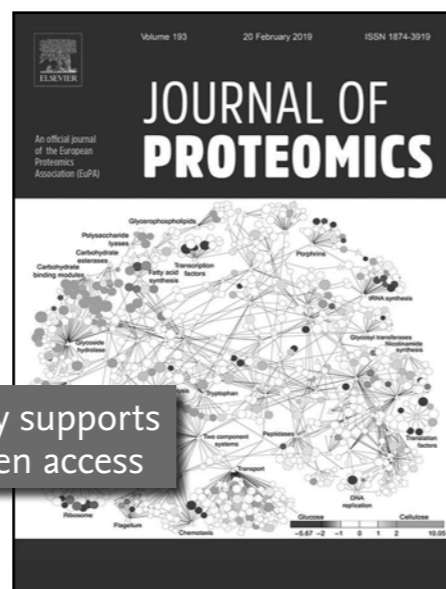
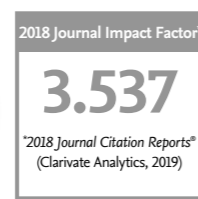
### Australasian Proteomics Society (APS) Student/ECR Travel Award Winners

Subash Adhikari  
Kathirvel Alagesan  
Ritchlynn Aranha  
Deanna Ayupova  
Ali Azimi  
Craig Barry  
Tara Bartolec  
Fiona Bicknell  
Joel Cain  
Sayantani Chatterjee  
Yanfang Chen  
Phil Choi  
Ashleigh Dale  
Keshava Datta  
Mriga Dutt  
Danila Elango  
Sophia Escobar-Correas  
Dilanka Fernando  
Shawn Goh  
Joshua Hamey  
Dylan Harney  
Daniella Hock  
Ashfaqu Hoque  
William Klare  
Naomi Koh Belic  
Rebecca Lane  
Chen Li  
Desmond Li  
Terry Lim Kam Sian  
Shivanjali Lingam  
Evelyn Maes  
Lok Man  
Shutao Mei  
Sonali Mohan  
Heather Murray  
Elise Needham  
Elizabeth Nguyen  
Mitchell Nye-Wood  
Kirti Pandey  
Selvam Paramasivan  
Cassandra Pegg  
Ruby Pelingon  
Toan Phung  
Rebecca Poulos  
Md Arifur Rahman  
Laura Rantanen  
Halley Ravuri  
Harley Robinson  
Alexander Rookyard  
Katherine Scull  
Ryan Separovich  
Mohammad Shahbazy  
David Skerrett-Byrne  
Daniela-Lee Smith  
Nestor Solis  
Joel Steele  
Pascal Steffen  
Arineh Tahmasian  
Xinle Tan  
Zeynep Sumer-Bayraktar  
Julie Webster  
Bradley Wright  
Rebekah Ziegman



# Journal of Proteomics

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 Instituto de Biomedicina de Valencia, Spain

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## Program at a Glance

Sunday, 15th September 2019

Room	Hall E1	Hall E2	Hall E3	Riverbank Room 5	Hall B	Hall A	Hall C
8:30							
9:00	The Early Career Researcher Initiative of the Human Proteome Organization (Mentoring Day)					HPP Investigators Meeting	
9:30							
10:00							
10:30							
11:00							
11:30							
12:00							
12:30							
13:00				Inaugural Australasian Core Facilities Meeting			
13:30				Cancer Biomarkers: The Things You Should Consider When Working on Biomarkers			
14:00							
14:30							
15:00							
15:30							
15:45							
16:00							
16:30		HUPO Council Meeting					
17:00							
17:30							
17:45							
18:00						HUPO 2019 Official Welcome	
18:30						Plenary 1 Rudolf Aebersold	
19:00						Plenary 2 Glenn F. King	
19:15							
19:30							
20:00	Welcome Function Exhibition Hall						
20:30							
21:00							
21:30							
22:00							

■ Pre Congress Workshops ■ Plenary Sessions ■ Social Functions



Monday, 16th September 2019

Room	Hall E1	Hall E2	Hall E3	Hall B	Hall A	Hall C	Innovation Stage (Exhibition Hall)	
7:15								
7:30	ECR Initiative Meet & Greet							
8:00								
8:15								
8:30					Plenary 3 Fuchu He			
9:00								
9:15								
9:30					Plenary 4 Nicolle Packer			
10:00	Morning Tea & Poster Viewing Exhibition Hall							
10:40	Theme 3 Beyond the Proteome Glycoimmunology and Clinical Glycobiology (AGS 1)	Theme 4 HPP 1: Rheumatic and Autoimmune Disorders	Theme 5 Our Human Environment Veterinary and Animal Health	Theme 6 Enabling Technologies Single Cell Proteomics	Theme 2 Biological Application of the Proteome Post-Translational Modifications I	Theme 1 Health and Disease Hereditary Disease and Aging		
11:00								
11:30								
12:00								
12:40	Lunch (12:40 – 2:00pm) Exhibition Hall							
12:45	ThermoFisher Advancing Quantitative Proteomics: Multiplexing, Accuracy, and Precision	Waters Addressing the analytical rigor of omics measurements for clinical research	Agilent Differentiated Approaches to Omics challenges in Translational Research		Bruker DIA with near 100% Ion Usage: Introducing diaPASEF on the timsTOF Pro			
13:00								
13:30								
13:45	Lunch Concludes Exhibition Hall							
14:00					Plenary 5 Matthias Uhlen			
14:30								
14:45	Afternoon Tea Exhibition Hall							
15:00								
15:15	Theme 3 Beyond the Proteome Chemical Glycobiology (AGS 2)	Theme 4 HPP 2: Towards the Complete Cardiac Proteome and Beyond	Theme 5 Our Human Environment Food and Nutrition	Theme 6 Enabling Technologies MS Imaging	Theme 2 Biological Application of the Proteome The Surfaceome and Extracellular Vesicles	Theme 1 Health and Disease Immunology and Inflammation	The HUPO External Development Initiative (HEDI)	
15:30								
15:45								
16:00								
16:30								
17:00								
17:20							HUPO AGM	
17:30								
18:00								
18:30	Poster Session 1 Exhibition Hall							
19:00								
19:15								

- Pre Congress Workshops ■ Plenary Sessions
- Sponsored Symposia ■ Social Functions ■ Catering Breaks
- Theme 1 ■ Theme 2 ■ Theme 3 ■ Theme 4 ■ Theme 5 ■ Theme 6

Tuesday, 17th September 2019

Room	Hall E1	Hall E2	Hall E3	Hall B	Hall A	Hall C	Innovation Stage (Exhibition Hall)
7:15	Bruker Tools for high productivity proteomics: timsTOF Pro, EvoSep One and MaxQuant						
7:30							
8:00							
8:15							
8:30					Plenary 6 Jim Paulson		
9:00							
9:15							
9:30					Plenary 7 Yu-Ju Chen		
10:00	Morning Tea Exhibition Hall						
10:40	Theme 3 Beyond the Proteome Microbial and Plant Glycobiology (AGS 3)	Theme 4 HPP3: P3: Plasma, Pediatrics and Proteomics	Theme 5 Our Human Environment Plant and Crop Proteomics I (AOAPO I)	Theme 6 Enabling Technologies Bioinformatics and Statistics	Theme 2 Biological Application of the Proteome Degradomics, Proteases and Enzymes	Theme 1 Health and Disease Cancer	
11:00							
11:30							
12:00							
12:40	Lunch (12:40 – 2:00pm) Exhibition Hall						
12:45	ThermoFisher Adapting EasyPep™ MS Sample Preparation and TMT labeling for higher throughput and larger volume formats	ThermoFisher Integrative Structural Biology, The Next Frontier of MS-Based Proteomics		Olink Driving personalized medicine through targeted protein biomarker discovery - taking proteomics beyond mass spectrometry	Bruker Clinical Research Applications of the timsTOF Pro		
13:00							
13:30							
13:45	Lunch Concludes Exhibition Hall						
14:00					Plenary 8 Albert Heck		
14:30							
14:45	Afternoon Tea Exhibition Hall						
15:00							
15:15	Theme 3 Beyond the Proteome Analytical Glycobiology (AGS 4)	Theme 6 Enabling Technologies Top-Down and Structural Proteomics	Theme 5 Our Human Environment Plant and Crop Proteomics II	Theme 4 HPP4: Pathology and the Cancer Proteome: Towards Precision Medicine	Theme 1 Health and Disease Infectious Diseases	Theme 2 Biological Application of the Proteome Proteogenomics	
15:30							
16:00							
16:30							
17:00							
17:15							
17:30	Poster Session 2 Exhibition Hall						PhD Poster Competition
18:00							
18:30							
19:30	Congress Dinner Adelaide Oval						
23:30							

- Pre Congress Workshops ■ Plenary Sessions
- Sponsored Symposia ■ Social Functions ■ Catering Breaks
- Theme 1 ■ Theme 2 ■ Theme 3 ■ Theme 4 ■ Theme 5 ■ Theme 6



Room	Hall E1	Hall E2	Hall E3	Hall B	Hall A	Hall C	Innovation Stage (Exhibition Hall)	
8:30								
9:00					Plenary 9 Kathryn Lilley			
9:15	Catering Break							
9:30	Morning Tea & Poster Viewing Exhibition Hall							
9:45	Catering Break							
10:00	Theme 4 HPP5: High Connectivity: Neuroproteomics at the Interface of Bench and Bedside	Theme 3 Beyond the Proteome Special Session: The ICPC Initiative	Theme 5 Our Human Environment Microbial Proteomics and the Microbiome	Theme 6 Enabling Technologies New Technological Advancements in Proteomics (HUPO IAB)	Theme 2 Biological Application of the Proteome Post-Translational Modifications II	Theme 1 Health and Disease Cardiovascular and Metabolic Disease		
10:30								
11:00								
11:30								
12:00	Lunch (12:00 - 1:30pm) Exhibition Hall							
	Sciex Big Data, Fast Data, Smart Data	ThermoFisher The Next Era in Pathway Proteomics - Towards Turnkey Targeted Quantitation Workflows	Evosep High-throughput proteomics with Evosep One					
	Lunch Concludes Exhibition Hall							
13:30	Theme 3 Beyond the Proteome Metabolomics and Lipidomics	Theme 4 HPP6: Moving proteomics into pharmaceutical discovery and application	Theme 6 Enabling Technologies Chemical Proteomics	Theme 5 Our Human Environment Special Session: Disease Biomarkers, Assays and Diagnostic Proteomics	Theme 2 Biological Application of the Proteome The Interactome	Theme 1 Health and Disease Precision Medicine and Clinical Proteomics		
14:00								
14:30								
15:00								
15:30	Afternoon Tea Exhibition Hall							
16:00					HUPO 2019 Awards Ceremony			
16:30					Plenary 10 Mike Snyder			
17:00					Plenary 10 Mike Snyder			
17:30					Plenary 10 Mike Snyder			
17:45					Closing Ceremony & HUPO 2020 Introduction			
18:00								

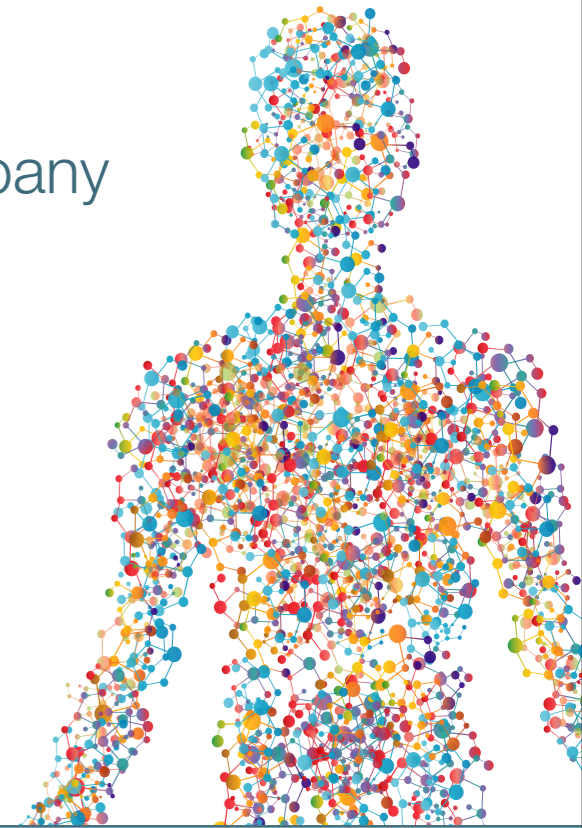
- Pre Congress Workshops ■ Plenary Sessions
- Sponsored Symposia ■ Catering Breaks
- Theme 1 ■ Theme 2 ■ Theme 3 ■ Theme 4 ■ Theme 5 ■ Theme 6



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# Program

## 15th September 2019

**Welcome to Country**  
6:00PM – 6:30PM Halls A & C

**Plenary 1**  
6:30PM – 7:15PM Halls A & C

6:30PM  
**Rudolf Aebersold**  
The modular proteome and its significance **abs# 1**

**Plenary 2**  
7:15PM – 8:00PM Halls A & C

7:15PM  
**Glenn F King**  
Deadly proteomes: the central role of proteomics in dissecting the chemical arsenal of animal venoms **abs# 2**

**Welcome Function**  
8:00PM – 9:30PM Hall H

## 16th September 2019

**ECR Initiative Meet and Greet**  
7:15AM – 8:15AM Room E1

**Plenary 3**  
8:30AM – 9:15AM Halls A & C

8:30AM  
**Fuchu He**  
Proteomics driven precision medicine for the early-stage hepatocellular carcinoma **abs# 3**

**Plenary 4**  
9:15AM – 10:00AM Halls A & C

9:15AM  
**Nicolle H. Packer**  
The elephant in the room: glycomics and glycoproteomics **abs# 4**

**Morning Tea & Poster Viewing**  
10:00AM – 10:40AM Hall H

**Hereditary Disease and Aging**  
10:40AM – 12:40PM Hall C

10:40AM  
**Marius Ueffing**  
Gene editing based analysis of functional protein networks in human disease **abs# 5**

11:05AM  
**Birgit Schilling**  
Proteomic Tools to Decipher Mechanisms of Senescence in Aging and Age-related Diseases **abs# 6**

11:30AM  
**Ryan R Julian**  
Spontaneous chemical modifications in long-lived proteins prevent lysosomal degradation: implications for age-related diseases **abs# 7**

11:50AM  
**Benjamin L Parker**  
Proteome-wide systems genetics to interrogate metabolism **abs# 8**

12:10PM  
**Yaoyang Zhang**  
Multidimensional proteomic study identifies decreased protein synthesis and increased histone 2A ubiquitylation during aging **abs# 9**

12:25PM  
**Nikeisha J Caruana**  
Endurance training of human skeletal muscle results in extensive mitochondrial biogenesis and remodelling of the mitochondrial proteome **abs# 10**

**Post-Translational Modifications I**  
10:40AM – 12:40PM Hall A

10:40AM  
**Chuna Choudhary**  
Proteomic analysis of lysine acetylation dynamics and stoichiometry **abs# 11**

11:05AM  
**Martin R. Larsen**  
Dissecting signaling pathways using PTMomics **abs# 12**

11:30AM  
**Anna Andrejeva**  
Subcellular distribution of post-translational modifications in human proteome **abs# 13**

11:50AM  
**Michael L. Nielsen**  
Systems-wide analysis of ADP-ribosylation in human cells using quantitative mass spectrometry **abs# 14**

12:05PM  
**Dorte B. Bekker-Jensen**  
Rapid and site-specific deep phosphoproteome profiling by data-independent acquisition (DIA) without the need for spectral libraries **abs# 15**

12:20PM  
**Albert Lee**  
Pathogenic mutations in ALS/FTD gene, CCNF, causes increased Lys48-ubiquitylation and defective autophagy leading to proteostasis dysfunction **abs# 16**

**Glycoimmunology and Clinical Glycobiology (AGS 1)**  
10:40AM – 12:40PM Room E1

10:40AM  
**Hans H Wandall**  
Contextualized functions of glycans in human tissue formation **abs# 17**

11:05AM  
**Tadashi Suzuki**  
Generation and Degradation of Free Oligosaccharides **abs# 18**

11:30AM  
**Pengyuan Yang**  
Highly efficient and precise glycoproteomic analysis **abs# 19**

11:50AM  
**Anand Mehta**  
Glycan analysis from tissue to serum – identification and validation of a biomarker for the early detection of hepatocellular carcinoma **abs# 20**

12:05PM  
**Julie Webster**  
Functional characterization of complement component C9 C-mannosylation in oesophageal adenocarcinoma **abs# 21**

12:20PM  
**Sayantani Chatterjee**  
Protein paucimannosylation is an enriched N-glycosylation signature of human cancers **abs# 22**

**HPP 1: Rheumatic and Autoimmune Disorders**  
10:40AM – 12:40PM Room E2

10:40AM  
**Stephen R Pennington**  
Clinical evaluation of a multiplexed protein panel to discriminate patients with psoriatic arthritis from those with rheumatoid arthritis **abs# 23**

11:05AM  
**Peter Nilsson**  
Affinity proteomics for array based profiling of autoantibody repertoires **abs# 24**

11:30AM  
**Ralf B Schittenhelm**  
Allelic association with ankylosing spondylitis fails to correlate with HLA-B27 homodimer formation **abs# 25**

11:50AM  
**Tianfu Wu**  
Development of an autoantigen microarray for the screening of novel autoantibodies in psoriatic arthritis **abs# 26**

12:05PM  
**Terry C.C Lim Kam Sian**  
HLA-B27 immunopeptidome: Understanding the connection between Salmonella typhimurium infection and ankylosing spondylitis **abs# 27**

12:20PM  
**Yaoting Sun**  
ThyroProt: a robust protein classification system for thyroid disease based on deep learning of proteome data **abs# 28**



## Program

### Veterinary and Animal Health 10:40AM – 12:40PM Room E3

10:40AM

#### Emøke Bendixen

Exploring farm animal proteomes, and their relevance to human health **abs# 29**

11:05AM

#### Brigitte BP Picard

Proteomics applied to beef productions: from the discovery of biomarkers to the development of evaluation tools **abs# 30**

11:30AM

#### Denise Dittmar

Proteome analysis of *Streptococcus suis* under stress conditions and in host-pathogen interaction **abs# 31**

11:50AM

#### Pawel Sadowski

Leveraging of extensive inter-species homologies to study plasma proteomes of bovinds using data-independent acquisition **abs# 32**

12:05PM

#### David A Skerrett-Byrne

Proteomic profiling of crocodile spermatozoa refutes the tenet that posttesticular maturation is restricted to mammals **abs# 33**

12:20PM

#### Paul A. Haynes

Proteomic characterisation of Ancient Egyptian skin, bones and textiles **abs# 34**

### Single Cell Proteomics 10:40AM – 12:40PM Hall B

10:40AM

#### Jonathan V Sweedler

High throughput Single Cell Chemical Characterization of the Cells in the Brain **abs# 35**

11:05AM

#### Emma Lundberg

Single cell proteome variability **abs# 36**

11:30AM

#### Sudhir Srivastava

Proteomic Cartography and Biomarkers at the Single-Cell Level: Interrogation of Premalignant and Early Stage Lesions **abs# 37**

11:50AM

#### Cecilia Lindskog

Integration of transcriptomics and antibody-based proteomics for spatial localization of cell type-specific expression patterns **abs# 38**

12:05PM

#### Christopher M Rose

A Offset Mass Triggered Data Acquisition Approach to Single Cell Proteomics Experiments **abs# 39**

12:20PM

#### Yu (Tom) Gao

Super-resolution proteomics method to explore cell heterogeneity at single-cell level **abs# 40**

### Lunch

12:40PM – 2:00PM Hall H

### Advancing Quantitative Proteomics: Multiplexing, Accuracy, and Precision 12:45PM – 1:45PM Room E1

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#### Addressing the analytical rigor of omics measurements for clinical research 12:45PM – 1:45PM Room E2

Proudly sponsored by Waters

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#### Differentiated Approaches to Omics challenges in Translational Research 12:45PM – 1:45PM Room E3

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#### DIA with near 100% Ion Usage: Introducing diaPASEF on the timsTOF Pro 12:45PM – 1:45PM Hall A

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#### Plenary 5 2:00PM – 2:45PM Halls A & C

Session sponsored by Molecular & Cellular Proteomics

**MCP** MOLECULAR & CELLULAR PROTEOMICS

2:00PM

#### Mathias Uhlen

The Human Protein Atlas – Implications for Human Biology, Drug Development and Precision Medicine **abs# 41**

### Afternoon Tea 2:45PM – 3:15PM Hall H

#### Immunology and Inflammation 3:15PM – 5:15PM Hall C

3:15PM

#### Aleksandra Nita-Lazar

Studies of innate immune signaling regulation through quantification of proteoforms and modeling of the TLR pathway **abs# 42**

3:40PM

#### Nicola Ternette

Value and limitations of LC-MS HLA-ligandome data for antigen discovery and vaccine development **abs# 43**

4:05PM

#### Anthony Purcell

Mass spectrometry- teaching us new lessons in immunity **abs# 44**

4:25PM

#### Julian A Hiscox

Proteomic analysis of a small animal model for ricin exposure reveals underlying pathways and responses to toxicity **abs# 45**

4:40PM

#### Sofia Farkona

Proteomics of laser-captured microdissected glomeruli and tubulointerstitium reveals extracellular matrix remodelling of kidney allografts with antibody-mediated rejection **abs# 46**

4:55PM

#### Richard Wilson

Identification of key pro-survival proteins in isolated colonic goblet cells of *Winnie*, a murine model of spontaneous colitis **abs# 47**

### The Surfaceome and Extracellular Vesicles 3:15PM – 5:15PM Hall A

3:15PM

#### Bernd Wollscheid

The in silico human surfaceome & technologies for the elucidation of the surfaceome nanoscale organization **abs# 48**

3:40PM

#### Daniel Kolarich

Protein glycosylation – an overlooked feature impacting Stem cell factor and Stem cell factor receptor function **abs# 49**

4:05PM

#### Maik Mueller

LUX-MS enables the light-controlled elucidation of ligand-receptor interactions and functional surfaceome nanoscale organization on living cells **abs# 50**

4:25PM

#### Christoph Krisp

Quantitative Proteome Profiling of Stage I – IV colorectal carcinoma tissues and serum based extracellular vesicles for early onset biomarker detection **abs# 51**

4:40PM

#### Mark E Graham

Phosphoproteomics of activity-dependent phospho-signalling in synaptosomes and cultured neurons **abs# 52**

4:55PM

#### Matthew Waas

SurfaceGenie: A web-based application for prioritizing cell-type specific marker candidates **abs# 53**

### MS Imaging 3:15PM – 5:15PM Hall B

3:15PM

#### Nathalie Agar

Mass spectrometry imaging applications for neurosurgery and neurooncology **abs# 54**

3:40PM

#### Richard R Drake

Combined glycan and extracellular matrix protein workflows for FFPE prostate cancer tissues **abs# 55**

4:05PM

#### Per E. Andren

Imaging age-induced perturbations of mitochondrial function, neurotransmission and lipid signaling in specific brain structures **abs# 56**

4:25PM

#### Gus Grey

Visualising the physiological biochemistry of human ocular lens transparency and cataract with imaging mass spectrometry **abs# 57**

4:40PM

#### Cristina Ruiz-Romero

Integrative proteomic and metabolomic analysis reveals altered molecular pathways for therapeutic target development in osteoarthritis **abs# 58**

4:55PM

#### Peter P.L. Horvatovich

Exploring the limits of high-resolution mass spectrometry imaging data **abs# 59**

## Program

### Chemical Glycobiology (AGS 2)

3:15PM – 5:15PM Room E1

3:15PM

#### Mark von Itzstein

Targeting respiratory viruses using structure-guided inhibitor design on glycoenzymes **abs# 60**

3:40PM

#### Lara K. Mahal

Systematically decoding glycosylation in disease **abs# 61**

4:05PM

#### Koichi Fukase

Synthesis of glycoconjugate vaccines and antibodies for new cancer immunotherapies **abs# 62**

4:25PM

#### Hironune Ando

Stereo-selective synthesis of sialic acid containing glycoconjugates **abs# 63**

4:40PM

#### Nima Sayyadi

Site-specific conjugation of dendrimer probes to the Fc glycans of monoclonal antibodies **abs# 64**

4:55PM

#### Kaori Sakurai

Development of gold nanoparticle-based multivalent photoaffinity probes toward exploration of carbohydrate-protein interaction **abs# 65**

### HPP2: Towards the Complete Cardiac Proteome and Beyond

3:15PM – 5:15PM Room E2

3:15PM

#### Rebekah L Gundry

Chamber and cell type specific views of the human heart glycoproteome and glycome in health and disease **abs# 66**

3:40PM

#### Melanie Y White

Delving Deeper into the Cardiac Proteome - Analyzing the Heart "Modificome" **abs# 67**

4:05PM

#### Stefan Lehr

Proteomic profiling of plasma lipoprotein particles as a tool to identify novel subspecies **abs# 68**

4:25PM

#### Sandra Goetze

Relating high density lipoprotein (HDL) particle composition to clinical signaling capacity **abs# 69**

4:40PM

#### Marika Mokou

Cross-species tissue proteomics analyses in cardiovascular disease: unraveling Ariadne's thread **abs# 70**

4:55PM

#### Ling Lin

An anatomically resolved human heart transcriptome and proteome landscapes reveal molecular signatures and disease-relevant pathways of end-stage dilated cardiomyopathy **abs# 71**

### Food and Nutrition

3:15PM – 5:15PM Room E3

3:15 PM

#### Paola Roncada

The Central Role Of Milk Proteomics In One Health Approach **abs# 72**

3:40PM

#### Michelle Colgrave

Food safety assessment in genetically engineered canola - LC-MS/MS as an alternative to antibody-based approaches **abs# 73**

4:05PM

#### Ben Schulz

Bottoms Up Proteomics! The Dynamic Beer Proteome **abs# 74**

4:25PM

#### Evelyne Maes

Insights in food digestion: tracking peptides from meat and meat hydrolysates by simulated gastrointestinal digestion and label-free proteomics **abs# 75**

4:40PM

#### Xuezhi Bi

Development of an ESI-MS based serotyping assay for Salmonella **abs# 76**

4:55PM

#### Mitchell G. Nye-Wood

Leavening it for later: Proteomics of gluten-free bread **abs# 77**

### The HUPO External Development Initiative (HEDI)

3:15PM – 5:15PM Innovation Stage (Exhibition Hall)

Panelists will discuss their interactions with the funding institutions and shed lights on their experience with the successful negotiation.

Panel Discussions: Robert Moritz, Rudolf Aebersold, Matthias Uhlen, Fuchu He, YM Park

3:15PM

#### Sudhir Srivastava

How are the scientific concepts evolved at the National Institutes of Health? **abs# 78**

3:40PM

#### Tesshi Yamada

How Does Japan's Agency for Medical Research and Development fund proteomic research? **abs# 79**

4:05PM

#### Henry Rodriguez

Perspectives on International Consortium on Proteogenomic: Interactions between Funders and Investigators **abs# 80**

4:30PM

#### Michael Snyder

HubMap: Partnership between the Funders and Investigators **abs# 81**

**HUPO General Assembly**  
5:20PM – 6:00PM Innovation Stage (Exhibition Hall)

**Poster Session 1**  
6:00PM – 7:15PM Hall H

## 17th September 2019

**Tools for high productivity proteomics: timsTOF Pro, Evosep One and MaxQuant**  
7:15AM – 8:15AM Hall E1

Proudly sponsored by Bruker



### Plenary 6

8:30AM – 9:15AM Halls A & C

Session sponsored by Bioplatforms



8:30AM

#### James C Paulson

Impact of the glycoproteome on B cell responses: From checkpoint inhibitors to HIV vaccines **abs# 82**

### Plenary 7

9:15AM – 10:00AM Halls A & C

9:15AM

#### Yu-Ju Chen

Taiwan Cancer Proteogenomics Moonshot: Pathway to Next Generation Precision Medicine in Cancer **abs# 83**

### Morning Tea

10:00AM – 10:40AM Hall H

### Cancer

10:40AM – 12:40PM Hall C

10:40AM

#### Jeroen Krijgsveld

Characterization and turnover of RNA-binding proteins: novel insights into ribosome maintenance **abs# 84**

11:05AM

#### Hyun Joo An

Sugar Code Cracking of Serum Haptoglobin for the Diagnosis of Gastric Cancer by Targeted Glycoproteomic Approach **abs# 85**

11:30AM

#### Mark P Molloy

Integrative multi-omics analysis from minimally invasive colorectal cancer FFPE tissue **abs# 86**

11:50AM

#### Fernando Corrales

Understanding liver regeneration. Proteomics and phosphoproteomics analysis **abs# 87**

12:05PM

#### Kailun Xu

Proteomic dynamics of colorectal cancer evolution identifies PLOD2-mediated microenvironmental regulation as a novel drug target **abs# 88**

12:20PM

#### Pouya Faridi

Spliced epitopes are abundant and highly immunogenic components of the melanoma immunopeptidome **abs# 89**



## Program

### Degradomics, Proteases and Enzymes

10:40AM – 12:40PM Hall A

10:40AM

#### Christopher M Overall

Protein TAILS Tell Remarkable Tales: Positional Proteomics Reveals Diverse N-Terminomes and Proteolytic Landscapes in Disease **abs# 90**

11:05AM

#### Merry L Lindsey

Proteomics of Extracellular Matrix Remodeling Following Myocardial Infarction **abs# 91**

11:30AM

#### Thierry Rabilloud

Is the mitochondrial protein processing system robust? Lessons from a combined N-terminomics and shotgun proteomics approach on human cells treated with rapamycin or zinc **abs# 92**

11:50AM

#### Thomas Hauser

Measuring protein functional states in central carbon metabolism by limited proteolysis coupled to mass spectrometry **abs# 93**

12:05PM

#### Nestor Solis

Integrated TAILS terminomics, shotgun, and transcriptomics analysis of macrophage polarization and activation **abs# 94**

12:20PM

#### Robert J Beynon

The degrading business: Measurement of proteome turnover in intact animals **abs# 95**

### Bioinformatics and Statistics

10:40AM – 12:40PM Hall B

10:40AM

#### Lydie Lane

neXtProt: a SPARQLing light in the dark human proteome **abs# 96**

11:05AM

#### Juergen Cox

Computational proteomics enhancements in MaxQuant by (deep) machine learning and ion mobility awareness **abs# 97**

11:30AM

#### Zhixin TIAN

Intact N-glycopeptide database search using GPSeeker **abs# 98**

11:50AM

#### Maggie Pui Yu Lam

Identifying high-priority proteins across the human diseasome using semantic similarity **abs# 99**

12:05PM

#### Tim Van Den Bossche

ReScoring peptide-to-spectrum-matches based on predicted fragment ion intensities leads to an increased identification rate in metaproteomics **abs# 100**

12:20PM

#### Henning Hermjakob

Reactome Pathway Analysis and Visualization **abs# 101**

### Microbial and Plant Glycobiology (AGS 3)

10:40AM – 12:40PM Room E1

Session sponsored by Griffith University



10:40AM

#### Katharina Paschinger

Drilling into the N-glycomes of parasites and their vectors **abs# 102**

11:05AM

#### Giuseppe Palmisano

Comprehensive characterization of protein glycosylation in Leishmania spp **abs# 103**

11:30AM

#### Joshua L Heazlewood

Application of glycoproteomics to identify the plant Golgi localized UDP-GlcNAc transporter and mining the data for novel plant O-linked glycans **abs# 104**

11:50AM

#### Eiji Miyoshi

Glycomic approach for detection of Enterococcus infection in chronic pancreatic diseases **abs# 105**

12:05PM

#### Nichollas Scott

Analysis of In vivo Arginine-glycosylation targets of the NleB/SseK family of effectors reveals discrete effector substrate specificities **abs# 106**

12:20PM

#### Atsushi Shimoyama

Systematic chemical synthesis and immunological function of Campylobacter jejuni lipid As **abs# 107**

### HPP 3: P3: Plasma, Pediatrics and Proteomics

10:40AM – 12:40PM Room E2

10:40AM

#### Petter Brodin

Systems-level analysis of immune development early in life **abs# 108**

11:05AM

#### Qibin Zhang

Temporal profiles of plasma proteome during childhood development and natural progression of Type 1 Diabetes **abs# 109**

11:30AM

#### Cristina Al-Khalili Szigyarto

Orthogonal validation of Duchenne Muscular Dystrophy biomarkers using targeted proteomics **abs# 110**

11:50AM

#### Valentina Siino

Mass spectrometry workflow for characterization of plasma proteome changes related to ageing **abs# 111**

12:05PM

#### Esther Willems

The sweet separation between bacterial and viral infections by glycopeptide profiling **abs# 112**

12:20PM

#### Sanjeeva Srivastava

A comprehensive proteomic analysis of medulloblastoma subtypes reveals mechanistic insights of Group 3 tumors **abs# 113**

### Plant and Crop Proteomics I (AOAPO I)

10:40AM – 12:40PM Room E3

10:40AM

#### Leslie M Hicks

Investigating plant derived antimicrobial peptides using “PepSAVI-MS” **abs# 114**

11:05AM

#### Pengcheng Wang

Mapping proteome-wide targets of protein kinases in plant stress responses **abs# 115**

11:30AM

#### Subhra Chakraborty

Chitosan remodels Extracellular Matrix Integrity and regulate Stomatal Function leading to Immunity against Wilt disease **abs# 116**

11:50AM

#### Setsuko Komatsu

Elucidation of tolerant mechanism in soybean treated with plant-derived smoke under flooding stress using omics technique **abs# 117**

12:05PM

#### Pingfang Yang

Morphological and proteomics analyses of petioles rigidity in sacred Lotus **abs# 118**

12:20PM

#### Sixue Chen

Molecular changes in the course of ice plant C3 to CAM transition revealed by proteomics and metabolomics **abs# 119**

#### Lunch

12:40PM – 2:00PM Hall H

### Clinical Research Applications of the timsTOF Pro

12:45PM – 1:45PM Hall A

Proudly sponsored by Bruker



### Driving personalized medicine through targeted protein biomarker discovery – taking proteomics beyond mass spectrometry

12:45PM – 1:45PM Hall B

Proudly sponsored by Olink



### Adapting EasyPep™ MS Sample Preparation and TMT labeling for higher throughput and larger volume formats

12:45PM – 1:45PM Room E1

Proudly sponsored by Thermo Fisher Scientific



### Integrative Structural Biology, The Next Frontier of MS-Based Proteomics

12:45PM – 1:45PM Room E2

Proudly sponsored by Thermo Fisher Scientific



### Plenary 8

2:00PM – 2:45PM Halls A & C

2:00PM

#### Albert Heck

Proteome and proteoform diversity exposed and quantified by hybrid mass spectrometry approaches **abs# 120**

## Program

### Afternoon Tea

2:45PM – 3:15PM Hall H

### Infectious Diseases

3:15PM – 5:15PM Hall A

3:15PM

#### Ileana M Cristea

Organelle shape and function in the context of viral infections **abs# 121**

3:40PM

#### Darren Creek

A multi-omics approach to drug target discovery for novel bis-triazine antimalarials **abs# 122**

4:05PM

#### Nathan P Croft

Systems immunology reveals factors driving anti-viral CD8 T cell immunity **abs# 123**

4:25PM

#### Amir Banaei-Esfahani

A Mycobacterium tuberculosis protein atlas **abs# 124**

4:40PM

#### Fabian Wendt

Spatiotemporal proteotype analysis of vaccinia virus infected cells reveals dynamic host surfaceome repopulation with viral proteins **abs# 125**

4:55PM

#### Xiaoyun Liu

Salmonella proteomic profiling during infection distinguishes the intracellular environment of host cells **abs# 126**

### Proteogenomics

3:15PM – 5:15PM Hall C

3:15PM

#### Akhilesh Pandey

PASS-DIA: A novel data-independent acquisition approach for discovery studies **abs# 127**

3:40PM

#### Janne Lehtio

Proteogenomics – connecting cancer genotype with molecular phenotype **abs# 128**

4:05PM

#### Henry Rodriguez

Implementing ProteoGenome-Driven Oncology and Global Data Sharing **abs# 129**

4:25PM

#### Chris R Kinsinger

Proteomic Data Commons: a resource for proteogenomic analysis **abs# 130**

4:40PM

#### Ankit Sinha

The proteogenomic landscape of curable prostate cancer **abs# 131**

4:55PM

#### Andrei Drabovich

Mapping functional interactions of testis germ cell-specific proteins with proteogenomic assays **abs# 132**

### Analytical Glycobiology (AGS 4)

3:15PM – 5:15PM Room E1

Session sponsored by Centre for Nanoscale BioPhotonics



3:15PM

#### Henrik Clausen

A Genetic Dissection Approach to Functional Glycomics **abs# 133**

3:40PM

#### Katalin F. Medzihradzky

Negotiating the labyrinth of O-glycopeptide analysis **abs# 134**

4:05PM

#### Kay-Hooi Khoo

Strategic applications of data dependent and targeted multistage fragmentation in dual modes to expedite mass spectrometry-based sequencing of glycopeptides **abs# 135**

4:25PM

#### Miyako Nakano

Development of cancer biomarker for biliary tract cancer and pancreatic cancer with serum haptoglobin glycan analyses **abs# 136**

4:40PM

#### Erdmann Rapp

glyXboxCE: A powerful tool in the glycoanalytical toolbox – improving biologics development and biomarker discovery for personalized diagnostics **abs# 137**

4:55PM

#### Ieva Bagdonaite

Isoform-specific functions of polypeptide GalNAc-transferases probed with glycoengineered human skin organoids and mass spectrometry **abs# 138**

### Pathology and the Cancer Proteome: Towards Precision Medicine

3:15PM – 5:15PM Hall B

3:15PM

#### Michael H. Roehrl

Proteome-Based Diagnostics: The Next Revolution in Medicine and Pathology **abs# 139**

3:40PM

#### Danni Li

Enabling Precision Medicine for Alzheimer's Disease through Biofluid-Based Biomarkers **abs# 140**

4:05PM

#### Qing Kay Li

Heterogeneity study of pancreatic tumor tissue: Proteomic characterization of tumor cells obtained by laser micro-dissection (LMD), coring, and bulk sampling techniques **abs# 141**

4:25PM

#### Rosemary Balleine

Intra- and inter-individual variation in the proteome of high-grade serous ovarian cancer **abs# 142**

4:40PM

#### Jacob Kagan

Proteomic Tissue Biomarkers for Early Prediction of Prostate Cancer Progression **abs# 143**

4:55PM

#### Soren Naaby Hansen

Oxygen-sensitive interactions between glycolytic enzymes and a cancer-testis antigen established signaling scaffold are regulated by lysine acetylation **abs# 144**

### Plant and Crop Proteomics II

3:15PM – 5:15PM Room E3

3:15PM

#### Hirofumi Nakagami

Proteomic dissection of the plant immune system **abs# 145**

3:40PM

#### Harvey Millar

Quantitative analysis of protein synthesis and degradation rates in plants using progressive labeling with stable isotopes **abs# 146**

4:05PM

#### Ghasem Hosseini Salekdeh

Systems Biology Analysis of Root Tips: Towards Bioengineering of Rice Root Structure to Enhance Drought Stress Tolerance **abs# 147**

4:25PM

#### Shaojun Dai

Na<sub>2</sub>CO<sub>3</sub>-responsive mechanism in alkaligrass revealed from redox proteomic analysis **abs# 148**

4:40PM

#### Niranjan Chakraborty

Global profiling of dehydration-induced mitochondrial dynamics and defense response in rice **abs# 149**

4:55PM

#### James A. Broadbent

Wheat pan-proteomics: Unifying data-independent LC-MS proteome measurements across diverse genetic backgrounds for trait prediction **abs# 150**

### Top-Down and Structural Proteomics

3:15PM – 5:15PM Room E2

3:15PM

#### Neil Kelleher

Single ion mass spectrometry to measure proteoforms and their complexes with complete molecular specificity **abs# 151**

3:40PM

#### Ying Ge

Novel Strategies in Top-Down Proteomics **abs# 152**

4:05PM

#### Lissa C. Anderson

Extending the upper mass range for top-down proteomics with proton-transfer reactions, parallel ion parking, and 21 tesla FT-ICR MS **abs# 153**

4:25PM

#### Hartmut Schlüter

Identification of the functional status of proteoforms and their interactomes in blood plasma **abs# 154**

4:40PM

#### Blaine R Roberts

Application of a novel electron capture dissociation (ECD) mass spectrometry to top-down and bottom-up proteoform characterization on a QTOF **abs# 155**

4:55PM

#### Alexandre A Shvartsburg

High-Resolution Differential Ion Mobility Separations with Orbitrap Mass Spectrometry for Middle-Down Analyses of Histone Proteoforms **abs# 156**



## Program

**Poster Session 2**  
5:15PM – 6:30PM Hall H

**Early Career Researcher (ECR) PhD Abstract Competition**  
5:30PM – 6:15PM  
Innovation Stage

**Congress Dinner**  
7:30PM – 11:00PM The Adelaide Oval, William Magarey Room

### 18th September 2019

**Plenary 9**  
8:30AM – 9:15AM Halls A & C

8:30AM  
**Kathryn Lilley**  
Cellular atlas of the transcriptome and proteome  
**abs# 157**

**Morning Tea and Poster Viewing**  
9:15AM – 10:00AM Hall H

**Cardiovascular and Metabolic Disease**  
10:00AM – 12:00PM Hall C

10:00AM  
**Jennifer Van Eyk**  
Reverse Engineering to Identify the Next Therapeutic in Heart Failure with Preserved Ejection Fraction? **abs# 158**

10:25AM  
**John R Yates**  
The Use of LC/MS and Bio-orthogonal Chemistry to Study Protein Dynamics in Cardiac Remodeling **abs# 159**

10:50AM  
**Jochen M Schwenk**  
Integrative analysis of plasma proteomes from prediabetes and diabetes progression: An IMI DIRECT study **abs# 160**

11:10AM  
**Mark Larance**  
Systems proteomics of the intermittent fasting response highlights the importance of hnf4a **abs# 161**

11:25AM  
**Daniella H. Hock**  
From disease to biology: how quantitative proteomics can resolve the molecular diagnosis of mitochondrial disease patients and provide insights into mitochondrial biology **abs# 162**

11:40AM  
**Alexander W. Rookyard**  
Multi-omic profiling of metabolic dysfunction caused by myocardial ischemia / reperfusion (I/R) injury **abs# 163**

**Post-Translational Modifications II**  
10:00AM – 12:00PM Hall A

10:00AM  
**Jesper V Olsen**  
Rapid, sensitive and site-specific phosphoproteome profiling of EGFR signaling by data-independent acquisition **abs# 164**

10:25AM  
**David James**  
Global redox proteome and phosphoproteome analysis reveals novel insights into the Insulin Signaling Network **abs# 165**

10:50AM  
**Justyna Fert-Bober**  
Hyper-citrullinated library workflow to support demand-driven correct identification of citrullinated residues **abs# 166**

11:10AM  
**Naoyuki Sugiyama**  
In Vitro Profiling of Ser/Thr/Tyr Selectivity of Human Protein Kinome **abs# 167**

11:25AM  
**Nuno Bandeira**  
Multi-stage discovery of hypermodified peptides and hundreds of post translational modifications from open modification search **abs# 168**

11:40AM  
**Susan Weintraub and Michael Hoopmann**  
HUPO Proteome Project Phosphopeptide Challenge Report **abs# 169**

**Special Session: The ICPC Initiative**  
10:00AM – 12:00PM Room E2

10:00AM  
**Ana I Robles**  
The International Cancer Proteogenome Consortium (ICPC): innovation and collaboration inspired by the Cancer Moonshot<sup>SM</sup> **abs# 170**

10:05AM  
**Johan Malm**  
Large Scale Melanoma Cancer Studies at the European Cancer Moonshot Lund Center in Partnership with Five International Hospitals **abs# 171**

10:30AM  
**René P. Zahedi**  
Proteogenomics of colorectal cancer liver metastases: complementing precision oncology with phenotypic data **abs# 172**

10:55AM  
**David J Clark**  
Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma **abs# 173**

11:15AM  
**Tadashi Kondo**  
Patient-derived cancer model for proteogenomics: Report by ICPC JAPAN team **abs# 174**

11:30AM  
**Yang Du**  
Proteogenomic Characterization of Human Gastric Cancer **abs# 175**

11:45AM  
**Iulia M. Lazar**  
Proteogenomic Analysis of Cancer Point Mutations - A Chromosomal Map **abs# 176**

**HPP 5: High Connectivity: Neuroproteomics at the Interface of Bench and Bedside**  
10:00AM – 12:00PM Room E1

10:00AM  
**Melanie Foecking**  
The use of proteomics to identify blood-based protein changes in childhood that are associated with increased risk for later psychosis **abs# 177**

10:25AM  
**Lingjun Li**  
Comparative glycoproteomic analyses of cerebrospinal fluids reveal novel molecular players in Alzheimer's disease **abs# 178**

10:50AM  
**K. Oliver Schubert**  
Autoantibody Profiling of Schizophrenia and related Psychotic Disorders in the Australian National Survey of High Impact Psychosis (SHIP) **abs# 179**

11:10AM  
**Sanjeeva Srivastava**  
Human brain proteome draft atlas to understand biological function and reference for brain tumour investigations **abs# 180**

11:25AM  
**Kelly L Stauch**  
Proteomic and bioenergetic analyses demonstrate synaptic mitochondrial alterations due to age-related pathologic tau accumulation **abs# 181**

11:40AM  
**Nathan Basisty**  
A Proteomic Atlas of Senescence-Associated Secretomes for Aging Biomarker Development **abs# 182**

**Microbial Proteomics and the Microbiome**  
10:00AM – 12:00PM Room E3

10:00AM  
**Daniel Figeys**  
Microbiome in diseases and health **abs# 183**

10:25AM  
**Simone Lemeer**  
Histidine phosphorylation: a new dimension in the phosphoproteome **abs# 184**

10:50AM  
**Stuart J Cordwell**  
Aligning label-based discovery and global DIA validation proteomics to explore bacterial virulence phenotypes **abs# 185**

11:10AM  
**Jonathan M Blackburn**  
An unbiased metaproteomic approach to describe the mucosal microbiome of an HIV-exposed African infant cohort **abs# 186**

11:25AM  
**Joshua J Hamey**  
Methylation throughout the proteome: the methyltransferases tell the story **abs# 187**

11:40AM  
**Nadine Prust**  
Phosphoproteomic study on Staphylococcus aureus to identify phosphoproteins involved in virulence **abs# 188**

## Program

**New Technological Advancements in Proteomics (HUPO IAB)**  
10:00AM – 12:00PM Hall B

10:00AM

**Michael MacCoss**

How do we make quantitative proteomics quantitative?  
**abs# 189**

10:25AM

**Stephanie M. Cologna**

Differential Proteomics and Lipidomics in Niemann-Pick Disease, Type C **abs# 190**

10:50AM

**Phillip J Robinson**

Rapid and robust high throughput cancer proteomics across multiple instruments in a single facility **abs# 191**

11:10AM

**Ryan Bomgarden**

Going Beyond 11: TMTpro 16plex Regents for Higher Quantitative Proteomic Sample Multiplexing **abs# 192**

11:25AM

**Gary Kruppa**

Diapasef: Toward The Ideal Mass Analyzer With Data-Independent Acquisition And Parallel Accumulation – Serial Fragmentation **abs# 193**

11:40AM

**Dylan Xavier**

Heat and Beat: A one-pot rapid tissue sample preparation for proteomics in under an hour **abs# 194**

**Lunch**

12:00PM – 1:30PM Hall H

**Big Data, Fast Data, Smart Data**  
12:15PM – 1:15PM Room E1

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**The Next Era in Pathway Proteomics – Towards Turnkey Targeted Quantitation Workflows**  
12:15PM – 1:15PM Room E2

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**High-Throughput Proteomics With Evosep One**

12:15PM – 1:15PM Room E3

Proudly sponsored by Evosep

**EVOSEP**

**Precision Medicine and Clinical Proteomics**  
1:30PM – 3:30PM Hall C

1:30PM

**Bing Zhang**

Onco-proteogenomics: toward a more complete understanding of cancer biology **abs# 195**

1:55PM

**Karin Rodland**

Pathway-level analysis of comprehensive proteogenomic and phosphoproteomic data to predict clinical outcomes **abs# 196**

2:20PM

**Joshua Labaer**

Multiplex In-Solution Protein Array (MISPA) for high throughput, quantitative profiling of protein interactions and detection of immune responses to pathogen induced cancers **abs# 197**

2:40PM

**György Marko-Varga**

Improved Survival Prognostication of Node-Positive Malignant Melanoma Patients applying Shotgun Proteomics Guided by Histopathological Characterization and Genomic data **abs# 198**

2:55PM

**Harsha Gowda**

Delineating mechanisms that confer resistance to kinase inhibitors in head and neck squamous cell carcinoma and melanoma **abs# 199**

3:10PM

**Darragh P O'Brien**

Integrative -Omics Reveals Novel Targets Underlying the Pathomechanisms of Uterine Fibroids and Associated Heavy Menstrual Bleeding **abs# 200**

**The Interactome**  
1:30PM – 3:30PM Hall A

1:30PM

**Juri Rappsilber**

Cellular Cartography at Molecular Detail: in Situ Crosslinking Mass Spectrometry **abs# 201**

1:55PM

**Meng-Qiu Dong**

Amine-selective Di-ortho-phthalaldehyde (DOPA) Cross-linking Captured the Conformational Change Associated with the Unfolding of Ribonuclease A **abs# 202**

2:20PM

**Marc Wilkins**

Crosslinking mass spectrometry analysis of the yeast nucleus reveals extensive protein-protein interactions not detected by systematic two-hybrid or affinity purification-mass spectrometry **abs# 203**

2:40PM

**Ben C Collins**

Complex-centric proteome profiling in one day with SEC-SWATH-MS and short gradient analysis **abs# 204**

2:55PM

**Eneko Villanueva**

Comprehensive identification of RNA-protein interactions in any organism using orthogonal organic phase separation (OOPS) **abs# 205**

3:10PM

**Claudia Martelli**

High-throughput protein-protein interaction profiling for clinical applications **abs# 206**

**Metabolomics and Lipidomics**  
1:30PM – 3:30PM Room E1

1:30PM

**Erin S Baker**

A Multi-Omic Investigation into the Molecular Signatures of Preeclampsia and Gestational Diabetes Mellitus **abs# 207**

1:55PM

**Ute Roessner**

The role of lipids in plant stress biology **abs# 208**

2:20PM

**Gavin E Reid**

A 'Systems-omics' Strategy to Uncover the Role of Brain Tissue Derived Exosomal Lipids in Alzheimer's Disease **abs# 209**

2:40PM

**Igor Popov**

MS-based tissue profiling for assistance on neurosurgery operations of brain cancer **abs# 210**

2:55PM

**Stephan Klatt**

Comparative targeted and high-throughput metabolomics workflow of small-volume plasma samples **abs# 211**

3:10PM

**Hiroshi W.L. Koh**

Identifying predictive network of lipids and proteins among individuals at high and low risk of coronary artery disease using iOmicsPASS **abs# 212**

**HPP6: Moving Proteomics into Pharmaceutical Discovery and Application**  
1:30PM – 3:30PM Room E2

1:30PM

**Anne Claude Gingras**

Proximity dependent sensors define a role for HOPS in macropinocytosis-dependent control of cell growth **abs# 213**

1:55PM

**Paul Alewood**

Venoms to Drugs **abs# 214**

2:20PM

**Wint Wint Phoo**

Unveiling protein targets involved in haptentation during allergic contact dermatitis via high resolution mass spectrometry **abs# 215**

2:40PM

**Sung Min Cho**

Reverse chemical proteomics identifies unanticipated human target of anti-malarial drug, Artesunate, for drug repositioning **abs# 216**

2:55PM

**David R. Spiciarich**

Proteome profiling of multiple sclerosis cerebrospinal fluid by data independent acquisition reveals changes in proteins involved in adaptive immunity **abs# 217**

3:10PM

**Xiaolu Zhao**

Thermostable potassium channel-inhibiting neurotoxins in processed scorpion medicinal material revealed by proteomic analysis: implications of its pharmaceutical basis in traditional Chinese medicine **abs# 218**



## Program

### Special Session: Disease Biomarkers, Assays and Diagnostic Proteomics 1:30PM – 3:30PM Hall B

1:30PM

#### Robert Moritz

Standardizing the performance of SWATH/DIA-MS software tools for label-free quantification using public repository spectral ion libraries **abs# 219**

1:55PM

#### Je-Yoel Cho

Development of clinically applicable lung cancer proteome biomarkers for in vitro diagnostics-multivariate index assay **abs# 220**

2:20PM

#### Jarrod Marto

Multidimension LC-MS/MS analysis of CSF samples in the biofind cohort for biomarker discovery in Parkinson's disease **abs# 221**

2:40PM

#### Young-Ki Paik

Human complement factor B: a new pancreatic cancer biomarker with multiple functions **abs# 222**

2:55PM

#### Charles Pineau

The eutopic endometrium proteome in endometriosis reveals candidate markers and molecular mechanisms of physiopathology **abs# 223**

3:10PM

#### Allan Stensballe

Phenotyping of multiple biofluids for liquid biomarkers for diagnostics and personalized medicine **abs# 224**

### Chemical Proteomics

1:30PM – 3:30PM Room E3

1:30PM

#### HoJeong Kwon

Unraveling protein targets of bioactive small molecules using label-free chemical proteomics **abs# 225**

1:55PM

#### Sheng-ce Tao

An Array of 60,000 Antibodies for Proteome-Scale Antibody Generation and Target Discovery **abs# 226**

2:20PM

#### Ruzanna Mnatsakanyan

Proteome-wide detection of cysteine nitrosylation targets and motifs using bioorthogonal cleavable-linker-based enrichment and switch technique (Cys-BOOST) **abs# 227**

2:40PM

#### Amir Ata Saei

System-wide identification of enzyme substrates by thermal analysis **abs# 228**

2:55PM

#### Tae young Kim

Mass Spectrometry Imaging of RTKi with protein target in human lung cancer tumor xenograft mouse **abs# 229**

3:10PM

#### Tao Liu

An enhanced boosting to amplify signal with isobaric labeling (eBASIL) approach toward comprehensive quantitative single-cell proteomics analysis **abs# 230**

### Afternoon Tea

3:30PM – 4:00PM Hall H

### HUPO Awards Ceremony

4:00PM – 5:00PM

### Plenary 10

5:00PM – 5:45PM Halls A & C

5:00 PM

#### Michael Snyder

Big Data And Health And World Wide Omics Profiling **abs# 231**

### Closing Ceremony and Introduction of HUPO 2020

5:45PM – 6:00PM Halls A & C

# timsTOF Pro

Ushering in the Era of 4D Proteomics with PASEF and diaPASEF



## timsTOF Pro and PASEF Winner of the EuPA Technology Award 2019

The timsTOF Pro with PASEF technology delivers revolutionary improvements in scan speed and sensitivity while maintaining ultra-high resolution for both precursor and MS/MS spectra. At the same time the timsTOF Pro with Trapped Ion Mobility (TIMS) adds a 4th ion mobility dimension to retention time, m/z, and intensity measured by other instruments. CCS-aware match between runs and CCS aligned DIA analysis are just the first of many powerful new applications that will be enabled by the timsTOF Pro.

- Near 100% duty cycle using dual TIMS technology with MS/MS at >120 Hz
- Discover, characterize and quantify more proteins with PASEF and 4D Proteomics

**NEW** Now with TIMS based DIA analysis capabilities - diaPASEF

For more information please visit [www.bruker.com/timstofpro](http://www.bruker.com/timstofpro)

TIMS-QTOF MS

Innovation with Integrity

For research use only. Not for use in clinical diagnostic procedures

## Congress Session Chairs

### Sunday 15th September

**Welcome Address**  
Stuart Cordwell  
and Peter Hoffmann

**Plenary 1**  
Peter Hoffmann

**Plenary 2**  
Stuart Cordwell

### Monday 16th September

**Plenary 3**  
Michelle Hill

**Plenary 4**  
Andrew Webb

**Concurrent Sessions**  
10:40AM - 12:40PM

**Hereditary Disease and Aging**  
Laura Dagley and Andrea Urbani

**Post-Translational Modifications I**  
Phil Robinson and  
Justyna Fert-Bober

**Glycoimmunology and  
Clinical Glycobiology (AGS I)**  
Morten Thaysen-Andersen  
and Naoyuki Taniguchi

**HPP1: Rheumatic Diseases  
and Autoimmune Disorders**  
Cristina Ruiz-Romero  
and Alex Rai

**Veterinary and Animal Health**  
Nana Satake and  
Omar Mendoza-Porras

**Single Cell Proteomics**  
Radoslaw Sabota  
and Susan Weintraub

**Plenary 5**  
Mark Baker

**Concurrent Sessions**  
15:15PM - 17:15PM

**Immunology and Inflammation**  
Patricia Illing and  
Manuela Klinger-Hoffman

**The Surfaceome and  
Extracellular Vesicles**  
Ben Parker and David Greening

**MS Imaging**  
Peter Hoffmann  
and Lissa Anderson

**Chemical Glycobiology (AGS II)**  
Giuseppe Palmisano  
and Yasuhiro Kajihara

**HPP2: Towards the Complete  
Cardiac Proteome and Beyond**  
Ying Ge and Maggie Lam

**Food and Nutrition**  
James Broadbent  
and Subhra Chakraborty

### Tuesday 17th September

**Plenary 6**  
Morten Thaysen-Andersen

**Plenary 7**  
Mark Molloy

**Concurrent Sessions**  
10:40AM - 12:40PM

**Cancer**  
Karin Rodland and Charles Pineau

**Degradomics, Proteases  
and Enzymes**  
Anthony Purcell and  
Valerie Wasinger

**Bioinformatics and Statistics**  
Yasushi Ishihama  
and Dana Pascovici

**Microbial and Plant  
Glycobiology (AGS III)**  
Ben Schulz and  
Zeynep Sumer-Bayraktar

**HPP3: Plasma, Pediatrics  
and Proteomics**  
Jochen Schwenk and  
Cristina Al-Khalili Szigyarto

**Plant and Crop Proteomics I**  
Michelle Colgrave  
and Harvey Millar

**Plenary 8**  
Anthony Purcell

**Concurrent Sessions**  
15:15PM - 17:15PM

**Infectious Diseases**  
Stuart Cordwell  
and Simone Lemeer

**Proteogenomics**  
Harsha Gowda and Ana Robles

**Analytical Glycobiology (AGS IV)**  
Daniel Kolarich and  
Terry Nguyen-Khuong

**HPP4: Pathology and  
the Cancer Proteome**  
Daniel Chan and Hui Zhang

**Plant and Crop Proteomics II**  
Setsuko Komatsu and Paul Haynes

**Top-Down and  
Structural Proteomics**  
Gus Grey and Tara Pukala

### Wednesday 18th September

**Plenary 9**  
Marc Wilkins

**Concurrent Sessions**  
10:00AM - 12:00PM

**Cardiovascular and  
Metabolic Disease**  
Rebekah Gundry and Uwe Volker

**Post-Translational  
Modifications II**  
Melanie White and Michelle Hill

**Special Session: The ICPC  
Initiative**  
Yu-Ju Chen and Henry Rodriguez

**HPP 5: High Connectivity:  
Neuroproteomics at the  
Interface of Bench and Bedside**  
Oliver Schubert and Peter Nilsson

**Microbial Proteomics  
and the Microbiome**  
Frank Schmidt and  
Emoke Bendixsen

**New Technological  
Advancements in  
Proteomics (IAB)**  
Katherine Tran and Mark Duncan

**Concurrent Sessions**  
13:30PM - 15:30PM

**Precision Medicine  
and Clinical Proteomics**  
Mark Molloy and Tiannan Guo

**The Interactome**  
Maxey Chung and  
Meng-Qiu Dong

**Metabolomics and Lipidomics**  
Darren Creek and Ute Roessner

**HPP 6: Moving Proteomics  
into Pharmaceutical Discovery  
and Application**  
Jenny Van Eyk and  
Ferdinando Cerciello

**Special Session: Disease  
Biomarkers, Assays and  
Diagnostic Proteomics**  
Andrew Webb and Ed Nice

**Chemical Proteomics**  
Terence Poon and Mingliang Ye

**Plenary 10**  
Stephen Pennington

## Hosted Lunchtime Workshops

### Addressing the analytical rigor of omics measurements for clinical research

#### Day

Monday 16th September, 12:45pm - 1:45pm

#### Room

Hall E2

#### Speakers

Dr. Marten F. Snel, SAHMRI,  
Head of MS Core Facility

A/Prof Robert Trengove, Murdoch University,  
Director Separation Science and Metabolomics  
Laboratory

#### Synopsis

The translation of discovery biomarker studies has been plagued with obstacles in the path to clinical utility. Small study sizes, poor experimental reproducibility and inappropriate analytical technique continue to confound the efficient translation from bench to bedside. Waters Corporation continues purposeful innovation in biomedical research with these challenges in mind. SONAR data independent acquisition was developed to improve reproducibility, increase speed of analysis for compatibility with large study cohorts whilst maintaining data quality and quantitative accuracy.

In this lunchtime workshop we will hear from two leading researchers who have been successfully addressing the analytical challenges of protein biomarker discovery in clinical research applications.

#### Topics

Biomarker Discovery, Translational Research, Reproducibility and accuracy of measurements, SONAR data independent acquisition

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**Waters**  
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### DIA with near 100% Ion Usage: Introducing diaPASEF on the timsTOF Pro

#### Day

Monday 16th September, 12:45pm - 1:45pm

#### Room

Hall A

#### Speakers

Prof. Dr. Ruedi Aebersold, Head of the Institute  
of Molecular Systems Biology, ETH, Zurich,  
Switzerland

#### Synopsis

The timsTOF Pro with PASEF was introduced as a shotgun proteomics solution at the International HUPO Congress in Dublin in 2017. The unique trapped ion mobility (TIMS) front end of the instrument enables usage of nearly 100% of the ions entering the instrument. However, as in any DDA method the precursor selection is automated, based on the data user adjustable parameters. The precursors that are targeted for MS/MS can vary from run to run due to biological variation and the semi-stochastic nature of the precursor selection process. DIA methods can improve the data completeness by fragmenting all ions in a wider window, but suffer from inefficient usage of the ions as the window must be cycled over the entire mass range of interest. In this workshop the use of a new scan mode called diaPASEF will show how virtually all of the peptide ions can be covered with highly efficient usage of the ions present. Dr. Gary Kruppa will present a brief introduction to the diaPASEF method. Then our featured speaker, Prof. Ruedi Aebersold will present a talk on "SWATH/DIA Proteomics and its Role in Biology".

#### Topics

DDA and DIA approaches to proteomics; The new diaPASEF approach; The importance of DIA/SWATH methods in biological applications.

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## Hosted Lunchtime Workshops

### Advancing Quantitative Proteomics: Multiplexing, Accuracy, and Precision

#### Day

Monday 16th September, 12:45pm – 1:45pm

#### Room

Hall E1

#### Speakers

Khatereh Motamed, Vertical Marketing Specialist (Thermo Fisher Scientific)

Kathryn Lilley, Professor, Department of Biochemistry (University of Cambridge)

#### Synopsis

Quantitative proteomics strategies using Tandem Mass Tags (TMT) enable precise measurement of protein abundance from multiple samples into a single high-resolution LC-MS analysis. Increasingly, various biological experiments demand higher multiplexing and sample throughput with accurate quantitation. In this workshop, our expert speakers will lay out strategies that combine next generation technologies in multiplexing chemistry, hardware, and software to achieve increased quantitative performance and throughput efficiency on Thermo Scientific Orbitrap Mass Spectrometers. Together, these advances allow for intelligent acquisition methods that improve quantitation accuracy, precision, and proteome depth.

#### Topics

- Quantitative proteomics strategies using Tandem Mass Tags (TMT)
- Strategies that combine next generation technologies in multiplexing chemistry, hardware, and software to achieve increased quantitative performance and throughput efficiency on Thermo Scientific Orbitrap Mass Spectrometers

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SCIENTIFIC

### Differentiated Approaches to Omics challenges in Translational Research

#### Day

Monday 16th September, 12:45pm – 1:45pm

#### Room

Hall E3

#### Speakers

A/Prof Michelle Hill of QIMR Berghofer Medical Research Institute and The University of Queensland Diamantina Institute, Brisbane, Australia

A/Prof Blaine Roberts, Florey Institute of Neuroscience and Mental Health, Melbourne, Australia

#### Synopsis

##### A/Prof Michelle Hill

**More information reproducibly from limited clinical samples: the power of clinical multi-omics**  
Combining multiple omics analyses can provide unparalleled insight for disease pathology and biomarker discovery. For clinical studies, the often limited amount of clinical material poses technical challenges. Furthermore, large clinical cohorts are required to achieve statistical power in view of the expected broad inter-patient variability. Therefore, high throughput and robust processing methods are essential for clinical multi-omics studies, preferably extracting multiple molecular types from the same limited patient sample. This presentation will highlight solutions of the concurrent extraction of metabolites, lipids and proteins from a single biopsy/clinical material, methods for quantitating lipids and high throughput sample preparation. In addition, bioinformatics workflows for integrating multi-omics data will also be discussed.

##### A/Prof Blaine Roberts

**Top-down Proteomics and PTM retention using an electron capture dissociation (ECD) fragmentation in a Q-ToF.**

#### Abstract

Fragmentation of intact proteins with mass spectrometry can better characterize endogenous post-translational modifications (PTMs), and allows for the complete characterization of biotherapeutics. However, collision induced dissociation limits current Q-ToF instruments to analyzing trypsin-sized peptides while frequently destroying labile PTMs. We evaluated an efficient electron-based fragmentation on an Agilent 6550 Q-TOF made possible by retrofitting e-MSion's ExD cell with a shortened collision cell. The modification took an hour to install and did not degrade the mass spectrometer's performance. The ExD cell provided efficient electron fragmentation and dissociation to yield nearly complete coverage of intact proteins up to ~30kDa. The fragmentation is fast and allowed human brain lysates to be analyzed on LC time scales with sequence coverage typically greater than 80%.

#### Topics

- Multi-Omics Challenges Overview
- The Power of Clinical Multi-Omics
- Top-Down Proteomics and PTM Retention with ECD Fragmentation in a LC-QTOF

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### Tools for high productivity proteomics: timsTOF Pro, Evosep One and MaxQuant

#### Day

Tuesday 17th September, 7:15am – 8:15am

#### Room

Hall E1

#### Speakers

Dr. Nicolai Bache, Head of Applications, Evosep, Denmark.

Prof. Jürgen Cox, PhD, Group Leader of the Computational Systems Biology group at the Max Planck Institute of Biochemistry, Martinsried, Germany.

#### Synopsis

With the trend toward clinical research and translational proteomics, the measurement of ever larger sample cohorts is needed for e.g. biomarker validation. Other emerging research areas, such as single cell proteomics, require running large numbers of samples. These trends place increasing demand on not just speed and sensitivity, of instrumentation, but also robustness and reproducibility. Since its introduction in 2017, the timsTOF Pro has proven to be not only an exceptionally fast and sensitive instrument for shotgun proteomics, but has also proven to have exceptional robustness. The combination of high sample throughput with robustness, and computational tools to get the most out of the acquired data, yields what we term "high productivity" proteomics.

In this workshop the combination of the Evosep One, a highly robust microflow LC system with the timsTOF Pro will be presented by Dr. Nicolai Bache of Evosep, with the title, "High productivity proteomics with the timsTOF Pro and Evosep One". Then Prof. Juergen Cox of the Max Planck Institute in Martinsried, Germany will present on recent developments for getting the most out of such data, with the title, "Unlocking the power of the fourth dimension: MaxQuant for timsTOF pro".

#### Topics

Trapped ion mobility coupled to a QTOF for shotgun proteomics. Robust LC operation at microflow rates using a combination of high flow sample preparation and injection, followed by microflow chromatography. Computational methods for efficiently analyzing 4-dimensional shotgun proteomics.

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## Hosted Lunchtime Workshops

### Adapting EasyPep™ MS Sample Preparation and TMT labeling for higher throughput and larger volume formats

#### Day

Tuesday 17th September, 12:45pm – 1:45pm

#### Room

Hall E1

#### Speakers

Ryan Bomgarden, Sr. Staff Scientist  
(Thermo Fisher Scientific)

#### Synopsis

Advances in mass spectrometry (MS) instrumentation have enabled routine analysis of complex protein samples. However, sample preparation methods are not standardized with many protocols taking 8-24hrs in addition to suffering from low peptide yields, poor digestion efficiency and limited scalability. Recently, we developed a new, simplified sample prep kit containing pre-formulated reagents and a standardized protocol for processing 10Qg to 100Qg protein samples in less than 2 hours. In this study, we adapted our chemistry to use an automated liquid handling system for sample preparation, TMT labeling, and a 96-well filter plate for peptide clean up.

#### Topics

- Introduce a new, simplified sample prep kit containing pre-formulated reagents and a standardized protocol
- Using an automated liquid handling system for sample preparation, TMT labeling, and a 96-well filter plate for peptide clean up

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S C I E N T I F I C

### Integrative Structural Biology, The Next Frontier of MS-Based Proteomics

#### Day

Tuesday 17th September, 12:45pm – 1:45pm

#### Room

Hall E2

#### Speakers

Ruedi Aebersold, Professor, Department of Biology, Institute of Molecular Systems Biology (University of Zurich)

#### Synopsis

To understand protein functioning in the cellular environment, it is essential that researchers determine protein complex assembly and structure beyond that of individual proteins. Solving the structure of large dynamic complexes often requires integrating several complementary mass spectrometry techniques—an approach known as integrative structural biology. Thermo Fisher Scientific leads the way in accelerating protein structure-function studies with its Integrative Structural Biology solutions. In this workshop, our expert speaker will share new approaches for structural proteomics workflows.

#### Topics

- To understand protein functioning in the cellular environment
- Solving the structure of large dynamic complexes
- Sharing new approaches for structural proteomics workflows

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S C I E N T I F I C

### Driving personalized medicine through targeted protein biomarker discovery – taking proteomics beyond mass spectrometry

#### Day

Tuesday 17th September, 12:45pm – 1:45pm

#### Room

Hall B

#### Speakers

Professor Matthias Uhlén (Royal Institute of Technology, Stockholm). Other speakers to be confirmed.

#### Synopsis

As proteomics takes an increasingly central role in driving precision medicine forwards, many new technologies are coming through to complement mass spectrometry, and in some cases, broaden the possibilities for protein biomarkers in this area. Olink has developed one such enabling technology for protein biomarker discovery, providing high throughput, sensitive analysis of multiple proteins direct from very small volumes of plasma/serum without the need for further sample preparation. Olink technology has been used widely in both the pharma-biotech and clinical research sectors in Europe and the U.S., generating around 90 million protein measurements from over a million samples, and resulting in over 250 peer-reviewed publications. These studies cover many types of applications, from the search for novel drug targets, to protein profiles for patient stratification and risk assessment, as well as to gain invaluable pathophysiological insights across a broad range of disease areas. As Olink expands into the wider Asia region, we are delighted to arrange this workshop at HUPO 2019 in Australia, and to have the opportunity to present a few examples of the many successful protein biomarker studies that have been carried out to date in both wellness and disease. Please come and join the discussion.

#### Topics

Professor Uhlén will describe how he has utilized Olink protein analysis in a major longitudinal wellness study.

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P R O T E O M I C S

### Clinical Research Applications of the timsTOF Pro

#### Day

Tuesday 17th September, 12:45pm – 1:45pm

#### Room

Hall A

#### Speakers

Catherine CL Wong, Ph. D., Director, Center for Precision Medicine Multi-omics Research, and Associate Professor, Health Science Center, Peking University, China.

Prof. Andrew Webb, Ph. D., Laboratory Head in the Advanced Technology and Biology Division of the Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia.

#### Synopsis

The timsTOF Pro with PASEF was introduced as a shotgun proteomics solution at the International HUPO Congress in Dublin in 2017. The unique trapped ion mobility (TIMS) front end of the instrument enables usage of nearly 100% of the ions entering the instrument. This leads to superb sensitivity when combined with the time and space focusing provided by the TIMS device. When used with the PASEF scan method, very high MS/MS speeds >100 Hz also become routine. Since its introduction, the speed, sensitivity and robustness of the timsTOF Pro have proven attractive to researchers working in clinical proteomics research. After a brief introduction to the unique features of the timsTOF Pro with PASEF, by Dr. Gary Kruppa, Prof. Catherine Wong will present a talk on "Mapping the Q-glycoproteome Using the timsTOF Pro". Following this Prof. Andrew Webb will speak on, "High throughput Proteomics on the timsTOF Pro: Applications to clinical research and beyond".

#### Topics

Unique features and principles of operation of the timsTOF Pro with TIMS and PASEF. Clinical research proteomics applications of the timsTOF Pro. Glycoproteomics applications of the timsTOF Pro.

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## Hosted Lunchtime Workshops

### High-Throughput Proteomics with Evosep One

#### Day

Wednesday 18th September, 12:15pm – 1:15pm

#### Room

Hall E3

#### Speakers

Dr Nicolai Bache, Head of Application, Evosep

#### Synopsis

Evosep aims to improve quality of life and patient care by radically innovating protein based clinical diagnostics. Making sample preparation and separation before MS analysis 10 times faster and 100 times more robust will enable truly large cohort studies for biomarker validation and provide the foundation for precision medicine.

This will be highlighted in the talk: “Increasing throughput with DIA and diaPASEF: from pre-clinical models to protein complexes”

#### Topics

Clinical proteomics, large cohort studies, DIA, diaPASEF, protein complexes, high throughput, robust proteomics

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### The Next Era in Pathway Proteomics – Towards Turnkey Targeted Quantitation Workflows

#### Day

Wednesday 18th September, 12:15pm – 1:15pm

#### Room

Hall E2

#### Speakers

Emily Chen, Senior Director (Thermo Fisher Scientific)

Lauren Stopfer, PhD Student (Koch Institute for Integrative Cancer Research, Massachusetts Institute of Technology)

#### Synopsis

Accurate monitoring of cell signaling pathway proteins has proven challenging due to the low cellular abundance of these targets and lack of standardized targeted proteomic methodologies and reagents. In this workshop, our expert speakers will share the latest advances and newest technologies in targeted peptide quantitation and pathway analysis, including our panel of Thermo Scientific SureQuant multiplex immunoprecipitation targeted mass spectrometry kits. They will also introduce the novel SureQuant internal standard triggered parallel reaction monitoring (IS-PRM) methodology for more reproducible and sensitive quantitation on Thermo Scientific Orbitrap mass spectrometers.

#### Topics

- Sharing the latest advances and newest technologies in targeted peptide quantitation and pathway analysis
- Panel of Thermo Scientific SureQuant multiplex immunoprecipitation targeted mass spectrometry kits
- Introduce the novel SureQuant internal standard triggered parallel reaction monitoring (IS-PRM) methodology

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### Big Data, Fast Data, Smart Data

#### Day

Wednesday 18th September, 12:15pm – 1:15pm

#### Room

Hall E1

#### Speakers

Tony Purcell, Larkin's Professorial Fellow and NHMRC Senior Research Fellow Head Immunoproteomics Laboratory

Tiannan Guo, Tenure Track Assistant Professor, Westlake Institute for Advanced Studies, Hangzhou, China

#### Synopsis

In the post-HeLa era of proteomics, precise quantitative measurements that can be made quickly and reproducibly across large datasets are required for Big Data approaches to precision medicine and in the advancement of human wellness.

In this workshop we introduce Scanning SWATH(R) Acquisition: the newest chapter in the SWATH(R) Acquisition story with the power to produce datasets containing the same level of information as all other acquisition strategies combined on a faster timescale than previously possible with SWATH (R) Acquisition.

The amount of data that can be collected on fast timescales and the multidimensional information that opens up the possibility of feasible and accessible Big Data approaches in clinical proteomics and beyond using the latest cloud-based informatics to allow translation of this data to advance healthcare and human wellness.

#### Topics

- Scanning SWATH Acquisition: DIA at lightning speed
- Systems level understanding of infectious immunity using targeted MS by Tony Purcell
- The emergence of proteomic big data research for precision medicine by Tiannan Guo

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# Bio-Informatics Hub

## Overview

The Bioinformatics Hub is a place where bioinformaticians gather together with three aims: (i) to provide their advice, knowledge, and support to anyone with a relevant question; (ii) to discuss current issues and challenges in proteomics informatics with the entire community; and (iii) to work on interesting, synergistic projects and to freely exchange tools, algorithms and know-how with each other, across all labs, seniorities and levels of experience.

This is achieved by specific sessions in the agenda. The Ask the Experts sessions (every day between 16h00 and 17h00) explicitly open the space to all with questions, and leverages the combined experience and expertise of all Hub participants to answer those questions. The Special Interest Topic sessions address a current problem or issue in proteomics informatics in a short (max 20 min) presentation, followed by an open discussion of the topic by all participants, moderated by the organizers. The last type of session, the workshop style sessions, allow participants to work on synergistic topics of their choice, or to exchange know-how, tools and algorithms with the other participants.

The Bioinformatics Hub operates under an open door policy, and that anyone is free to walk in at any time and participate in the work or the discussions, ask a question of someone, or just listen in on what is going on! The bioinformatics hub is meant to be inclusive, low threshold, and aimed at knowledge exchange across all levels of experience.

## Hashtags for Twitter

#BioinformaticsHub #HUPO2019

## Bioinformatics Hub Schedule

### Monday September 16

#### 08h30–10h00: Session #1

**Draft MassIVE input into HPP**  
(Nuno Bandeira, UCSD)

#### 10h30–11h00: Session #2a

**How to contribute to the C-HPP wiki**  
(Peter Horvatovich, Univ. of Groningen)

#### 11h00–12h30: Session #2b

**Stranded and Singleton Peptides**  
(Tadashi Yamamoto, Niigata University;  
Gil Omenn, U Michigan)

#### 12h30–14h00: Lunch break

#### 14h00–15h15: Session #3

**Human Membrane Proteome  
Tryptic Peptide Predictor**  
(Subash Adhikari, Macquarie University)

#### 15h15–17h15: Session #4

**Current advances in DIA data analysis**  
(Brian Searle, ISB)

#### 17h15–19h15: Session #5

**HPP Data Interpretation Guidelines 3.0**  
(Eric Deutsch, ISB) bioRxiv

### Tuesday September 17

#### 08h30–10h00: Session #6

**Quantifying the impact of public omics data**  
(Henning Hermjakob, EBI,  
Juan Antonio Vizcaíno, EBI)

#### 12h30–14h00: Lunch break

#### 14h00–15h15: Session #8

**SPARQL hands-on session**  
(Lydie Lane, SIB)

#### 15h15–16h00: Session #9a

**The need for bioinformatics tools  
in clinical settings**  
(Ferdinando Cerciello,  
University Hospital of Bern, Inselspital)

#### 16h00–17h15: Session #9b

**Computational predictions for uPE1  
protein functional annotation with  
I-TASSER and COFACTOR**  
(Gil Omenn, U Michigan; Lydie Lane, SIB;  
Chengxin Zhang, U Michigan; Yang Zhang,  
U Michigan)

#### 17h15–18h30: Ask the Experts session

### Wednesday September 18

#### 08h30–10h00: Session #10

**MS Pillar 96-phosphopeptides  
standard assay results**  
(Sue Weintraub, UTHSCSA;  
Michael Hoopmann, ISB)

#### 10h00–11h00: Session #11

**EuBIC (European Bioinformatics Community)  
Intro, discussion, developers meeting**  
(Julian Uszkoreit, Uni. Bochum;  
Tim Van Den Bossche, Ghent Univ.)

#### 11h00–12h00: Session #12

**Emerging PSI Standards: PEFF,  
USI, PROXI, SpecLib format**  
(Eric Deutsch, ISB, Juan Antonio Vizcaíno, EBI,  
Nuno Bandeira, UCSD, Luis Mendoza, ISB)

### Special Interest Topics to be scheduled

**HPP Data Interpretation Guidelines 3.0**  
(Eric Deutsch, ISB) bioRxiv

#### EuBIC session

(Julian Uszkoreit, Uni. Bochum;  
Tim Van Den Bossche, Ghent Univ.)

#### Human Membrane Proteome Tryptic Peptide Predictor

(Subash Adhikari, Macquarie University)

#### MS Pillar 96-phosphopeptides standard assay results

(Sue Weintraub, UTHSCSA)

#### Computational predictions for uPE1 protein functional annotation with I-TASSER and COFACTOR

(Gil Omenn, U Michigan)

#### Stranded and Singleton Peptides

(Tadashi Yamamoto, Niigata University;  
Gil Omenn, U Michigan)

**SPARQL hands-on session**  
(Lydie Lane, SIB)

**Draft MassIVE input into HPP**  
(Nuno Bandeira, UCSD)

#### PSI Standards in progress: PEFF, USI, SpecLib, PROXI

(Eric Deutsch, ISB; Juan Antonio Vizcaíno, EBI;  
Nuno Bandeira, UCSD, Luis Mendoza, ISB)

### Attending Organizers

- Eric Deutsch
- Juan Antonio Vizcaíno
- Lydie Lane
- Nuno Bandeira
- Henning Hermjakob
- Sandra Orchard
- EuBIC (proteomics-academy.org)
- Julian Uszkoreit
- Tim Van Den Bossche

### Ask the Experts

- Brian Searle
- Sandra Orchard
- Luis Mendoza

### Other Confirmed Participants

- Gil Omenn
- Luis Mendoza
- Subash Adhikari
- All others are welcome!



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## Poster Listings

### Poster Session 1 6:00PM – 7:15PM Hall H

**Jodie L Abrahams**  
Metastatic melanoma model  
system selection: implications  
for glyco-marker discovery  
**abs# 401**

**Brahim Achour**  
The Molecular Stethoscope:  
RNA of drug metabolising  
enzymes in circulating vesicles  
correlates with their specific  
protein content in the liver  
**abs# 402**

**Jun Adachi**  
System-wide characterization  
of esophageal squamous  
cell carcinoma cells by  
phosphoproteome analysis.  
**abs# 403**

**Subash Adhikari**  
Many multi-transmembrane  
domain-containing proteins  
can't conform to current  
high-stringency MS metrics  
solely after tryptic digestion  
**abs# 404**

**Eman Ahmed**  
Metabolomics Spectral Libraries  
for data-independent SWATH  
Liquid Chromatography-Mass  
Spectrometry Acquisition  
"SASA, a Novel SWATH Based  
Metabolomics tool" **abs# 405**

**Javed Akhtar**  
Autoantibody response against  
tumor-associated antigens in  
gallbladder carcinoma using  
immunoproteomics approach  
**abs# 406**

**Kazunari Akiyoshi**  
Glycan profiling on extracellular  
vesicles surface using  
evanescent-field fluorescence-  
assisted lectin array for  
biomarker discovery **abs# 407**

**Cristina Al-Khalili Szgyarto**  
Antibodypedia reveals trends  
in antibody validation **abs# 408**

**Kathirvel Alagesan**  
SynGp one-stop shop: synthetic  
glycopeptides assisted  
glycoproteomics **abs# 409**

**Dalal Alonazy**  
Analysis of proteome and  
phosphoproteome in response  
to higher temperatures in rice  
cultivars **abs# 410**

**Sandra I. Anjo**  
A different perspective of  
circulatory biomarker discovery  
in neurodegenerative diseases:  
combined use of alternative  
proteomics analyses to create  
a comprehensive "proteomics  
signature of the blood"  
**abs# 411**

**Brendan R. E. Ansell**  
Automated quality assessment  
for genome-wide protein  
structure prediction **abs# 412**

**Norie Araki**  
Integrated phospho-glycomics  
identified specific target  
networks of cancer stem  
cells **abs# 413**

**Ritchlynn Aranha**  
Novel sources of peptide  
antigens in the melanoma  
immunopeptidome **abs# 414**

**Alexander Archakov**  
Proteomics on the way to  
reverse Avogadro number  
as basis of precision medicine  
**abs# 415**

**Stuart D Armstrong**  
Plasma proteomic profiling  
of patients with haemorrhagic  
fever with renal syndrome  
from puumala and dobrava  
hantavirus infections **abs# 416**

**Tabiwang N. Arrey**  
Performance evaluation of a  
the new Orbitrap Exploris 480  
mass spectrometer **abs# 417**

**Deanna Ayupova**  
Unrevealed mystery of  
cell dust:extracellular vesicles  
and tumor-derived exosomes  
**abs# 418**

**Ali Azimi**  
SWATH-MS proteomic analysis  
can discriminate between  
actinic keratosis, Bowen's  
disease and cutaneous  
squamous cell carcinoma  
**abs# 419**

**Mahya Bahmani**  
Physiological and proteomic  
changes to heat and water  
stress in soybean leaf **abs# 420**

**Mark S. Baker**  
SWATH library construction  
including recombinant  
proteins allows identification  
and quantification of lower  
abundance human plasma  
cancer biomarkers **abs# 421**

**Nuno Bandeira**  
BloodKB: an open community-  
scale knowledge base for  
plasma proteome diversity  
**abs# 422**

**Dmitry Bandura**  
Analytical validation of  
run-to-run and site-to-site  
performance of a human  
immune profiling assay and  
automated data analysis  
solution for CyTOF mass  
cytometry technology  
**abs# 423**

**Geul Bang**  
DeepY: A deep learning model  
for biosimilarity evaluation  
of antibody drug using intact  
glycoproteins analysis by LC-  
MS **abs# 424**

**Craig Barry**  
Modelling life and death in  
mammalian cells to generate  
rational engineering strategies  
**abs# 425**

**Pragya Barua**  
Dehydration-responsive  
nuclear proteome and  
phosphoproteome profiling  
of a grain legume chickpea  
(*Cicer arietinum* L.) **abs# 426**

## Poster Listings

### Amani Batarseh

Enhancing extracellular vesicle isolation of human plasma verified by high resolution lipidomics **abs# 427**

### Mike Baynham

Powerful, standardized and versatile low-flow LCMS platform for deep dive proteomics and high-throughput analysis with maximum MS utilization **abs# 428**

### Aiden Beauglehole

Understanding complex post-translational modifications in CHO cells **abs# 429**

### Fiona Bicknell

Establishing the proteomic profile of human neuroblastoma cells during neuronal differentiation **abs# 430**

### Steve Binos

Improved middle-down characterization of antibodies using multiple ion activation techniques and Proton Transfer Charge Reduction on an Orbitrap Eclipse mass spectrometer **abs# 431**

### Alyson P Black

Antibody Panel Based N-glycan imaging of patient serum for cancer biomarker discovery **abs# 432**

### Jonathan Blackburn

Proteomic analysis of cellular secretory responses in a human lung-challenge model of tuberculosis disease **abs# 433**

### Jonathan Blackburn

Predicting immunotherapy treatment outcomes in melanoma patients **abs# 434**

### Jonathan Blackburn

Sub-lethal Rifampicin effects on the Mycobacterium smegmatis cell wall and on survival in macrophage infection models **abs# 435**

### Sascha Blankenburg

Enhanced protein identification using harsh cell disruption combined with bead-based protein preparation (SP3-protocol) in a Legionella pneumophila cell culture infection model **abs# 436**

### Jude J Bond

Proteins co-ordinating cell permeability and nutrient transport in the rumen epithelium of sheep. **abs# 437**

### Eva Borràs

Protein-based Cardiogenic Shock Patient Classifier **abs# 438**

### Utpal Bose

Understanding the storage protein biosynthesis and protein compensation in hordein double-null barley lines using SWATH mass spectrometry **abs# 439**

### Matthew T Briggs

Differential Glycosylation and Novel N-Glycan Site Analysis of ECM Proteins in Gynaecological Cancers **abs# 440**

### Scott Bringans

PromarkerD as an immunoaffinity mass spectrometry assay for diabetic kidney disease **abs# 441**

### Ann Brinkmalm

Synaptic dysfunction investigated in clinical cohorts by immunoprecipitation/mass spectrometry. **abs# 442**

### Gunnar Brinkmalm

Identification of covalently cross-linked A $\beta$  dimers in Alzheimer's disease brain by combining top-down and bottom-up mass spectrometry **abs# 443**

### Daniel A Broszczak

Proteome survey of wound fluid from non-healing wounds reveals key biological processes associated with poor healing outcomes **abs# 444**

### Richard Burchmore

A polyomic approach to understand the molecular basis of virulence in Leishmania **abs# 445**

### Keren Byrne

Applying LC-MS/MS to provide insights into eukaryotic nitrogenase engineering **abs# 446**

### Xue Cai

Pulse Data Independent Acquisition (PulseDIA) on Orbitraps for deeper proteomic profiling with relatively small sample consumption **abs# 447**

### Joel Cain

Identification of novel N-glycosylation sites from the bacterium Campylobacter jejuni **abs# 448**

### Joel Cain

Proteomics reveals multiple phenotypes associated with N-linked glycosylation in Campylobacter jejuni **abs# 449**

### Weiqian Cao

A comprehensive O-glycoprotein repository to facilitate O-glycosylation study **abs# 450**

### Tom TC Carew

Uncoupling the mechanisms of protein degradation **abs# 451**

### Annalisa Carli

DCLK1: a novel promoter of gastric cancer progression **abs# 452**

### Morgan Carlton

Monitoring Physical Healing and Psychological Wellbeing in Paediatric Burns through Proteomic Analysis of Saliva. **abs# 453**

### Rahul Chakraborty

Role of NCL1 in Cysteine induced toxicity **abs# 454**

### Zoon Chan

An Orbitrap Eclipse Tribrid mass spectrometer with real time search enhances multiplexed proteome coverage and quantitation accuracy. **abs# 455**

### Ian Yi-Feng Chang

AWVP: An automated workflow for variant peptide production **abs# 456**

### The Huong Chau

Circadian rhythm impacts the synaptic glycosylation machinery but not the N-glycosylation signatures in mice brains **abs# 457**

### Safee Chaudhary

PERCEPTRON - An Open-source GPU Accelerated Proteoform Identification Pipeline for Top-Down Proteomics **abs# 458**

### Chao-Jung Chen

Protein Biomarker Discovery for the identification of Methicillin-sensitive, heterogeneous Vancomycin-Intermediate and Vancomycin-Intermediate Staphylococcus aureus Strains by Data-Independent Acquisition Quantitative Proteomics **abs# 459**

### Ching-Tai Chen

WinProphet: a user-friendly pipeline management system for proteomics data analysis based on Trans-Proteomic Pipeline **abs# 460**

### Emily Chen

Scalable and Automated Plasma Workflow Based on the Thermo Scientific Q Exactive HF-X MS Platform **abs# 461**

### Gary G Chen

High-efficiency and low-cost production of pure home-brew Tn5 transposase protein and its application in the development of novel single cell resolution Next Generation Sequencing (NGS) methods. **abs# 462**

### Lei Chen

The Chinese immunopeptidome project and a platform for validation of naturally presented HLA-binding peptides **abs# 463**

### Sixue Chen

Proteomic and phosphoproteomic networks of Arabidopsis stomatal immune responses **abs# 464**

### Yanfeng Chen

Phosphoproteomics for Identification of Activated Signalling Pathways in Breast Cancers **abs# 465**

### Yet-Ran Chen

Study of plant systemic migrating proteins in response to nitrate, phosphate, and potassium deficiency using quantitative proteomics approach **abs# 466**

### Yi-Ju Chen

Proteogenomics landscape of early-stage lung adenocarcinoma patients identifies stratification hallmarks of early onset and progression **abs# 467**

### Heung-Chin Cheng

Quantitative N-terminomic and phosphoproteomic analyses of primary neurons and rodent models of neurotoxicity reveal distinct signalling networks governing neuronal death in excitotoxicity **abs# 468**

### Anastasia Chernykh

Site-Specific Glycoproteomics of Recombinant Human Corticosteroid-Binding Globulin **abs# 469**

### Jimmy Ka-Wai Cheung

Efficient sample preparation of human tears proteomic workflow using S-Trap™ **abs# 470**

### Lang-Ming Chi

Profiling the membrane and secretory proteomes to discover the signaling drives the malignancy of oral cavity cancers **abs# 471**

### Yasunori Chiba

MUC1 glycopeptides by chemoenzymatic synthesis revealed distinct specificities of anti-MUC1 antibodies **abs# 472**

### Chiew Foan Chin

Quantitative iTRAQ-based proteomic analysis of exogenous cytokinin induced callus and protocorm-like bodies (PLBs) formation from the root tips of Vanilla planifolia **abs# 473**

### Cristina Chiva

ImCal: Internal calibration curves for accurate quantitation in clinical proteomics. **abs# 474**

### Hyungwon Choi

MetaboKit: a comprehensive data processing workflow for DDA and DIA-MS data in untargeted metabolomics **abs# 475**

### Phil M Choi

Social, economic and demographic correlates of drug and food consumption identified by wastewater-based epidemiology **abs# 476**

### Seunghyuk Choi

Proteogenomic approach to UTR peptides identification **abs# 477**

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### Booth 37, 38, 39, 40

Bruker is enabling scientists to make breakthrough discoveries and develop new applications that improve the quality of human life. Bruker's high-performance scientific instruments and high-value analytical and diagnostic solutions enable scientists to explore life and materials at molecular, cellular and microscopic levels.

In close cooperation with our customers, Bruker is enabling innovation, improved productivity and customer success in life science molecular research, in applied and pharma applications, in microscopy and nanoanalysis, and in industrial applications, as well as in cell biology, preclinical imaging, clinical phenomics and proteomics research and clinical microbiology.

Bruker Daltonics, a division of the Bruker Corporation, provides cutting edge mass spectrometry solutions which include MALDI-TOF, UHR-QTOF, Ion Traps, FTMS as well as LC and GC systems to solve the most demanding analytical questions presented to these markets today.

For more information, please visit: [www.bruker.com](http://www.bruker.com).

## Evosep

### Booth 36

Evosep aims to improve quality of life and patient care by radically innovating protein based clinical diagnostics. Making sample preparation and separation before MS analysis 10 times faster and 100 times more robust will enable truly large cohort studies for biomarker validation and provide the foundation for precision medicine.

## Fluidigm

### Booth 30

*Deliver new insights in health and disease*

Improving life. It's what drives us each day. That's why we provide multi-omic solutions to study cancer, inflammatory diseases and immunotherapies in transformative new ways. Harnessing the power of CyTOF® and microfluidics technologies, we empower our customers to uncover new insights in health and disease, identify meaningful biomarkers and accelerate therapeutic development.

## HPOP

### Booth 24

Stanford University's Human Personalized Omics Profiling (hPOP) project studies the variance of omics profiles (proteome, genome, metabolome, microbiome and more) across a large number of participants. These measurements could be potentially used to diagnose disease early, monitor treatment progression and personalize healthcare. The hPOP project launched at the 2016 HUPO in Taipei.

## HUPO 2020

### Booth 33

The 19th Human Proteome Organization World Congress, HUPO 2020 will be held 18 Oct - 22 Oct 2020 in Stockholm, Sweden. The Swedish Proteomics Society and the Swedish Pharmaceutical Society cordially invite proteomic researchers from around the globe to attend this all-encompassing symposium on the latest proteomic research and technology.

## IonOpticks

### Booth 1

IonOpticks' high-performance plug-and-play nano capillary columns with integrated emitter tip are used by proteomics researchers globally. Our innovative columns provide a unique ability to enhance the sensitivity of biological sample analysis, enabling scientists to achieve over 25% more protein identifications than similar commercially available solutions.

## Korea Basic Science Institute

### Booth 19

Korea Basic Science Institute (KBSI) performs a role as a national institute with the world-class basic research infrastructure leading the innovation of research facilities and equipment.

Now, we are introducing a software tool (IQ-GPA) developed for identification and quantification of intact N- and O-linked glycopeptides from mass spectrometry data.

## Mass Dynamics

### Booth 4

Built for the #massgeek masses, we accelerate discoveries by intersecting smart data science, progressive technology, global knowledge and thoughtful design. Our intelligent research assistant removes typical pain points by encouraging straight-forward yet in-depth analysis, guiding quality control and standardising workflows. All while making the experimental process iterative, collaborative and fun.

## Mimotopes

### Booth 20

Mimotopes is 30 years a peptide synthesis industry leader.

Our one stop shop online offers:

- Custom peptides
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- Assay services
- Peptide arrays
- Off-the-shelf libraries
- Reagents
- Catalogue peptides
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## Molecular & Cellular Proteomics

The journal Molecular & Cellular Proteomics (MCP) fosters the development and applications of proteomics in both basic and translational research. It showcases cutting-edge advances in proteomics, metabolomics and informatics. The American Society for Biochemistry and Molecular Biology publishes MCP. Visit [www.mcponline.org](http://www.mcponline.org).



## Exhibitor Listings

### Oink Proteomics

#### Booth 9

Oink Proteomics provides the most efficient tool available for targeted human protein biomarker discovery & development, with high-throughput analysis, exceptional data quality, and minimal sample consumption. Disease/biology-focused panels allow rapid analysis of over 1,100 validated protein biomarkers with <15 QI of sample using kits or our Analysis Service.

### Peak Scientific

#### Booth 23

Peak Scientific is the market-leading nitrogen, hydrogen and zero air gas generator manufacturer for specialty laboratory equipment.

Our gas generators are safe, cost-effective alternative to cylinders and liquid Nitrogen. Our forte is providing hassle free; high quality, dependable gas without on-going gas delivery fees, decreasing environmental and safety concerns.

### PharmaFluidics

#### Booth 26

PharmaFluidics introduces the silicon revolution in liquid chromatography. The micro-Chip Pillar Array (QPAC™) column overcomes the physical limits of any packed bed alternative. The QPAC™ columns feature a perfectly ordered separation bed of free-standing pillars ensuring excellent separation power, unprecedented reproducibility and unrivalled robustness.

Whether you are analyzing trace amounts of compounds in complex biological samples for proteomics, metabolomics or lipidomics, or whether you are looking for subtle modifications in monoclonal antibodies: use plug-and-play QPAC™ columns to boost your biomarker and life sciences research. Our QPAC™ columns are compatible with all standard nano-LC equipment.

### Proteoform Scientific

#### Booth 34

Proteoform Scientific is empowering researchers with new technology to simplify protein sample preparation in both top-down and bottom-up proteomics. The ProTrap XG is a disposable cartridge that provides fast, reproducible and robust results. In just minutes, the ProTrap XG delivers unmatched protein purity of 99.5% and recovery greater than 95%.

### Proteomics International

#### Booth 29

Founded in 2001, Proteomics International is a medical technology company at the forefront of predictive diagnostics and bioanalytical services. Activities include the research into diagnostic tests for chronic diseases with an unmet medical need (PromarkerD for diabetic kidney disease); and providing ISO17025 accredited analytical services to industry and the research community.

### SCIEX

#### Booth 35

SCIEX provides a range of innovative instruments, software and reagents to help you examine the proteome more completely, addressing all needs across the research pipeline. Decades of innovative LC/MS/MS and CE solutions enable scientists around the world to find deeper insights in discovery proteomics, targeted peptide quantitation, lipidomics, metabolomics and protein characterization. We deliver technology at the leading edge of protein research to unlock knowledge to help advance your work. For information visit [www.sciex.com](http://www.sciex.com).

### Sengenics

#### Booth 27

Sengenics is a functional proteomics company that leverages its patented KREX technology for production of full-length, correctly folded and functional proteins. Invented at the University of Cambridge, the key application of KREX is autoantibody biomarker discovery for patient stratification and diagnosis of cancer, autoimmune or neurodegenerative conditions.

### Shimadzu Scientific Instruments

#### Booth 17, 18

Our products and solutions serve the research community and analysts in diverse fields such as chemistry, molecular biology, medical science environmental analysis and industry. It has resulted in our leadership in spectroscopy, chromatography, mass spectrometry, environmental analysers, medical systems, aircraft equipment, semiconductors and flat panel display equipment. Our Excellence is proven in the Science, Shimadzu.

### Synpeptide

#### Booth 7

Synpeptide is a leading provider of innovative peptide-based product & services, ranging from custom peptides, isotope labeled peptides, peptide library and peptide modifications, etc. Synpeptide's monthly capacity reaches >30,000 purified custom peptides. Global market share has been over 30%.

### Tecan Australia

#### Booth 10

Tecan is a leading global provider of automated laboratory instruments and solutions. Our systems and components help people working in clinical diagnostics, research and analytics bring their science to life.

In particular, we develop, produce, market and support automated workflow solutions that empower laboratories to achieve more.

We work side by side with a range of clients, including diagnostic laboratories, pharmaceutical and biotechnology companies and university research centres. Whatever the project - large or small, simple or complex - helping our clients to achieve their goals comes first.

### ThermoFisher Scientific

#### Booth 13, 14, 15, 16

Thermo Fisher Scientific is the world leader in serving science. Our mission is to enable our customers to make the world healthier, cleaner and safer. Through our Thermo Scientific brand, we help customers accelerate innovation and enhance productivity.

Thermo Fisher Scientific supplies innovative solutions for the world's proteomics community in academic research, clinical translational medicine, and pharmaceutical/ and biotech industries. With applications that span the mass spectrometry based proteomics and protein analysis workflows- we provide a broad range of products and services that support leading edge biological research from disease and biomarker discovery, drug development and clinical research.

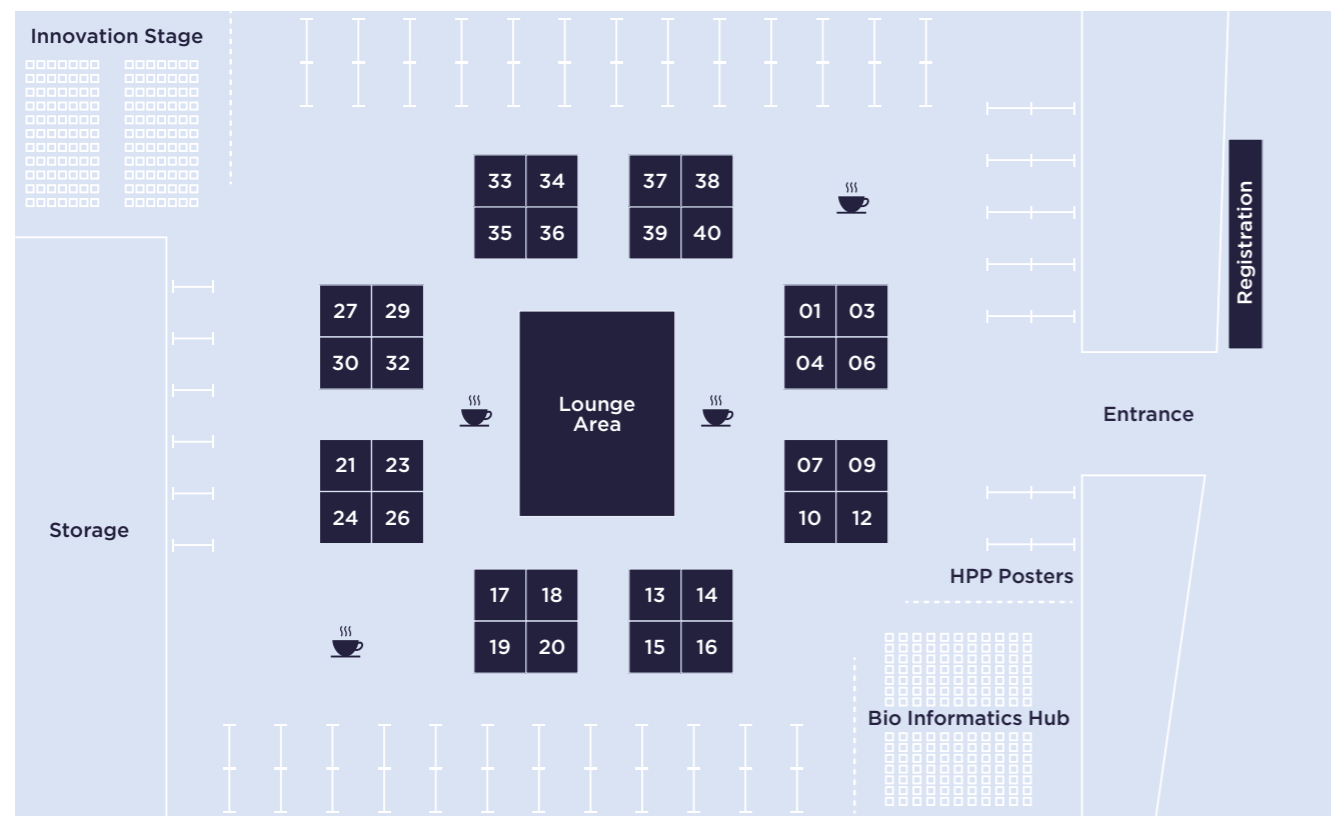
### Waters Corporation

#### Booth 32

Waters Corporation creates business advantages for laboratory-dependent organizations by delivering scientific innovation to enable customers to make significant advancements. Waters helps customers make profound discoveries, optimize laboratory operations, deliver product performance, and ensure regulatory compliance with a connected portfolio of separations and analytical science, laboratory informatics, mass spectrometry, as well as thermal analysis.



# HUPO 2019 Floor Plan



# Join us at the 25th Annual Lorne Proteomics Symposium, Cumberland Resort 6th – 9th of February 2020

*"Celebrating the silver jubilee of Proteomics in Australia"*

## Confirmed Invited Speakers

Professor Matthias Trost  
Newcastle University

Dr Stacy Malaker  
Stanford University

Dr Philipp Geyer  
Max Planck Institute of Biochemistry

Professor Anne-Claude Gringas  
Newcastle University

Dr Ben Collins  
University of Belfast

Professor Robert Moritz  
Institute for Systems Biology

Associate Professor Judit Villen  
University of Western Australia

Martin Krzywinski  
Canada's Michael Smith Genome  
Sciences Centre

Kylie Bemis  
Northeastern University

# HUPO 2019

Transition from basic research to translational research



## Program

**Booth  
#37-40**

Lunch Symposium: DIA with near 100% Ion Usage: Introducing diaPASEF on the timsTOF Pro

**Monday, September 16, 2019**

In this workshop the use of a new scan mode called diaPASEF will show how virtually all of the peptide ions can be covered with highly efficient usage of the ions present. Dr. Gary Kruppa will present a brief introduction to the diaPASEF method. Then, one of Bruker's featured speakers, Prof. Ruedi Aebersold will present a talk on "SWATH/DIA Proteomics and its Role in Biology".

Lunch Symposium: Clinical Research Applications of the timsTOF Pro

**Tuesday, September 17, 2019**

After a brief introduction to the unique features of the timsTOF Pro with PASEF, by Dr. Gary Kruppa, Prof. Catherine Wong will present a talk on "Mapping the Q-glycoproteome Using the timsTOF Pro". Following this Prof. Andrew Webb will speak on, "High throughput Proteomics on the timsTOF Pro: Applications to clinical research and beyond".

Breakfast Workshop: Tools for high productivity proteomics: timsTOF Pro, Evosep One and MaxQuant

**Tuesday, September 17, 2019**

In this workshop the combination of the Evosep One, a highly robust microflow LC system, with the timsTOF Pro will be presented by Dr. Nicolai Bache of Evosep, with the title, "High productivity proteomics with the timsTOF Pro and Evosep One." Then Prof. Juergen Cox of the Max Planck Institute in Martinsried, Germany will present on recent developments for getting the most out of such data, with the title, "Unlocking the power of the fourth dimension: MaxQuant for timsTOF Pro."

Innovation with Integrity

Proteomics

For more information please visit [www.bruker.com](http://www.bruker.com)

## Key Dates

Abstract Submission Deadline  
Friday 18th October 2019

Early Bird Registration Deadline  
Sunday 15th November 2019

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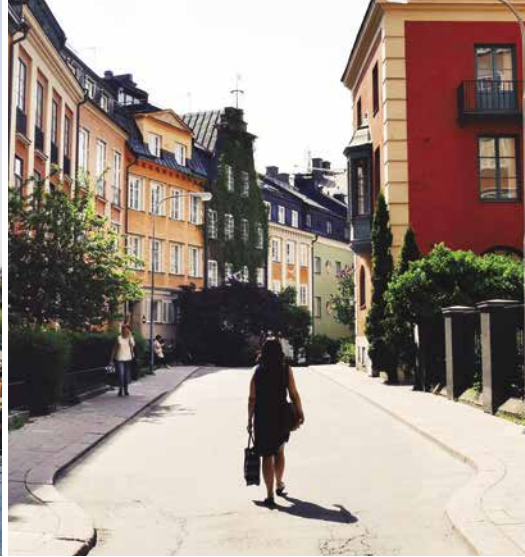
Walter+Eliza Hall  
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For more information, please visit our website:

<https://www.australasianproteomics.org/25th-annual-lorne-proteomics-symposium-2020>





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October 18 - 22, 2020

[www.hupo2020.org](http://www.hupo2020.org)



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19<sup>th</sup> Human Proteome Organization World Congress