Congress Handbook
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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Be surprised!

For more information: www.adelaideconvention.com.au
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 organizations 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 makeup 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)
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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
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/

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 ‘Curinda’ 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.

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

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.

• Monday 16th September, 8:00am – 7:30pm
• Tuesday 17th September, 7:30am – 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.

• Monday 16th September, 8:00am – 1:30pm
• Tuesday 17th September, 8:00am – 1:30pm
• Wednesday 18th September, 8:00am – 1:30pm

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

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
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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

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, Minneapolis, 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

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

Zhixin Tian
Tongji University, Shanghai, China

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

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

Melanie White
University of Sydney New South Wales, Australia

Bernd Wollscheid
ETH Zurich, Zurich, Switzerland

Zhixin Tian
Tongji University, Shanghai, China

Bing Zhang
Baylor College of Medicine, Texas, USA

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

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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)

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 postdoctoral 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)

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.
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 pharmaceutical 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 underpinning cystic fibrosis research, as well as her work on Alzheimer's disease.

John R. Yates III
Scripps Research Institute, USA

Professor Yates has significantly contributed to advances in proteomics and protein biochemistry throughout his 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 FS508 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 proteomics company. 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 oriented 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).

Sponsored by Institute for Systems Biology, USA

Robert Moritz
Institute for Systems Biology, USA

Dr. Moritz is a world leader in proteomics methods development with a focus on mass-spectrometry applications towards comprehensive proteome quantification and software development for the analysis of Big Data from these comprehensive resources. His group has developed both comprehensive 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 wider 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 similar congresses organized by HUPO. He is responsible for ensuring that 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 is dedicated with several companies to provide resources to enable HUPO members to freely participate in the HPP Phosphoproteome 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.
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 $3,000 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 predict mitochondrial protein phosphorylation and developed targeted proteomics workflows to quantify mitochondrial protein phosphorylation events. 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. Secondly, proteomics has the advantage of assaying secreted proteins in an accurate and unsupervised manner. Lastly, the flow of information in the dogma of biology can differ as genomics clusters converge to different proteomic clusters. 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.

Ankit Sinha

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 oncopgenes. 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 basis for 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 Welcome 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.

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 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/Early Career Researcher Travel Awards to support their participation at this year’s World Congress to be held in Adelaide, Australia from 15-19 September, 2019. We wholeheartedly congratulate these worthy recipients and look forward to welcoming you all to Adelaide.

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 process- and/or disease-relevant proteins2.

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 (Germany)
Christian Hentschker (Germany)
Antonia Pries (Netherlands)
Nadine Prust (Netherlands)
Louise Schelleter (Austria)
Jan Stöckl (Austria)
Julian Uszkoreit (Austria)
Julia Voll (Austria)

Japanese Proteomics Society (JPrOS) and HUPO 2019

Yuma Inamori (Japan)
Kaori Konno (Japan)
TomoYa Niinae (Japan)

Proteomics Society of India (PSI) and HUPO 2019

Hwangkyo Jeong (South Korea)
Hyeryeon Jung (South Korea)
Chae-Young Kim (South Korea)
HanByeal Kim (South Korea)
Dabin Lee (South Korea)
Jua Lee (South Korea)
Nari Seo (South Korea)
Seojin Yang (South Korea)
Jeonghun Yeom (South Korea)
Jiyoung Yu (South Korea)

Proteomics Society of India (PSI) and HUPO 2019

Javed Akhtar (India)
Arumina Sinha (India)
Boomathi Pandi (India)
Rahul Chakraborty (India)
Pragya Barua (India)

Singapore Society for Mass Spectrometry and HUPO 2019

Ian Loke (Singapore)
Wint Wint Phoo (Singapore)

Swiss Proteomics Society and HUPO 2019

Maik Müller (Switzerland)
Kathrin Nowak (Switzerland)
Fabian Wendt (Switzerland)

US-HUPO and HUPO 2019

Natan Basisty (USA)
Hiroki Koh (USA)
Xueshu Xi (USA)
Matthew Waas (USA)

HUPO 2019 Student/ ECR Travel Award Winners

Anna Andrejeva (UK)
Sandra Anjo (Portugal)
Christopher Ashwood (USA)
GL Balasubramani (India)
Ieva Bagdonasite (Denmark)
Kevin Erzo Castillo (USA)
Josie Christopher (UK)
David Clark (USA)
Alana Costa (Brazil)
Simon Davis (UK)
Benedict Dinberger (UK)
Penchat Diskul-Na-Auythayha (Thailand)
Mohamed Elizek (UK)
Sofie Farkona (Canada)
Andrea Fossati (Switzerland)
Anders Garlid (USA)
Ana Gill de Bona (USA)
Tianqi Gong (USA)
Andreas Hober (Sweden)
Yajun Hu (China)
John Janetzkio (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 Garief (South Africa)
Kanika Narula (India)
Jessica Nickerson (Canada)
Aya Osama (Egypt)
Matthys Potgieter (South Africa)
Rashmi Rana (India)
Divya Rathi (India)
Sushant Sadotra (Taiwan)
Catia Sant (Portugal)
Darien Schell (South Africa)
Wenguang Shao (Switzerland)
Ankit Sinha (Germany)
Sedighheh Shokri (Iran)
Margaret Simonian (USA)
Elizaveta Solovyeva (Russia)
Arun Tailer (UK)
Denise Utami Putri (Taiwan)
Tim Van Den Bossche (Belgium)
Valeria Vezzinčnik (Slovenia)
James Waddington (UK)
Ke Wang (China)
Churat Weerasap (Thailand)
Mengxi Wu (China)
Juanjuan Xie (China)
Yueting Xiong (China)
Junyue Xu (China)
Hailun Yang (China)
Yi Yang (China)
Yameng Zhang (China)

Australian Proteomics Society (APS) Student/ ECR Travel Award Winners

Subash Adhikari (Sri Lanka)
Kathirvel Alagesan (Sri Lanka)
Ritchlynn Aranha (Brazil)
Deanna Ayupova (Canada)
Ali Azimi (Australia)
Craig Barry (Australia)
Tara Bartolec (Australia)
Fiona Bicknell (Australia)
Joel Cain (Australia)
Sayantani Chatterjee (Australia)
Yanfang Chen (China)
Phil Choi (Australia)
Ashleigh Dale (Australia)
Keshava Datta (India)
Mirza Butt (Canada)
Daniela Espina (Switzerland)
Sophia Escobar-Correas (Australia)
Dilanka Fernando (Australia)
Shahid Go (Australia)
Joshua Hamy (Australia)
Dylan Hamy (Australia)
Daniella Hock (Canada)
Ashfaqul Hoque (Bangladesh)
William Klaire (Australia)
Naomi Koh Belic (Australia)
Rebecca Lane (Australia)
Chen Li (China)
Desmond Li (Australia)
Terry Lim Kam Sian (Australia)
Shivraj Lingam (India)
Eylene Maes (Australia)
Lok Man (Australia)
Shutao Mei (Australia)
Sonali Mohan (Australia)
Heather Murray (Australia)
Ellie Needham (Australia)
Elizabeth Nguyen (Australia)
Mitchell Nye-Wood (Australia)
Kirit Panda (Australia)
Selvam Paramasivam (Australia)
Cassandra Pegg (Australia)
Ruby Pelson (Australia)
Toan Phung (Australia)
Rebecca Poulos (Australia)
Md Ariful Rahman (Bangladesh)
Laura Rantanen (Australia)
Halley Ravuri (Australia)
Harley Robinson (Australia)
Alexander Rookyard (Australia)
Katherine Scull (Australia)
Ryan Separovich (Australia)
Mohammad Shahbazi (Australia)
David Skerrett-Byrne (Australia)
Daniela Lee Smith (Australia)
Nestor Solis (Australia)
Joel Steele (Australia)
Pascal Steffen (Australia)
Arineh Tahmasian (Australia)
Xinle Tan (Australia)
Zeynep Sumer-Bayraktar (Australia)
Julie Webster (Australia)
Bradley Wright (Australia)
Rebekah Ziegman (Australia)
## Program at a Glance

**Sunday, 15th September 2019**

<table>
<thead>
<tr>
<th>Room</th>
<th>Hall E1</th>
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Wednesday, 18th September 2019

**Room**

**Hall E1**  **Hall E2**  **Hall E3**  **Hall B**  **Hall A**  **Hall C**

<table>
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<th>Time</th>
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<tr>
<td>8:30</td>
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<td>Plenary 9</td>
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<td>Plenary 10</td>
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**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
  - New Technologies: New Technologies in Proteomics (HUPO IAB)
- Theme 1
  - Health and Disease: Cardiovascular and Metabolic Disease
- Theme 2
  - Biological Application of the Proteome: The Interactome
- Theme 3
  - Beyond the Proteome: Metabolomics and Lipidomics
- Theme 4
  - Moving proteomics into pharmaceutical discovery and application
- Theme 5
  - Chemical Proteomics
- Theme 6
  - Enabling Technologies: Chemical and Clinical Proteomics

**More Information**

- **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

- **Sponsored Symposia**
  - NEUROLOGY
  - IMMUNO-ONCOLOGY
  - CARDIOVASCULAR
  - and many more...

- **Visit us @ Booth #35 to enter the Virtual World of Scanning SWATH**
  - sciex.com/vipscanningswath

- **HUPO 2019 Awards Ceremony**
- **Plenary 10 Mike Snyder**
- **Closing Ceremony & HUPO 2020 Introduction**
### 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

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

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#### 16th September 2019

**ECR Initiative Meet and Greet**
7:15AM – 8:00AM Room E1

**Plenary 3**
8:00AM – 8:30AM Halls A & C
8:30AM
Fuchu He
Proteomics driven precision medicine for the early-stage hepatocellular carcinoma abs# 3

**Plenary 4**
8:30AM – 9:15AM Halls A & C
9:15AM
Nicolle H. Packer
The elephant in the room: glycomics and glycoproteomics abs# 4

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

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

**Post-Translational Modifications I**
10:40AM – 12:00PM Hall A
10:40AM
Chuna Choudhury
Proteomic analysis of lysine acetylation dynamics and stoichiometry in human disease abs# 5

**Plenary 5**
10:40AM – 12:00PM Room E1
10:40AM
Marius Ueffing
Gene editing based analysis of functional protein networks in human disease abs# 6

**Morning Tea & Poster Viewing**
11:15AM – 11:45AM Hall H

**Plenary 2**
11:45AM – 12:30PM Room E2
11:45AM
Birgit Schilling
Proteomic Tools to Decipher Mechanisms of Senescence in Aging and Age-related Diseases abs# 7

**Morning Tea & Poster Viewing**
12:30PM – 1:00PM Hall H

**Plenary 3**
12:00PM – 1:15PM Room E1
12:00PM
Michael L. Nielsen
Systems-wide analysis of ADP-ribosylation in human cells using quantitative mass spectrometry abs# 8

**Morning Tea & Poster Viewing**
1:15PM – 1:45PM Hall H

**Plenary 4**
1:45PM – 2:30PM Room E2
1:45PM
Benjamin L Parker
Proteome-wide systems genetics to interrogate metabolism abs# 9

**Morning Tea & Poster Viewing**
2:30PM – 3:00PM Hall H

**Plenary 5**
3:00PM – 4:15PM Room E1
3:00PM
Anna Andrejeva
Subcellular distribution of post-translational modifications in human proteome abs# 10

**Morning Tea & Poster Viewing**
4:15PM – 4:45PM Hall H

**Plenary 3**
4:45PM – 5:30PM Room E2
4:45PM
Ryan R Julian
Spontaneous chemical modifications in long-lived proteins prevent lysosomal degradation: implications for age-related diseases abs# 11

**Morning Tea & Poster Viewing**
5:30PM – 6:00PM Hall H

**Plenary 4**
6:00PM – 7:15PM Room E2
6:00PM
Martin R. Larsen
Dissecting signaling pathways using PTMomics abs# 12

**Morning Tea & Poster Viewing**
7:15PM – 8:00PM Hall H

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### Registration and Networking Opportunities

**HUPO 2019 Congress Handbook**

**Session 1:**
- **Welcome Session and Keynote:**
  - **6:00PM – 6:30PM:** Hall H
  - **Speaker:**
  - **Topic:**

**Session 2:**
- **ECR Initiative Meet and Greet:**
  - **7:15AM – 8:00AM:** Room E1

**Session 3:**
- **Plenary Talks:**
  - **8:00AM – 8:30AM:** Halls A & C
  - **Speaker:**
  - **Topic:**

**Session 4:**
- **Morning Tea & Poster Viewing:**
  - **10:00AM – 10:40AM:** Hall H

**Session 5:**
- **Post-Translational Modifications I:**
  - **10:40AM – 12:00PM:** Hall A

**Session 6:**
- **Morning Tea & Poster Viewing:**
  - **11:15AM – 11:45AM:** Hall H

**Session 7:**
- **Plenary Talks:**
  - **11:45AM – 12:30PM:** Room E2

**Session 8:**
- **Morning Tea & Poster Viewing:**
  - **12:30PM – 1:00PM:** Hall H

**Session 9:**
- **Plenary Talks:**
  - **1:45PM – 2:30PM:** Room E1

**Session 10:**
- **Morning Tea & Poster Viewing:**
  - **2:30PM – 3:00PM:** Hall H

**Session 11:**
- **Plenary Talks:**
  - **4:45PM – 5:30PM:** Room E2

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### Additional Information

**HUPO 2019 Congress Handbook**

**Conference Venue:**
Hall H, Hall A & C

**Conference Dates:**
15th September 2019 – 16th September 2019

**Conference Highlights:**
- **ECR Initiative Meet and Greet**
- **Plenary Talks**
- **Morning Tea & Poster Viewing**

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**Contact Information:**
For more information, please contact the conference organizers at info@hupo2019.com.
Veterinary and Animal Health
10:40AM – 12:40PM Room E3

10:40AM
Emke Bendixen
Exploring farm animal proteomes, and their relevance to human health abs# 29

10:50AM
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 bovids 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

12:40PM
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

12:45PM
Thermo Fisher Scientific
Advancing Quantitative Proteomics: Multiplexing, Accuracy, and Precision 12:45PM - 1:45PM Room E1

12:50PM
Paul A Haynes
The Human Protein Atlas - Implications for Human Biology, Drug Development and Precision Medicine abs# 41

1:45PM
Matthew Waas
SurfaceGenie: A web-based application for prioritizing cell-type specific marker candidates abs# 53

2:45PM
Cecilia Lindskog
Differentiated Approaches to Omics challenges in Translational Research 12:45PM - 1:45PM Room E3

2:50PM
Sophia Farkona
Proteomics of laser-captured microdissected glomeruli and tubulointerstitium reveals extracellular matrix remodelling of kidney allografts with antibody-mediated rejection abs# 46

3:15PM
Nicola Tornette
Value and limitations of LC-MS HLA-ligandome data for antigen discovery and vaccine development abs# 43

3:20PM
Anthony Purcell
Mass spectrometry- teaching us new lessons in immunity abs# 44

3:45PM
Mark E Graham
Phosphoproteomics of activity-dependent phospho-signalling in synaptosomes and cultured neurons abs# 52

4:05PM
Per E. Andren
Visualising the physiological biochemistry of human ocular lens transparency and cataract with imaging mass spectrometry abs# 56

4:10PM
Gus Grey
Mass spectrometry imaging of human colon cancer tissues abs# 57

4:25PM
Sofia Farkona
Phosphoproteomics of activity-dependent phospho-signalling in synaptosomes and cultured neurons abs# 52

4:30PM
Alexander Hiscox
Proteomic analysis of a small animal model for ricin exposure abs# 50

4:40PM
Julian A Hiscox
Proteomic analysis of a small animal model for ricin exposure abs# 45

4:50PM
Sudhir Srivastava
Proteomic Cartography and Biomarkers at the Single-Cell Level: Interrogation of Premalignant and Early Stage Lesions abs# 37

5:00PM
Matthew Waas
SurfaceGenie: A web-based application for prioritizing cell-type specific marker candidates abs# 53

Afternoon Tea
2:45PM – 3:15PM Hall H

2:50PM
Anton Melo
Proteomics and Precision Medicine abs# 49

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

4:55PM
Per E. Andren
Visualising the physiological biochemistry of human ocular lens transparency and cataract with imaging mass spectrometry abs# 56
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
Hiromune Ando
Stereo-selective synthesis of sialic acid containing glycoconjugates
abs# 63
4:25PM
Nima Sayyadi
Site-specific conjugation of dendrimer probes to the Fc glycans of monoclonal antibodies for new cancer immunotherapies
abs# 62
4:40PM
Koichi Fukase
Synthesis of glycoconjugate vaccines and antibodies to identify novel subspecies of lipoprotein particles as a tool to antibody-based approaches
abs# 64
4:55PM
Kaori Sakurai
Development of gold nanoparticle-based multivalent photoaffinity probes toward exploration of carbohydrate-protein interaction
abs# 65
Food and Nutrition
3:15PM – 5:15PM Room E3
3:15PM
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
How are the scientific concepts evolved at the National Institutes of Health?
abs# 78
4:25PM
Evelyne Maes
How Does Japan’s Agency for Medical Research and Development fund proteomic research?
abs# 79
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
1:15PM
Sudhir Srivastava
How are the scientific concepts evolved at the National Institutes of Health?
abs# 83
2:00PM
Jeroen Krijgsveeld
Characterization and turnover of RNA-binding proteins: novel insights into ribosome maintenance
abs# 84
3:15PM
Henry Rodriguez
Development fund proteomic for Medical Research and Institutes of Health?
abs# 85
4:05PM
Marc P Molloy
Integrative multi-omics analysis from minimally invasive colorectal cancer FFPE tissue
abs# 86
4:55PM
Kailun Xu
Proteomic dynamics of the microenvironmental regulation identifies PLOD2-mediated colorectal cancer as a novel drug target
abs# 88
5:40PM
Fernando Corrales
Understanding liver regeneration. Proteomics and phosphoproteomics analysis
abs# 87
6:20PM
Kailun Xu
Proteomic dynamics of colorectal cancer evolution identifies PLOD2-mediated microenvironmental regulation as a novel drug target
abs# 88
10:00AM – 10:40AM Hall H
Degradomics, Proteases and Enzymes
10:40AM - 12:40PM Hall A

10:40AM
Christopher M Overall
Protein TAILS Tell Remarkable Tales: Positional Proteomic 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-termiomics 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 approaches 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
Jurgen 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 Galgicolocalized UDP-GlcNAc transporter and mining the data for novel plant O-linked glycans abs# 104

11:50AM
Valentina Siino
Mass spectrometry workflow for characterization of plasma proteome changes related to ageing abs# 111

12:05PM
Eiji Miyoshi
Glycomic approach for detection of Enterococcus infection in chronic pancreatic diseases abs# 105

12:20PM
Nicholas 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 A 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
Mapping proteome-wide targets of protein kinases in Duchenne Muscular Dystrophy abs# 111

12:05PM
Esther Willems
The sweet separation between bacterial and viral infections by glycopeptide profiling abs# 112

12:20PM
Sanjeeta Srivastava
A comprehensive proteomic analysis of multidrug resistance subtypes reveals mechanistic insights of Group 3 tumours abs# 113

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

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

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

Ileana M Cristea
Organelli 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 proteonomic 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. Medzhiradszky
Negotiating the labyrinth of O-glycopeptide analysis abs# 134

4:05PM
Kay-Hooi Khoo
Strategic application 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 Bagdontaite
Isosform-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-tests 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
Na2CO3-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

Precision Medicine
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 interactions 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 proteome 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
### 18th September 2019

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

- **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

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

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

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

**11:00AM**

- **Mark Larance**
  Systems proteomics of the intermittent fasting response highlights the importance of hnf4a
  abs# 161

- **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

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

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

- **David James**
  Global redox proteome and phosphoproteome analysis reveals novel insights into the insulin signaling network
  abs# 165

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

- **Naoyuki Sugiyama**
  In Vitro Profiling of Ser/Thr/Tyr Selectivity of Human Protein Kinome
  abs# 167

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

- **Susan Weintraub** and **Michael Hoopmann**
  HUPO Proteome Project Phosphopeptide Challenge Report
  abs# 169

**11:40AM – 12:00PM**

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

- **Anna I Robles**
  The International Cancer Proteogenome Consortium (ICPC): innovation and collaboration inspired by the Cancer Moonshot
  abs# 170

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

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

- **David J Clark**
  Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma
  abs# 173

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

- **Yang Du**
  Proteogenomic Characterization of Human Gastric Cancer
  abs# 175

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

**10:00AM – 12:00PM**

**Room E1**

**Cancer MoonshotSM collaboration inspired by the International Cancer Proteogenomic Consortium (ICPC): innovation and health**

- **Iulia M. Lazar**
  Proteogenomic Analysis of Gastric Cancer
  abs# 177

- **Yang Du**
  Integrated Proteogenomic Studies at the European Cancer Moonshot Lund Center
  abs# 178

**10:00AM – 12:00PM**

**Room E2**

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

- **Daniel Figey**
  Microbiome in diseases and health
  abs# 183

- **Simone Lemeer**
  Histidine phosphorylation: a new dimension in the phosphoproteome
  abs# 184

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

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

- **Joshua J Hamey**
  Methylation throughout the proteome: the methyltransferases tell the story
  abs# 187

- **Nadine Prust**
  Phosphoproteomic study on Staphylococcus aureus to identify phosphoproteins involved in virulence
  abs# 188

**10:00AM – 12:00PM**

**Room E3**

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

- **Daniel Figey**
  Microbiome in diseases and health
  abs# 183

- **Simone Lemeer**
  Histidine phosphorylation: a new dimension in the phosphoproteome
  abs# 184

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

**10:00AM – 12:00PM**

**Room E3**

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

- **Daniel Figey**
  Microbiome in diseases and health
  abs# 183

- **Simone Lemeer**
  Histidine phosphorylation: a new dimension in the phosphoproteome
  abs# 184

- **Stuart J Cordwell**
  Aligning label-based discovery and global DIA validation proteomics to explore bacterial virulence phenotypes
  abs# 185
New Technological Advancements in Proteomics (HUPO 1AB) 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 Bomgardner
Going Beyond 11: TMTpro 16plex Regents for Higher Quantitative Proteomic Sample Multiplexing abs# 192

11:25AM
Gary Kruppa
Diapase: 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
Proudly sponsored by SCIEX

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

The Next Era in Pathway Proteomics – Towards Turnkey Targeted Quantitation Workflows
12:15PM - 1:15PM Room E2
Proudly sponsored by Thermo Fisher Scientific

ThermoFisher SCIENTIFIC
High-Throughput Proteomics With Evosep One
12:15PM - 1:15PM Room E3
Proudly sponsored by Evosep

Evosep

The Interactome
1:30PM - 3:30PM Hall A

1:30PM
Bing Zhang
Onco-proteogenomics: toward a more complete understanding of cancer biology abs# 195

1:55PM
Karín Rodríguez
Pathway-level analysis of comprehensive proteogenomic and phosphoproteomic data to predict clinical outcomes abs# 196

2:20PM
Joshua Labaeer
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 Markó-Varga
Improved Survival Prognostication of Node-Negative 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 -Omic Reveals Novel Targets Underlying the Pathomechanisms of Uterine Fibroids and Associated Heavy Menstrual Bleeding abs# 200

Metabolomics and Lipidomics
1:30PM - 3:30PM Room E1

1:30PM
Juri Rappisbier
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 (OPPS) abs# 205

3:10PM
Claudia Martelli
High-throughput protein–protein interaction profiling for clinical applications abs# 206

HHPP6: 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 macrophagy-cytosis-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 haptation 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
**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 Ic-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

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**timsTOF Pro**

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

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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
- Now with TIMS based DIA analysis capabilities - diaPASEF

For more information please visit www.bruker.com/timstofpro

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**timsTOF Pro and PASEF**

Winner of the EuPA Technology Award 2019

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**Innovation with Integrity**

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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
- Plenary 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
- 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
- Fused Proteomics
  - 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 Cerelli
- 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

**Proudly sponsored by Waters**

**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 precursor selection process. DiazPASEF 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 precursor selection process. DiazPASEF 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. 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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
Khaterem 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

Proudly sponsored by Thermo Fisher 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/cutaneous tissue, using different 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%.

Proudly sponsored by Agilent Technologies

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 in 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. Jürgen 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-dimenosional shotgun proteomics.

Proudly sponsored by Bruker
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

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 directly 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.

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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Proudly sponsored by Olink

Proudly sponsored by Bruker
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.
Topics
Clinical proteomics, large cohort studies, DIA, diaPASEF, protein complexes, high throughput, robust proteomics
Proudly sponsored by Evosep

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
Proudly sponsored by Thermo Fisher Scientific

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
Proudly sponsored by SCIEX
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)
**Tuesday September 17**
08h30–10h00: Session #6
Quantifying the impact of public omics data
(Henning Hermjakob, EBI; Juan Antonio Vizcaino, 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 Cericiello, University Hospital of Bern, Inselspital)
**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, SpecLib, PROXI
(Eric Deutsch, ISB; Juan Antonio Vizcaino, EBI; Nuno Bandeira, UCSD, Luis Mendoza, ISB)
**Thursday September 19**
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

Attending Organizers
• Eric Deutsch
• Juan Antonio Vizcaino
• 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!

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.

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Hashtags for Twitter
#BioinformaticsHub #HUPO2019

Bio-Informatics 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)
**Tuesday September 17**
08h30–10h00: Session #6
Quantifying the impact of public omics data
(Henning Hermjakob, EBI; Juan Antonio Vizcaino, 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 Cericiello, University Hospital of Bern, Inselspital)
**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, SpecLib, PROXI
(Eric Deutsch, ISB; Juan Antonio Vizcaino, EBI; Nuno Bandeira, UCSD, Luis Mendoza, ISB)
**Thursday September 19**
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

Attending Organizers
• Eric Deutsch
• Juan Antonio Vizcaino
• 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!

Bio-Informatics Hub
Overview
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The Molecular Stethoscope: RNA of drug metabolising enzymes in circulating vesicles correlates with their specific protein content in the liver abs# 402

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Subash Adhikari
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Eman Ahmed
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Cristina Al-Khalili Szigyarto
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Norie Araki
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Mahya Bahmani
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Dmitry Bandura
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Atlas Antibodies is a Swedish manufacturer and supplier of advanced research reagents targeting all human proteins. With a focus in targeted proteomics, we are now proudly launching QPREST - Stable isotope-labeled protein standards for absolute quantification using mass spectrometry.

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Bioinformatics Solutions
Booth 3
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Bruker
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 nanoaanalysis, and in industrial applications, as well as in cell biology, preclinical imaging, clinical phenomics and proteomics research and clinical microbiology.

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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
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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 straightforward yet in-depth analysis, guiding quality control and standardising workflows. All while making the experimental process iterative, collaborative and fun.

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• Antibody services
• Assay services
• Peptide arrays
• Off-the-shelf libraries
• Reagents
• Catalogue peptides
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Call us to coordinate your requirements at every stage.

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.
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 92%.

SCIEX
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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 components help people working in clinical laboratories, 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.
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6th – 9th of February 2020

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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

Key Dates

Abstract Submission Deadline
Friday 18th October 2019

Early Bird Registration Deadline
Sunday 15th November 2019

For more information, please visit our website: