15th September 2019

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

Plenary 1
6:30PM - 7:15PM Halls A & C
6:30 PM Rudolf Aebersold
The modular proteome and its significance abs# 1

Plenary 2
7:15PM - 8:00PM Halls A & C
7:15 PM Glenn F King
Deadly proteomes: the central role of proteomics in dissecting the chemical arsenal of animal venoms abs# 2

Welcome Function
8:00PM - 10:00PM Hall H
16th September 2019

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

Plenary 3
8:30AM - 9:15AM Halls A & C
8:30 AM  Fuchu He
  Proteomics driven precision medicine for the early-stage hepatocellular carcinoma abs# 3

Plenary 4
9:15AM - 10:00AM Halls A & C
9:15 AM  Nicolle H. Packer
  The elephant in the room: glycomics and glycoproteomics abs# 4

Morning Tea
10:00AM - 10:40AM Hall H

Hereditary Disease and Aging
10:40AM - 12:40PM Hall C
10:40 AM  Marius Ueffing
  Gene editing based analysis of functional protein networks in human disease abs# 5

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

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

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

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

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

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

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

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

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

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

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

Glycoimmunology and Clinical Glycobiology (AGS 1)

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

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

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

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

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

12:20 PM Sayantani Chatterjee
Protein paucimannosylation is an enriched N-glycosylation signature of human cancers abs# 22
**HPP 1: Rheumatic and Autoimmune Disorders**

10:40AM - 12:40PM Room E2

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

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

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

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

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

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

**Veterinary and Animal Health**

10:40AM - 12:40PM Room E3

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

11:05 AM **Brigitte BP Picard**  
Proteomics applied to beef productions: from the discovery of biomarkers to the development of evaluation tools *abs# 30*

11:30 AM **Denise Dittmar**  
Proteome analysis of *Streptococcus suis* under stress conditions and in host-pathogen interaction *abs# 31*

11:50 AM **Pawel Sadowski**  
Leveraging of extensive inter-species homologies to study plasma proteomes of bovids using data-independent acquisition *abs# 32*

12:05 PM **David A Skerrett-Byrne**  
Proteomic profiling of crocodile spermatozoa refutes the tenet that posttesticular maturation is restricted to mammals *abs# 33*

12:20 PM **Paul A. Haynes**  
Proteomic characterisation of Ancient Egyptian skin, bones and textiles *abs# 34*
**Single Cell Proteomics**

10:40 AM - 12:40PM Hall B

10:40 AM **Jonathan V Sweedler**  
High throughput Single Cell Chemical Characterization of the Cells in the Brain *abs# 35*

11:05 AM **Emma Lundberg**  
Single cell proteome variability *abs# 36*

11:30 AM **Sudhir Srivastava**  
Proteomic Cartography and Biomarkers at the Single-Cell Level: Interrogation of Premalignant and Early Stage Lesions *abs# 37*

11:50 AM **Cecilia Lindskog**  
Integration of transcriptomics and antibody-based proteomics for spatial localization of cell type-specific expression patterns *abs# 38*

12:05 PM **Christopher M Rose**  
A Offset Mass Triggered Data Acquisition Approach to Single Cell Proteomics Experiments *abs# 39*

12:20 PM **Yu (Tom) Gao**  
Super-resolution proteomics method to explore cell heterogeneity at single-cell level *abs# 40*

**Lunch**

12:40PM - 2:00PM Hall H

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

12:45PM - 1:45PM Room E1

Proudly sponsored by Thermo Fisher Scientific

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

12:45PM - 1:45PM Room E2

Proudly sponsored by Waters

**Differentiated Approaches to Omics challenges in Translational Research**

12:45PM - 1:45PM Room E3

Proudly sponsored by Agilent Technologies
DIA with near 100% Ion Usage: Introducing diaPASEF on the timsTOF Pro
12:45PM - 1:45PM Hall A
Proudly sponsored by Bruker

Plenary 5
2:00PM - 2:45PM Halls A & C

Session sponsored by

2:00 PM Mathias Uhlen
The Human Protein Atlas - Implications for Human Biology, Drug Development and Precision Medicine abs# 41

Afternoon Tea
2:45PM - 3:15PM Hall H

Immunology and Inflammation
3:15PM - 5:15PM Hall C

3:15 PM Aleksandra Nita-Lazar
Studies of innate immune signaling regulation through quantification of proteoforms and modeling of the TLR pathway abs# 42

3:40 PM Nicola Ternette
Value and limitations of LC-MS HLA-ligandome data for antigen discovery and vaccine development abs# 43

4:05 PM Anthony Purcell
Mass spectrometry- teaching us new lessons in immunity abs# 44

4:25 PM Julian A Hiscox
Proteomic analysis of a small animal model for ricin exposure reveals underlying pathways and responses to toxicity abs# 45

4:40 PM Sofia Farkona
Proteomics of laser-captured microdissected glomeruli and tubulointerstitium reveals extracellular matrix remodelling of kidney allografts with antibody-mediated rejection abs# 46

4:55 PM Richard Wilson
Identification of key pro-survival proteins in isolated colonic goblet cells of Winnie, a murine model of spontaneous colitis abs# 47
The Surfaceome and Extracellular Vesicles

3:15PM - 5:15PM Hall A

3:15 PM **Bernd Wollscheid**
The *in silico* human surfaceome & technologies for the elucidation of the surfaceome nanoscale organization *abs# 48*

3:40 PM **Daniel Kolarich**
Protein glycosylation – an overlooked feature impacting Stem cell factor and Stem cell factor receptor function *abs# 49*

4:05 PM **Maik Mueller**
LUX-MS enables the light-controlled elucidation of ligand-receptor interactions and functional surfaceome nanoscale organization on living cells *abs# 50*

4:25 PM **Christoph Krisp**
Quantitative Proteome Profiling of Stage I – IV colorectal carcinoma tissues and serum based extracellular vesicles for early onset biomarker detection *abs# 51*

4:40 PM **Mark E Graham**
Phosphoproteomics of activity-dependent phospho-signalling in synaptosomes and cultured neurons *abs# 52*

4:55 PM **Matthew Waas**
SurfaceGenie: A web-based application for prioritizing cell-type specific marker candidates *abs# 53*

MS Imaging

3:15PM - 5:15PM Hall B

3:15 PM **Nathalie Agar**
Mass spectrometry imaging applications for neurosurgery and neurooncology *abs# 54*

3:40 PM **Richard R Drake**
Combined glycan and extracellular matrix protein imaging mass spectrometry workflows for FFPE prostate cancer tissues *abs# 55*

4:05 PM **Per E. Andren**
Imaging age-induced perturbations of mitochondrial function, neurotransmission and lipid signaling in specific brain structures *abs# 56*

4:25 PM **Gus Grey**
Visualising the physiological biochemistry of human ocular lens transparency and cataract with imaging mass spectrometry *abs# 57*

4:40 PM **Peter Hoffmann**
Mass Spectrometry Imaging in Cancer Diagnostics and Cancer Spheroids as Drug Testing Model *abs# 58*

4:55 PM **Peter P.L. Horvatovich**
Exploring the limits of high-resolution mass spectrometry imaging data *abs# 59*
Chemical Glycobiology (AGS 2)

3:15PM - 5:15PM Room E1

3:15 PM  **Mark von Itzstein**
Targeting respiratory viruses using structure-guided inhibitor design on glycoenzymes    *abs*# 60

3:40 PM  **Lara K. Mahal**
Systematically decoding glycosylation in disease. *abs*# 61

4:05 PM  **Koichi Fukase**
Synthesis of glycoconjugate vaccines and antibodies for new cancer immunotherapies *abs*# 62

4:25 PM  **Hiromune Ando**
Stereo-selective synthesis of sialic acid containing glycoconjugates *abs*# 63

4:40 PM  **Nima Sayyadi**
Site-specific conjugation of dendrimer probes to the Fc glycans of monoclonal antibodies *abs*# 64

4:55 PM  **Kaori Sakurai**
Development of gold nanoparticle-based multivalent photoaffinity probes toward exploration of carbohydrate-protein interaction *abs*# 65

HPP 2: Towards the complete cardiac proteome and beyond

3:15PM - 5:15PM Room E2

3:15 PM  **Rebekah L Gundry**
Chamber and cell type specific views of the human heart glycoproteome and glycome in health and disease *abs*# 66

3:40 PM  **Melanie Y White**
Delving Deeper into the Cardiac Proteome – Analyzing the Heart “Modificome” *abs*# 67

4:05 PM  **Stefan Lehr**
Proteomic profiling of plasma lipoprotein particles as a tool to identify novel subspecies. *abs*# 68

4:25 PM  **Sandra Goetze**
Relating high density lipoprotein (HDL) particle composition to clinical signaling capacity *abs*# 69

4:40 PM  **Marika Mokou**
Cross-species tissue proteomics analyses in cardiovascular disease: unraveling Ariadne’s thread *abs*# 70

4:55 PM  **Ling Lin**
An anatomically resolved human heart transcriptome and proteome landscapes reveal molecular signatures and disease-relevant pathways of end-stage dilated cardiomyopathy *abs*# 71
Food and Nutrition

3:15PM - 5:15PM Room E3

3:15 PM  **Paola Roncada**
The Central Role Of Milk Proteomics In One Health Approach  *abs# 72*

3:40 PM  **Michelle Colgrave**
Food safety assessment in genetically engineered canola – LC-MS/MS as an alternative to antibody-based approaches  *abs# 73*

4:05 PM  **Ben Schulz**
Bottoms Up Proteomics! The Dynamic Beer Proteome  *abs# 74*

4:25 PM  **Evelyne Maes**
Insights in food digestion: tracking peptides from meat and meat hydrolysates by simulated gastrointestinal digestion and label-free proteomics  *abs# 75*

4:40 PM  **Xuezhi Bi**
Development of an ESI-MS based serotyping assay for *Salmonella*  *abs# 76*

4:55 PM  **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

Panelists will discuss their interactions with the funding institutions and shed lights on their experience with the successful negotiation.
Panel Discussions: Rob Moritz, Ruedi Aebersold, Matthias Uhlen, Fuchu He, YM Park

3:15 PM  **Sudhir Srivastava**
How are the scientific concepts evolved at the National Institutes of Health?  *abs# 78*

3:40 PM  **Tesshi Yamada**
How Does Japan’s Agency for Medical Research and Development fund proteomic research?  *abs# 79*

4:05 PM  **Henry Rodriguez**
Perspectives on International Consortium on Proteogenomic: Interactions between Funders and Investigators  *abs# 80*

4:30 PM  **Michael Snyder**
HubMap: Partnership between the Funders and Investigators  *abs# 81*

HUPO General Assembly

5:20PM - 6:00PM Innovation Stage (Exhibition Hall)

Poster Session 1

6:00PM - 7:15PM Hall H
17th September 2019

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

7:15AM - 8:15AM Hall E1

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Plenary 6

8:30AM - 9:15AM Halls A & C

Session sponsored by

8:30 AM **James C Paulson**
Impact of the glycoproteome on B cell responses: From checkpoint inhibitors to HIV vaccines. *abs# 82*

Plenary 7

9:15AM - 10:00AM Halls A & C

9:15 AM **Yu-Ju Chen**
Taiwan Cancer Proteogenomics Moonshot: Pathway to Next Generation Precision Medicine in Cancer *abs# 83*

Morning Tea

10:00AM - 10:40AM Hall H

Cancer

10:40AM - 12:40PM Hall C

10:40 AM **Jeroen Krijgsveld**
Characterization and turnover of RNA-binding proteins: novel insights into ribosome maintenance *abs# 84*

11:05 AM **Hyun Joo An**
Sugar Code Cracking of Serum Haptoglobin for the Diagnosis of Gastric Cancer by Targeted Glycoproteomic Approach *abs# 85*

11:30 AM **Mark P Molloy**
Integrative multi-omics analysis from minimally invasive colorectal cancer FFPE tissue *abs# 86*

11:50 AM **Fernando Corrales**
Understanding liver regeneration. Proteomics and phosphoproteomics analysis *abs# 87*
12:05 PM Kailun Xu
Proteomic dynamics of colorectal cancer evolution identifies PLOD2-mediated microenvironmental regulation as a novel drug target abs# 88

12:20 PM Pouya Faridi
Spliced epitopes are abundant and highly immunogenic components of the melanoma immunopeptidome abs# 89

Degradomics, Proteases and Enzymes

10:40AM - 12:40PM Hall A

10:40 AM Christopher M Overall
Protein TAILS Tell Remarkable Tales: Positional Proteomics Reveals Diverse N-Terminomes and Proteolytic Landscapes in Disease abs# 90

11:05 AM Merry L Lindsey
Proteomics of Extracellular Matrix Remodeling Following Myocardial Infarction abs# 91

11:30 AM Thierry Rabilloud
Is the mitochondrial protein processing system robust? Lessons from a combined N-terminomics and shotgun proteomics approach on human cells treated with rapamycin or zinc abs# 92

11:50 AM Thomas Hauser
Measuring protein functional states in central carbon metabolism by limited proteolysis coupled to mass spectrometry abs# 93

12:05 PM Nestor Solis
Integrated TAILS terminomics, shotgun, and transcriptomics analysis of macrophage polarization and activation abs# 94

12:20 PM Robert J Beynon
The degrading business: Measurement of proteome turnover in intact animals abs# 95

Bioinformatics and Statistics

10:40AM - 12:40PM Hall B

10:40 AM Lydie Lane
neXtProt: a SPARQLing light in the dark human proteome abs# 96

11:05 AM Juergen Cox
Computational proteomics enhancements in MaxQuant by (deep) machine learning and ion mobility awareness. abs# 97

11:30 AM Zhixin TIAN
Intact N-glycopeptide database search using GPSeeker abs# 98

11:50 AM Maggie Pui Yu Lam
Identifying high-priority proteins across the human diseasome using semantic similarity abs# 99
12:05 PM **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*

12:20 PM **Henning Hermjakob**  
Reactome Pathway Analysis and Visualization *abs# 101*

### Microbial and Plant Glycobiology (AGS 3)

10:40AM - 12:40PM Room E1

**Session sponsored by**

**10:40 AM Katharina Paschinger**  
Drilling into the N-glycomes of parasites and their vectors *abs# 102*

**11:05 AM Giuseppe Palmisano**  
Comprehensive characterization of protein glycosylation in *Leishmania spp.* *abs# 103*

**11:30 AM Joshua L Heazlewood**  
Application of glycoproteomics to identify the plant Golgi localized UDP-GlcNAc transporter and mining the data for novel plant O-linked glycans *abs# 104*

**11:50 AM Eiji Miyoshi**  
Glycomic approach for detection of *Enterococcus* infection in chronic pancreatic diseases *abs# 105*

**12:05 PM Nicholas Scott**  
Analysis of *In vivo* Arginine-glycosylation targets of the NleB/SseK family of effectors reveals discrete effector substrate specificities *abs# 106*

**12:20 PM Atsushi Shimoyama**  
Systematic chemical synthesis and immunological function of *Campylobacter jejuni* lipid As *abs# 107*

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

10:40AM - 12:40PM Room E2

**10:40 AM Petter Brodin**  
Systems-level analysis of immune development early in life *abs# 108*

**11:05 AM Qibin Zhang**  
Temporal profiles of plasma proteome during childhood development and natural progression of Type 1 Diabetes *abs# 109*

**11:30 AM Cristina Al-Khalili Szigyarto**  
Orthogonal validation of Duchenne Muscular Dystrophy biomarkers using targeted proteomics *abs# 110*
11:50 AM **Valentina Siino**  
Mass spectrometry workflow for characterization of plasma proteome changes related to ageing *abs# 111*

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

12:20 PM **Sanjeeva Srivastava**  
A comprehensive proteomic analysis of medulloblastoma subtypes reveals mechanistic insights of Group 3 tumors *abs# 113*

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

10:40AM - 12:40PM Room E3

10:40 AM **Leslie M Hicks**  
Investigating plant derived antimicrobial peptides using “PepSAVI-MS” *abs# 114*

11:05 AM **Pengcheng Wang**  
Mapping proteome-wide targets of protein kinases in plant stress responses *abs# 115*

11:30 AM **Subhra Chakraborty**  
Chitosan remolds Extracellular Matrix Integrity and regulate Stomatal Function leading to Immunity against Wilt disease *abs# 116*

11:50 AM **Setsuko Komatsu**  
Elucidation of tolerant mechanism in soybean treated with plant-derived smoke under flooding stress using omics technique *abs# 117*

12:05 PM **Pingfang Yang**  
Morphological and proteomics analyses of petioles rigidity in sacred Lotus *abs# 118*

12:20 PM **Sixue Chen**  
Molecular changes in the course of ice plant C₃ to CAM transition revealed by proteomics and metabolomics *abs# 119*

### Lunch

12:40PM - 2:00PM Hall H

### Clinical Research Applications of the timsTOF Pro

12:45PM - 1:45PM Hall A

Proudly sponsored by Bruker
Driving personalized medicine through targeted protein biomarker discovery - taking proteomics beyond mass spectrometry

12:45PM - 1:45PM Hall B

Proudly sponsored by Olink

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

12:45PM - 1:45PM Room E1

Proudly sponsored by Thermo Fisher Scientific

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

12:45PM - 1:45PM Room E2

Proudly sponsored by Thermo Fisher Scientific

Plenary 8

2:00PM - 2:45PM Halls A & C

2:00 PM  Albert Heck
Proteome and proteoform diversity exposed and quantified by hybrid mass spectrometry approaches abs# 120

Afternoon Tea

2:45PM - 3:15PM Hall H

Infectious Diseases

3:15PM - 5:15PM Hall A

3:15 PM  Ileana M Cristea
Organelle shape and function in the context of viral infections  abs# 121

3:40 PM  Darren Creek
A multi-omics approach to drug target discovery for novel bis-triazine antimalarials abs# 122

4:05 PM  Nathan P Croft
Systems immunology reveals factors driving anti-viral CD8 T cell immunity abs# 123

4:25 PM  Amir Banaei-Esfahani
A Mycobacterium tuberculosis protein atlas  abs# 124
4:40 PM  **Fabian Wendt**  
Spatiotemporal proteotype analysis of vaccinia virus infected cells reveals dynamic host surfaceome repopulation with viral proteins  
*abs# 125*

4:55 PM  **Xiaoyun Liu**  
*Salmonella* proteomic profiling during infection distinguishes the intracellular environment of host cells  
*abs# 126*

**Proteogenomics**

3:15 PM - 5:15PM Hall C

3:15 PM  **Akhilesh Pandey**  
PASS-DIA: A novel data-independent acquisition approach for discovery studies  
*abs# 127*

3:40 PM  **Janne Lehtio**  
Proteogenomics — connecting cancer genotype with molecular phenotype  
*abs# 128*

4:05 PM  **Henry Rodriguez**  
Implementing ProteoGenome-Driven Oncology and Global Data Sharing  
*abs# 129*

4:25 PM  **Chris R Kinsinger**  
Proteomic Data Commons: a resource for proteogenomic analysis  
*abs# 130*

4:40 PM  **Ankit Sinha**  
The proteogenomic landscape of curable prostate cancer  
*abs# 131*

4:55 PM  **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

3:15 PM  **Henrik Clausen**  
A Genetic Dissection Approach to Functional Glycomics  
*abs# 133*

3:40 PM  **Katalin F. Medzihradszky**  
Negotiating the labyrinth of O-glycopeptide analysis  
*abs# 134*

4:05 PM  **Kay-Hooi Khoo**  
Strategic applications of data dependent and targeted multistage fragmentation in dual modes to expedite mass spectrometry-based sequencing of glycopeptides  
*abs# 135*
4:25 PM  **Miyako Nakano**  
Development of cancer biomarker for biliary tract cancer and pancreatic cancer with serum haptoglobin glycan analyses  
abs# 136

4:40 PM  **Erdmann Rapp**  
glyXbox\textsuperscript{CE}: A powerful tool in the glycoanalytical toolbox - improving biologics development and biomarker discovery for personalized diagnostics  
abs# 137

4:55 PM  **Ieva Bagdonaitė**  
Isoform-specific functions of polypeptide GalNAc-transferases probed with glycoengineered human skin organoids and mass spectrometry  
abs# 138

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

3:15PM - 5:15PM Hall B

3:15 PM  **Michael H. Roehrl**  
Proteome-Based Diagnostics: The Next Revolution in Medicine and Pathology  
abs# 139

3:40 PM  **Danni Li**  
Enabling Precision Medicine for Alzheimer’s Disease through Biofluid-Based Biomarkers  
abs# 140

4:05 PM  **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

4:25 PM  **Rosemary Balleine**  
Intra- and inter-individual variation in the proteome of high-grade serous ovarian cancer  
abs# 142

4:40 PM  **Jacob Kagan**  
Proteomic Tissue Biomarkers for Early Prediction of Prostate Cancer Progression  
abs# 143

4:55 PM  **Soren Naaby Hansen**  
Oxygen-sensitive interactions between glycolytic enzymes and a cancer-testis antigen established signaling scaffold are regulated by lysine acetylation  
abs# 144

**Plant and Crop Proteomics II**

3:15PM - 5:15PM Room E3

3:15 PM  **Hirofumi Nakagami**  
Proteomic dissection of the plant immune system  
abs# 145

3:40 PM  **Harvey Millar**  
Quantitative analysis of protein synthesis and degradation rates in plants using progressive labeling with stable isotopes  
abs# 146

4:05 PM  **Ghasem Hosseini Salekdeh**  
Systems Biology Analysis of Root Tips: Towards Bioengineering of Rice Root Structure to Enhance Drought Stress Tolerance  
abs# 147
4:25 PM  **Shaojun Dai**  
Na$_2$CO$_3$-responsive mechanism in alkaligrass revealed from redox proteomic analysis  *abs# 148*

4:40 PM  **Niranjan Chakraborty**  
Global profiling of dehydration-induced mitochondrial dynamics and defense response in rice  *abs# 149*

4:55 PM  **James A. Broadbent**  
Wheat pan-proteomics: Unifying data-independent LC-MS proteome measurements across diverse genetic backgrounds for trait prediction  *abs# 150*

**Top-Down and Structural Proteomics**

3:15PM - 5:15PM Room E2

3:15 PM  **Neil Kelleher**  
Single ion mass spectrometry to measure proteoforms and their complexes with complete molecular specificity  *abs# 151*

3:40 PM  **Ying Ge**  
Novel Strategies in Top-Down Proteomics  *abs# 152*

4:05 PM  **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*

4:25 PM  **Hartmut Schlüter**  
Identification of the functional status of proteoforms and their interactomes in blood plasma  *abs# 154*

4:40 PM  **Blaine R Roberts**  
Application of a novel electron capture dissociation (ECD) mass spectrometry to top-down and bottom-up proteoform characterization on a QTOF.  *abs# 155*

4:55 PM  **Alexandre A Shvartsburg**  
High-Resolution Differential Ion Mobility Separations with Orbitrap Mass Spectrometry for Middle-Down Analyses of Histone Proteoforms  *abs# 156*

**Poster Session 2**

5:15PM - 6:30PM Hall H

**Early Career Researcher (ECR) PhD Abstract Competition**

5:30PM - 6:15PM Innovation Stage

**Conference Dinner**

7:30PM - 11:00PM The Adelaide Oval, William Magarey Room
18th September 2019

Plenary 9

8:30AM - 9:15AM Halls A & C

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

Morning Tea and Final Poster Session

9:15AM - 10:00AM Hall H

Cardiovascular and Metabolic Disease

10:00AM - 12:00PM Hall C

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

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

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

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

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

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

Post-Translational Modifications II

10:00AM - 12:00PM Hall A

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

10:25 AM David James
Global redox proteome and phosphoproteome analysis reveals novel insights into the Insulin Signaling Network abs# 165
10:50 AM **Justyna Fert-Bober**
Hyper-citrullinated library workflow to support demand-driven correct identification of citrullinated residues abs# 166

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

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

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

**Special Session: The ICPC Initiative**

10:00AM - 12:00PM Room E2

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

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

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

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

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

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

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

**HPP 5: High Connectivity: Neuroproteomics at the Interface of Bench and Bedside**

10:00AM - 12:00PM Room E1

10:00 AM **Melanie Foecking**
The use of proteomics to identify blood-based protein changes in childhood that are associated with increased risk for later psychosis abs# 177
10:25 AM Lingjun Li
Comparative glycoproteomic analyses of cerebrospinal fluids reveal novel molecular players in Alzheimer’s disease abs# 178

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

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

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

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

Microbial Proteomics and the Microbiome

10:00AM - 12:00PM Room E3

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

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

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

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

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

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

New Technological Advancements in Proteomics (HUPO IAB)

10:00AM - 12:00PM Hall B

10:00 AM Michael MacCoss
How do we make quantitative proteomics quantitative? abs# 189
10:25 AM **Stephanie M. Cologna**
Differential Proteomics and Lipidomics in Niemann-Pick Disease, Type C *abs# 190*

10:50 AM **Phillip J Robinson**
Rapid and robust high throughput cancer proteomics across multiple instruments in a single facility *abs# 191*

11:10 AM **Ryan Bomgarden**
Going Beyond 11: TMTpro 16plex Regents for Higher Quantitative Proteomic Sample Multiplexing *abs# 192*

11:25 AM **Gary Kruppa**
Diapasef: Toward The Ideal Mass Analyzer With Data-Independent Acquisition And Parallel Accumulation – Serial Fragmentation *abs# 193*

11:40 AM **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

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

12:15PM - 1:15PM Room E2

Proudly sponsored by Thermo Fisher Scientific

**HIGH-THROUGHPUT PROTEOMICS WITH EVOSEP ONE**

12:15PM - 1:15PM Room E3

Proudly sponsored by Evosep

**Precision Medicine and Clinical Proteomics**

1:30PM - 3:30PM Hall C

1:30 PM **Bing Zhang**
Onco-proteogenomics: toward a more complete understanding of cancer biology *abs# 195*
1:55 PM **Karin Rodland**  
Pathway-level analysis of comprehensive proteogenomic and phosphoproteomic data to predict clinical outcomes *abs# 196*

2:20 PM **Joshua Labaer**  
Multiplex In-Solution Protein Array (MISPA) for high throughput, quantitative profiling of protein interactions and detection of immune responses to pathogen induced cancers *abs# 197*

2:40 PM **György Marko-Varga**  
Improved Survival Prognostication of Node-Positive Malignant Melanoma Patients applying Shotgun Proteomics Guided by Histopathological Characterization and Genomic data *abs# 198*

2:55 PM **Harsha Gowda**  
Delineating mechanisms that confer resistance to kinase inhibitors in head and neck squamous cell carcinoma and melanoma *abs# 199*

3:10 PM **Darragh P O’Brien**  
Integrative -Omics Reveals Novel Targets Underlying the Pathomechanisms of Uterine Fibroids and Associated Heavy Menstrual Bleeding *abs# 200*

**The Interactome**

1:30 PM - 3:30PM Hall A

1:30 PM **Juri Rappsilver**  
Cellular Cartography at Molecular Detail: *in Situ* Crosslinking Mass Spectrometry *abs# 201*

1:55 PM **Meng-Qiu Dong**  
Amine-selective Di-ortho-phthalaldehyde (DOPA) Cross-linking Captured the Conformational Change Associated with the Unfolding of Ribonuclease A *abs# 202*

2:20 PM **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*

2:40 PM **Ben C Collins**  
Complex-centric proteome profiling in one day with SEC-SWATH-MS and short gradient analysis *abs# 204*

2:55 PM **Eneko Villanueva**  
Comprehensive identification of RNA–protein interactions in any organism using orthogonal organic phase separation (OOPS) *abs# 205*

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

**Metabolomics and Lipidomics**

1:30PM - 3:30PM Room E1
1:30 PM  Erin S Baker  
A Multi-Omic Investigation into the Molecular Signatures of Preeclampsia and Gestational Diabetes Mellitus  abs# 207

1:55 PM  Ute Roessner  
The role of lipids in plant stress biology  abs# 208

2:20 PM  Gavin E Reid  
A ‘Systems-omics’ Strategy to Uncover the Role of Brain Tissue Derived Exosomal Lipids in Alzheimer’s Disease  abs# 209

2:40 PM  Igor Popov  
MS-based tissue profiling for assistance on neurosurgery operations of brain cancer  abs# 210

2:55 PM  Stephan Klatt  
Comparative targeted and high-throughput metabolomics workflow of small-volume plasma samples  abs# 211

3:10 PM  Hiromi W.L. Koh  
Identifying predictive network of lipids and proteins among individuals at high and low risk of coronary artery disease using iOmicsPASS  abs# 212

HPP 6: Moving proteomics into pharmaceutical discovery and application

1:30PM - 3:30PM Room E2

1:30 PM  Anne Claude Gingras  
Proximity dependent sensors define a role for HOPS in macropinocytosis-dependent control of cell growth  abs# 213

1:55 PM  Paul Alewood  
Venoms to Drugs  abs# 214

2:20 PM  Wint Wint Phoo  
Unveiling protein targets involved in haptenation during allergic contact dermatitis via high resolution mass spectrometry  abs# 215

2:40 PM  Sung Min Cho  
Reverse chemical proteomics identifies unanticipated human target of antimalarial drug, Artesunate, for drug repositioning  abs# 216

2:55 PM  David R. Spiciarich  
Proteome profiling of multiple sclerosis cerebrospinal fluid by data independent acquisition reveals changes in proteins involved in adaptive immunity  abs# 217

3:10 PM  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

1:30 PM Robert Moritz
Standardizing the performance of SWATH/DIA-MS software tools for label-free quantification using public repository spectral ion libraries abs# 219

1:55 PM Je-Yoel Cho
Development of clinically applicable lung cancer proteome biomarkers for in vitro diagnostics-multivariate index assay abs# 220

2:20 PM Jarrod Marto
Multidimension lc-ms/ms analysis of csf samples in the biofind cohort for biomarker discovery in Parkinson's disease abs# 221

2:40 PM YOUNG-KI PAIK
Human complement factor B: a new pancreatic cancer biomarker with multiple functions abs# 222

2:55 PM Charles Pineau
The eutopic endometrium proteome in endometriosis reveals candidate markers and molecular mechanisms of physiopathology abs# 223

3:10 PM Allan Stensballe
Phenotyping of multiple biofluids for liquid biomarkers for diagnostics and personalized medicine abs# 224

Chemical Proteomics

1:30PM - 3:30PM Room E3

1:30 PM HoJeong Kwon
Unraveling protein targets of bioactive small molecules using label-free chemical proteomics abs# 225

1:55 PM Sheng-ce Tao
An Array of 60,000 Antibodies for Proteome-Scale Antibody Generation and Target Discovery abs# 226

2:20 PM Ruzanna Mnatsakanyan
Proteome-wide detection of cysteine nitrosylation targets and motifs using bioorthogonal cleavable-linker-based enrichment and switch technique (Cys-BOOST) abs# 227

2:40 PM Amir Ata Saei
System-wide identification of enzyme substrates by thermal analysis abs# 228

2:55 PM Tae young Kim
Mass Spectrometry Imaging of RTKi with protein target in human lung cancer tumor xenograft mouse abs# 229
3:10 PM  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