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

10:40AM - 12:40PM Hall A

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)

10:40AM - 12:40PM Room E1

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

10:40AM - 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 MCP MOLECULAR & CELLULAR PROTEOMICS

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 S*almonella 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

Griffith UNIVERSITY
Institute for Glycomics
Queensland, Australia

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 **Nichollas 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 remodels 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 C_3 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

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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

3:15PM - 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^{CE}: A powerful tool in the glycoanalytical toolbox - improving biologics development and biomarker discovery for personalized diagnostics *abs# 137*

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

Pathology and the Cancer Proteome: Towards Precision Medicine

3:15PM - 5:15PM Hall B

3:15 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_2CO_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^{SM} *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

1:30PM - 3:30PM Hall A

1:30 PM **Juri Rappsilber**
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 anti-malarial 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