

All times in UTC (Coordinated Universal Time)

HUPO 2021 ReCONNECT

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MONDAY, NOVEMBER 8, 2021 (PRE-CONGRESS)

14:00 - 15:00 (UTC) Pre-Congress Training 1 (PT01): Proteomics 101

Characterization of complex proteomes is the key to reveal their composition and functions. This session will present an overview of the current methodology used to identify and quantify proteins. Three experts will cover the basic principles and practice of proteomics, analytical workflows and data interpretation of mass spectrometry based proteomics, global (isotopic labeling, label-free, DIA) and targeted quantitative proteomics methods [e.g., selected reaction monitoring (SRM) and parallel reaction monitoring (PRM)].

Chairs: Marc Wilkins & Maike Langini

14:00 Live Q&A with Chairs and Speakers

Watch the following pre-recorded presentations, available as of October 25 on the Virtual Platform in the Education Session Area. They will not be played during the Live Session.

- PT01.01 Introduction to Proteomics and Mass Spectrometry – Lindsay Pino
- PT01.02 From Mass Spectrum to Protein – David Tabb
- PT01.03 Quantitative and Targeted Proteomics – Michael MacCoss

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TUESDAY, NOVEMBER 9, 2021 (PRE-CONGRESS)

14:00 – 15:00 (UTC) **Pre-Congress Training 2 (PT02): Statistics and Experimental Design**

Tutorials covering statistics essential for proteomics experiments, and considerations for proteomics experimental design will be presented in this session. Attendees will learn the basics of designing a proteomics experiment for biological research and biomarker discovery, as well as issues related to analysing (large) quantitative proteomic data sets generated by data-dependent acquisition (DDA; including label-free and label-based-methods), data-independent acquisition (DIA), and targeted proteomics. The session will also cover the statistical principles for peptide and protein identification and quantification, taking into account the specific challenges of large data sets and cohorts.

Chairs: Tiannan Guo & Mathieu Lavallée-Adam

14:00 **Live Q&A with Chairs and Speakers**

Watch the following pre-recorded presentations, available as of October 25 on the Virtual Platform in the Education Session Area. They will not be played during the Live Session.

- PT02.01 Statistical Considerations for Biomarker Discovery Experiments - Meena Choi
- PT02.02 Statistics for Peptide and Protein Identification and Quantification - Alexey I. Nesvizhskii
- PT02.03 Experimental Design and Data-analysis in Label-free Quantitative LC/MS Proteomics: A Tutorial with MSqRob - Lieven Clement

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WEDNESDAY, NOVEMBER 10, 2021 (PRE-CONGRESS)

14:00 - 15:00 (UTC) **Pre-Congress Training 3 (PT03): Interactomics Approaches**

Proteins do not function in isolation, but rather, they associate with other proteins to form complexes and interaction networks with distinct structures and compositions to execute their function. Moreover, disease-causing genetic mutations may lead to alterations in protein function by modulating the interactions of the mutated proteins. Thus, a fundamental part of understanding a protein's function in health and disease is to systematically study the proteins and other molecules that it interacts with and their dynamic changes in a cellular or disease state. Proteomics is the premier method for mapping protein-protein and protein-ligand interactions. This session will highlight approaches for the identification and characterization of protein-protein interactions and complexes.

Chairs: Ileana Cristea & Ruth Hüttenhain

14:00 **Live Q&A with Chairs and Speakers**

Watch the following pre-recorded presentations, available as of October 25 on the Virtual Platform in the Education Session Area. They will not be played during the Live Session.

- PT03.01 Thermal Protein Profiling - Mikhail M Savitski
- PT03.02 Complex Centric Proteome Profiling - Isabel Bludeau
- PT03.03 Protein-protein Interactions/Spatial Proteomics - Anne-Claude Gingras

16:00 – 19:00 (UTC) **Bioinformatics Hub**

Chair: Eric Deutsch

16:00 Proteogenomics - Current State of the Art and Future Directions
David Fenyö & Sam Payne

17:00 ProteomeXchange - Current Status and Future Directions – Discussion
Juan Antonio Vizcaino

17:30 Proteomics Standards Initiative - Ongoing Projects and Future Directions – Discussion
Eric Deutsch & Dave Tabb

18:00 Human Proteome Project - Human Proteins Absent from Swiss-Prot/neXtProt
Sandra Orchard, Maria Martin, Gil Omenn

18:30 Human Proteome Project - PE1 Validation with Protein-protein Interaction and Similar Data
Sandra Orchard, Lydie Lane

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Wednesday, November 10, 2021

20:00 - 23:00 (UTC) BD-HPP Session - SARS-CoV-2 Through the Lens of Proteomics

20:00 Introductory Remarks

20:05 Peptide Vaccination for COVID19

Speaker: Juliane Walz | **Chair:** Michal Bassani-Sternberg

20:30 Insights from Mapping the HLA Class II-presented Peptidome of the SARS-CoV2 Spike Glycoprotein

Speaker: Nicola Ternette | **Chair:** Maggie Lam

20:55 Molecular Effects of SARS-CoV-2 Infections in a General and Undiagnosed Population

Speaker: Jochen Schwenk | **Chair:** Fernando Corrales

21:20 Sex Differences in Autoantibodies Response to SARS-CoV-2 Infection

Speaker: Justyna Fert-Bober | **Chair:** Ileana Cristea

21:45 Virus-Receptor Interactions of Glycosylated SARS-CoV-2 Spike and Human ACE2 Receptor

Speaker: Oliver Grant | **Chair:** Nicki Packer

22:05 Drug-induced Phospholipidosis Confounds Drug Repurposing for SARS-CoV-2

Speaker: Matthew O' Meara | **Chair:** Aleksandra Nita-Lazar

22:30 Integrated Proteogenomic Characterization Across Seven Histological Types of Pediatric Brain Tumors

Speaker: Francesca Petralia | **Chair:** Ferdinando Cerciello

22:55 Concluding Remarks

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THURSDAY, NOVEMBER 11 (PRE-CONGRESS)

10:00 - 12:00 (UTC) **Bioinformatics Hub**

10:00 **Deep Learning in Proteomics**

Mathias Wilhelm & Cheng Chang & Wassim Gabriel

11:00 **EuBIC-MS: Ongoing Projects and Future Directions**

Tim Van Den Bossche & Ralf Gabriels & Julian Uszkoreit

11:30 **Tutorial: Proteomics in R**

Christian Panse & Tobias Kockmann

14:00 - 15:00 (UTC) **Pre-Congress Training 4 (PT04): Proteomics Informatics Workflows**

Managing the informatics pipeline of a typical proteomics experiment is as important and challenging as managing the experimental and analytical workflows. This session will provide examples of large scale computational workflows for proteomics data management and analysis.

Chairs: Eric Deutsch & Cheng Chang

14:00 **Live Q&A with Chairs and Speakers**

Watch the following pre-recorded presentations, available as of October 25 on the Virtual Platform in the Education Session Area. They will not be played during the Live Session.

- PT04.01 MaxQuant and Perseus Workflows - Jürgen Cox
- PT04.02 DIA Workflows - Brian Searle
- PT04.03 ProteORE for Proteomics Data Interpretation in Galaxy - Yves Vandenbrouck

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FRIDAY, NOVEMBER 12 (PRE-CONGRESS)

14:00 - 15:00 (UTC) **Pre-Congress Training 5 (PT05): Biological Context and Interpretation**

Large-scale proteomics experiments generate an immense amount of data that need to be comprehensively interpreted to extract biological meaning after computational/statistical analyses are completed. This crucial step is required in order to select targets for functional follow-up which could take months to years of work. More specialized mass spectrometry-based experiments (such as interactome identification) also bring specific challenges for biological interpretation. This session will focus on use of large-scale datasets for elucidation of biological function, highlighting tools and strategies that can aid in these steps.

Chairs: Jennifer Geddes-McAlister & Andreas Hober

14:00 **Live Q&A with Chairs and Speakers**

Watch the following pre-recorded presentations, available as of October 25 on the Virtual Platform in the Education Session Area. They will not be played during the Live Session.

- PT05.01 BioPlex 2.0 Project, Interactome - Ed Huttlin
- PT05.02 HPA for Proteomics Data Interpretation - Cecilia Lindskog Bergström
- PT05.03 (Large-scale) Multi-omics Data Analysis - Johannes Griss

14:00 - 15:20 (UTC) **HPP: Session 1 - HPP Project**

Chair: Ileana Cristea

14:00 The Human Proteome Project “Grand Project” A Function for Every Protein
Robert Moritz, Chair HPP

14:15 Translating Proteomics to the Clinical Arena
Tom Montine

14:35 The Pharma Proteomics Project
Chris Whelan

14:55 Target 2035 - Pharmacological Modulators for The Human Proteome Project “Grand Project”
Cheryl Arrowsmith

15:05 Expanding Proteomics Beyond the Proteomic Community with the Human Proteome Project “Grand Project” - Open Discussion

15:15 Wrap up

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Friday, November 12, 2021

16:00 - 17:40 (UTC) HPP: Session 2 - Breakout Group Discussions

Chair: Fernando Corrales

16:00 Questions to Each of the Breakout Session

16:05 Breakout Sessions

- Breakout I - Scientific Advisory Board session - Ruedi Aebersold
- Breakout II - Pathology Pillar "Clinical relevance of the Grand Project" - Michael Roehrl
- Breakout III - Chromosome Centric-HPP "Providing Evidence to Function" – Chris Overall
- Breakout IV - Biology/Disease-HPP "Organizing Functional Consequences" - Ileana Cristea
- Breakout V - MS Pillar/Knowledgebase Pillar/Antibody Pillar – Contribution of Pillars to the Grand Project - Susan Weintraub, Eric Deutsch, Cecilia Lindskog

16:50 Summary - Reports

18:00 - 19:40 (UTC) HPP: Session 3 - Progress and Plans

Chair: Susan Weintraub

18:00 Review and Updates from 2021 (Outcomes and Developments)

- C-HPP - Chris Overall
- B/D-HPP - Ileana Cristea
- Resource Pillar: Ab - Cecilia Lindskog
- Resource Pillar: KB - Eric Deutsch & Nuno Bandeira & Lydie Lane
- Resource Pillar: PP - Michael Roehrl & Ed Nice
- Resource Pillar: MS - Susan Weintraub

18:30 ECR Involvement in HPP and the Grand Challenge
Ferdinando Cerciello

18:40 Open Session – Grand Project Discussion

19:00 Other Opportunities – Questions from Floor

19:10 Final Summary
Rob Moritz

19:15 Incoming HPP Chair Address
Charles Pineau

19:25 Closing Address
Rob Moritz & Ruedi Aebersold

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MONDAY, NOVEMBER 15

11:30 - 12:30 (UTC) HUPO Council Meeting Session 1 (By Invitation Only)

12:45 - 14:15 (UTC) Opening Session & Plenary 1 (PL01) - Visualizing the Cell Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

For a complete understanding of a system's processes and each protein's role in health and disease, it is essential to study protein expression with a spatial resolution, as the exact location of proteins at the tissue, cellular or subcellular levels is tightly linked to protein function. This session highlights new discoveries and emerging efforts based on different spatial technologies.

Chairs: Stephen Pennington & Cecilia Lindskog

12:45 Opening Remarks
Yu-Ju Chen

12:50 Introduction to the HUPO 2021 ReCONNECT Program and Virtual Platform
Henning Hermjakob

13:00 Highlights of the Year
Benjamin Garcia

13:05 PL01.01 Spatiotemporal Dissection of the Human Proteome
Emma Lundberg

13:35 PL01.02 The Dynamic Spatial Organisation of the Cell
Kathryn Lilley

14:05 Live Q&A

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Monday, November 15, 2021

14:30 - 15:45 (UTC) **Session 1 (KN01) - Combating COVID-19**

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

COVID-19 infections have changed the world as we know it, possibly permanently in several ways. Research on coronaviruses has in record time led to a great understanding of the biology and pathology of this modern-day plague, including the development of vaccines. Proteomics has been instrumental in our full understanding of this virus's mechanism and this session will highlight the latest proteomics research in this emergent area.

Chairs: Aleksandra Nita-Lazar & Mehdi Bouhaddou

14:30 KN01.01 Glycomics of Sars-Cov-2: From Structural Biology to Vaccines

Max Crispin

14:50 KN01.02 Chasing SARS-CoV2 and Finding More

Jennifer Van Eyk

15:10 KN01.03 Profiling SARS-CoV-2 HLA-I Peptidome Reveals T Cell Epitopes From Out-of-Frame ORFs

Susan Klaeger

15:20 KN01.04 SARS-CoV-2 Structural Coverage Map Reveals Viral Protein Assembly, Mimicry, and Hijacking Mechanisms

Sean O'Donoghue

15:30 Live Q&A

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16:00 - 17:00 (UTC) **Mentoring Session (MS01): How to Successfully Balance a Personal Life While in Academia**

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

In addition to managing their daily lab work, young researchers are increasingly facing strenuous hurdles, such as maintaining a work-life balance, unclear career prospects, publication pressure, and writing blockades. Organized by HUPO's Early Career Researcher Initiative in partnership with the European Proteomics Association's Young Proteomics Investigators Club, the mentoring sessions extend the scope of HUPO ReCONNECT 2021 from pure science and technology to the topics that indirectly affect our research.

Chairs: Maurine Fucito & Blandine Chazarin

Mentors:

- Christine Carapito, University of Strasbourg
- Harry Whitwell, Imperial College London
- Jennifer Geddes-McAlister, University of Guelph

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Monday, November 15, 2021

17:15 - 18:15 (UTC) **Industry-Supported Seminar (ISS1) - Thermo Fisher Scientific: Roadmap for Translational Proteomics Research and Precision Medicine**



Platform Location: Industry Hub | Industry Hub Auditorium 2

Proteomics has for a long time been expected to shine in the discovery of protein biomarkers in plasma and tissues advancing our understanding of diagnosing diseases such as cancer, monitoring their progression, predicting recurrence and supporting the identification of therapeutic treatment. Topics such as longitudinal studies, targeted assays as well as standardization have been at the forefront of discussion, publications, meetings and task forces. In addition, pushing proteomics technologies to demonstrate the value of proteogenomics for defining the molecular signature of human tumors, and translation to other areas of biomedicine and life sciences has been ongoing. This session will focus on recent research achievements from leaders in the community that delivers a roadmap for translational proteomics research.

17:15 - 18:15 (UTC) **Industry-Supported Seminar (ISS2) - SCIEX: Powerful New Proteomic Workflows Enabled by the SCIEX ZenoTOF System**



Platform Location: Industry Hub | Industry Hub Auditorium 1

Join SCIEX for an exciting session highlighting new innovations and proteomics applications made possible using the [SCIEX ZenoTOF 7600 system](#). Dr. Christie Hunter (SCIEX) will provide a short technology overview and introduce the innovations. Then, Professor Jerome Lemoine from the Institute of Analytical Sciences at the University of Lyon and Professor Anthony Whetton from the Stoller Biomarker Discovery Centre at the University of Manchester will share some exciting early results from the platform that highlight the use of the ZenoTOF 7600 system for biomarker research.

Chair: Dr. Christie Hunter, Director, Application and Technical Marketing, SCIEX

Speakers:

- Dr. Christie Hunter, Director, Application and Technical Marketing, SCIEX
- Professor Jerome Lemoine, Institute of Analytical Sciences at the University of Lyon
- Professor Anthony Whetton, Stoller Biomarker Discovery Centre at the University of Manchester

All times in UTC (Coordinated Universal Time)

Monday, November 15, 2021

18:30 - 19:45 (UTC) Session 2 (KN02) - Precision Pathology: Proteomics for Patients
Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

Precision Medicine is now entering an era that reaches beyond genomics. Pathology, in particular, is transforming to diagnose the precise and quantitative changes of proteins as the machines of life and disease. Proteome-based diagnostic pathology will address crucial clinical needs, and there is an urgent need to develop stringent, fit-for-purpose proteomic assays that can be implemented in the clinic for the benefit of patients. This session will discuss high-impact clinical areas that will be transformed by proteomics and hopes to bring together physicians and scientists to drive this proteomic evolution of health care.

Chairs: Ed Nice & Justyna Fert-Bober

18:30 KN02.01 Proteomics For Patients: How Proteomics Will Transform Medicine

Michael Roehrl

18:50 KN02.02 A Protein-Based Classifier for Thyroid Nodule Diagnosis

Tiannan Guo

19:10 KN02.03 Multiomics Identification and Validation of Novel Blood-Based Alzheimer's Disease Autoantibody Biomarkers

Miren Alonso-Navarro

19:20 KN02.04 Beyond Fibril-Forming Proteins: Developing a More Holistic Approach on Amyloid Formation

Juliane Gottwald

19:30 Live Q&A

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Monday, November 15, 2021

20:00 - 21:00 (UTC) Graduate Student Poster Competition

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

The graduate student poster competition serves as a platform to highlight the important contributions that graduate and PhD students make to the proteomics field. In this session eighth preselected finalists will present their posters and will be evaluated by an expert committee to select a winner and two runner-ups. Each presentation will consist of a 4min presentation and 2min Q&A.

Chairs: Giuseppe Palmisano & Jessica Brandi

20:00 P11.17 MAGPIE: A Machine Learning Approach for Deciphering Protein-Protein Interactions in Human Plasma

Emily Hashimoto-Roth

20:06 P08.14 Identification of Protein Biomarkers in FFPE Primary Tissues to Predict Recurrence in Endometrial Cancer

Carlos López Gil

20:12 P11.42 SAPID-MSI: Spatially-Aware Protein Identification Algorithm for Mass Spectrometry Imaging

Soroush Shahryari Fard

20:18 P10.04 Cell Surface Phenotyping of the Human Heart Reveals Cardiomyocyte-Specific Targets and Surfaceome Dynamics of Explanted Cardiac Fibroblasts

Linda Berg Luecke

20:24 P12.C11 Data-Independent Acquisition Method for Ubiquitinome Analysis Reveals Regulation of Circadian Biology

Fynn Hansen

20:30 P08.12 Species-Specific Cutaneous Protein Signatures of Incision Injury and Correlation with Distinct Pain-Related Phenotypes in Humans

Christin Kappert

20:36 P10.09 The Proteomic Analysis of High Grade Serous Ovarian Cancer Reveals the Role of Tumor Microenvironment in Chemoresistance

Kruttika Dabke

20:42 Live Q&A

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Monday, November 15, 2021

21:15 - 22:15 (UTC)

Industry- Supported Seminar (ISS3) - BSI: Towards an In-depth Understanding of the HLA Immunoepitome Using MS-based Workflows



Platform Location: Industry Hub | Industry Hub Auditorium 1

Chair: Katherine Tran, Sales Department Manager at Bioinformatics Solutions Inc.

Speakers:

- Curtis McMurtrey, Ph.D., Director of Immunoepitomics at PureMHC
- Jonathan R. Krieger, Ph.D., Applications Manager at Bioinformatics Solutions Inc.
- Hieu Tran, Senior Research Scientist at Bioinformatics Solutions Inc.

23:00 - 00:00 (UTC)

HUPO Council Meeting Session 2 (By Invitation Only)

All times in UTC (Coordinated Universal Time)

TUESDAY, NOVEMBER 16

13:00 - 14:15 (UTC) **Plenary Session 2 (PL02) - Omics at Single-Cell Resolution**

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

Single-cell omics is taking a quantum leap to dissect biology at individual cell resolution. This session will present emerging technologies and applications in single-cell omics.

Chairs: Catherine CL Wong & Blandine Chazarin

13:00 PL02.01 Single Cell/Deep Visual Proteomics
Matthias Mann

13:30 PL02.02 Increasing the Sensitivity, Reliability, Reproducibility and Throughput of Single-Cell Proteomics
Nikolai Slavov

14:00 Live Q&A



This session is sponsored by:

14:30 - 15:45 (UTC) **Session 3 (KN03) - Technological Advancements in Proteomics**

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

This session will focus on new technologies for proteomics, highlighting improved ways to handle challenging samples, cutting-edge approaches and instrumentation for sample analysis, and enhanced strategies for data processing. Presentations will include examples of biological and/or clinical applications that illustrate the performance of the new technology.

Chairs: Gary Kruppa & Maurine Fucito

14:30 KN03.01 Ultra-Fast Proteomics and How It Opens New Doors for Gene Function Prediction, Drug Screens, and Clinical Proteomics Using AI
Markus Ralser

14:50 KN03.02 MONTE: A Multiomics Suite Enabling Serial Immunopeptidome, Ubiquitylome, Proteome, Phosphoproteome, Acetylome Analyses of Sample-Limited Tissues
Steven Carr

15:10 KN03.03 Next-generation Serology by Mass Spectrometry: Ig-MS Readout of the SARS-CoV-2 Antibody Repertoire
Rafael Melani

15:20 KN03.04 In-depth Plasma Proteomics Profiling with ProteographTM Product Suite: A Performance Evaluation of Label Free and TMT Multiplexing Approaches
Alex Rosa Campos

15:30 Live Q&A

All times in UTC (Coordinated Universal Time)

Tuesday, November 16, 2021

16:00 - 17:00 (UTC) Poster Session

Platform Location: Posters Sections 1 - 8

Poster presenters are available at their posters to present their work, chat with you and answer your questions.

17:15 - 18:15 (UTC) Industry-Supported Seminar (ISS4) - Bruker: Advances in 4D-Proteomics™: Plasma Proteomics and Targeted Quantitative Biology



Platform Location: Industry Hub | Industry Hub Auditorium 1

Chair: Chris Adams, Bruker Daltonics

17:15 prm-PASEF-based Biomarker Discovery in Serum from Colon Cancer Patients
Prof. Gunnar Dittmar, Head of Quantitative Biology, Luxembourg Institute of Health (LIH)

Patient serum is a preferred biofluid for diagnostic purposes as it is readily available. The biomarker detection in serum is usually hindered by the enormous dynamic range of protein abundance, making the reliable measurement of lower abundant proteins challenging. Targeted proteomic analysis of selected proteins offers an alternative to dig deeper and detect low abundant protein in this complex matrix. The development of PRM-PASEF combines the advantages of PRM with the additional selectivity of ion-mobility. Using an extensive collection of isotope-labeled reference peptides, we systematically screened patient serum for biomarkers with a high dynamic range in a very short time using fast liquid chromatography.

17:45 Toward Comprehensive Plasma Proteomics by Orthogonal Protease Digestion
Asst. Prof. Danielle Swaney, Cellular and Molecular Pharmacology, University California San Francisco (UCSF)

Rapid and consistent protein identification across large clinical cohorts is an important goal for clinical proteomics. Here we apply a simple and accessible tip-based workflow for the generation of DIA spectral libraries to provide a comprehensive overview on the plasma proteome in individuals with and without active tuberculosis (TB). To boost protein coverage, we utilized non-conventional proteases together with the gold standard trypsin, identifying more than 30,000 peptides mapping to 3,309 proteins. Application of this library to quantify plasma proteome differences in TB infection recovered more than 400 proteins in 50 minutes of MS-acquisition, including the direct detection of diagnostic Mycobacterium tuberculosis (Mtb) proteins.

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Tuesday, November 16, 2021

17:15 - 18:15 (UTC) Industry-Supported Seminar (ISS5) - Biognosys: Unearth the Full Potential of DDA Proteomics with SpectroMine 3



Platform Location: Industry Hub | Industry Hub Auditorium 2

Chair: Maximilian J. Helf (Biognosys)

17:15 What's New in SpectroMine 3

Tikira Temu (Biognosys)

Lead developer Tikira Temu is presenting new features in SpectroMine 3, the latest version of our all-in-one software solution for DDA proteomics. Learn how to make the most of your isobaric labeling quantification (ILQ) data, including TMTpro 18-plex experiments. The new PTM workflow makes it easy to extract valuable information about peptide modifications while taking full advantage of Pulsar, our industry-leading search engine. SpectroMine 3 also comes with improved fractionation support, specialized immunopeptidomics functionalities, and dramatically increased processing speed, especially for analyses with multiple variable modifications.

17:45 Improving Single Cell Proteomics with Advanced Data Acquisition and Data Analysis

Erwin M. Schoof (Technical University of Denmark)

Blood cells are a prime example of complex cellular hierarchy, with Hematopoietic Stem Cells (HSC) as the origin of many cell lineages. The Schoof lab subjected healthy and malignant hematopoietic cells to fluorescence-activated cell sorting (FACS) combined with novel single-cell proteomics (scMS) strategies. Using the latest LC-MS instrumentation with intelligent data acquisition and advanced data analytics provided by Spectromine 3.0, this approach resulted in unprecedented maps of protein expression in individual cells. Furthermore, they developed a computational workflow (SCeptre) for effective MS data post-processing and FACS data integration to extract cell-specific proteins. Results show enrichment of cell-type-specific proteins in various compartments, and protein signatures that clearly distinguish the differentiation stages within their respective hierarchies.

20:00 - 21:00 (UTC) HUPO General Assembly of Members Session 1

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

All times in UTC (Coordinated Universal Time)

Tuesday, November 16, 2021

21:15 - 22:15 (UTC) ECR Networking Hour

Platform Location: ECR Lounge

The ECR Networking Hour is an open forum to bridge the digital, cultural, and continental gaps so that early-stage researchers can meet, share, and create bridges for future collaboration. Participants are encouraged to engage with their cameras and join in both the ice-breaker and proteomics-related networking. In preparation for the ECR Networking Hour, participants are encouraged to set up a LinkedIn or Twitter handle to keep the engagement going beyond November 16.

Chairs: Rob Rivers & Omar Mendoza Porras

Mentors are encouraged to attend

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WEDNESDAY, NOVEMBER 17

13:00 - 14:15 (UTC) **Plenary Session 3 (PL03) - Proteome-wide Structural Biology** Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

A fundamental understanding of how proteins function in biology and disease requires a detailed characterization of their structures and the structural dynamics through protein interactions and post-translational modifications. This session will highlight emerging proteomics approaches to globally map protein structure alterations.

Chair: Juri Rappsilber & Ruth Ruth Hüttenhain

13:00 PL03.01 3D Proteomics: From Structural to Functional Screens
Paola Picotti

13:30 PL03.02 Structural Biology on the Proteome-Wide Scale Using Protein Footprinting
Lisa Jones

14:00 Live Q&A

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14:30 - 15:45 (UTC) **Session 4 (KN04) - Translating Proteomics into the Clinic** Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

Proteomics has led to the discovery of new biomarkers in a wide range of diseases. This session will present new technologies to accelerate detection and prediction of diseases, and assay development from discovery to clinical use.

Chairs: Bernd Wollscheid & Chia Jung Yu

14:30 KN04.01 Development and Delivery of Protein Biomarkers for Patient Benefit: "It's Easy"
Stephen Pennington

14:50 KN04.02 Approach to Hypothesis Building from Multi-Omics Using Human Plasma Samples
Yoshiya Oda

15:10 KN04.03 Approaching a Non-invasive Diagnosis of Endometrial Cancer by the Analysis of Protein Biomarkers in Pap-Smears
Eva Coll-de la Rubia

15:20 KN04.04 Health Surveillance Panel Multiplexed MRM-Based Protein Assay for the Identification of Multiple Biomarkers of Disease Severity in Human Coronary Disease
Esthelle Hoedt

15:30 Live Q&A

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Wednesday, November 17, 2021

16:00 - 17:00 (UTC) Hot Topic Discussion 1: Future Preparedness for Pandemics: Role of Proteomics & Multi-omics Technologies

Platform Location: Education Sessions & Recordings | Hot Topic Room Future Preparedness...

Coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has rapidly spread throughout the globe. What has compounded the problem is the non-availability of robust detection methods as well as lack of knowledge of how to treat the disease. There has never been a more urgent situation ever before to review our preparedness for future pandemics. The panellist will discuss role of proteomics, multi-omics technologies, big data and ML for COVID-19 rapid detection methods, disease prognosis and therapeutic approaches.

Moderator: Sanjeeva Srivastava

Discussants: Joshua LaBaer, Graham Ball, Tiannan Guo, Shantanu Sengupta

16:00 - 17:00 (UTC) Hot Topic Discussion 2: Moms in Proteomics

Platform Location: Education Sessions & Recordings | Hot Topic Room Moms in Proteomics...

Supporting women in STEM, and in particular, the rapidly expanding field of proteomics, needs to go beyond traditional methods of mentorship and promotion by recognizing and encouraging mothers to pursue careers in STEM. The intricate balance between managing a successful research program, writing grant applications, teaching and mentoring trainees, and fulfilling institutional and external service commitments, all while raising young children and caring for their needs, is demanding, challenging, and daunting for many women and mothers. This Hot Topic will provide an opportunity to connect with other mothers in STEM, share stories of success and failure, and build a network for success of mothers in highly productive and influential careers.

Moderator: Jennifer Geddes-McAlister

Discussants: Francesca Sacco, Maria Pavlou, Scarlet Koch, Natalie Krahmer, Ruth Hüttenhain

16:00 - 17:00 (UTC) Hot Topic Discussion 3: Standardization is Key

Platform Location: Education Sessions & Recordings | Hot Topic Room Standardization is Key...

Reviewing the methods sections in published papers, it looks like everybody has their own standard or optimized solution. But the variety makes it difficult to reproduce the experiments, makes it harder to compare results, and slows down knowledge transfer. The question then is whether standardization will hurt innovation or enable a deeper focus on the biological mechanisms under study.

Moderator: Nicolai Bache

Discussants: Jennifer Van Eyk, Phil Robinson, Martin Overgaard, Nicolai Albrechtsen

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Wednesday, November 17, 2021

17:15 - 18:15 (UTC) **Industry-Supported Seminar (ISS6) - Olink: Exploring Molecular Phenotypes of Incident Breast Cancer Through Population-based Proteogenomics**



Platform Location: Industry Hub | Industry Hub Auditorium 2

Speaker: Anders Malarstig, Director Target Sciences, Pfizer Worldwide Research, Development & Medical, Stockholm & Senior Researcher, Department of Medical Epidemiology and Biostatistics, Karolinska Institute, Sweden

Proteins play key roles in malignant transformation and represent an important hub for oncogenic signaling. Elevated levels of circulating proteins can be identified years before onset of cancer diagnoses. This session will focus on exploring the power of proteomic discoveries at the population scale in breast cancer cohort, and integration of proteogenomics to generate key biological insights into risk prediction of breast cancer that may lead to translational applications for breast cancer prevention.

17:15 - 18:15 (UTC) **Industry-Supported Seminar (ISS7) - Somalogic: New Insights and Discoveries from Massive Scale Proteomics**



Platform Location: Industry Hub | Industry Hub Auditorium 1

Speaker: Dr. Kári Stefánsson, CEO deCode Genetics

In this 45-minute talk, Dr. Stefánsson will discuss the largest population proteomics study ever performed to help provide more insight on disease and health outcomes. This collaborative research assembled expertise from deCode Genetics and SomaLogic to combine the study of genetic and protein diversity to characterize disease biomarkers in the human population. The data from this type of proteomic study will inform drug discovery and development as well as improvements in health management.

You will learn about:

- The high-throughput technologies (e.g., mass spectrometry) that made this study possible
- The application of population proteomics in diagnosis and management of common and rare diseases

All times in UTC (Coordinated Universal Time)

Wednesday, November 17, 2021

18:30 - 19:45 (UTC) Session 5 (KN05) - Brain Rewiring in Neurological Disorders

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

As the world's population ages, age-related neurological disorders will continue to increase in numbers affected. Proteomics technologies will continue to play a central role in understanding how perturbations in protein modification, protein interactions, and localization in the brain propagate disease states. This session will illuminate recent findings that hold promise for new therapeutic targets and biomarkers.

Chairs: Renā A. S. Robinson & Ling Hao

18:30 KN05.01 Mass Spectrometry in the Pandemic: Translation and Collaboration for Diagnostics and Prognostics

Perdita Barran

18:50 KN05.02 Using Large Data Approaches to Diagnose and Drug Dementia

Judith Steen

19:10 KN05.03 Parallel Proteomic and Microscopy Analyses Identify Protein Networks Associated with Synapse Loss Across Aging in the Human Brain

Matthew MacDonald

19:20 KN05.04 Proteomic/PTMomic Screening of Human Parkinson's Disease iPSC-derived Neurons Identifies Disease Phenotypes and Potential Therapeutic Targets

Helle Bogetofte

19:30 Live Q&A

20:00 - 21:00 (UTC) Mentoring Session (MS02) - Scientific Integrity

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

In addition to managing their daily lab work, young researchers are increasingly facing strenuous hurdles, such as maintaining a work-life balance, unclear career prospects, publication pressure, and writing blockades. Organized by HUPO's Early Career Researcher Initiative in partnership with the European Proteomics Association's Young Proteomics Investigators Club, the mentoring sessions extend the scope of HUPO ReCONNECT 2021 from pure science and technology to the topics that indirectly affect our research.

Chairs: Andreas Hober & Emily Hashimoto-Roth

Mentors: Stephen Pennington & Suzanne Farley & Anne-Claude Gingras

All times in UTC (Coordinated Universal Time)

Wednesday, November 17, 2021

21:15 - 22:15 (UTC) Industry-Supported Seminar (ISS8) - ThermoFisher Scientific: Post-translational Modifications - The Third Disruptive Wave in Proteomics



Platform Location: Industry Hub | Industry Hub Auditorium 2

We have lived through two waves of disruptions in proteomics, the “identification ID” disruption where the large number of identified proteins enabled by LC/MS and bioinformatics. The second wave became “quantitative” enabling 1000’s of proteomes to be quantitatively compared among each other.

Now, we are about to enter the third disruptive wave, where deciphering protein function is key to push the understanding of biology further. To that end, the study of “post-translational modifications PTMs” is becoming more important due to their contribution to the regulation of protein function and exponentially growing the functional diversity of the proteome and even efforts to generate PTM atlases.

This session will focus on several approaches to PTM analysis from leaders in the community, on the path for the elucidation of the biological function of proteins or protein groups and classes on a proteome-wide level. To understand the physiological processes by pushing MS approaches and seeing the complete picture of the modified proteome.

21:15 - 22:15 (UTC) Industry-Supported Seminar (ISS9) - Seer: Advances in Untargeted Plasma Proteomics Analysis with the Proteograph™ Product Suite



Platform Location: Industry Hub | Industry Hub Auditorium 1

Chair: Khatereh Motamedchaboki, Seer Inc.

21:15 Enhanced Protein Coverage and Analysis Scale with New Nanoparticle-based Technology for Plasma Proteomics

Daniel Hornburg, Ph.D. Sr. Director of Research and Tech Development, Seer Inc.

- Current challenges in scaling plasma proteomics
- Enhanced depth of coverage and throughput with Seer’s Proteograph platform
- Exploration of physicochemical properties of engineered nanoparticles with protein selectivity enabling deeper proteome coverage

21:45 Large-Scale, Deep and Untargeted Plasma Proteomics for a Multi-Cancer Biomarker Discovery Study
 Bruce E. Wilcox, Ph.D. VP of Proteomics, PrognoMiQ

- The importance of plasma proteomics in multi-omics research and biomarker discovery
- Advantages of Seer’s Proteograph Product Suite to analyze the plasma proteome at scale
- Experience with the Proteograph platform for a large-scale plasma proteomics project in multi-cancer clinical research

All times in UTC (Coordinated Universal Time)

Wednesday, November 17, 2021

23:00 - 00:00 (UTC) ECR Manuscript Competition

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

The manuscript competition serves as a platform to highlight the important contributions that postdoctoral fellows, young clinicians, and junior faculty members make to the proteomics field. In this session, three preselected finalists will present their publications and will be evaluated by an expert committee to select the "Proteomics Highlight of the Year". Each presentation will consist of a 12min talk and 8min live Q&A. Awards along with cash prizes (\$1,000 to winner, \$500/each to two runners ups) will be presented to the finalists during the Closing Ceremony & Awards Session on November 19, 2021. In addition, the three finalists will receive complimentary registration for HUPO ReCONNECT 2021.

Chairs: Maike Langini & Christian Moritz

23:00 The Global Phosphorylation Landscape of SARS-CoV-2 Infection

Mehdi Bouhaddou

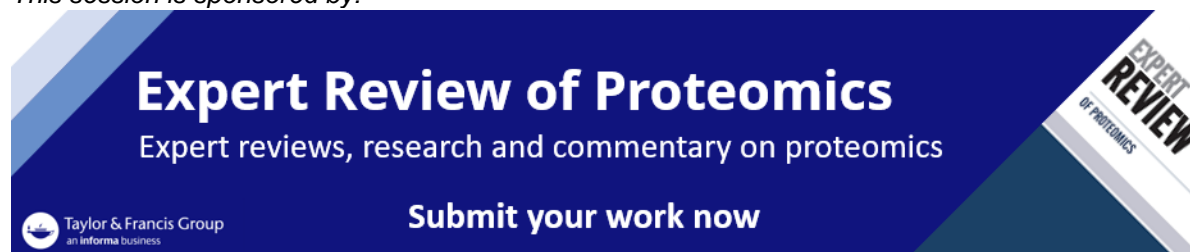
23:20 Benefits of Chemical Sugar Modifications Introduced by Click Chemistry for Glycoproteomic Analyses

Stacy Malaker

23:40 Global and Site-specific Effect of Phosphorylation on Protein Turnover

Yansheng Liu

This session is sponsored by:



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THURSDAY, NOVEMBER 18

00:15 - 01:30 (UTC) Session 6 (KN06) - Proteomics-guided Therapeutics

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

Compared to gene-centric measurements, proteomics accurately reflects the action, mechanism, and effect of therapy. This session will highlight proteomics technologies to guide immuno-oncology, accelerate pharmaceutical research and development, and technological advancements in chemical proteomics.

Chairs: Bernhard Kuster & Teck Yew Low

00:15 KN06.01 Insights into the Tumour Immunopeptidome and its Role in Personalized Immunotherapy
Anthony Purcell

00:35 KN06.02 Exploring Drug-Target Interaction Using Label-Free Darts and Lc-MS/Ms. Method and Its Translational Impact
Hojeong Kwon

00:55 KN06.03 Proteomic Markers Predict Response to Methotrexate in Patients with Early Rheumatoid Arthritis
Rocío Paz González

01:05 KN06.04 Warp-speed Selectivity Profiling of Small Molecule Inhibitors Using μ SPE Chip-based CE-MS with PRM-LIVE Acquisition on an Ion Mobility Mass Spectrometer
Jarrod Marto

01:15 Live Q&A



This session is sponsored by:

01:30 – 03:00 (UTC) Poster Viewing and Networking Time

All times in UTC (Coordinated Universal Time)

Thursday, November 18, 2021

03:00 - 04:15 (UTC) Plenary Session 4 (PL04) - Proteomics-driven Precision Medicine

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

The promise of precision medicine aims to deliver customized medication to subgroups of patients based on molecular or cellular analysis. This section will highlight proteomics-driven translational studies with diagnostic and/or therapeutic impacts.

Chairs: Henry Rodriguez & Rob Rivers

03:00 PL04.01 Proteomics-driven Precision Medicine

Fuchu He

03:30 PL04.02 Tackling Cancer Proteomic Heterogeneity Towards Early Diagnostics and Precision Medicine

Tamar Geiger

04:00 Live Q&A



This session is sponsored by:

04:30 - 05:30 (UTC) Poster Session

Platform Location: Poster Sections 1 - 8

Poster presenters are available at their posters to present their work, chat with you and answer your questions.

05:45 - 06:45 (UTC) HUPO General Assembly Session 2

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

23:00 - 00:00 (UTC) Hot Topic Discussion 4: Metaproteomics

Platform Location: Education Sessions & Recordings | Hot Topic Room Metaproteomics

Metaproteomics – measuring the composite proteome from multiple organisms in a community — touches upon all aspects of conventional proteomics workflows, but much more intensely. Real or perceived challenges that are uniquely related to metaproteomics can create obstacles for newcomers to this endeavor. We will discuss these obstacles – ranging from sample acquisition and storage to instrumentation and computational complexities – and how to approach them for applications related to human health and environmental studies.

Discussants: Daniel Figey, Robert Hettich, Mary Lipton

All times in UTC (Coordinated Universal Time)

Thursday, November 18, 2021

23:00 - 00:00 (UTC) Hot Topic Discussion 5: Glycoproteomics Needs Glycobioinformatics

Platform Location: Education Sessions & Recordings | Hot Topic Room Glycoproteomics...

Recent developments in sample preparation, mass spectrometry and associated software tools facilitate the analysis of intact glycopeptides. However, bioinformatic tools for glycoproteomics are in their infancy compared to those available for more traditional proteomics, and considerable variation in performance metrics and interpretation currently exist among available tools and users. The lack of established guidelines and workflows for applying basic principles of glycobiology and tools for false-discovery rate estimation currently present challenges to accurate data reporting. In this session, experts in glycobiology and bioinformatics will discuss challenges and pose solutions to increase accuracy and reproducibility when interpreting mass spectrometry-based glycoproteomics data.

Moderator: Rebekah Gundry

Discussants: Frederique Lisacek, Robert Chalkley, Morten Andersen

23:00 - 00:00 (UTC) Hot Topic Discussion 6: Top-down MS and Native Proteomics

Platform Location: Education Sessions & Recordings | Hot Topic Room Top-down MS...

This session will focus on current challenges, applicable solutions, and future directions of top-down MS and native proteomics. Several proposed topics include native top-down, data analysis/statistics/quantitation, and application/sample preparation in top-down proteomics. We will have an open and robust discussion between the audience and the discussants (panelists) after a brief introduction of each topic from the moderator/discussant.

Moderator: Si Wu

Discussants: Ljiljana Pasa-Tolic, Ying Ge, Neil Kelleher, Joseph Loo

23:00 - 00:00 (UTC) Hot Topic Discussion 7: Next Generation Proteomics Technologies: NGS, Microarray and Other Technology Platform Read Out

Platform Location: Education Sessions & Recordings | Hot Topic Room Next Generation...

Discuss emerging proteomics technologies and their applications. What are the advantages and limitations of those technologies and future trending? What are the main application areas, what will be enabled by these technologies? How do these technologies add value to drug development pipelines?

Moderator: Fiona Kaper

Discussants: Towia Liberman, Carl Barrett, Addeb Rahman

All times in UTC (Coordinated Universal Time)

Thursday, November 18, 2021

23:00 - 00:00 (UTC)

Hot Topic Discussion 8: The Human Proteome Project Grand Project – Advancing the Human Proteome

Platform Location: Education Sessions & Recordings | Hot Topic Room The Human Proteome...

Discussants: Charles Pineau, Gil Omenn, Robert Moritz, Ruedi Aebersold, Ileana Cristea, Cecilia Lindskog, Lydie Lane

All times in UTC (Coordinated Universal Time)

FRIDAY, NOVEMBER 19

00:15 - 01:30 (UTC) **Session 7 (KN07) - Proteomics Data Science and AI**

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

Proteomics data science has developed from an appendix of data generation to the center stage, often requiring as much planning, time, and resources as the experimental component. This session will present current challenges and approaches, from proteogenomics to AI.

Chairs: Tiannan Guo & Kun-Hsing Yu

00:15 KN07.01 Connecting Tumor Histopathology Images With Molecular Features Using Multi-Resolution Deep Learning Models

David Fenyö

00:35 KN07.02 Pride and Proteomexchange: Enabling “Big Data” Approaches in the Proteomics Field

Juan Antonio Vizcaino

00:55 KN07.03 Ionbot: A Novel, Innovative and Sensitive Machine Learning Approach to LC-MS/MS Peptide Identification

Sven Degroove

01:05 KN07.04 Systematic Detection of Functional Proteoform Groups from Bottom-up Proteomic Datasets

Isabell Bludau

01:15 Live Q&A

01:30 – 03:00 (UTC) **Poster Viewing and Networking Time**

03:00 - 04:15 (UTC) **Plenary Session 5 (PL05) - The Future of Proteomics**

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

Proteomics is mature for system-wide measurement and quantification of protein expression levels, but also for comprehensive analyses at the single cell level. This session will highlight and discuss the future of proteomics and what is the place of the technology in precision medicine and precision health.

Chairs: Lennart Martens & Mathieu Lavallée-Adam

03:00 PL05.01 Thoughts on the Future of Proteomics

Mike Snyder

03:30 PL05.02 Exploring Uncharted Facets of the Proteome

Ruedi Aebersold

04:00 Live Q&A



This session is sponsored by:

All times in UTC (Coordinated Universal Time)

Friday, November 19, 2021

04:30 - 05:30 (UTC) Mentoring Session (MS03): Getting Started on Writing Manuscripts, Grants, and Fellowships

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

In addition to managing their daily lab work, young researchers are increasingly facing strenuous hurdles, such as maintaining a work-life balance, unclear career prospects, publication pressure, and writing blockades. Organized by HUPO's Early Career Researcher Initiative in partnership with the European Proteomics Association's Young Proteomics Investigators Club, the mentoring sessions extend the scope of HUPO ReCONNECT 2021 from pure science and technology to the topics that indirectly affect our research.

Chairs: Mio Iwasaki & Justyna Fert-Bober & Robert Rivers

Mentors: Yasushi Ishihama, Kyoto University | Rebekah L. Gundry, University of Nebraska | Molecular Omics Representative

This session is supported by:



05:45 - 06:45 (UTC) Industry-Supported Seminar (ISS10) - Bruker: Advances in 4D-Proteomics™: Single Cell Proteomics and PaSER Real-Time Search



Platform Location: Industry Hub | Industry Hub Auditorium 1

Chair: Gary Kruppa, Bruker Daltonics

05:45 Single Cell Proteome (SCP) using Glass-Oil-Air-Droplet (GOAD) Nano Chip Device and its Application on Embryo Development

Prof. Catherine C.L. Wong, School of Basic Medical Sciences, Peking University Health Science Center, Center for Precision Medicine Multi-Omics Research

Deep single-cell proteome has great biological significance for understanding cellular heterogeneity. To overcome the barriers along the processes of shotgun SCP, we firstly developed a nanoliter-scaled glass-oil-air-droplet (GOAD) chip using miniaturized stationary droplet microreaction and manipulation techniques for multi-step sample pretreatment. We identified more than 1300 protein groups from a 200pg standard cell digest using timsTOF mass spectrometer in parallel-accumulation-serial-fragmentation (PASEF) scanning mode. We further demonstrate the application of GOAD chip device for the first time SCP analysis on embryo development. This method has great potential for achieving ultrasensitive proteomic analysis on single-cell level.

All times in UTC (Coordinated Universal Time)

Friday, November 19, 2021

06:15 PaSER and CCS-aware 4D Informatics

Robin Park, Director of Bioinformatics, Bruker Daltonics

PaSER is a real time GPU-based search engine designed to take advantage of the massive parallelization possible on GPUs to enable real time search. Real-time database search means that bottom-up shotgun proteomics data can be processed as quickly as it is acquired by the mass spectrometer. This results in "Run and Done", meaning that when your sample run is done the database search results are ready and can be used for making real time decisions about the next steps in your sample queue. PaSER will also implement the use of CCS values obtained with 4D-Proteomics methods for improving the FDR in database searches and in particular to improving de novo peptide identification. Additional late breaking developments in PaSER portfolio will be discussed.

07:00 - 08:30 (UTC) Closing Ceremony & Award Lectures

Platform Location: Education Sessions & Recordings | Education Sessions Auditorium

07:00 Congress Summary & Thank You

Henning Hermjakob

07:05 Announcement of Graduate Poster and ECR Manuscript Competition Winners

Ruth Hüttenhain & Mathieu Lavallée-Adam

07:15 Clinical & Translational Proteomics Sciences Award

Ying Ge

07:25 Discovery in Proteomic Sciences Award

Paola Picotti

07:35 Distinguished Achievement in Proteomic Sciences Award

Nicolle H. Packer

07:45 Distinguished Service Award

Stephen Pennington

07:55 Science & Technology Award

Nicolai Bache & Ole Vorm

08:10 HUPO 2022 Cancun Invite

Sergio Encarnacion Guevera & Luis Manuel Teran

08:15 Closing Remarks

Yu-Ju Chen