

Program

OL: Opening Lectures

Saturday, September 14 17:30-18:30 Main Hall

Chair:

Pierre Legrain

Ecole Polytechnique, France

OL-01 17:30-18:00

Innovative Technology for Sequence Analysis of Intact Proteins on a Chromatographic Time-Scale

Donald F. Hunt

Departments of Chemistry and Pathology, University of Virginia, USA

OL-02 18:00-18:30

New Gene Expression Regulation World Based on Transcriptome Network

Yoshihide Hayashizaki

RIKEN Preventive Medical Innovation Program, Japan

PL01: Plenary Lecture 01

Sunday, September 15 9:40-10:50 Main Hall

Chair:

Gilbert S. Omenn

University of Michigan, USA

PL01-01 9:40-10:10

New Technologies for MS-Based Proteomics and their Application in Biology and Biomedicine

Matthias Mann

Max-Planck Institute of Biochemistry, Germany

Novo Nordisk Foundation Center for Protein Research, Denmark

PL01-02 10:15-10:45

Defining the Human Tissue-Specific Proteomes Based on Transcriptomics and the Human Protein Atlas

Mathias Uhlen

Science for Life Laboratory, Royal Institute of Technology (KTH), Sweden

PL02: Plenary Lecture 02

Sunday, September 15 17:30-18:05 Main Hall

Chair:

Catherine Fenselau

University of Maryland, USA

PL02-01 17:30-18:00

Proteomics and Neurobiology

John R. Yates III, Jeffrey Savas

Department of Chemical Physiology, The Scripps Research Institute, USA

PL03: Plenary Lecture 03
(Co-organized by Yokohama City University)

Monday, September 16 9:40-10:50 Main Hall

Chair:

Tesshi Yamada

National Cancer Center Research Institute, Japan

PL03-01 9:40-10:10

SWATH-MS: Principles and Applications to Quantitative Biology

Rudolf H. Aebersold

Department of Biology, Institute of Molecular Systems Biology, ETH Zurich and Faculty of Science,
University of Zurich, Switzerland

PL03-02 10:15-10:45

neXtProt: The Human Protein Knowledge Platform in the Context of HPP

Amos Bairoch

Swiss Institute of Bioinformatics and University of Geneva, Switzerland

PL04: Plenary Lecture 04

Tuesday, September 17 9:40-10:50 Main Hall

Chair:

Kazuyuki Nakamura

Yamaguchi University, Japan

PL04-01 9:40-10:10

Unleashing the Power of Proteomics to Develop Blood Based Cancer Markers

Samir Hanash

MD Anderson Cancer Center, USA

PL04-02 10:15-10:45

A Decade of Adventures of CNHUPO and HLPP

Fuchu He^{1,2}

¹State Key Laboratory of Proteomics, Beijing Proteome Research Center, Beijing Institute of Radiation
Medicine, China, ²National Engineering Research Center for Protein Drugs, China

PL05: Plenary Lecture 05
(Organized by the Human Proteome Project)

Wednesday, September 18 13:45-14:55 Room 303+304

Chair:

Young-Ki Paik

Yonsei University, Korea

PL05-01 13:45-14:15

Metabolic Phenotyping and Systems Medicine in the Real World

Jeremy K. Nicholson

Imperial College London, UK

PL05-02 14:20-14:50

Evolution of Alternative Splicing and Transcriptional Regulation by Transposable Elements

Heui-Soo Kim

Department of Biological Sciences, College of Natural Sciences, Pusan National University, Korea

PS01: New Technology in Mass Spectrometry 1

[Technology Session]

Sunday, September 15 11:00-12:50 Main Hall

Chairs:

Georgy Marko-Varga
Juan Pablo Albar

Lund University, Sweden
Centro Nacional de Biotecnología - CSIC, ProteoRed-ISCIII, Spain

PS01-01 11:00-11:25

Proteomic Approaches for Quantitative Protein Complex Analysis

Marius Ueffing^{1,2}, Andreas Vogt¹, Yves Texier¹, Bettina Fuerholzner¹, Grischa Toedt³,
Toby Gibson³, Norbert Kinkl¹, Karsten Boldt¹

¹Medical Proteome Center, Centre for Ophthalmology, University of Tübingen, Germany, ²Department of Protein Science, Helmholtz Zentrum München, German Research Center for Environmental Health, Germany, ³Structural and Computational Biology Unit, European Molecular Biology Laboratory, Germany

PS01-02 11:30-11:55

Workflows and Solutions for Targeted Quantification to Increase Throughput and Sensitivity

Amol Prakash
Thermo Fisher Scientific, USA

PS01-03 12:00-12:25

Proteomic Analysis of Colon Cancer Phenotypes

Robbert J. C. Slebos
Vanderbilt University Medical School, USA

PS01-04 12:30-12:45 (POS-03-154)

Quantitative CID Cleavable Crosslink Strategy on a Benchtop Instrument Using All-Ion-Fragmentation and SILAC

Richard A. Scheltema, Herbert Schiller, Matthias Mann
Max-Planck Institute for Biochemistry, Germany

PS02: Antibody Proteomics and Protein Atlas

[Technology Session]

Sunday, September 15 11:00-12:50 Room 303+304

Chairs:

Mathias Uhlen
Tadashi Kondo

Royal Institute of Technology (KTH), Sweden
National Cancer Center Research Institute, Japan

PS02-01 11:00-11:25

Design, Operation and Application of an Automated High Throughput Monoclonal Antibody Facility to Support Global Proteomics Initiatives

Edouard Nice, Daniel Layton, Caroline Laverty
Monash Antibody Technologies Facility, Monash University, Australia

PS02-02 11:30-11:55

Exploration of the Protein Coding Genome

Caroline Kampf¹, Fredrik Ponten¹, Linn Fagerberg², Bjorn Hallstrom², Emma Lundberg²,
Kalle Jonasson², Mathias Uhlen²

¹Department of Immunology, Genetics and Pathology, Science for Life Laboratory, Sweden, ²Science for Life Laboratory, Department of Proteomics, KTH - Royal Institute of Technology, Sweden

PS02-03 12:00-12:25

Chemical Proteomics for Target Identification and for the Development of Therapeutic Antibodies: From the Bench to the Clinic

Dario Neri

Swiss Federal Institute of Technology (ETH Zürich), Switzerland

PS02-04 12:30-12:45 (POS-01-033)

Development of an Automated Immuno-MALDI Assay for the Clinical Measurement of Plasma Renin Activity

Robert Popp¹, David Malmstrom¹, Alexander G. Camenzind¹, Daniel T. Holmes², J. Grace van der Gugten², Christoph H. Borchers^{1,3}

¹University of Victoria, Genome BC Proteomics Centre, Canada, ²St. Pauls Hospital, University of British Columbia, Canada, ³University of Victoria, Dept. of Biochemistry and Microbiology, Canada

PS03: Single Cell Proteomics

Sunday, September 15 11:00-12:50 Room 301

Chairs:

Mark S. Baker

Macquarie University, Australia

David Klug

Imperial College London, UK

PS03-01 11:00-11:25

Single Cell Membrane Protein-Protein Interactions on Human Cancer Cells May Change Antigen Availability to Immunohistochemical Detection

Mark S. Baker, David Cantor, Harish Cheruku, Rohit Saldanha, Leon McQuade, Abidali Mohamedali, Charlie Ahn, Iveta Slapetova, Samuykta Anand, Shoba Ranganathan, Ed Nice

Dept. of Chemistry & Biomolecular Sciences, Macquarie University, Australia

PS03-02 11:30-11:55

Single Cell Analysis of Proteins from Clinical Samples Relevant to Human Health

David R. Klug

Department of Chemistry, Imperial College London, UK

PS03-03 12:00-12:25

Analysis of Single Cell Signaling Through Time and Space by Mass Cytometry

Bernd Bodenmiller

IMLS, University of Zürich, Switzerland

PS03-04 12:30-12:45 (POS-02-166)

Monitoring Protein Synthesis in Living Cells with Fluorescent Labeled tRNA FRET Pairs

Zeev Smilansky¹, Sima Barhoom², Ian Farrell³, Dvir Dahary¹, Andrew Leask³, Peter Vanderklisch⁴, Marcelo Ehrlich², Barry S. Cooperman⁵, Ornal Elroy-Stein²

¹Anima Cell Metrology, Inc., USA, ²Department of Cell Research and Immunology, George S. Wise Faculty of Life Sciences, Tel Aviv University, Israel, ³Department of Dentistry, Schulich School of Medicine and Dentistry, University of Western Ontario, Canada, ⁴Department of Neurobiology, The Scripps Research Institute, USA, ⁵Department of Chemistry, University of Pennsylvania, USA

PS04: New Tide of Biomarker Discovery

Sunday, September 15 11:00-12:50 Room 302

Chairs:

Jean-Charles Sanchez University of Geneva, Switzerland
Visith Thongboonkerd Mahidol University, Thailand

PS04-01 (Keynote) 11:00-11:25

Importance of Systems Glycobiology for Understanding Disease Onset, Biomarker and Therapeutics

Naoyuki Taniguchi
RIKEN Global Research Cluster, Japan

PS04-02 11:30-11:55

Challenges of Disease Biomarker Discovery: A Perspective from Developing Countries

Sanjeeva Srivastava
Wadhvani Research Centre for Biosciences and Bioengineering Department of Biosciences and Bioengineering, Indian Institute of Technology Bombay, India

PS04-03 12:00-12:25

Proteomics and Nephrolithiasis

Visith Thongboonkerd
Siriraj Hospital, Mahidol University, Thailand

PS04-04 12:30-12:45 (PO5-02-182)

High Throughput Cell-Based Studies and Protein Microarrays for Biomarker and Target Discovery

Joshua Labaer
Virginia G. Piper Center for Personalized Diagnostics, Biodesign Institute, Arizona State University, USA

PS05: Top-Down Proteomics

[Technology Session]

Sunday, September 15 15:30-17:20 Main Hall

Chairs:

William S. Hancock Northeastern University, USA
Catherine E. Costello Boston University School of Medicine, USA

PS05-01 (Keynote) 15:30-15:55

Towards Novel Separation and Fragmentation Techniques for Top-Down Proteomics

Mohammad Pirmoradian, Juan Astorga-Wells, Bob Zhang, Oleksii Rebrov, Alexey Chernobrovkin, Roman A. Zubarev
Department of Medical Biochemistry and Biophysics, Karolinska Institutet, Sweden

PS05-02 (Keynote) 16:00-16:25

Top-Down Analysis of Modified Proteins and Glycoproteins Using Various Dissociation Methods

Mark E. McComb, Roger Theberge, Sandrine Bourgoin-Voillard, Yan Jiang, Stephen A. Whelan, Xiaobin Xu, Xiang Yu, Christian F. Heckendorf, Jean L. Spencer, Cheng Lin, Catherine E. Costello
Center for Biomedical Mass Spectrometry, Boston University School of Medicine, USA

PS05-03 16:30-16:50 (POS-03-225)

Top-Down and Flexible Analysis of Protein Using MALDI In-Source Decay

Mitsuo Takayama

Yokohama City University, Japan

PS05-04 16:55-17:15 (POS-02-218)

Top-Down Proteomic Analysis of Enzymes and Complexes in *Trichoderma* Fungal Secretomes

Luis Henrique F. Do Vale^{1,2}, Adam Catherman², Ryan Tal Fellers², Paul Thomas²,

Edivaldo Ximenes F. Filho³, Carlos Andre O. Ricart¹, Neil L. Kelleher²,

Marcelo Valle de Sousa¹

¹Brazilian Center of Protein Research, Department of Cell Biology, University of Brasilia, Brazil,

²Proteomics Center of Excellence, Departments of Chemistry and Molecular Biosciences Northwestern University, USA, ³Laboratory of Enzymology, Department of Cell Biology, University of Brasilia, Brazil

PS06: Imaging Mass Spectrometry

[Technology Session]

Sunday, September 15 15:30-17:20 Room 303+304

Chairs:

Mitsutoshi Setou

Hamamatsu University School of Medicine, Japan

David C. Muddiman

North Carolina State University, USA

PS06-01 15:30-16:00

Molecular Tissue Imaging Under Ambient Conditions Using a Novel Imaging Source Coupled to High Resolving Power Mass Spectrometry

David C. Muddiman

North Carolina State University, USA

PS06-02 16:05-16:35

Imaging Mass Spectrometry of Clinical Samples

Mitsutoshi Setou

Hamamatsu University School of Medicine, Department of Cell Biology and Anatomy, Japan

PS06-03 16:40-16:55 (POS-02-008)

A Study of Drug Distribution in Malignant Melanoma Tissue by MALDI Mass Spectrometry Imaging for Evaluation of Drug Efficacy

Yutaka Sugihara¹, Charlotte Welinder¹, Ákos Végvári², György Marko-Varga^{2,3}

¹Department of Oncology and Cancer Epidemiology, Clinical Sciences, Lund University, Sweden, ²Clinical Protein Science & Imaging, Biomedical Center, Department of Measurement Technology and Industrial Electrical Engineering, Lund University, ³First Department of Surgery, Tokyo Medical University, Japan

PS06-04 17:00-17:15 (POS-02-009)

Peptide MALDI Imaging - How to Get Most out of Your Sample?

Hanna C. Diehl¹, Julian Elm¹, Judith Baronner¹, Dennis Trede², Herbert Thiele²,

Helmut E. Meyer¹, Corinna Henkel¹

¹Medizinisches Proteom-Center, Ruhr-University Bochum, Germany, ²Steinbeis Innovation Center SCILS, Bremen, Germany

PS07: Membrane Proteomics

Sunday, September 15 15:30-17:30 Room 301

Chairs:

Connie R. Jimenez
Bernd Wollscheid

VU University Medical Center, Netherlands
ETH Zurich, Switzerland

PS07-01 15:30-15:55

Global Mapping of Mitochondrial Interaction Networks Connects Mitochondrial Function to Neurodegenerative Disease

Sandy Kassir¹, Vishaldeep Sidhu¹, Ke Jin^{1,2}, James Vlasblom¹, Sadhna Phanse², Zhaolei Zhang², Mohan Babu¹

¹Department of Biochemistry, Research and Innovation Centre, University of Regina, Canada, ²Terrence Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Canada

PS07-02 16:00-16:25

Decoding Ligand Receptor Interactions

Bernd Wollscheid

Institute of Molecular Systems Biology (IMSB), Department of Health Sciences and Technology, ETH Zurich, Switzerland

PS07-03 16:30-16:55 (POS-02-109)

A Plasma Membrane Proteomic Analysis of Mouse and Human Cardiovascular Proteins

Parveen Sharma, Nicolas Bousette, Savo Lazic, Cynthia Abbasi, Nicole Dubois, Alex Ignatchenko, Vladimir Ignatchenko, Jie Liu, Allen Teng, Melissa Noronha, Robert Hamilton, Peter P. Liu, Peter H. Backx, Gordon Keller, Igor Stagljjar, Ian C. Scott, Thomas Kislinger, Anthony Gramolini

University of Toronto, Canada

PS07-04 17:00-17:15 (POS-01-053)

Development of Novel Membrane Protein Marker for Lung Cancer Diagnosis and Therapy

Boram Lee, Jooyoung Chung, Hanyoung Chung, Taiyoun Rhim

Department of Bioengineering, Hanyang University, Korea

PS07-05 17:15-17:30 (POS-02-104)

Proteomic Profiling of Ganglioside-Associated Microdomain in Malignant Melanomas

Noboru Hashimoto¹, Kazunori Hamamura¹, Norihiro Kotani², Yuki Ohkawa¹, Keiko Furukawa³, Koichi Honke², Koichi Furukawa³

¹Department of Biochemistry II, Nagoya University Graduate School of Medicine, Japan, ²Department of Biochemistry, Kochi University School of Medicine, Japan, ³Department of Biomedical Sciences, Chubu University College of Life and Health Sciences, Japan

PS08: Cancer Proteomics

Sunday, September 15 15:30-17:20 Room 302

Chairs:

Jong-Shin Yoo
Alexander Archakov

Korea Basic Science Institute, Korea
Institute of Biomedical Chemistry of RAMS, Russia

PS08-01 15:30-15:55

Integrated Site Specific Mapping of N-Linked Glycopeptides for Cancer Biomarker Discovery in Human Plasma by Mass Spectrometry

Jong-Shin Yoo

Mass Spectrometry Research Center, Korea Basic Science Institute, Korea

PS08-02 16:00-16:25

**Nerve Growth Factor and Its Precursor as Cancer Biomarkers and Targets:
Using Proteomics from Discovery to Validation**

Severine Roselli¹, Jay Pundavela¹, Genevieve Choquet², Jordane Biarc³, Jerome Lemoine³,
Ralph A. Bradshaw⁴, Hubert Hondermarck¹

¹School of Biomedical Sciences & Pharmacy, University of Newcastle, Australia, ²Department of Biomarker Identification and Validation, BioMerieux, Marcy l'Etoile, France, ³CNRS UMR-5280 University of Lyon, France, ⁴Department of Pharmaceutical Chemistry, University of California San Francisco, USA

PS08-03 16:30-16:50

**Convergence of Genomics with Proteomics to Better Understand Cancer Biology - The
NCI Clinical Proteomic Tumor Analysis Consortium**

Henry Rodriguez

National Cancer Institute, National Institutes of Health, USA

PS08-04 16:55-17:15 (POS-01-108)

**Label-free Quantitative Personalized Tissue Membrane Proteomics and Targeted
Membrane Glycoprotein Profiling for Gastric Cancer Biomarker**

Tai-Du Lin^{1,2}, Chia-Li Han¹, Chih-Wei Chien¹, Pei-Mien Chen¹, Chi-Huey Wong^{2,3},
Yu-Ju Chen¹

¹Institute of Chemistry, Academia Sinica, Taiwan, ²Institute of Biochemical Sciences, National Taiwan University, Taiwan, ³Genomics Research Center, Academia Sinica, Taiwan

PS09: New Technology in Phosphoproteomics (Co-organized by Yokohama City University)

[Technology Session]

Monday, September 16 11:00-12:50 Main Hall

Chairs:

Brigitte Wittmann-Liebold WITA, Teltow, Germany

Yasushi Ishihama Kyoto University, Japan

PS09-01 11:00-11:30

Towards a Comprehensive Characterization of a Human Cancer Cell Phosphoproteome

Shabaz Mohammed^{1,2}

¹Biomolecular Mass Spectrometry and Proteomics, Bijvoet Center for Biomolecular Research and Utrecht Institute for Pharmaceutical Sciences, Utrecht University, The Netherlands, ²Departments of Chemistry and Biochemistry, University of Oxford, UK

PS09-02 11:35-12:00

**Sequential Phosphoproteomic Enrichment through Complementary Metal-Directed
Immobilized Metal Ion Affinity Chromatography**

Chia-Feng Tsai^{1,2}, Chuan-Chih Hsu², Jo-Nan Hung¹, Yi-Ting Wang^{3,4}, Wai-Kok Choong⁵,
Ming-Yao Zeng², Pei-Yi Lin², Ting-Yi Sung⁵, Yu-Ju Chen^{1,2,3}

¹Department of Chemistry, National Taiwan University, Taiwan, ²Institute of Chemistry, Academia Sinica, Taiwan, ³Chemical Biology and Molecular Biophysics Program, Taiwan International Graduate Program, Taiwan, ⁴Institute of Biochemical Sciences, National Taiwan University, Taiwan, ⁵Institute of Information Science, Academia Sinica, Taiwan

PS09-03 12:05-12:20 (POS-02-250)

**Enhanced Phosphopeptide Identification in Escherichia Coli by Stepwise Hydroxy Acid-
Modified Metal Oxide Chromatography with Elevated Sample Loading Capacity**

Miao-Hsia Lin, Shunsuke Takagi, Masaki Wakabayashi, Naoyuki Sugiyama,
Yasushi Ishihama

Graduate School of Pharmaceutical Sciences, Kyoto University, Japan

PS09-04 12:25-12:40 (POS-02-288)

Unravelling Cell Signaling Events with Sub-Minute Temporal Resolution

Evgeny Kanshin^{1,4}, Louis-Philippe Sandoval-Bergeron¹, Pierre Thibault^{1,2,4},
Stephen Michnick^{1,3}

¹Departement of Biochemistry, University of Montreal, Canada, ²Departement of Chemistry, University of Montreal, Canada, ³Centre Robert-Cedergren, Bio-Informatique et Genomique, University of Montreal, Canada, ⁴Institute for Research in Immunology and Cancer, University of Montreal, Canada

PS10: New Technology in Mass Spectrometry 2

[Technology Session]

Monday, September 16 11:00-12:50 Room 303+304

Chairs:

Roman Zubarev

Karolinska Institutet, Sweden

Satoko Akashi

Yokohama City University, Japan

PS10-01 11:00-11:25

Dissecting the Sub-Cellular Proteome

Kathryn S. Lilley

Cambridge Centre for Proteomics, Department of Biochemistry and Cambridge Systems Biology Centre, University of Cambridge, UK

PS10-02 11:30-11:55

How to Submit MIAPE Compliant Data to ProteomeXchange Repository in the Context of the Human Proteome Project

Juan P. Albar

Centro Nacional de Biotecnología - CSIC, ProteoRed-ISCIII, Spain

PS10-03 12:00-12:25 (POS-02-136)

SOMAmr Capture Coupled to Mass Spectrometry for Plasma Protein Quantification

Thomas O. Joos¹, Frederik Weiss¹, Sheri Wilcox³, Jeff Carter³, Stephan Kraemer³,
Nick Saccomano³, Larry Gold³, Bart H.J. van den Berg¹, Martin Gamer²,
Peter Schulz-Knappe², Oliver Poetz¹

¹NMI Natural and Medical Sciences Institute at the University of Tübingen, Germany, ²Protagen AG, Germany, ³Somalogic, USA

PS10-04 12:30-12:45

Protein Quantitative Trait Locus (pQTL) Analysis in Mouse by Targeted Proteomics

Yibo Wu¹, Evan G. Williams², Johan Auwerx², Ruedi Aebersold¹

¹Department of Biology, Institute of Molecular Systems Biology, ETH Zurich, Switzerland, ²Laboratory of Integrative and Systems Physiology, School of Life Sciences, Switzerland

PS11: Proteomics of Protein Degradation

Monday, September 16 11:00-12:50 Room 301

Chairs:

Keiichi Nakayama

Kyushu University, Japan

Hiroyuki Yokota

Astellas Pharma Inc., Japan

PS11-01 (Keynote) 11:00-11:25

The Ubiquitin-Proteasome System

Keiji Tanaka

Tokyo Metropolitan Institute of Medical Science, Japan

PS11-02 (Keynote) 11:30-11:55

Molecular Dissection of Autophagy - Intracellular Recycling System

Yoshinori Ohsumi

Tokyo Institute of Technology, Japan

PS11-03 12:00-12:25

How Unspecific is Protein Degradation by Stress-Induced Autophagy?

Joern Dengjel^{1,2}

¹Freiburg Institute for Advanced Studies (FRIAS)-LifeNet, Albert-Ludwigs-University, Germany,

²Center for Biological Systems Analysis (ZBSA), Albert-Ludwigs-University, Germany

PS11-04 12:30-12:45

The True Story of How MHC Peptides are Produced

Arie Admon¹, Lilach Gutter-Kapon¹, Elena Milner¹, Eilon Barnea¹, Ilan Beer²

¹Technion - Israel Institute of Technology, Israel, ²IBM Haifa Research Lab., Israel

PS12: Proteomics for Diseases Other than Cancer (Co-organized by Cambridge Isotope Laboratories, Inc.)

Monday, September 16 11:00-12:50 Room 302

Chairs:

Tomohiro Kato

St. Marianna University School of Medicine

Masayasu Okochi

Osaka University, Japan

PS12-01 11:00-11:25

Quantitative Assessment of the Interactome, Phosphoproteome and Regulome in Bacterial Infection

Leonard J. Foster

Centre for High-Throughput Biology, Department of Biochemistry & Molecular Biology, University of British Columbia, Canada

PS12-02 11:30-11:50

Surrogate Markers for Aβeta as Biomarkers for Alzheimer and T-ALL

Masayasu Okochi

Department of Neuropsychiatry and Neurochemistry, Osaka University Graduate School of Medicine, Japan

PS12-03 11:55-12:10

In Deep Characterization of the Host Pathogen Interaction During Internalization of *Staphylococcus aureus* by A549 Cells

Kristin Surmann¹, Marjolaine Simon¹, Maren Depke², Petra Hildebrandt², Henrike Pfortner¹, Sebastian Stentzel³, Stephan Michalik³, Vishnu Dhople¹, Jörg Bernhardt⁴, Rabea Schlüter⁴, Leif Steil¹, Barbara Bröker³, Uwe Völker¹, Frank Schmidt²

¹Department of Functional Genomics and ZIK-FunGene, Interfaculty Institute for Genetics and Functional Genomics, University of Greifswald, Greifswald, Germany, ²ZIK-FunGene, Junior Research Group Applied Proteomics, Interfaculty Institute for Genetics and Functional Genomics, University of Greifswald, Greifswald, Germany, ³Department of Immunology, Institute of Immunology and Transfusion Medicine, University of Greifswald, Greifswald, Germany, ⁴Institute for Microbiology, University of Greifswald, Greifswald, Germany

PS12-04 12:15-12:30 (POS-01-161)

Proteomic Study of Biomarkers for Amyotrophic Lateral Sclerosis in Human Muscle Biopsies

Konstantin Artemenko¹, Ganna Shevchenko¹, Kristin Elf², Hakan Askmark², Jonas Bergquist¹

¹Department of Chemistry - Biomedical center, Uppsala University, Sweden, ²Department of Neuroscience, Uppsala University, Sweden

PS12-05 12:35-12:50 (POS-01-151)

Mass Spectrometry Methods for Surrogate Biomarker Discovery in Duchenne Muscular Dystrophy

Ramya L. Marathi¹, Sree Rayavarapu¹, Kristy J. Brown¹, Jenny Mac¹, Kanneboyina Nagaraju¹, Eric P. Hoffman¹, Erik Henricson², Craig M. McDonald², Yetrib Hathout¹

¹Center for Genetic Medicine, Children's National Medical Center, USA, ²University of California, Davis, USA

PS13: Proteomic Application of Multiple (Selected) Reaction Monitoring

Monday, September 16 15:30-17:00 Room 303+304

Chairs:

Hubert Hondermarck University of Newcastle, Australia
Young Mok Park Korea Basic Science Institute, Korea

PS13-01 15:30-15:55 (POS-01-224)

Quantitative Mass Spectrometry (SRM/MRM) to Amyloid Peptides, Tau Protein, and Apolipoprotein E in Human Cerebrospinal Fluid for Alzheimer Disease Diagnosis

Sylvain Lehmann¹, Nicolas Barthelemy², Jérôme Vialaret¹, Susanna Schraen-Maschke³, Laurent Tiers¹, Constance Delaby¹, Christophe Junot², Jacques Touchon¹, Nicolas Sergent³, Audrey Gabelle¹, François Becher², Christophe Hirtz¹

¹CHU Montpellier, Université MONTPELLIER 1, France, ²DSV/iBiTec-S/SPI, CEA Saclay, France, ³INSERM UMR 837, France

PS13-02 16:00-16:15 (POS-03-105)

High Resolution MRM Quantification of 300 Tear Proteins Using MS/MS^{ALL} with SWATHTM Acquisition and Its Application to Biomarker Discovery

Lei Zhou^{1,2,3}, Louis Tong^{1,4}, Tina Wong^{1,4}, Jocelyn Chua⁴, Siew Kwan Koh¹, Justin Lim⁵, Jason Neo⁵, Roger W Beuerman^{1,2,3}

¹Singapore Eye Research Institute, Singapore, ²Department of Ophthalmology, Yong Loo Lin School of Medicine, National University of Singapore, Singapore, ³SRP Neuroscience and Behavioral Disorder, DUKE-NUS Graduate Medical School, Singapore, ⁴Singapore National Eye Centre, Singapore, ⁵AB SCIEX, Singapore

PS13-03 16:20-16:35 (POS-01-227)

Development of an LC-MRM Based Assay of Prostate Specific Antigen (PSA) in Blood Samples

Zicheng Yang¹, Robert Maxwell¹, Paul Shieh¹, Helen Sun¹, Kefei Wang¹, Qing Zhang², Yixue Li²

¹Bruker Daltonics Inc., USA, ²Shanghai Bio-Medicine Research Institute, China

PS13-04 16:40-16:55 (POS-02-277)

Improved PhosphoTau SRM Assay Sensitivity Enables Multi-Site Tau Phosphorylation Quantitation in a Preclinical Model of AD Treated with Novel Small Molecule Inhibitors of Casein Kinase 1 Delta

Emma L. Lahert, Claire L. Russell, Ian Pike, Malcolm Ward
Proteome Sciences plc, London, UK

**PS14: Structural Proteomics of Post-translational Modification
(Co-organized by Yokohama City University)**

Monday, September 16 15:30-17:00 Room 301

Chairs:

Andrew H.-J. Wang
Kazuhiro Ogata

Institute of Biological Chemistry, Academia Sinica, Taiwan
Yokohama City University, Japan

PS14-01 15:30-15:55

The Structural Proteomics of Glycoproteins

Raymond J. Owens

The Oxford Protein Production Facility-UK, Research Complex at Harwell, Rutherford Appleton Laboratory and Division of Structural Biology, Wellcome Trust Centre for Human Genetics, University of Oxford, UK

PS14-02 16:00-16:25

Structural Insights into the EGFR Pathway Substrate Dephosphorylation by Protein Tyrosine Phosphatase N3

Kai-En Chen¹, Meng-Yen Lee^{1,2}, Abirami Santhanam¹, Guang-Chao Chen^{1,2},
Tzu-Ching Meng^{1,2}, Andrew H.-J. Wang^{1,2,3}

¹Institute of Biological Chemistry, Academia Sinica, Taiwan, ²Institute of Biochemical Sciences, National Taiwan University, Taiwan, ³Core Facilities for Protein Structural Analysis, Academia Sinica, Taiwan

PS14-03 16:30-16:55

Cooperative Formation of a Multiple Transcription Factor Assembly on an Enhancer DNA and Its Regulation by Phosphorylation of a Transcription Factor via a Cell Signaling

Masaaki Shiina, Keisuke Hamada, Taiko Inoue-Bungo, Mariko Shimamura,
Akiko Uchiyama, Shiho Baba, Ko Sato, Kazuhiro Ogata

Department of Biochemistry, Yokohama City University Graduate School of Medicine, Japan

PS15: Drug Target Proteomics

Monday, September 16 15:30-17:00 Room 302

Chairs:

Maxey C. M. Chung
Bruno Domon

National University of Singapore, Singapore
Luxembourg Clinical Proteomics Center, Luxembourg

PS15-01 15:30-15:55

Chemical Proteomics for Drug Discovery: Drug Targets, Drug Selectivity, Drug Mechanism of Action and Drug Resistance

Bernhard Kuster

Technische Universität München, Germany

PS15-02 16:00-16:25

Systems-Level Analysis of Inflammatory Proteolytic Events *In Vivo* by N-Terminomics Analyses

Christopher M. Overall

UBC Centre for Blood Research, University of British Columbia, Canada

PS15-03 16:30-16:55

Cell-Surface Proteins as Drug Targets

Bruno Domon, Panchali Goswami, Yeoun Jin Kim, Antoine Lesur, Jan van Oostrum
Luxembourg Clinical Proteomics Center, Luxembourg

PS16: Systems Biology

Monday, September 16 15:30-17:00 Room 311+312

Chairs:

Michael Snyder
Marc Wilkins

Stanford University, USA
University of New South Wales, Australia

PS16-01 15:30-15:55

Integrative Multi-Platform Analysis of Cancer Kinome Networks

Rune Linding

Technical University of Denmark (DTU), Denmark

PS16-02 16:00-16:25

The Genetic Landscape of a Cell

Charlie Boone

Donnelly Centre, Banting and Best Department of Medical Research, Department of Molecular Genetics, University of Toronto, Canada

PS16-03 16:30-16:55

Ca²⁺ Induced Phosphorylation Signalling in Nerve Terminals

Phillip Robinson

Cell Signalling Unit, Children's Medical Research Institute, Australia

PS17: Mass Spectrometry for Protein Complex

[Technology Session]

Tuesday, September 17 11:00-12:50 Main Hall

Chairs:

Toshifumi Takao
Nobuhiro Takahashi

Osaka University, Japan
Tokyo University of Agriculture and Technology, Japan

PS17-01 11:00-11:25

Conformational Changes of Multi-Protein Complexes Determined by Mass Spectrometry

Juri Rappsilber

Wellcome Trust Centre for Cell Biology, Institute of Cell Biology, University of Edinburgh, UK

PS17-02 11:30-11:55

Protein-Phosphoprotein Complexes in DNA Damage and Cancer Signalling

Ming-Daw Tsai

Academia Sinica, Taiwan

PS17-03 12:00-12:25

From the Top Down; Mass Spectrometry and Its Role in Studying Intact Proteins and Protein Complex Structure, Dynamics, and Assembly

Albert J. R. Heck^{1,2}

¹Faculty of Sciences, Utrecht University, The Netherlands, ²Netherlands Proteomics Centre, The Netherlands

PS17-04 12:30-12:45 (POS-02-191)

In Vivo Crosslinking Combined with Label-Free Quantitative Proteomics to Determine the Subcellular Distribution and Stoichiometry of Proteasome Complexes

Bertrand Fabre, Thomas Lambour, Manuelle Ducoux-Petit, Luc Garrigues, Francois Amalric, Bernard Monsarrat, Marie-Pierre Bousquet-Dubouch, Odile Burllet-Schiltz

Institute of Pharmacology and Structural Biology (IPBS), CNRS, University of Toulouse, France

PS18: Mass Spectrometry for Glycomics and Glycoproteomics

[Technology Session]

Tuesday, September 17 11:00-12:50 Room 303+304

Chairs:

Nicki H. Packer
Yoshinao Wada

Macquarie University, Australia

Osaka Medical Center for Maternal and Child Health, Japan

PS18-01 11:00-11:25

Utilizing Carbohydrate Fragmentation Database (UniCarb-DB) for Glycoresearch Discovery

Niclas Karlsson

University of Gothenburg, Sweden

PS18-02 11:30-11:55

Challenges & Solutions for Glycoproteomics

Daniel Kolarich

Department of Biomolecular Systems, Max Planck Institute of Colloids and Interfaces, Germany

PS18-03 12:00-12:25

Connecting Proteomics with Glycomics

Nicolle H. Packer¹, Morten Thaysen-Andersen¹, Niclas Karlsson³, F. Lisacek², M.P. Campbell¹

¹Biomolecular Frontiers Research Centre, Macquarie University, Australia, ²Proteome Informatics Group, Swiss Institute of Bioinformatics, Switzerland, ³Department of Medical Biochemistry, University of Gothenburg, Sweden

PS18-04 12:30-12:45

N-Glycoproteome Analysis from Identification of Glycosylation Sites to Intact Glycopeptides

Hanfa Zou¹, Kai Cheng¹, Rui Chen^{1,2}, Fangjun Wang¹, Mingliang Ye¹, Daniel Figeys^{2,3}

¹Key Lab of Separation Science for Analytical Chemistry, National Chromatography R&A Center, Dalian Institute of Chemical Physics, the Chinese Academy of Science, ²Ottawa Institute of Systems Biology, Department of Biochemistry, Microbiology and Immunology, Faculty of Medicine, University of Ottawa, ³Department of Chemistry, Faculty of Science, University of Ottawa

PS19: Proteomics of Exosome and Other Organelles

Tuesday, September 17 11:00-12:50 Room 301

Chairs:

Richard J. Simpson
Pei Pei Ping

La Trobe University, Australia

UCLA School of Medicine, USA

PS19-01 (Keynote) 11:00-11:25

Exploring Communication in the Tumor Microenvironment

Catherine Fenselau¹, Meghan Burke¹, Waeowalee Choksawangkarn¹, Rebecca Rose¹, Avantika Dhabaria¹, Yan Wang¹, Nathan Edwards², Suzanne Ostrand-Rosenberg³

¹University of Maryland, USA, ²Georgetown University Medical Center, USA, ³UMBC, USA

PS19-02 11:30-11:55

Oncogenic H-Ras Reprograms Madin-Darby Canine Kidney (MDCK) Cell-Derived Exosomes During Epithelial-Mesenchymal Transition

Richard J. Simpson

La Trobe Institute for Molecular Sciences (LIMS), La Trobe University, Australia

PS19-03 12:00-12:25

EVpedia: An Integrated Proteome Database for Systemic Analyses of Prokaryotic and Eukaryotic Exosomes

Dae-Kyum Kim, Yong Song Gho

Department of Life Sciences, POSTECH, Korea

PS19-04 12:30-12:45 (POS-02-186)

Extracellular Vesicle (EV) Array: Microarray Capturing of Exosomes and Other Extracellular Vesicles for Multiplexed Phenotyping

Malene Joergensen¹, Shona Pedersen², Rikke Baek¹, Evo Soendergaard¹,
Soeren R. Kristensen², Kim Varming¹

¹Department of Clinical Immunology, Aalborg University Hospital, Denmark, ²Department of Clinical Biochemistry, Aalborg University Hospital, Denmark

PS20: Disease Phosphoproteomics

Tuesday, September 17 11:00-12:50 Room 302

Chairs:

Pierre Thibault

Universite de Montreal, Canada

Takeshi Tomonaga

National Institute of Biomedical Innovation, Japan

PS20-01 11:00- 11:25

Phosphoproteomics and Cancer

Scott Gerber

Geisel School of Medicine at Dartmouth, USA

PS20-02 11:30- 11:55

How Targeted Therapies Exploit Signaling (Src) and Metabolic (Glucose) Over-Dependencies in Cancer Homeostasis

Thomas G. Graeber

University of California Los Angeles, USA

PS20-03 12:00-12:15 (POS-03-188)

Development of Universal Protocols for Clinical Tissue Phosphoproteomics Optimized for Formalin-Fixed Paraffin-Embedded Specimens

Mayu Ogura, Masaki Wakabayashi, Naoyuki Sugiyama, Yasushi Ishihama

Kyoto University, Japan

PS20-04 12:20-12:35 (POS-02-259)

Identification of Dysregulated Kinase-Mediated Pathways in Hepatocellular Carcinoma by a Quantitative Phosphoproteome Approach

Yu-Tsun Lin¹, Kun-Yi Chien¹, Chau-Ting Yeh^{1,2}, Jau-Song Yu¹

¹Graduate Institute of Biomedical Sciences, Chang Gung University, Taiwan, ²Liver Research Center, Chang Gung Memorial Hospital, Taiwan

PS21: Proteome Informatics

Tuesday, September 17 11:00-12:50 Room 311+312

Chairs:

Henning Hermjakob
Ravi Sirdeshmukh

The European Bioinformatics Institute, UK
Institute of Bioinformatics, India

PS21-01 11:00-11:20

Integration and Data-Mining of Human Transcriptome and Proteome Databases in H-InvDB

Tadashi Imanishi

Tokai University School of Medicine / molprof, AIST, Japan

PS21-02 11:25-11:50

What is a Proteomic Publication?

Robert Chalkley

University of California San Francisco, USA

PS21-03 11:55-12:10 (POS-01-258)

Estimation of Protein Species Number for Mammalian, Bacteria, Insecta and Yeast

Elena Ponomarenko, Stanislav Naryzhny, Ekaterina Poverennaya, Mikhail Pyatnitskii,

Andrey Lisitsa, Alexander Archakov

Institute of Biomedical Chemistry of RAMS, Russia

PS21-04 12:15-12:30 (POS-01-272)

Isobar: Making Sense out of Protein and Modified Peptide iTRAQ/TMT Quantitative Data

Florian P. Breitwieser, Jacques Colinge

CeMM - Research Center for Molecular Medicine of the Austrian Academy of Sciences, Austria

PS21-05 12:35-12:50 (POS-01-273)

FindPairs - The Protein Quantification Module of the PeakQuant Software Suite

Martin Eisenacher¹, Michael Kohl¹, Sebastian Wiese², Romano Hebel^{1,3},
Helmut E. Meyer¹, Bettina Warscheid^{2,4}, Christian Stephan^{1,5}

¹Medizinisches Proteom-Center, Ruhr-Universitaet Bochum, Germany, ²Funktionelle Proteomik, Fakultae fuer Biologie und BIOSS Centre for Biological Signalling Studies, Universitaet Freiburg, Germany, ³Brucker Daltonik GmbH, Germany, ⁴Zentrum fuer Biosystemanalyse (ZBSA), Universitaet Freiburg, Germany, ⁵Kairos GmbH, Germany

PS22: Sample Preparation for Mass Spectrometry

[Technology Session]

Tuesday, September 17 15:30-17:25 Main Hall

Chairs:

Robert L. Moritz
Terence Chuen Wai Poon

Institute for Systems Biology, USA
Chinese University of Hong Kong, China

PS22-01 15:30-15:55

Immunoaffinity Separations and Intelligent PRISM Fractionation for Achieving Ultrasensitive Targeted Protein Quantification

Tujin Shi¹, Thomas L. Fillmore², Rui Zhao², Yuqian Gao¹, Carrie D. Nicora¹, Jacob Kagan³,
Sudhir Srivastava³, Karin D. Rodland¹, Tao Liu¹, Keqi Tang¹, Richard D. Smith¹,
David G. Camp¹, Alvin Y. Liu⁴, Wei-Jun Qian¹

¹Biological Sciences Division, Pacific Northwest National Laboratory, USA, ²Enviornmental Molecular Sciences Laboratory, USA, ³Division of Cancer Prevention, National Cancer Institute (NCI), USA,

⁴Department of Urology, University of Washington, USA

PS22-02 16:00-16:25

A High-Throughput and Reproducible Workflow for Targeted Mass Spectrometry Applied to Large Scale Analysis of Clinical Samples

Qin Fu¹, Michael P Kowalski², Weihua Ji¹, Jie Zhu¹, Pingbo Zhang¹, Eric Grote¹, Graham J. Threadgill³, Christie Hunter⁴, Jennifer E. Van Eyk¹

¹Johns Hopkins Bayview Proteomics Center, Division of Cardiology, Department of Medicine, School of Medicine, Johns Hopkins University, USA, ²Beckman Coulter Life Sciences, USA, ³Beckman Coulter, Inc, USA, ⁴AB SCIE, USA

PS22-03 16:30-16:55

Mark Twain: How to Fathom the Depth of Your Pet Proteome

Pier G. Righetti

Department of Chemistry, Politecnico di Milano, Italy

PS22-04 16:45-17:10

Automated Native Sample Preparation for Proteome Analysis

Heidrun Rhode¹, Sindy Wendler¹, Baerbel Tautkus¹, Sabine Nemitz¹, Jelena Pesek¹, Thomas Krueger¹, Stefan Opitz¹, Steffen Richter², Heiko Oehme², Stefan Kreusch³, Bendikt Hanf⁴, Lutz Schmidt⁴

¹Institute of Biochemistry I, Jena University Hospital, Friedrich Schiller University Jena, Germany, ²CyBio-AG, Germany, ³Scienova GmbH, Germany, ⁴X-CASE GmbH, Germany

PS23: New Technology in Integrated Omics

[Technology Session]

Tuesday, September 17 15:30-17:20 Room 303+304

Chairs:

Akhilesh Pandey

Johns Hopkins University School of Medicine, USA

Norie Araki

Kumamoto University, Japan

PS23-01 (Keynote) 15:30-15:55

New Technology in Integrated Omics: Challenges: Concepts, Methods and Tools

Pierre Legrain

Ecole Polytechnique, France

PS23-02 16:00-16:25

Insights from a Multi-Omic Analysis of a Single Human Cell Type

Akhilesh Pandey

Johns Hopkins University School of Medicine, USA

PS23-03 16:30-16:55

Chr 18 Quantitative Proteome and Transcriptome

Victor Zgoda, Arthur Kopylov, Olga Tikhonova, Alexander Moisa, Nadezhda Pyndyk, Tatyana Farafonova, Svetlana Novikova, Andrey Lisitsa, Alexander Archakov

Orekhovich Institute of Biomedical Chemistry of the Russian Academy of Medical Sciences, Russia

PS23-04 17:00-17:15 (POS-01-270)

Firmiana: An Integrated Platform for Mass Spectrometry-Based Proteomics Studies Based on Galaxy Framework

Jun Qin², Bingxin Lu¹, Peng Li¹, Ruichao Xue¹, Lihong Diao², Wei Zhang², Chen Ding², Jinwen Feng¹, Ruifang Cao¹, Juan Yang¹, Dong Li², Wanlin Liu², Cheng Chang², Naiqi Qiu¹, Yu Du², Tieliu Shi¹

¹Center for Bioinformatics and Computational Biology, Shanghai Key Laboratory of Regulatory Biology, the Institute of Biomedical Sciences and School of Life Science, East China Normal University, China,

²State Key Laboratory of Proteomics, Beijing Proteome Research Center, Beijing Institute of Radiation Medicine, China

PS24: Disease Glycoproteomics (Co-organized by AIST)

Tuesday, September 17 15:30-17:20 Room 301

Chairs:

Hisashi Narimatsu
Stuart J. Cordwell

National Institute of Advanced Industrial Science and Technology, Japan
The University of Sydney, Australia

PS24-01 15:30-15:55

A Robust Method for the Relative Quantitative Analysis of Dual Labeled N-Glycans

Weiqian Cao, Wei Zhang, Jiangming Huang, Pengyuan Yang
Fudan University, China

PS24-02 15:55-16:20

An Integrated Approach of Proteomics, Glycoproteomics and Glycomics for the Structural and Functional Study of Glycoproteins

Hui Zhang, Daniel W. Chan
Department of Pathology, Johns Hopkins University, USA

PS24-03 16:20-16:45

Use of Zinc Finger Nuclease Gene Targeting for Functional Glycomics

Catharina Steentoft¹, Sergey Y. Vakhrushev¹, Hiren J. Joshi¹, Yun Kong¹,
Malene B. Vester-Christensen¹, Katrine T-B.G. Schjoldager¹, Kirstine Lavrsen¹,
Sally Dabelsteen¹, Nis B. Pedersen¹, Lara Marcos-Silva³, Ramneek Gupta²,
Eric Paul Bennett¹, Ulla Mandel¹, Søren Brunak², Hans H. Wandall¹, Steven B. Lavery¹,
Henrik Clausen¹

¹Copenhagen Center for Glycomics, Departments of Cellular and Molecular Medicine and School of Dentistry, Faculty of Health and Medical Sciences, University of Copenhagen, Denmark, ²Center for Biological Sequence Analysis, Department of Systems Biology Technical University of Denmark, ³IPATIMUP, Institute of Molecular Pathology and Immunology of the University of Porto, Portugal

PS24-04 16:45-17:10 (POS-03-028)

Breast Cancer Tumour Transformation from Primary Tumour to Secondary Site

Emila Kurbasic¹, Sofia Waldemarson¹, Peter James¹, Emma N. Malmstrom²

¹Department of Immunotechnology, BMC D13, Lund University, Sweden, ²Department of Oncology, Institute of Clinical Sciences, University Hospital, Sweden

PS25: Animal Models for Human Diseases

Tuesday, September 17 15:30-17:20 Room 302

Chairs:

Shigeo Ohno
Fernando J. Corrales

Yokohama City University, Japan
University of Navarra, Spain

PS25-01 15:30-15:55

Functional Validation of Biomarker Discovery from Mouse Models to Translational Research

Je-Kyung Seong
Laboratory of Developmental Biology and Genomics, College of Veterinary Medicine, Seoul National University, Korea

PS25-02 16:00-16:15 (POS-01-006)

Biomarkers of Diabetes in Plasma of NOD Mice

Juliana A. Colucci¹, Juliana Perez¹, Maisa Mayumi Sakata¹,
Regina L. H. Watanabe³, Fernando C. Bizerra², Dulce E. Casarini¹

¹Universidade Federal de Sao Paulo, Departamento de Medicina, Disciplina de Nefrologia, Brazil,

²Universidade Federal de Sao Paulo, Departamento de Medicina, Disciplina de Doencas Infecciosas Parasitarias, Brazil, ³Universidade Federal de Sao Paulo, Departamento de Fisiologia, Disciplina de Fisiologia da Nutricao, Brazil

PS25-03 16:20-16:35 (POS-01-008)

Proteomic Analysis of Left Ventricular Tissues in Dilated Cardiomyopathy Mouse Models

Mitsuhiro Nishigori¹, Hiroaki Yagi¹, Akikazu Mochizuki¹, Kazuki Sasaki¹, Yuko Iwata²,
Shigeo Wakabayashi², Naoto Minamino¹

¹National Cerebral and Cardiovascular Center, Department of Molecular Pharmacology, Japan, ²National Cerebral and Cardiovascular Center, Department of Molecular Physiology, Japan

PS25-04 16:40-16:55 (POS-01-009)

Plasma Proteomic Pattern Analysis for Murine Experimental Autoimmune Encephalomyelitis (EAE) Model

Tomohito Sakai¹, Takayuki Kondo², Takashi Nirasawa³, Kazunori Yokoi¹, Kei Tashiro⁴,
Masaya Ikegawa^{1,4}

¹Department of Genomic Medical Sciences, Kyoto Prefectural University of Medicine, Japan, ²Department of Neurology, Kyoto University, Japan, ³Bruker Daltonics KK, Japan, ⁴Department of Medical Life Systems, Doshisha University, Japan

PS25-05 17:00-17:15 (POS-01-004)

Integrated Proteomics for the Study of Metastatic Human Tongue Cancer Development in a Heterogeneous Microenvironment

Masayo W. Morifuji, Akiko N. Nambu, Daiki Kobayashi, Norie Araki
Dept. Tumor Gen. Biol., Grad. Sch. Med. Sci., Kumamoto Univ., Japan

PS26: High Quality Disease Proteomics

Tuesday, September 17 15:30-17:20 Room 311+312

Chair:

Helmut E. Meyer

Ruhr-University of Bochum, Germany

PS26-01 15:30-15:50

Label-Free Proteomics for Biomarker Discovery and Validation in Proximal Fluids: Applications in Colon Cancer and Alzheimer's Disease

Connie R. Jimenez

OncoProteomics Laboratory, Department Medical Oncology, VU University Medical Center, Netherlands

PS26-02 15:50-16:10

Clinical Proteomics MRM

Christoph H. Borchers

University of Victoria, Canada

PS26-03 16:10-16:30

Proteomics Strategies for Analysis of Liver Cancer

Juliet Padden¹, Dominik A. Megger¹, Thilo Bracht¹, Michael Kohl¹, Martin Eisenacher¹,
Stephanie Tautges¹, Hideo A. Baba², Jörg F. Schlaak³, Christian Gerges⁴,
Helmut E. Meyer¹, Barbara Sitek¹

¹Medizinisches Proteom-Center, Ruhr-Universität Bochum, Germany, ²Institut für Pathologie, Universitätsklinikum Essen, Germany, ³Klinik für Gastroenterologie und Hepatologie, Universitätsklinikum Essen, Germany, ⁴Evangelisches Krankenhaus Düsseldorf, Germany

PS26-04 16:30-16:50

**From a Brain Damage Proteomics Model to a Blood Time Indicator of Stroke Onset:
The Glutathione S-Transferase-Pi Proof of Concept**

Natacha Turck¹, Xavier Robin^{1,2}, Alexandre Hainard¹, Roman Sztajzel³, Ghislaine Wagner³, Denis F. Hochstrasser¹, Joan Montaner⁴, Pierre R. Burkhard³, Jean-Charles Sanchez¹

¹Biomedical Proteomics Research Group, Department of Human Protein Sciences, Faculty of Medicine, Switzerland, ²Swiss Institute of Bioinformatics, Medical University Centre, Switzerland, ³Department of Neurology, Geneva University Hospitals and Faculty of Medicine, University of Geneva, Switzerland, ⁴Neurovascular Research Laboratory, VHIR & Stroke Unit, Vall d'Hebron Hospital, Autonomous University of Barcelona (UAB), Spain

PS26-05 16:50-17:10

Diagnosis of Male Reproductive System Disorders with Protein Biomarkers Quantified in Seminal Plasma

Andrei P. Drabovich¹, Punit Saraon², Ihor Batruch³, Keith Jarvi⁴, Eleftherios P. Diamandis¹⁻³

¹Samuel Lunenfeld Research Institute, Mount Sinai Hospital, Canada, ²Department of Laboratory Medicine and Pathobiology, University of Toronto, Canada, ³Pathology and Laboratory Medicine Department, Mount Sinai Hospital, Canada, ⁴Department of Surgery, Division of Urology, Mount Sinai Hospital, Canada

**PS27: Nobel Prize Memorial Lecture (Co-Organized by Daiichi-Sankyo) :
iPS and ES Cell Proteomics**

Tuesday, September 17 17:30-19:00 Main Hall

Chairs:

Albert J. R. Heck Utrecht University, Netherlands
Netherlands Proteomics Centre, Netherlands

Ghasem Hosseini Salekdeh Royan Institute for Stem Cell Biology and Technology, Iran

PS27-01 GUEST 17:30-17:35

Shinya Yamanaka
Kyoto University, Japan

PS27-02 17:35-18:00

Development of iPS Cell Technology for Clinical Application

Masato Nakagawa
Center for iPS Cell Research and Application (CiRA), Kyoto University, Japan

PS27-03 18:00-18:25

Directed Differentiation of Stem Cells by Changing Protein Dynamics

Bonghee Lee
Center for Genomics and Proteomics & Institute for Regenerative Medicine, Lee Gil Ya Cancer and Diabetes Institute, Gachon University, Korea

PS27-04 18:25-18:50

Deep Proteome Profiling Identifies Distinct Pluripotent Cellular Populations During Somatic Cell Reprogramming into Induced Pluripotent Stem Cells

Marco Benevento^{1,2}, Javier Munoz Peralta^{1,2,3}, Peter Tonge⁴, Mira Puri⁴, Andras Nagy⁴, Albert J.R. Heck^{1,2}

¹Biomolecular Mass Spectrometry and Proteomics, Bijvoet Center for Biomolecular Research and Utrecht Institute for Pharmaceutical Sciences, Utrecht University, The Netherlands, ²Netherlands Proteomics Centre, the Netherlands, ³Proteomics Unit, Spanish National Cancer Research Centre (CNIO), Spain, ⁴Samuel Lunenfeld Research Institute, Mount Sinai Hospital, Canada

PS28: Computational Proteomics

[Technology Session]

Tuesday, September 17 17:30-19:00 Room 303+304

Chairs:

Masaya Ono

National Cancer Center Research Institute, Japan

Robert L. Moritz

Institute for Systems Biology, USA

PS28-01 17:30-17:55

Whole Proteome Resources: Access and Sharing of Data Through the Peptide and SRMAtlas Proteomics Suites

Robert L. Moritz

Institute for Systems Biology, USA

PS28-02 18:00-18:25

Building Your Knowledge Base of Empirically Measured Peptides with Skyline and Panorama

Brendan MacLean

University of Washington, USA

PS28-03 18:30-18:55

Computational Proteomics Enables Accurate Label Free Quantification of Proteins and Posttranslational Modifications

Jürgen Cox

Max-Planck Institute for Biochemistry, Germany

PS29: Biology-Oriented Glycoproteomics (Co-organized by AIST)

Tuesday, September 17 17:30-19:00 Room 301

Chairs:

Pengyuan Yang

Fudan University, China

Henrik Clausen

University of Copenhagen, Technical University of Denmark, Denmark

PS29-01 17:30-17:55

Site-Specific Glycan-Peptide Analysis for Determination of *N*-Glycoproteome Heterogeneity in Bacteria and Mammalian Systems

Benjamin L. Parker, Nicholas E. Scott, Stuart J. Cordwell

School of Molecular Bioscience and Discipline of Pathology, School of Medical Sciences, The University of Sydney, Australia

PS29-02 18:00-18:25

Tackling Sulfoglycomics and Realizing the Prospects of Sulfoglycoproteomics

Kai-Hooi Khoo

Institute of Biological Chemistry, Academia Sinica, Taiwan

PS29-03 18:30-18:55

A New Method for Glycopeptide Assignment by Duplex-LC/MS Analyses

Hiroiyuki Kajii, Azusa Tomioka, Toshihide Shikanai, Hisashi Narimatsu

Research Center for Medical Glycoscience, AIST, Japan

PS30: Chemical Proteomics and Proteomics for Drug Effects

Tuesday, September 17 17:30-19:00 Room 302

Chairs:

Ho Jeong Kwon Yonsei University, Korea
Peter Karuso Macquarie University, Australia

PS30-01 17:30-17:55

Target Deconvolution of Bioactive Small Molecules via Multi-Omics Based Approach

Ho Jeong Kwon

Department of Biotechnology, Translational Research Center for Protein Function Control, College of Life Science & Biotechnology, Yonsei University, Korea

PS30-02 18:00-18:25

Reverse Chemical Proteomics as a Tool in Drug Discovery

Peter Karuso

Department of Chemistry & Biomolecular Sciences, Macquarie University, Australia

PS30-03 18:30-18:55

Target Identification of Novel Anti-inflammatory Compound Using Chemical Proteomics Approach with Bait Compound

Takashi Yamamoto¹, Ayatoshi Andou¹, Nobuhiko Hayakawa¹, Masatsugu Noguchi¹, Sen Takeshita¹, Ryohei Yokoyama¹, Agung Eviryanti¹, Yukie Seki¹, Hikaru Nishio¹, Manami Shuto¹, Misato Noguchi¹, Yoichiro Shima¹, Kanna Kuribayashi¹, Shunsuke Kageyama¹, Hiroyuki Eda¹, Shun-ichiro Iemura², Tohru Natsume², Tomohisa Hatta², Masataka Shoji¹

¹Exploratory Research Laboratories, Ajinomoto Pharmaceuticals Co. Ltd., Japan, ²Biomedical Information Research Center (BIRC); National Institute of Advanced Industrial Science and Technology (AIST), Japan

PS31: Frontiers in Agriculture Proteome Research

Tuesday, September 17 17:30-19:00 Room 311+312

Chairs:

Gilberto Domont Federal University of Rio de Janeiro, Brazil
Setsuko Komatsu National Institute of Crop Science, Japan

PS31-01 17:30-17:55

An Overview of Label-Free Quantitative Shotgun Proteomics in Rice and Grapes

Paul A. Haynes¹, Iniga S. George¹, Mehdi Mirzaei¹, Karlie A. Neilson¹, Shila Shabhzian¹, Chumithri G. Gammulla¹, Michael Symons¹, Steve Van Sluyter¹, Brian Atwell², Ghassem H. Salekdah³, Anne Fennell⁴, Grant Cramer⁵

¹Chemistry and Biomolecular Sciences, Macquarie University, Australia, ²Biological Sciences, Macquarie University, Australia, ³Agricultural Biotechnology Institute of Iran, Iran, ⁴South Dakota State University, USA, ⁵University of Nevada, USA

PS31-02 18:00-18:25

Green Systems Biology - From Single Genomes, Proteomes and Metabolomes to Ecosystems Research and Biotechnological Applications

Wolfram Weckwerth

Department for Ecogenomics and Systems Biology, University of Vienna, Austria

PS31-03 18:30-18:55

Golgi Proteomics in Plants and Application for Biofuel Plant Development

Harriet T. Parsons, Vibe Gondolf, Carsten Rautengarten, Christopher J. Petzold,
Henrik V. Scheller, Joshua L. Heazlewood

Joint BioEnergy Institute and Physical Biosciences Division, Lawrence Berkeley National Laboratory, USA

PS32: Miscellaneous Post-Translational Modifications

Wednesday, September 18 10:00-11:50 Room 302

Chairs:

Chunaram Choudhary

University of Copenhagen, Denmark

Toshihiko Utsumi

Yamaguchi University, Japan

PS32-01 10:00-10:25

Quantitative Proteomics of Lysine Acetylation, Succinylation, and Ubiquitylation

Chunaram Choudhary

The Novo Nordisk Foundation Center for Protein Research, Faculty of Health Sciences, University of Copenhagen, Denmark

PS32-02 10:30-10:50

Comprehensive Identification of Human N-Myristoylated Proteins Using cDNA Resource and Cell-Free Protein Synthesis System

Toshihiko Utsumi

Applied Molecular Bioscience, Graduate School of Medicine, Yamaguchi University, Japan

PS32-03 10:55-11:10

Identification and Characterization of the Posttranslational Modifications of Yeast 26S Proteasome

Ayuko Kimura¹, Yu Kato¹, Yoichi Kurata^{1,2}, Yayoi Kimura¹, Hisashi Hirano¹

¹Adv. Med. Res. Center, Yokohama City Univ., Japan, ²National Cancer Center Research Institute, Japan

PS32-04 11:15-11:30 (POS-02-224)

Mapping the Human Methyltransferasome Reveals the Existence of a Posttranslational Modification Code that Targets Molecular Chaperones to Regulate Functional Organization of the Human Proteome

Philippe Cloutier¹, Anais Aulas³, Mathieu Lavallee-Adam², Mathieu Blanchette²,
Christine VandeVelde³, Benoit Coulombe¹

¹Institut de Recherches Cliniques de Montreal, Universite de Montreal, Canada, ²McGill Centre for Bioinformatics, McGill University, Canada, ³Centre de Recherche du CHUM, Universite de Montreal, Canada

PS32-05 11:35-11:50 (POS-03-172)

A Proteomic Investigation of Proteasome Malfunctioning

Karen A. Sap, Karel Bezstarosti, Dick H. W. Dekkers, Olaf Voets, Erikjan Rijkers,
C. Peter Verrijzer, Jeroen A. A. Demmers

Erasmus University Medical Center, The Netherlands

PS33: Plant and Food Proteomics

Wednesday, September 18 9:00-11:50 Room 311+312

Chairs:

Yoichi Sakakibara
Toshiaki Mitsui

University of Miyazaki, Japan
Niigata University, Japan

PS33-01 9:00-9:20

Tracking Protein Turnover in Plant Cells and Intact Plants: A New Frontier is Understanding the Energy Efficiency of Plant Growth

A. Harvey Millar¹, Clark Nelson, Lei Li, Ralitzia Alexova, Richard Jacoby

ARC Centre of Excellence in Plant Energy Biology and Centre for Comparative Analysis of Biomolecular Networks, The University of Western Australia, Australia

PS33-02 9:25-9:45

Functional Proteomics and Plant Signaling and Metabolic Networks

Sixue Chen¹, Mengmeng Zhu¹, Yan He¹, Johanna Strul¹, Haiying Li², Shaojun Dai³, Xiufeng Yan³, Alice Harmon¹

¹Department of Biology, Genetics Institute, University of Florida, USA, ²College of Life Sciences, Heilongjiang University, China, ³Alkali Soil Natural Environmental Science Center, Northeast Forestry University, China

PS33-03 9:50-10:10

Comparative Analysis of the Proteomes of *Ricinus communis* and *Jatropha curcas* Seeds

Francisco A. P. Campos

Department of Biochemistry and Molecular Biology, Federal University of Ceará, Brazil

PS33-04 10:15-10:35

Proteomic Analysis Showing the Features of Metabolism Regulation During Rice Seed Germination

Pingfang Yang, Dongli He, Chao Han

Key Laboratory of Plant Germplasm Enhancement and Speciality Agriculture, Wuhan Botanical Garden, Chinese Academy of Sciences, China

PS33-05 10:40-11:00

Involvement of the Plasma Membrane in Plant Cold Adaptation: A Proteomics Perspective

Daisuke Takahashi¹, Takato Nakayama², Yushi Miki², Yukio Kawamura^{1,2}, Matsuo Uemura^{1,2}

¹United Graduate School of Agricultural Sciences, Iwate University, Japan, ²Cryobiofrontier Research Center, Faculty of Agriculture, Iwate University, Japan

PS33-06 11:05-11:25 (POS-02-089)

Characterization of Muscadine Berry Proteome Using Label and Label Free Mass Spectrometry Approaches

Ramesh Katam¹, Devaiah M. Kambiranda¹, Katsumi Sakata², Tiratharaj Singh⁴, Steve V. Sluyter³, Paul A. Haynes³, Mehboob B. Sheikh¹, Lekan M. Latinwo¹

¹Florida A&M University, USA, ²Maebashi Institute of Technology, Japan, ³Macquarie University, Australia, ⁴Bioclu.es.org

PS33-07 11:30-11:50 (POS-02-065)

Quantitative MSE Proteomics as a Tool for the Determination of Clinically Relevant Proteins in Wheat Grain

Lubica Uvackova¹, Ludovit Skultety^{2,3}, Slavka Bekesova², Scott McClain⁴, Martin Hajduch¹

¹Institute of Plant Genetics and Biotechnology, Slovak Academy of Sciences, Slovakia, ²Institute of Virology, Slovak Academy of Sciences, Slovakia, ³Center for Molecular Medicine, Slovak Academy of Sciences, Slovakia, ⁴Syngenta Crop Protection, LLC, USA

JHUPO-Organized Session Topics of Biomarker Research

Monday, September 16 15:30-17:00 Room 313+314

Chairs:

Sudhir Srivastava
Akihide Ryo

National Cancer Institute, USA
Yokohama City University, Japan

JHP-01 15:30- 15:55

Molecularly-Informed Discovery of Proteomic Biomarkers for Cancer Detection

Sudhir Srivastava

Cancer Biomarkers Research Group, National Cancer Institute, USA

JHP-02 16:00- 16:25

A Proteomic Approach to Decipher the Molecular Link between HIV-1 Gag and Host Proteins

Akihide Ryo

Department of Microbiology, Yokohama City University School of Medicine, Japan

JHP-03 16:30- 16:45 (POS-01-221)

Phosphoproteomics of Human Liver Cancer Analyzed by 2-Dimensional Image-Converted Analysis of Liquid Chromatography and Mass Spectrometry (2DICAL)

Masaya Ono¹, Masahiro Kamita¹, Tomohiro Sakuma², Miho Banno², Tesshi Yamada¹

¹National Cancer Center Research Institute, Japan, ²Mitsui Knowledge Industry Co., Ltd., Japan

SS: Human Proteome Project

Wednesday, September 18 9:00-11:50 Room 303+304

Chair:

Young-Ki Paik

Yonsei Proteome Research Center, Yonsei University, Korea

SS-01 9:00-9:15

Vision of Genome-Wide HPP

Young-Ki Paik

Yonsei Proteome Research Center, Yonsei University, Korea

SS-02 (Keynote) 9:15- 9:45

The Strategy, Organization, and Progress of the Human Proteome Project

Gilbert S. Omenn

University of Michigan, USA

SS-03 (Keynote) 9:50- 10:20

Genome-wide Proteomics: The Role the C-HPP Initiative to Study Cancer Gene Amplicons and Proteomic Signatures

W. Hancock¹, G. Omenn², M.Snyder³, R.Beavis⁴, Y-K. Paik⁵, Hoguen Kim⁵

¹Northeastern University, USA, ²University of Michigan, USA, ³Stanford University, USA, ⁴University of British Columbia, Canada, ⁵Yonsei University, Korea

SS-04 10:25- 10:55

Protein Post-Translational Modifications and their Regulation of Cardiovascular Disease

Melanie Y. White^{1,2}, Benjamin L. Parker², Jana Paulech¹, Kiersten A. Liddy¹,

Lauren E. Smith², Alistair V.G. Edwards², Stuart J. Cordwell^{1,2}

¹School of Molecular Bioscience, The University of Sydney, Australia, ²Discipline of Pathology, The University of Sydney, Australia

SS-05 11:00-11:50

Panel of HPP Leaders and General Discussion

William S. Hancock
Northeastern University, USA

YI01: Young Investigator Session 1

Sunday, September 15 11:00-12:50 Room 311+312

Chair:

Tosifusa Toda Yokohama City University, Japan
Norie Araki Kumamoto University, Japan

YI01-01 11:05-11:18 (POS-02-229)

Role of CYLD Deubiquitinase in EGF Signaling Pathway

Virginia Sanchez-Quiles, Vyacheslav Akimov, Inigo Barrio-Hernandez, Blagoy Blagoev
Center for Experimental Bioinformatics, Department of Biochemistry and Molecular Biology, University of Southern Denmark, Denmark

YI01-02 11:18-11:32 (POS-01-165)

ATP Accessibility Screening (AAS), A High-Throughput and High-Resolution Kinase Analysis Platform for Signaling Research

Jun Adachi¹, Daisuke Higo², Shio Watanabe¹, Masayoshi Kuwano¹, Yuki Hashimoto¹, Takeshi Tomonaga¹
¹Laboratory of Proteome Research, National Institute of Biomedical Innovation, Japan, ²Thermo Fisher Scientific K.K., Japan

YI01-03 11:33-11:46 (POS-03-143)

Hidden Proteome: Multiplex Quantitation of Low- and Ultralow-Copy Number Proteins in HepG2 Cells and Human Plasma

Arthur T. Kopylov, Zgoda G. Victor, Lisitsa V. Andrei, Elena Ponomarenko, Ekaterina Poverennaya, Ekaterina Ilgisonis, Alexander A. Moisa, Alexey D. Filimonov, Alexander I. Archakov
Orekhovich Institute of Biomedical Chemistry of the Russian Academy of Medical Sciences, Russia

YI01-04 11:47-12:00 (POS-03-076)

Targeted Proteomics to Validate and Quantify One-Hit Wonders Proteins in Human Liver

Chen Chen
Department of Chemistry, Fudan University, China

YI01-05 12:01-12:14 (POS-01-115)

Basic Fetoprotein is Homologous with G6PI/AMF/NLK/MF/PGI/PHI/SA-36 by the Identification of 99% AA Sequence for BFP Using MALDI-MS

Mutsumi Hosako, Hiroki Kuyama, Chihiro Nakajima, Shin-ichirou Kawabata, Koichi Tanaka
Koichi Tanaka Laboratory of Advanced Science and Technology, Shimadzu Corporation, Japan

YI01-06 12:15-12:28 (POS-01-203)

Systematic Characterization of Human Platelets in Arterial Vascular Disorders by Quantitative Proteomics

Julia M. Burkhardt¹, Marc Vaudel¹, Joerg Geiger³, Kristin Becker¹, Stepan Gambaryan², Walter Ulrich², Lennart Martens⁴, Rene P. Zahedi¹, Albert Sickmann¹
¹Leibniz-Institut fuer Analytische Wissenschaften - ISAS - e.V., Germany, ²Institute fuer Klinische Biochemie und Pathobiochemie, Germany, ³ibdw - Interdisciplinary Bank of Biomaterials and Data, Germany, ⁴VIB Department of Medical Protein Research, Germany

YI01-07 12:29-12:42 (POS-01-063)

Secretome Analysis of Three-Dimensional In Vitro Model Cholangiocarcinoma

Phanthakarn Tit-oon¹, Phannee Sawangareetrakul², Daranee Chokchaichamnankit²,
Jisnusun Svasti^{1,2}, Chantragan Srisomsap²

¹Applied Biological Sciences Program, Chulabhorn Graduate Institute, Thailand, ²Laboratory of Biochemistry, Chulabhorn Research Institute, Thailand

YI02: Young Investigator Session 2

Sunday, September 15 15:30-17:20 Room 311+312

Chair:

Pier Giorgio Righetti Politecnico di Milano, Italy

Masamichi Ohishi Kitasato University, Japan

YI02-01 15:35-15:47 (POS-02-058)

Applying SWATH-MS to Dissect the Variability and Heritability of the Human Plasma Proteome

Yansheng Liu¹, Ben Collins¹, Ludovic CJ Gillet¹, Ruth Huttenhain¹,
Emmanouil T Dermitzakis², Ruedi Aebersold^{1,3}

¹Department of Biology, Institute of Molecular Systems Biology, ETH Zurich, Switzerland, ²Department of Genetic Medicine and Development, University of Geneva Medical School, Switzerland, ³Faculty of Science, University of Zurich, Switzerland

YI02-02 15:48-16:00 (POS-02-144)

Plasma Proteome Analysis Using LC-MS/MS with Travelling Wave Ion Mobility and an Alternative Computational Solution to Protein Quantitation

Charlotte E. Daly^{1,2}, Amirmansoor Hakimi¹, Leong L. Ng², Don J. L. Jones¹

¹Department of Cancer Studies and Molecular Medicine, University of Leicester, UK, ²Department of Cardiovascular Sciences, University of Leicester, UK

YI02-03 16:01-16:13 (POS-02-233)

Quantifying the Dynamics of a 14-3-3 Protein Interaction Network by Affinity Purification and SWATH Mass Spectrometry

Ben C. Collins¹, Ludovic C. Gillet¹, George Rosenberger^{1,2}, Hannes L. Rost^{1,2},
Matthias Gstaiger¹, Ruedi Aebersold^{1,2,3,4}

¹Department of Biology, Institute of Molecular Systems Biology, ETH Zurich, Switzerland, ²Ph.D. Program in Systems Biology, University of Zurich and ETH Zurich, Switzerland, ³Competence Center for Systems Physiology and Metabolic Diseases, Switzerland, ⁴Faculty of Science, University of Zurich, Switzerland

YI02-04 16:14-16:26 (POS-02-231)

Investigation of Time Dependent Competitive Protein Adsorption to Surfaces Using Mass Spectrometry

Torgny Undin, Andreas Dahlin, Jonas Bergquist, Magnus Wetterhall
Uppsala University, Sweden

YI02-05 16:27-16:39 (POS-03-096)

Establishment and Application of a High-Quality Comparative Analysis Strategy of Low-Abundance Biomarker Peptide in Serum Based on Optimized Novel Peptide Extraction Method

Tatsuya Saito¹, Kawashima Yusuke^{1,2}, Minamida Satoru³, Kazumasa Matsumoto³, Takashi Matsui⁴, Mamoru Satoh⁵, Fumio Nomura^{5,6}, Masatsugu Iwamura³, Tadakazu Maeda^{1,2}, Shiro Baba³, Yoshio Kodera^{1,2,5}

¹Laboratory of Biomolecular Dynamics, Department of Physics, Kitasato University School of Science, Japan, ²Center for Disease Proteomics, Kitasato University School of Science, Japan, ³Department of Urology, Kitasato University School of Medicine, Japan, ⁴Division of Natural Products Chemistry, Department of Medicinal Resources, Institute of Natural Medicine, University of Toyama, Japan, ⁵Clinical Proteomics Research Center, Chiba University Hospital, Japan, ⁶Department of Molecular Diagnosis (F8) Graduate School of Medicine, Chiba University, Japan

YI02-06 16:40-16:52 (POS-03-164)

Quantitative Proteomic Approach to Identify Proteins Signalling Pathways in Human Cerebral Microvascular Endothelial Cells Modified with 17β-Estradiol

Nurul F. Jufri^{1,2}, Mark Baker¹, Jian Tu¹

¹Macquarie University, Australia, ²National University of Malaysia, Malaysia

YI02-07 16:53-17:06 (POS-02-213)

Defining the Structure of Mitotic Chromosomes Using Multi-Classifer Combinatorial Proteomics Together with DT40 Genetics

Shinya Ohta^{1,2}, Laura Wood², Itaru Samejima², Luis Fernando Montano², Juri Rappsilber², William C. Earnshaw²

¹Center for Innovative and Translational Medicine, Medical School, Kochi University, Japan, ²Wellcome Trust Centre for Cell Biology, University of Edinburgh, UK

YI02-08 17:07-17:20 (POS-03-079)

Targeted Analysis of *Salmonella* Effector Proteins Using Multiple Reaction Monitoring

Joost W. Gouw, Nat F. Brown, Leonard J. Foster

Centre for High-Throughput Biology, University of British Columbia, Canada

YI03: Young Investigator Session 3

Monday, September 16 11:00-12:50 Room 311+312

Chairs:

Naoyuki Taniguchi

RIKEN Global Research Cluster, Japan

Fumio Nomura

Chiba University & Chiba University Hospital, Japan

YI03-01 11:03-11:15 (POS-01-088)

Differentially Glycosylated Circulating Protein Biomarker Discovery for Barretts Esophagus and Esophageal Adenocarcinoma

Alok K. Shah¹, David Chen², Kim-Anh Le Cao³, Eunju Choi¹, Derek Nancarrow⁴, David Whiteman⁴, Nicholas A. Saunders¹, Andrew Barbour⁵, Michelle M. Hill¹

¹The University of Queensland Diamantina Institute, The University of Queensland, Australia, ²School of Information and Communication Technology, Griffith University, Australia, ³Queensland Facility of Advanced Bioinformatics, The University of Queensland, Australia, ⁴Queensland Institute of Medical Research, Australia, ⁵School of Medicine, The University of Queensland, Australia

YI03-02 11:16-11:28 (POS-02-263)

A Novel Titanium Dioxide Plate (TiO₂ Plate) for Phosphopeptide Enrichment and On-Target MALDI-TOF Analysis

Chao-Jung Chen

China Medical University, Taiwan

YI03-03 11:29-11:41 (POS-03-016)

Site-Specific N-Linked Glycosylation Analysis by Nano-LC Tandem Mass Spectrometry Coupled with a Spectral Library Searching Approach

Pei-Jing Pai, Yingwei Hu, Henry Lam

Department of Chemical and Biomolecular Engineering, The Hong Kong University of Science and Technology, Hong Kong SAR, China

YI03-04 11:41-11:53 (POS-03-070)

Proteome-Wide Identification of Poly (ADP-Ribosyl)ation Targets in Different Genotoxic Stress Responses

Stephanie Jungmichel¹, Florian Rosenthal², Michael O. Hottiger², Michael L. Nielsen¹

¹Department of Proteomics, The Novo Nordisk Foundation Center for Protein Research, University of Copenhagen, Faculty of Health Sciences, Denmark, ²Institute of Veterinary Biochemistry and Molecular Biology, University of Zurich, Switzerland

YI03-05 11:56-12:08 (POS-01-222)

Synthesis of Galactose-Deficient IgA1 O-glycans by GalNAc-transferases: Implications for the Pathogenesis of IgA Nephropathy

Kazuo Takahashi^{1,2}, Milan Raska^{1,3}, Tyler J. Stewart¹, Milada Stuchlova Horynova^{1,3}, Audra Hargett¹, Alena Kasperova^{1,3}, Stacy D. Hall¹, Yoshiyuki Hiki², Yukio Yuzawa², Bruce A. Julian¹, Zina Moldoveanu¹, Matthew B. Renfrow¹, Jan Novak¹

¹University of Alabama at Birmingham, USA, ²Fujita Health University, Japan, ³Palacký University in Olomouc, Czech Republic

YI03-06 12:09-12:21 (POS-01-197)

A SILAC-based Approach Defines an Angiotensin II- Regulated Proteome in Primary Human Kidney Cells

Ana Konvalinka^{1,2}, Eleftherios Diamandis^{3,4}, James Scholey^{1,2}

¹Division of Nephrology, Toronto General Hospital, University Health Network, University of Toronto, Canada, ²Department of the Institute of Medical Science, University of Toronto, Canada, ³Department of Pathology and Laboratory Medicine, Mount Sinai Hospital, University of Toronto, Canada, ⁴Department of Clinical Biochemistry, University Health Network, University of Toronto, Canada

YI03-07 12:24-12:36 (POS-01-113)

An Improved Protocol for the Enrichment of Plasma Membrane Proteins Allows the Identification of Accessible Antibody Targets on Trastuzumab-Resistant Breast Cancer Cells

Yohei Mukai^{1,2,3}, Danilo Ritz⁴, Dario Neri¹, Tim Fugmann⁴

¹Institute of Pharmaceutical Sciences, ETH Zurich, Switzerland, ²Graduate School of Pharmaceutical Sciences, Osaka University, Japan, ³Laboratory of Biopharmaceutical Research, National Institute of Biomedical Innovation (NiBio), Japan, ⁴Philochem AG, Switzerland

YI03-08 12:37-12:50 (POS-03-044)

Mass Isotopomer Analysis of Metabolically Labeled Nucleotide Sugars and N- and O-Glycans for Tracing Nucleotide Sugar Metabolisms

Kazuki Nakajima

Systems Glycobiology Research Group, RIKEN, Japan