Luncheon Seminar 1

Sunday, September 15
13:00-14:00
Room 303+304

Sponsored by Bruker Daltonics Inc.

LS-01

Quantitative and Targeted Proteomics: MRM or Accurate Mass?

LS-01-1

The New EVOQ Elite ER: Highest Sensitivity and Selectivity for Absolute Quantitation and Targeted Proteomics

Rohan Thakur
Bruker Corporation, USA

LS-01-2

Proteomic Profiling and Imaging for the Studies of Neurological Diseases

Professor Masaya Ikegawa
Doshisya University, Japan

LS-01-3

The Power of Accurate Mass Screening and DIA in Quantitative Proteomics

Pierre-Olivier Schmit
Bruker Daltonique S.A., France

Luncheon Seminar 2

Sunday, September 15
13:00-14:00
Room 301

Sponsored by
GE Healthcare Japan Corporation

LS-02

Fluorescent Detection Overcomes the Challenges in Quantitative Western Blotting (tentative)

Susanne Grimsby, B.S.
Senior Research Engineer, GE Healthcare Life Sciences

To overcome the challenges in quantitative Western blotting, we report on;
- Ways to use chemiluminescent and fluorescent Western blotting for confirmatory and quantitative detection
- What the prerequisites are for achieving quantitative results, and how those can be fulfilled using fluorescent Western blotting detection
- Tips on how to overcome common challenges in Western blotting, in order to achieve consistent results

Luncheon Seminar 3

Sunday, September 15
13:00-14:00
Room 302

Sponsored by Thermo Fisher Scientific

LS-03

HRAM Quantification Using Orbitrap Technology

Thermo Fisher Scientific

Luncheon Seminar 4

Sunday, September 15
13:00-14:00
Room 311+312

Sponsored by
KIKO TECH CO., LTD./ ProteinSimple

LS-04

The Simple Western: A Fully Automated and Quantitative Tool for Protein, Biotherapeutic, and Vaccine Research

John Proctor, Ph.D.
Director of Corporate Development, ProteinSimple

The Simple Western is a fully automated walk-away solution that is a gel-free and blot-free reinvention of the traditional Western blot for protein separation and characterization. As an automated instrument, it drastically reduces the hands-on time traditionally required when performing an immunoassay. It delivers reproducibility and true quantitation while addressing the major challenges that researchers face on a daily basis-unreliable data, delayed time to results, reduced productivity and, ultimately, more costly research programs. In this seminar, I will illustrate examples of how the Simple Western has been applied to protein quantitation, cell signaling analysis, biotherapeutic characterization, and vaccine research. This sensitive technology measures either protein molecular weight or charge in complex samples and provides this critical information without the need for sample purification. Whether you' re doing protein research in biotech, pharma, or academia there is a Simple Western application for you.

Luncheon Seminar 5

Monday, September 16
13:00-14:00
Room 303+304

Sponsored by AB SCIEX

LS-05

Deep and Efficient Acquisition of Human Proteome/Phosphoproteome Data by One-Shot Proteomic LC-MS with Long Monolithic Columns

Yasushi Ishihama
Kyoto University, Kyoto, Japan

Because peptide samples for shotgun proteomics exhibit extremely high complexity with a wide dynamic range of concentration, the separation capability of the current nanoLC is not sufficient enough to reduce the complexity. Recently, by using one-dimensional nanoLC-MS with meter-long, monolithic silica-C18 capillary column, we successfully identified 9,510 proteins in human induced pluripotent stem cells and fibroblasts [Yamana et al, JPR2013]. In this presentation, we will also present deep and efficient acquisition of phosphoproteomes by one-shot proteomic LC-MS approach.

Luncheon Seminar 6

Monday, September 16
13:00-14:00
Room 301

Sponsored by Bruker Daltonics Inc.

LS-06

Top-Down Sequencing for Full Protein Characterization in Proteomics and Biopharma

LS-06-1

A paradigm Change in Mass Resolution - The New solariX XR

Mike Easterling
Bruker Daltonics Inc., USA

LS-06-2

Top-down Proteomics with Ultra-high Resolution QTOF Instruments

Peter Brechlin
Bruker Daltonik GmbH, Germany

LS-06-3

MALDI-TDS of the Biooriginator Cetuximab Providing 100% Sequence Coverage and Complete Glycosylation Elucidation

Detlev Suckau
Bruker Daltonik GmbH, Germany

Luncheon Seminar 7

Monday, September 16
13:00-14:00
Room 302

Sponsored by
SHIMADZU CORPORATION

LS-07

Quantitative Analysis by LC/MS/MS of Progranulin as a Marker for Insulin Resistance

Susumu Seino
Division of Molecular and Metabolic Medicine, and The Integrated Center for Mass Spectrometry, Kobe University, Graduate School of Medicine

Obesity and diabetes are diseases that afflict enormous populations in the 21st century. Insulin resistance is a characteristic feature in both obesity and diabetes. Adipose tissue secretes various cytokines or hormone-like substances called "adipokines". We have recently identified progranulin as a key adipokine that links high fat diet to obesity, suggesting that progranulin can be a biomarker for insulin resistance as well as a therapeutic target of obesity. Progranulin has been shown to be processed to granulin peptides (GRNs). In this lecture, we will discuss a novel method for selective quantification of GRNs in the blood, based on our recent data.

Luncheon Seminar 8

Monday, September 16
13:00-14:00
Room 311+312

Sponsored by
Bio-Rad Laboratories K.K.

LS-08

Innovative Technologies for Increased Confidence in Proteomic and Protein Analysis Workflows

Anton Posch
Staff Scientist, Bio-Rad Laboratories, Hercules, USA

Proteomic analysis of biological systems requires the integration of multiple technologies into robust work-flows for protein separation, analysis, and detection. Gel-based protein separations are widely used in these workflows and frequently followed by protein visualization/staining, mass spectrometry and/or immunodetection applications. Currently, these applications suffer from at least two important limitations: First, standard methods of protein visualization/staining are time-consuming and the associated manual handling adds to overall variability between experiments. Second, the quality of antibodies used for immunodetections are often unsatisfactory, affecting confidence in final outcome. Here, we present innovative technologies to address each of these limitations.
To address the first limitation, we present TGX Stain-Free SDS-PAGE gels which contain unique trihalo compounds formulated into the gel chemistry for immediate visualization of proteins across the entire gel without staining. When activated, these compounds covalently bind to tryptophan residues in proteins and emit a fluorescent signal that is easily detectable with suitably matched imager systems. We will illustrate benefits of stain-free technology for increased confidence in two dimensional electrophoresis, western blotting, mass spectrometry (MS), and protein purification/visualization applications. To address the second limitation, we introduce HuCAL - a novel technology for high quality antibody generation for western blotting, immuno-MS and diagnostics.

Luncheon Seminar 9

Tuesday, September 17
13:00-14:00
Room 303+304

Sponsored by Thermo Fisher Scientific

LS-09

Advanced Proteomic Discovery Workflows Using Novel Multiplexing Methods

Thermo Fisher Scientific

If cannot be prepared by deadline, then will not put abstract.

Luncheon Seminar 10

Tuesday, September 17
13:00-14:00
Room 301

Sponsored by GlycoTechnica Ltd. / Sysmex Corporation

LS-10-1

Introduction of a Powerful Lectin Microarray Platform for Biomarker Discovery and Screening

Masao Yamada, Ph.D.
Cheif Exective Scientific Officer, GlycoTechnica Ltd.

LS-10-2

Development of Quantitative Glyco-indices for Hepatic Diseases

Atsushi Kuno, Ph.D.
Team Leader, Glycodiagnosis Translation Team, Research Center for Medical Glycomics, National Institute of Industrial Science and Technology

LS-10-3

Introduction of HISCL Automated Analysis System

Tomoyuki Nishida
Manager, Product Development, Immunology & Chemical Product Engineering, ICH Business Unit, Sysmex Corporation

Glycomics opens up a novel strategy for searching new biomarkers, screening the candidates, and ending up to developing clinical inspection assays. A lectin microarray platform presented here named "GlycoStation" (GlycoTechnica Ltd.) is very powerful in biomarker development, and has the highest sensitivity and quantitative feature comparing with any other similar systems. In this seminar, new biomarker developments for human liver fibrosis and cholangiocarcinoma are highlighted as typical examples of this success (National Institute of Advanced Industrial Science and Technology). Finally, practical clinical inspection assay designed on HISCL Automated Analysis System (Sysmex Corp.) is introduced as one the most successful results of this strategy.

Luncheon Seminar 11

Tuesday, September 17
13:00-14:00
Room 302

Sponsored by Waters Corporation

LS-11

Innovations in High-resolution Mass Spectrometry for Protein Quantification

James Langridge
Waters Corporation, Manchester, UK

Multiple Reaction Monitoring (MRM) mass spectrometry has emerged as a sensitive and robust method for the quantification of target analytes, particularly those in biological matrices. However, for the quantification of putative protein biomarkers sensitivity and specificity are paramount. For this reason increasing the selectivity of the MRM assay is crucial and high-resolution approaches have been suggested.

We will compare and contrast results from a new high resolution MRM approach (high-definition MRM) on a Synapt G2-Si mass spectrometer with the classical tandem quadrupole approach.

Luncheon Seminar 12

Tuesday, September 17
13:00-14:00
Room 311+312

Sponsored by Funakoshi Co., Ltd.

LS-12-1

Absolute Quantification of Human Proteome by Large-Scale Targeted Proteomics

Professor Keiichi Nakayama
Kyushu University

We have developed a new technology termed information-based multiple reaction monitoring (iMRM) to measure the absolute abundance of all human proteins. With the use of iMRM system, we have now measured the absolute abundance of all metabolic enzymes in normal and cancer cells and uncovered the secret underlying "Warburg effect."

LS-12-2

Products for MRM

Dr Akihiro Yoshida
Funakoshi Co.,Ltd.

- Peptide probes for Human protein
- Proteomics Sample preparation Kit
- Retention Time Markers for iMRM Analysis

Luncheon Seminar 13

Tuesday, September 17
12:00-13:00
Room 303+304

Sponsored by
Wako Pure Chemical Industries, Ltd.

LS-13

Phos-tag-Based Technological Advances for Studies on Signal Transduction in the Coming Generation

Eiji Kinoshita
Hiroshima University, Japan

We have been involved in developing a technology known as Phos-tag to permit the analysis of phosphorylated biomolecules. The Phos-tag technology has made contributions to the development of several procedures for research on the phosphoproteome, including a phosphate-affinity chromatography technique for the separation and enrichment of phosphopeptides and phosphoproteins, a phosphate-affinity electrophoresis technique for the detection of shifts in the mobilities of phosphoproteins, and microarray techniques for the detection of protein phosphorylation multiplexes. In this seminar, I discuss the impact of Phos-tag-based technological advances for studies on signal transduction in the coming generation.

Luncheon Seminar 14

Tuesday, September 17
12:00-13:00
Room 302

Sponsored by Nihon Pall Ltd.

LS-14

Hit Identification and Lead Confirmation in the Discovery of Drugs Targeting Bromodomain Proteins

Liu Liu, PhD
Comprehensive Cancer Center, University of Michigan

Luncheon Seminar 15

Tuesday, September 17
12:00-13:00
Room 311+312

Sponsored by
Agilent Technologies, Inc.

LS-15-1

QC or Bust: Performance Assessment for Quantitative Plasma Proteomics by MRM

Christoph Borchers, Ph.D.
University of Victoria - Genome BC Proteomics Centre, Victoria, BC, Canada

LS-15-2

Defining the Next Experiment: Pathway-directed Analysis from Protein Discovery Data

Christine Miller
Senior Application Scientist, Agilent Technologies

Learn how pathway knowledge can be used to create targeted proteomics experiments to verify and validate candidate disease biomarkers in complex matrices. Examples are shown in the seminar. For some targeted assays, absolute quantitation is key to finding the true biological differences. In order to enable the acquisition of more precise and accurate quantitative data, two reference kits were developed by MRM Proteomics using SIS peptide approach for undepleted and non-enriched human plasma.

Evening Seminar 1

Sunday, September 15
18:00-19:30
Exhibition Hall Session Space

Sponsored by Tanaka ms3d Project

ES-01

Development of the Next Generation Mass Spectrometry System, and Contribution Toward Drug Discovery and Diagnostics - Focus on Software Development

ES-01-1

FIRST ms3d Project

Koichi Tanaka
Koichi Tanaka Laboratory of Advanced Science and Technology, Shimadzu Corporation

"FIRST" <http://first-pg.jp/english/> is a major project funded by the Cabinet Office of Japan (100 billion JPY). One of the 30 "FIRST" projects is "ms3d project" (core-researcher: Koichi Tanaka) <http://www.first-ms3d.jp/> whose objective is to develop all MS systems from "Sample Preparation", "Ionization", "MS Hardware" up to "Software" mainly for Drug Discovery and Diagnostics. One of the foremost achievement is "Improved selectivity and sensitivity by >10,000 folds".

ES-01-2

Introduction of MS Analysis Software Mass++

Satoshi Tanaka
Koichi Tanaka Laboratory of Advanced Science and Technology, Shimadzu Corporation

Mass++ is freeware for viewing and manipulating various types of mass spectrometric data. Its primary objectives are: 1. To provide essential functionality mass for proteomics and metabolomics analysis. 2. To support a wide range of vendors' data file formats. 3. To be easily extendible using plug-in technology. In this section, we will introduce and demonstrate some functions of Mass++ such as identification and quantitation.

ES-01-3

Biomarker Discovery Using Mass++ Software

Ken Aoshima
Eisai Co., Ltd Biomarkers and Personalized Medicine

Mass++ is an universal mass spectrometry data analysis software, which allows to develop plug-ins for different types of research needs. Recently we have developed a label free quantitation algorithm called AB3D as a new plug-in of Mass++, and we have successfully applied our algorithm to biomarker research and drug discovery. In this presentation, we will introduce our recent biomarker discovery results by utilizing quantitative features of Mass++ software.

Evening Seminar 2

Sunday, September 15
18:15-19:45
Room 315

Sponsored by
Agilent Technologies, Inc.

ES-02

2013 HUPO Meeting of the Minds

This unique event provides the opportunity to meet with HUPO keynote speakers and dignitaries during Agilent's cocktail reception.
This unique gathering's format will consist of 15-20 minute intervals for personal discussions with one or two dignitaries at a time, and then rotate to another table for additional discussions with other thought leaders in the proteomics field.

Evening Seminar 3

Tuesday, September 17
19:00-20:30
Exhibition Hall Session Space

Sponsored by Matrix Science Ltd.

ES-03

Mascot Insight: A New Application to Organise, Analyse and Report Mascot Search and Quantitation Results

Dr. Patrick Emery
Matrix Science Ltd. Senior Bioinformatician

As proteomics experiments become larger scale and more complex, one of the main challenges facing researchers and core facilities is the management and data mining of the generated data sets. Mascot Insight is a new platform which can take the results of Mass Spectrometry based sequence database searches, either from a Mascot server or from an MzIdentML export, and allows users to merge, filter, compare and annotate datasets and incorporate additional information from sources such as GO and molecular interaction databases. A variety of reports are supplied which facilitate analysis of discovery searches, quantitation experiments and de novo searches. Users can create additional reports using a simple Java based API.