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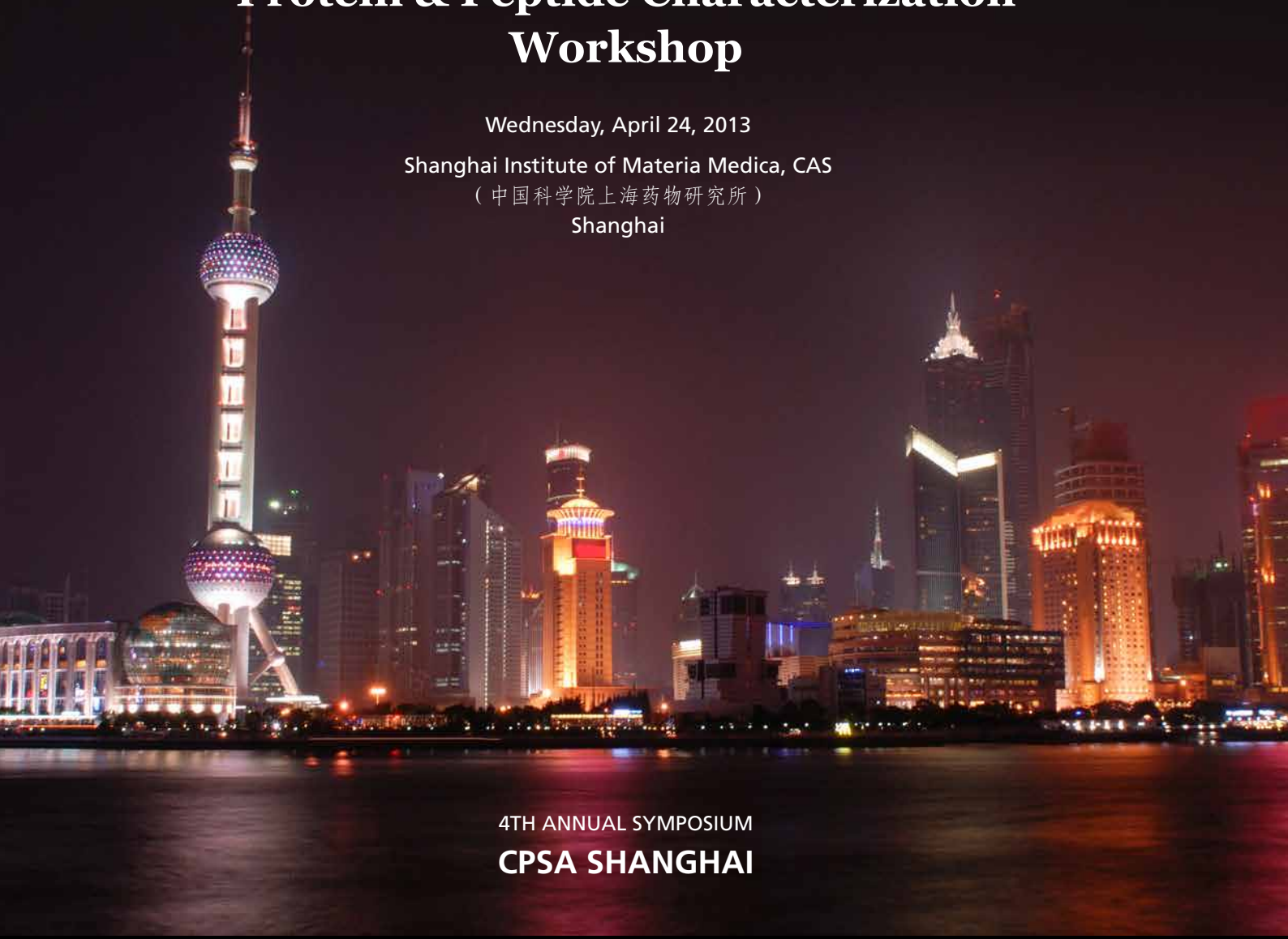
PRE-CONFERENCE EVENT

Held in conjunction with CPSA SHANGHAI 2013

Protein & Peptide Characterization Workshop

Wednesday, April 24, 2013

Shanghai Institute of Materia Medica, CAS
（中国科学院上海药物研究所）
Shanghai



4TH ANNUAL SYMPOSIUM

CPSA SHANGHAI

Where Technology and Solutions Meet
Where East Meets West

Milestone Development Services

Protein & Peptide Characterization Workshop

Wednesday, April 24, 2013
1:00 PM - 4:00 PM

CPSA SHANGHAI 2013

Shanghai Institute of Materia Medica, CAS (中国科学院上海药物研究所)
Yi-Sheng Hall, Building 1 555 Zu-Chong-Zhi Road (上海市浦东张江祖冲之路555号)
Pudong New District, Shanghai
www.simm.cas.cn

JOIN US for this engaging and informative afternoon workshop with leaders in the fields of proteomics research and technology

Data Independent Acquisition in Proteomics Analysis

Nathan A. Yates, Ph.D *Scientific Director, Biomedical Mass Spectrometry Center, University of Pittsburgh*

Traditionally, shotgun proteomics experiments have used data dependent acquisition wherein the mass spectrometer performed an initial scan of precursor ions and selected a sampling of those ions for fragmentation and generation of MS/MS spectra. Because instruments can't scan quickly enough to acquire all the precursors entering at a given moment, however, many ions – particularly low-abundance ions – are never selected for MS/MS fragmentation and so are not detected. In DIA, the mass spec selects broad m/z windows and fragments all precursors in that window, allowing the machine to collect MS/MS spectra on all ions in a sample. In combining qualitative and quantitative proteomics analysis, DIA techniques have been employed by a number of proteomics researchers using a variety of different platforms.

Nanospray Technologies for Proven Characterization with Established and Emerging Technologies

Gary A. Valaskovic, Ph.D. *CEO of New Objective Inc.*

Workflows for proteomics based on liquid chromatography/mass-spectrometry (LC-MS) typically fall along a qualitative or quantitative path. MS based proteomics is typically accomplished in a bottom-up fashion using enzymatic digestion. Peptides are identified by matching of molecular ion fragmentation patterns, resulting in the inferred identification of the representative protein. For either the qualitative or quantitative workflow, the resulting mixtures are highly complex, typically containing tens of thousands of chemically distinct peptides for analysis. To provide adequate analytical sensitivity and selectivity, nanospray ionization for mass spectrometry is combined with nanobore LC. The considerable need for dynamic range in qualitative analysis and the high throughput demands of quantitative analysis places strict emphasis on no-compromise system performance. High performance nanospray requires control of emitter geometry, spray voltage, emitter position, flow rate, column chemistry, column temperature, and perhaps most importantly a combination or robustness and ease-of-use. Optimization of these parameters will be highlighted and discussed. Based on these needs, a newly developed and innovate platform technology (PicoChip™) has been developed. The PicoChip system combines high-performance robustness and outstanding ease-of-use combined with flexibility of column chemistry, column format, and temperature control. A prototype multiplexed system will be shown that enables a greater than 95% duty cycle for the mass spectrometer with sufficient throughput to enable quantitative proteomics workflows.

Multi PTM Analysis on LTQ-Orbitrap Hybrid Mass Spectrometer

Min-Jia Tan, Ph.D. *Shanghai Institute of Materia Medica, CAS*

Protein translational modifications (PTMs) of proteins are complex and fundamental mechanisms of cellular regulation, and have been associated with almost all known cellular pathways and disease processes. Among them, phosphorylation, ubiquitination, acetylation have been by far the most well-characterized. With the advancement of high-resolution mass spectrometry (MS) technologies, MS-based have been the fundamental tool for detecting, mapping and quantifying protein covalent modifications, and large-scale modification-specific proteomics studies. Here we describe and applications of MS-based strategies and bioinformatics tool used to detect common PTMs, map protein modification sites, quantitive global profiling of PTMs, noting the advantages and drawbacks of different approaches.

REGISTRATION

Early Registration (before April 6, 2013)	$75.00
Regular Registration: (after April 6, 2013)	$100.00

MORE INFORMATION

Visit the CPSA Shanghai website to register, for directions, or for more information: **www.cpsa-shanghai.com**

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