# HUPO 2013 ERRATA

## Correction in the Program Book

- Corrections with * applies to Program Book and Abstract USB
- Information on the Program Book and Abstract are based on the submitted information.

**p. 22 Time Correction**

Program Overview for HUPO2013
Sunday, Sep.15, 2013 Main Hall
PLENARY LECTURE2 17:20-18:05
→ 17:30-18:05

**p. 23 Time Correction**

Program Overview for HUPO2013
Sunday, Sep. 15, 2013
Luncheon Seminar 4 14:00-15:30
KIKO TECH CO., LTD./
ProteinSimple
→ 13:00-14:00

**p. 23 Speaker Change***

PS21-03 11:55-12:10
Estimation of Protein Species Number for Mammalian, Bacteria, Insecta and Yeast
Elena Ponomarenko, Stanislav Naryzhny, Ekaterina Poverennaya, Mikhail Pyatnitskii, Andrey Lisitsa, Alexander Archakov
→
Elena Ponomarenko, Stanislav Naryzhny, Ekaterina Poverennaya, Mikhail Pyatnitskii, Andrey Lisitsa, Alexander Archakov

**P. 30 Speaker Change***

PS01-02
Amol Prakash
→
Barbara Frewen

**P. 55 Additional Chair**

YI03: Young Investigator Session 3
Chair:
Naoyuki Taniguchi RIKEN Global Research Cluster, Japan
→Chairs:
Naoyuki Taniguchi RIKEN Global Research Cluster, Japan
Fumio Nomura Chiba University & Chiba University Hospital, Japan

**P. 87 Correction on Affiliation***

POS-01-047

Search and Identification of Peptide Biomarkers of Colorectal Cancer in Sera

Igor Azarkin[1], Rustam Ziganshin[1], Georgy Arapidi[1], Sergey Kovalchuk[1,2], Victoria Shender[1], Olga Ivanova[1], Vadim Govorun[1,2], Vadim Ivanov[1]

[1]Shemyakin-Ovchinnikov Institute of Bioorganic Chemistry of the Russian Academy of Sciences, Russia,

[2]Research Institute for Physico-Chemical Medicine Federal Medical-Biological Agency of the Russia

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[2]Research Institute for Physico-Chemical Medicine Federal Medical-Biological Agency of the Russian Federation, Russia

**p. 89 Correction on Affiliation***

POS-01-059

Biomarker Proteins in Head and Neck Squamous Cell Carcinoma. A Brief Review

Rachel Conrad[1], Marnelli Bautista[1], Cliff Herrmann[2], Mia Perez[1], Lawrence Sandberg[2], Ravi Raghavan[1]

*[1]Pathology, [2]Biochemistry*

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[1] *Department of Pathology, Loma Linda University Medical Center, USA*

[2] *Department of Biochemistry, Loma Linda University Medical Center, USA*

**P. 99 Correction on Title***

POS-01-066

Lactoylglutathione (Glo1)

→ Lactoylglutathione Lyase (GLO1)

**P. 107 Speaker Change***

POS-01-184

Proteomic Analysis on the Mechanism of LDL Apheresis Therapy in the Steroid-Resistant Nephrotic Syndrome

Emiko Kuribayashi-Okuma[1,2]

*[1]Department of Nephrology, School of Medicine, Teikyo University, Japan, [2]Department of Biochemistry, School of Medicine, Teikyo University, Japan*

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Emiko Kuribayashi-Okuma[1], Harumi Hisaki[2], Tomoki Okazaki[2], Shunya Uchida[1]

*[1]Department of Nephrology, School of Medicine, Teikyo University, Japan, [2]Department of Biochemistry, School of Medicine, Teikyo University, Japan*

**P. 114 Speaker Change***

POS-01-224 / PS13-01

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

Sylvain Lehmann[1], Nicolas Barthelemy[2], Jérôme Vialaret[1], Susanna Schraen-Maschke[3], Laurent Tiers[1], Constance Delaby[1], Christophe Junot[2], Jacques Touchon[1],Nicolas Sergent[3], Audrey Gabelle[1], François Becher[2], Christophe Hirtz[1]

→

Sylvain Lehmann[1], Nicolas Barthelemy[2], Jérôme Vialaret[1], Susanna Schraen-Maschke[3], Laurent Tiers[1], Constance Delaby[1], Christophe Junot[2], Jacques Touchon[1],Nicolas Sergent[3], Audrey Gabelle[1], François Becher[2], Christophe Hirtz[1]

**P. 123 Additional Co-author***

POS-02-001

Bridging the Gap Between Imaging Mass Spectrometry and LC-MS/MS Identification

Ove Johan Ragnar Gustafsson[1], Stephan Meding[1], Karina Martin[1], James S Eddes[1], Sandra Hack[1], Tomas Koudelka[1], Martin K Oehler[2], Shaun R McColl[1], Peter Hoffmann[1]

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Ove Johan Ragnar Gustafsson[1], Stephan Meding[1], Karina Martin[1], James S Eddes[1], Sandra Hack[1], Tomas Koudelka[1], **Carmen E. Pyragius**[2], Shaun R McColl[1], Martin K Oehler[2], Peter Hoffmann[1]

**P. 126 Speaker Change***

POS-02-020

Extensive Phenotypically Characterization of Exosomes Derived from Activated,
Non-Activated APCs and T-Cells Using an Extracellular Vesicle (EV) Array

Anne Louise S. Revenfeld[1,2], Allan Stensballe[1], Malene Joergensen[2]

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Anne Louise S. Revenfeld[1,2], Allan Stensballe[1], Malene Joergensen[2]

**P. 145 Speaker Change***

POS-02-158

Amol Prakash

→

Barbara Frewen

## CANCELLATIONS

**P. 98** POS-01-119*

**P. 149** POS-02-189*

**P.188** POS-03-184*

## NEW PRESENTTIONS

**P. 101** POS-01-140*

Proteomic Analysis of the Monkey Hippocampal DG after the Ischemia-Reperfusion

Yuki Kitamura [1], Shota Kurimoto [1], Tetsumori Yamashima [2],
Mariko Murata [1], Shinji Oikawa[1]

*[1] Department of Environmental and Molecular Medicine, Mie University Graduate School of Medicine*

*[2] Department of Restorative Neurosurgery, Kanazawa University Graduate School of Medical Science*

**P. 206** POS-03-LB-069*

Deciphering human-microbe proteome interactions using an E. coli proteome chip

Chen Chien-Sheng

*Graduate Institute of Systems Biology and Bioinformatics, National Central University*

POS-03-LB-070

E-Learning Platform for Proteomics as a Part of National Program on Technology Enhanced Learning in India; Proteomics Education as a Community Effort

Sanjeeva Srivastava, Sandipan Ray, Rekha Jain, Kaustav Dasgupta,
Avani Yeola, Prajakta Kulkarni, Samridhi Sharma, Darpan Malhotra, Jaipal Panga Reddy, Saurabh Yadav, Parvez Syed

*[1]Department of Biosciences and Bioengineering, Indian Institute of Technology Bombay, Mumbai, India*

# Correction in the Abstracts USB

**POS-01-066 Corrections on Title/Contents***

Lactoylglutathione (Glo1)

→ Lactoylglutathione Lyase (GLO1)

**POS-01-079 Correction on Affiliation**

[4]*Pharmaceutical Chemistry, University of California San Francisco, USA*

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[4]*Department of Pharmaceutical Chemistry, University of California San Francisco, USA*

## ADDITIONAL ABSTRACTS

**POS-01-140**

Proteomic Analysis of the Monkey Hippocampal DG after the Ischemia-Reperfusion

Yuki Kitamura [1], Shota Kurimoto [1], Tetsumori Yamashima [2],
Mariko Murata [1], Shinji Oikawa[1]

[1] *Department of Environmental and Molecular Medicine, Mie University Graduate School of Medicine*

[2]*Department of Restorative Neurosurgery, Kanazawa University Graduate School of Medical Science*

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Ischemia-reperfusion is known to cause oxidative stress through the excessive generation of reactive oxygen species (ROS). It has been reported that ROS causes extensive cell death in the cornu ammonis (CA) 1 region but not in the dentate gyrus (DG) of the hippocampus, which is known to be involved in learning and memory processes. In this study, to elucidate the mechanism of resistance to oxidative stress in DG, we examined the alternations of protein expression in DG isolated from the Japanese monkeys after the ischemia-reperfusion insult by 2D DIGE.

Nicotinamide adenine dinucleotide (NAD)-dependent protein deacetylase sirtuin-2 (SIRT2) was significantly increased in DG after the ischemia-reperfusion. It is reported that deacetylation of the forkhead box protein O3a (FOXO3a) by SIRT2 regulates cellular response to oxidative stress through the activation of manganese superoxide dismutase (MnSOD), known as an antioxidant enzyme. In addition, we performed the identification and characterization of carbonylated protein, protein oxidation products, in DG after the ischemia-reperfusion by using 2DE with immunochemical detection of protein carbonyls (2D Oxyblot). The specific oxidation level of dihydropyrimidinase related protein 2 (DRP-2) was greatly increased in DG at 5 days after the ischemia-reperfusion insult, although slightly increased in CA1. It is known that knockdown of DRP-2 plays a neuroprotective role in primary rat hippocampal neuron under the excitotoxic conditions. Therefore, our result raises the possibility that up-regulated SIRT2 and carbonylated DRP-2 may exert its neuroprotective effect in DG after the ischemia-reperfusion.

Keywords: oxidative stress, dentate gyrus (DG), protein oxidation

**POS-03-LB-069**

Deciphering Human-Microbe Proteome Interactions Using an *E. coli* Proteome Chip

Chen Chien-Sheng

*Graduate Institute of Systems Biology and Bioinformatics, National Central University*

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We developed a new high-throughput protein purification protocol that allows us to purify 4,256 *Escherichia coli* proteins and to spot them on glass slides to form an *E. coli* proteome microarray (chip). We detected the interactions between human serum antibodies and genome-wide *E. coli* proteins using this *E. coli* proteome chip. Thus, we identified new

serological biomarkers for inflammatory bowel disease (IBD). Each protein array was screened using individual serum from healthy controls and clinically well-characterized patients with IBD [Crohn's disease (CD) and ulcerative colitis (UC)]. Surprisingly, SAM analysis identified a total of 417 *E. coli* proteins that were differentially recognized by serum antibodies between healthy controls and CD or UC. We also identified two sets of serum antibodies that were novel biomarkers for specifically distinguishing CD from healthy controls, and CD from UC, respectively. We also detected the interactions between a human antimicrobial peptide exiting in the gut (Lactoferricin B, Lfcin B) and *E. coli* proteome using this chip. The result showed that Lfcin B binds to bacterial response regulators, BasR and CreB of two-component system (TCS). The electrophoretic mobility shift assays and kinase assays indicate that Lfcin B inhibited the phosphorylation between response regulators (BasR and CreB) and their cognate sensor kinases (BasS and CreC). These results indicate that this *E. coli* proteome microarray is a powerful tool for the study of human-microbe proteome interactions.

Keywords: host-microbe interaction, Proteome microarray, antimicrobial peptide

**POS-03-LB-070**

E-Learning Platform for Proteomics as a Part of National Program on Technology Enhanced Learning in India; Proteomics Education as a Community Effort

Sanjeeva Srivastava, Sandipan Ray, Rekha Jain, Kaustav Dasgupta,
Avani Yeola, Prajakta Kulkarni, Samridhi Sharma, Darpan Malhotra, Jaipal Panga Reddy, Saurabh Yadav, Parvez Syed
[1]*Department of Biosciences and Bioengineering, Indian Institute of Technology Bombay, Mumbai, India*

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National Program on Technology Enhanced Learning (NPTEL) is a timely attempt from India to establish high-quality educational materials for global distribution. As part of this program, the 'Advanced Clinical Proteomics' developed by the researchers from IIT Bombay, attempts to identify the problems associated with proteomic analysis of clinical samples, devising strategies to overcome such limitations and emerging sophisticated high-throughput techniques to generate and analyze a large number of data. This web-based learning approach intends to provide comprehensive details of different proteomics technologies; including 2D-DIGE, SILAC, iTRAQ, ICAT, protein microarrays, SPR and other label-free detection methods, and nanoproteomics approaches using videos and interactive simulations. The overall course content has been divided into six different modules, to encompass both traditional and advanced proteomic approaches and explicitly cover the crux of the proteomic technologies, advantages and challenges, along with an attempt to analyze real experimental data, in terms of interesting assignments for the learners. A great deal of light has also been shed into tackling different biological samples like serum, cerebrospinal fluids, urine, etc, which come up with their own set of challenges. Apart from this curriculum, we have also developed a Static Virtual Proteomics Lab and Clinical Proteomics Remote Triggering Virtual Laboratory (available at http://iitb.vlab.co.in/?sub=41) for providing the learners an experience of practical proteomics experimental procedures without any direct physical involvement in real bench works. These proteomics education resources have been included as a tutorial for the International Proteomics Tutorial Programme supported by HUPO and EuPA.

Keywords: Proteomics Education, E-learning, Virtual Proteomics Lab