

## **Human Kidney & Urine Proteome Project “Towards Standards for Urine Proteomics”**

Co-Chairs: Mark A Knepper (NHLBI, NIH, Bethesda, MD, USA) and Robyn G Langham (Department of Medicine, Vincent's Hospital, University of Melbourne, Australia),  
Saturday, Oct 6, 14:00-16:00, Jangbo Hall 333

14:00-14:05 **Introduction**

Tadashi Yamamoto, Chair of HKUPP, Niigata University

14:05-14:20 **Urinary proteomics of high-molecular-mass proteins by 2-DE with agarose gels in the first dimension (Agarose 2-DE) and LC-MS/MS**

Hiroshi Okusa<sup>1</sup>, Yoshio Kodera<sup>2,3</sup>, Ryojiro Kondo<sup>2</sup>, Kazumasa Matsumoto<sup>1</sup>, Masatsugu Iwamura<sup>1</sup>, Masamichi Oh-Ishi<sup>2</sup>, Shiro Baba<sup>1</sup>, and Tadakazu Maeda<sup>2,3</sup>

<sup>1</sup> Department of Urology, Kitasato University School of Medicine, <sup>2</sup> Department of Physics, Kitasato University School of Science, and <sup>3</sup>Center for Disease Proteomics, Kitasato University School of Science, Sagami-hara, Japan

14:20-14:35 **The human urinary proteome contains more than 1500 proteins, including a large proportion of membrane proteins**

Jun Adachi<sup>1,2</sup>, Nagaraj, Nagarjuna<sup>1</sup>

<sup>1</sup>Department of Proteomics and Signal Transduction, Max-Planck Institute for Biochemistry, Germany, and <sup>2</sup>Current address: Graduate School of Global Environmental Studies, Kyoto University, Japan

14:35-14:50 **An attempt to understand kidney functions by comparing serum and urine proteomes**

Lulu Jia, Ling Zhang, Chen Shao, Eli Song, Wei Sun and Youhe Gao

Department of Pathophysiology, Proteomics Research Center, Institute of Basic Medical Sciences, Peking Union Medical College, Beijing, China

14:50-15:05 **Identification of a processed ubiquitin form as differentially excreted protein in diabetic nephropathy patients by urinary proteomics**

Hassan Dihazi, and Gerhard A. Müller

Nephrology & Rheumatology, Georg-August University Goettingen, Goettingen, Germany

15:05-15:20 **Two-dimensional gel electrophoresis-based proteome analysis of normal human urine proteome: optimization of urine sample handling and quantitative difference between healthy children and adults**

Yutaka Yoshida<sup>1</sup>, Yoshimi Nagasaka<sup>1</sup>, Izumi Taguchi<sup>1</sup>, Masahito Miyamoto<sup>1</sup>, Bo Xu<sup>1</sup>, Ying Zhang<sup>1</sup>, Kenji Miyazaki<sup>2</sup>, Akira Tsugita<sup>2</sup>, Eishin Yaoita<sup>1</sup>, Hidehiko Fujinaka<sup>1,3</sup>, Tadashi Yamamoto<sup>1</sup>

<sup>1</sup>Department of Structural Pathology, Institute of Nephrology, Niigata University, Niigata, <sup>2</sup>Proteomics Research Center, Fundamental and Environmental Res. Labs. NEC Corp., Tsukuba, and <sup>3</sup>Institute for Clinical Research, Niigata National Hospital, Kashiwazaki, Japan.

15:20-15:45 **Issues of concern in urinary proteomics and initial recommendations**

Visith Thongboonkerd

Medical Molecular Biology Unit, Office for Research and Development, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, Thailand.

15:45-16:00 **Discussion**