## Symposia of the 125<sup>th</sup> Annual Meeting of the Pharmaceutical Society of Japan

## S34 Bioinformatics for the Drug Discovery Research

## S34-1 Development of the quantitative analysing system "Zucchini" for identification of drug target pathway

Kappei Tsukahara (Laboratory of Seeds Finding Technology, Eisai Co., Ltd.)

S34-2 The role of bioinformatics in topdown proteomics.

Katsutoshi Takahashi (Computational Biology Research Center, AIST)

S34-3 Plasma proteomics for early detection of pancreatic cancer

Tesshi Yamada (Chemotherapy Division and Cancer Proteomics Project, National Cancer Center Research Institute)

S34-4 A New Method for Metabolome Analysis and Application to Biosciences.

Tomoyoshi Soga (Institute for Advanced Biosciences, Keio University, Human Metabolome Technologies Inc.)

S34-5 Genome-wide association mapping to identify susceptible loci of common diseases for genome-based drug discovery

Hidetoshi Inoko (Department of Molecular Life Science, Division of Molecular Medical Science and Molecular)

S34-6 Methods of mass spectrometry and a search system for effective identification of lipid metabolites in lipidomics

Ryo Taguchi (Department of Metabolome Graduate School of Medicine The University of Tokyo)

S34-7 - Amyloid Enhances Glutamate Uptake Activity of Astrocytes

Yuji Ikegaya (Laboratory of Chemical Pharmacology, Graduate School of Pharmaceutical Sciences, The University of Tokyo.)

S34-8 Rotation mechanism for transmembrane signaling by theatrial natriuretic peptide receptor

Haruo Ogawa (Department of Biochemistry and Molecular Biology, University of Nevada,
Reno)