FIRST Program： Tanaka ms3d Project Evening Seminar

Date & Time: Sunday, Sep. 15, 2013, 6:00pm - 7:30pm
Venue: Presentation Area, Hall B, Pacifico Yokohama
Entrance: Free
(*) The registration to the congress is separately required.

Title :

Development of the next generation mass spectrometry system, and contribution toward drug discovery and diagnostics – focus on software development

Organizer :

Funding Program for World-Leading Innovative R&D on Science and Technology (FIRST) Tanaka ms3d Project

1. "FIRST ms3d project"

Speaker: 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".

2. Introduction of MS analysis software Mass++

Speaker: 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.

3. Biomarker discovery using Mass++ software

Speaker: 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.

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