

2016 Thermo Fisher Scientific Events

Mass Spectrometry Users Meeting Agenda

Start	End	August 17 (Wed), 2016	Room # 201 ~ 202
17:20	17:50	Facilitate Metabolite Biomarker Discovery Using HRAM LC-MS-MS Approach on a Orbitrap Mass Spectrometer Reiko Kiyonami, Thermo Fisher Scientific	
17:50	18:15	Metabolomics-driven integrative network analysis of unicellular microalga, <i>Chlamydomonas reinhardtii</i> Jung-Eun Lee, Kookmin University	
18:15	18:40	Introduction of recent smart processing software for small molecules applications Hansun Kwon, Thermo Fisher Scientific Korea	

Luncheon Seminar Agenda

Start	End	August 18 (Thu), 2016	Room # 201 ~ 202
11:50	12:15	The Power of the Orbitrap Mass Analyzer for Online Intact and Subunit Analysis Heewon Koh, Thermo Fisher Scientific Korea	
12:15	12:40	Introduction of Thermo Scientific Exactive GC-MS System – Redefining Routine Analysis Yeanwoong You, Thermo Fisher Scientific Korea	

Software Demo Schedule

Date	Time	Duration	Software
17 th	15:45	40 min	Biopharma Finder 1.0 Intact Protein deconvolution, Peptide mapping for Biopharmaceutical drug
18 th	09:50	60 min	Compound Discoverer 2.0 Metabolite ID / Metabolomics / Impurity Profiling / Natural Product ID / Statistics - small molecule compounds qualitative processing
18 th	14:50	40 min	TraceFinder 4.0 Small molecule / peptide Quan. / Target Screening (Library matching) - Easiest way to acquire, quantitate and confirm large sample set or large compounds set data
19 th	10:50	40 min	Proteome Discoverer 2.1 Protein Profiling / Modification Search / Peptide Quant - Easy and simple workflow for protein sample analysis