

ASMS 2006

Posters based on Seattle Proteome Center Research

Author	Institution	Title
Bryan J. Prazen	Insilicos	Instrument Specific Calibration of PeptideProphet
Sajani Swamy	Wellcome Trust Sanger Institute, Hinxtton, UK	MS/MS Database Search Strategies for High-accuracy Mass Spectrometry
Alexandre Panchaud	University of Lausanne	Protein identification and quantification based on C-terminal isotope-coded tagging
Armann A. Andaya	University of California Davis Genome Center,	A Mass Spectrometry Based Platform for Biomarker Discovery in Archived Prostate Tissues
Brendan MacLean	LabKey Software	An open-source framework for evaluating MS/MS score functions: "pluggable scoring" in X! Tandem
Alexey I. Nesvizhskii	University of Michigan Medical School	Reanalysis of Unassigned High Quality Spectra from Published Datasets Can Provide Biologically Interesting New Insights
Lilly Wong	Celgene, San Diego	Proteomic Biomarker Discovery Associated with the JNK Pathway and Fibrosis
Sau-Mei Leung	GenoLogics, Victoria, BC, Canada	The use of an open architecture LIMS solution to address the complexity of proteomic workflows, data management, and analysis
Patrick G.A. Pedrioli	Institute for Molecular Systems Biology, Zurich	The mzXML Schema version 3.0
Erik J Nilsson	Insilicos	A Novel Visualization Tool for Common Mass Spectrometric File Formats
Brian S Pratt	Insilicos	Recent Advances in Reliability, Performance and Usability of the Trans-Proteomic Pipeline (TPP) Software Tools
Bruce D Pascal	The Scripps Research Institute, Jupiter, Fl	Integrated proteomics environment for automated high throughput analysis of MS data
Minjie Guo	Purdue University, West Lafayette, IN	Developing soluble dendritic polymers for quantitative proteomics
Keller, Andrew	Rosetta Bioinformatics, Inc.	Improved automated validation of MS-MS search results employing high precursor mass accuracy