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Mass Spectrometry

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Thermo Fisher Scientific Launches Proteome Discoverer: Breakthrough Bio-Software for Advanced Proteomics Research

Mass informatics platform offers powerful analytics, open and flexible architecture, and easy-to-use interface

San Jose, CA (May 30, 2008) – Thermo Fisher Scientific Inc. (NYSE: TMO), the world leader in serving science, today announced the introduction, at ASMS 2008, of Thermo Scientific Proteome Discoverer, a new proteomics analysis software platform that provides the most comprehensive view of quantitative and qualitative proteomic data available. Proteome Discoverer enables researchers to combine and compare data from multiple search engines, public databases and dissociation methods on a larger scale than previously possible, in a program that is both easy-to-use and flexible. Proteome Discoverer's extensive quantitative analysis capabilities include industry-standard best practices, new Thermo Scientific solutions and isotopic labeling strategies, such as iTRAQ™ and TMT®.

Scientists have spent a decade perfecting protein sequencing only to find that current software produces little more than a qualitative data list. Proteome Discoverer, which replaces Thermo Scientific BioWorks™, is the first commercial proteomic data analysis software platform that enables researchers to combine, compare and analyze data from multiple sources with one program.

"Today's scientists want more than just a search engine and a protein sequence from their analysis programs, but they don't want to hire an entire bioinformatics team to get it," said Andreas Hühmer, proteomics marketing director, Thermo Fisher Scientific. "Proteome Discoverer is a complete workflow solution that offers a level of functionality that, up to now, would have required a complicated and expensive custom-built solution. Our software is elegant and easy to customize, so people can focus on research, not programming – science shouldn't be limited by software."

Proteome Discoverer analyzes data from all of the Thermo Scientific mass spectrometers and is compatible with all of the standard proteomic workflows. It is backwards compatible with results generated using BioWorks and offers a seamless upgrade path for current BioWorks users. Proteome Discoverer includes a license to the SEQUEST® search algorithm, the industry standard for confident protein identification.

Proteome Discoverer is an open and flexible platform that can integrate new tools, data sources and analysis methods.

A major advantage is the ability to analyze information from multiple dissociation methods to find more PTMs and increase the accuracy of peptide and protein identifications. For instance, CID

and ETD data can be analyzed simultaneously in a single operation, providing sequence, post-translational and cross-validation information about results. Moreover, information from the proprietary Thermo Scientific Z-Core algorithm, which analyzes the c-type and z-type ion spectra generated via ETD, easily merges with search data from CID spectra to increase protein coverage in a simple-to-read format.

Similarly, Thermo Scientific Proteome Discoverer enables researchers to combine search engine results and public database information using Proteome Discoverer's Workflow Engine, providing multiple methods of cross validation. For instance, data from different search engines, such as Mascot™ and SEQUEST, can be combined in a single report. Other software features include an automated false discovery rate calculation that allows direct comparison of database search engine results.

Proteome Discoverer is an open platform that is compatible with common bioinformatics tools, such as the InforSense KDE environment, and also supports all data standards developed by the Human Proteome Organization (HUPO), such as ProtXML and mzML file formats. A new developer's kit, to be released later this year, will enable researchers to customize the platform.

The Thermo Scientific Proteome Discoverer is now available as a client-server-enabled application with flexible licensing models and pricing. For more information on it, as well as other Thermo Fisher products, please visit the Thermo Scientific booth 41 at the 56th ASMS Conference on Mass Spectrometry and Allied Topics, in Denver, June 1-5. Alternatively, please call +1 800-532-4752, email analyze@thermofisher.com or visit www.thermo.com/proteomics.

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