

Advertisement feature



The Thermo Scientific LTQ Orbitrap Velos routinely deliver ultra-high resolution and accurate mass data

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Biomarkers MS Discovery!

Mass spectrometry (MS) is an analytical technique used to measure the characteristics and composition of samples and molecules. This technique is commonly used in the pharmaceutical industry as a tool for drug research and also has applications in the chemical, biotechnology, material sciences and medical industries. In recent years, mass spectrometry has been increasingly instrumental in proteomics research and the discovery of biomarkers to indicate diseases. As these research fields grow in strength, new mass spectrometers and software are being developed to increase sample throughput and improve laboratory productivity.

Mass Spectrometry for Proteomics and Biomarker Discovery

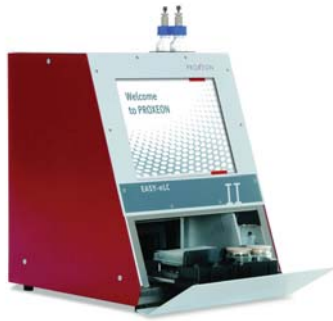
Instrumentation

Thermo Fisher Scientific's LTQ Orbitrap Velos™ system combines the industry-leading Orbitrap mass analyzer, a new Higher-Energy Collisional Dissociation (HCD) cell and dual pressure trap technology to routinely deliver ultra-high resolution and accurate mass data. The high mass accuracy of the Thermo Scientific LTQ Orbitrap Velos increases the speed and confidence of protein identification in complex samples by minimizing false positives. The ultra-high resolution delivers certainty in analytical results by enabling molecular weight determination for intact proteins and in-depth analysis of isobaric species. These capabilities enable the identification of more proteins with increased sequence coverage and higher confidence. The speed of the LTQ Velos-based mass spectrometer is ideal for coupling to U-HPLC systems, enabling researchers to identify more compounds in less time. The new HCD cell in the LTQ Orbitrap Velos is more efficient, resulting in improved quantitation of isobarically-labeled peptides, such as applications requiring tandem mass tags (TMT). These new features enable the Thermo Scientific LTQ Orbitrap Velos to perform confident protein and metabolite identification, characterization and quantitation.

Proxeon has released the company's second generation instrument, **EASY-nLC™ II**, optimized for LC-MS applications in proteomics and providing scientists with the opportunity to improve system productivity as a result of a new autosampler and

upgraded software. Proxeon's EASY-nLC platform utilizes a 'split-free' configuration to enhance sensitivity, reproducibility and system stability. The EASY-nLC II system offers the ease of use and excellent performance of its predecessor, but has been optimized to increase system productivity. The new autosampler features a fully insulated, refrigerated compartment with increased capacity for sample vials and wash-solvents, enabling the system to run unattended for longer. An 'intelligent flow control' feature enables runs to be preprogrammed to user-defined pressure limits, ensuring rapid build-up of pressure and flow, speeding up equilibration and sample loading steps and eliminating interruptions that can occur due to pressure fluctuations. In addition, the automated self-diagnostic tests of the EASY-nLC systems have been enhanced to ensure that users spend less time troubleshooting.

Shimadzu Scientific Instruments has developed the **Nanotrap™ Biomarker Discovery Platform** in partnership with **Ceres Nanosciences** and **Nonlinear Dynamics**, giving researchers the ability to enrich, preserve and screen low-level biomarkers directly from complex biological samples. Nanotraps are core shell hydrogel particles with porous interiors and size exclusion shells. By delivering affinity selection and size exclusion in one step, Shimadzu's Nanotrap Biomarker Discovery Platform easily amplifies low-level biomarkers directly from complex biological fluids. This enables the harvesting of low-



Proxeon's EASY-nLC™ II improves system productivity with new autosampler and upgraded software



The SORCERER from Sage-N Research, Inc. with Sequest 3Q software providing high throughput and sensitivity



Expressionist 5.3 from Genedata with advanced capabilities for mass spectrometry (MS)-based biomarker discovery

abundance biomarkers from complex samples, making early disease detection possible. Biomarkers in current clinical use have low sensitivity and specificity and limited use for early disease detection. Nanotraps meet this challenge by providing fractionation, concentration and protection of low-level biomarkers directly from complex biological fluids. When used with the AXIMA MALDI mass spectrometers, Nanotrap-enriched samples are analyzed rapidly and reproducibly in a fully automated format.

Software

Proteome Software has introduced its web-based mass spectrometry quality control tool, **MassQC**. MassQC is an online quality control tool that helps scientists to achieve more reproducible LC-MS/MS experiments, while reducing time spent assessing the performance of instruments. MassQC improves reproducibility by examining repeated, standard runs for a small number of known proteins and covers both width and breadth of LC-MS system performance. Researchers in the field suggest that rigorous, quantitative assessment of system performance is essential to proteomics' success. More replicates, better upstream preparatory methods, and a more thorough Quality Control protocol are among areas needing improvement. The design of MassQC makes Quality Control Proteomics more accessible to the LC-MS scientist. The tool is a powerful and approachable method to get more reproducible experiments.

Thermo Fisher Scientific has launched two new products designed to increase the productivity of quantitative proteomics research: **Intelligent Selected Reaction Monitoring (iSRM)**, which improves the throughput of SRM assays, and **Pinpoint software** for automated method development and quantitative analysis of

SRM-based targeted peptide assays. One of the biggest challenges in proteomics quantitation is to simultaneously verify and quantify low-level biomarkers. iSRM, which is available on all Thermo Scientific TSQ (triple stage quadrupole) instruments, increases the sensitivity and selectivity of targeted quantitation assays for simultaneously verifying and quantifying targeted proteins. The technology is designed to target as many as 1000 peptides and handle over 10,000 SRM transitions in a single experiment, which is higher than past technologies could deliver. As such, iSRM has the potential to significantly decrease labor and cost per analysis by increasing the number of peptides targeted in a single analysis. Thermo Fisher Scientific has also introduced Pinpoint software, designed to simplify the transition from early-stage biomarker discovery to larger-scale, quantitative verification of putative biomarkers and general quantitative proteomics.

Sage-N Research, Inc. (Sage-N) has developed the next generation SEQUEST standard search engine (SE) to provide the throughput and sensitivity required for translational proteomics research, particularly involving phosphorylation and protein post-translational modifications (PTMs) important to cancer and stem cell research. The new **SEQUEST 3G** defines a single common standard for similarity scores, search statistics and file formats to provide a robust foundation that meets the needs of translational research, including support for high-accuracy mass spectrometers and dissociation technologies such as electron-transfer dissociation (ETD). As translational proteomics technology has evolved to accurately characterize low-abundance proteins and protein PTMs in complex cell lysates, the SEQUEST 3G proteomics SE has been designed to include digital signal processing (DSP) to

improve sensitivity for noisy spectra, provide robust PTM search, include support for ETD, be able to support multiple similarity scores to improve specificity and be optimized for high-throughput searching of large data sets with 100K+ spectra.

Genedata has released **Expressionist 5.3** with advanced capabilities for mass spectrometry (MS)-based biomarker discovery. Designed on a powerful technology-hub concept for raw MS data processing, Expressionist's peak identification and annotation tools offer direct links to search engines and databases such as MASCOT, SEQUEST, HMDB and Chemspider. The Expressionist system includes advanced Refiner MS and Analyst modules, which process and analyze raw metabolomic and proteomic MS data and provide sophisticated statistical analysis capabilities for large and complex data sets. In addition to supporting ABI instruments, version 5.3 of Refiner MS supports Thermo Scientific Exactive, GC-MS instruments and Agilent Q-TOF, as well as instrumentation from all major MS vendors. Built on scalable architecture, Refiner MS removes all limitations from MS data analysis, allowing researchers to process thousands of samples and terabytes of raw MS data.

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