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Exploring new frontiers in biological science using Mass Spectrometry

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Innovation is shrinking industrial machines and medical devices to the scale of atoms and molecules. Mass spectrometry is one of the important and versatile tools that will drive the future of bio-science through its potential utility in R&D where pharmaceutical industries increase investment to achieve discovery of novel compounds. This technology will continue to drive high-throughput screening of candidate molecules together with advances in "omics" technologies (genomics, transcriptomics, proteomics, metabolomics) and biomarker identification.

Mass Spectrometry is used in industrial and academic fields for both routine and research purposes. Today, there is no single area of experimental science where mass spectroscopy is not being used. It is used to understand the fundamental atomic and molecular processes and, at the same time, those of immediate relevance to events within cells. As a technique, it helps to control processes in chemical and biological industries, diagnose diseases, discover new drugs, protect the environment and explore mysteries of nature.

Scientists and biologists face many challenges in functional biology studies that require the observation of proteomes over many time points, precise spatial distribution of proteins and different cellular states. These issues translated into the analytical challenge of performing reproducible and precise quantification of a few selected biological components in the presence of very complex background.
One of the major challenges in proteomics is the quantification of low abundance proteins and peptides of biological relevance such as transcription factors or low stoichiometry post translational modified proteins. The quantification of these analytes of interest is complicated by the very large dynamic range observed for cellular protein expression, especially in humans. With the development of new generations of mass spectrometry platforms providing high resolution and multiple detector versatility, new strategies are available to push the limits of quantification.

This new technology ensures that scientists don't miss anything in their area of research and provides a strong platform, combining next-generation screening techniques with advanced targeted methods for protein quantitation. It is designed to expand researchers' capabilities in advanced proteomics and metabolomics applications, including targeted, data-independent acquisition (DIA) and top-down analyses with the industry's highest level of sensitivity. This delivers more complete sequence coverage and allows scientists to perform more inclusive analyses.

On January 27, 2016, Thermo Fisher Scientific's Orbitrap Fusion Lumos Tribrid Mass Spectrometer received the SelectScience Scientists' Choice Award for Best New Drug Discovery Product of 2015. This award celebrates the new technologies that made the biggest impact in drug discovery and development research in 2015. The awards are unique in this industry as they empower scientists to nominate and vote for their favorite new product, allowing them to have their say about which manufacturers have truly enabled their work.
We're seeing firsthand how Orbitrap mass spectrometry is driving the future of bioscience, helping scientists push the limits of quantitation and protein characterization further and faster. It is ideal for laboratories that require more extensive and more profound analytical information from their sample, especially lower limits of detection and better sequence coverage when characterizing proteoforms, which was not possible with other high-resolution mass spectrometry systems.

This technology also enables scientists to:
Ã¢â?¬Â¢ Confidently quantify low-level analytes, low atomic LOQ in nLC analysis and fg in high flow analysis;
Ã¢â?¬Â¢ Be more selective about which instruments they perform their MS/MS experiments on;
Ã¢â?¬Â¢ Characterize intact proteins with top down on LC time scale, which means lower detection limits and higher throughput; and
Ã¢â?¬Â¢ Elucidate structures more thoroughly and easily by using any fragmentation mode, at any stage of MSn analysis, with detection by either analyzer, which maximizes structural information from metabolites, glycans, PTMs, and sequence polymorphisms.

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