Orbitrap Mass Spectrometry in Proteomics

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Since coming to market in 2005 the Orbitrap mass analyser, in the form of the LTQ Orbitrap, Q Exactive and Orbitrap Fusion products, has made a significant impact in the area of proteomics.

One of the latest additions to the Orbitrap family are the Orbitrap Fusion Tribrid mass spectrometer and the Q Exactive HF mass spectrometer, both containing the Ultra High Field Orbitrap mass analyzer. This new analyzer can deliver a resolution of up to half a million while facilitating to maintain a very high scan speed. These characteristics are mainly responsible for enabling to identify high numbers of proteins in a short time, like e.g., the complete yeast proteome in one hour only.

In addition the Orbitrap Fusion mass spectrometer contains a unique architecture of three mass analyzers, namely a mass resolving quadrupole, an Orbitrap cell and a linear ion trap, which can operate in complete parallel leading to new dimensions of analysis not only for protein identification but also for multiplexed protein quantification. Moreover, the system comes with a new, robust ETD source in the instrument's front region, providing also the possibility to study post-translational modifications with a much increased rate in high quality ETD spectra. Also the Orbitrap Fusion offers methods for intelligent precursor selection and the combination of CID, HCD and ETD fragmentation makes it the perfect tool for phosphopeptide and glycopeptide analysis.

During this presentation a short history of the development of the hybrid versions of orbitrap-based mass spectrometers and current generation performance characteristics will be described and explained on a technical level and the impact will be discussed in the field of proteomics.