

## Biognosys' Spectronaut™ software now supports Thermo Scientific™ Q Exactive™

### New Spectronaut™ software release to support data-independent acquisition (DIA) on Thermo Scientific™ Q Exactive™

**August 28, 2013 – Zurich-Schlieren (CH)** – Biognosys AG, a Swiss Proteomics Company, announced today the second release of its [Spectronaut™](#) software for analysis of Hyper Reaction Monitoring (HRM) data. [HRM](#) is a targeted proteomics technology that enables reproducible and accurate quantification of 1000s of proteins in a single instrument run. It thereby bridges the gap between the scale of shotgun proteomics with the ability to identify many proteins and the quantitation accuracy of MRM/SRM that allows high quality quantification of smaller number of proteins.

HRM is based on data-independent acquisition (DIA) performed on the new generation of mass spectrometric systems. DIA on the Thermo Scientific™ Q Exactive™ hybrid quadrupole-Orbitrap mass spectrometer enables acquiring MS/MS signals from all detected precursor ions present in the sample similar to SWATH™ Acquisition performed on AB SCIEX TripleTOF® 5600+ System. HRM combines DIA with high resolution MS/MS, large spectral libraries and a targeted approach for data deconvolution and analysis.

Spectronaut™ software was first launched by Biognosys in January 2013 for analysis of SWATH data. The new software release also supports analysis of DIA data generated on Q Exactive. Together with this release Biognosys provides an acquisition method for Q Exactive that has been optimized for high content quantification experiments.

Other new features of this Spectronaut™ release include advanced HRM-specific peak scoring and new visualization options like a multiple-run alignment view. Spectronaut™ uses a proprietary high speed data format that allows processing of 100'000s transitions within minutes. Furthermore, Spectronaut™ incorporates advanced mProphet algorithms (Nature Methods, 2011) adapted for HRM to enable accurate signal detection and statistically valid peak scoring. The powerful principle behind Spectronaut™ is the integration of the software algorithms with a reagent kit – [HRM Calibration Kit](#) – that provides optimal customized parameter calibration for any end-user system independently on the specific chromatography and mass spectrometer set-up. Spectronaut™ is a user-friendly desktop application that can be installed and run on a standard notebook.

Biognosys currently offers its [HRM](#) technology as a service for discovery applications and highly multiplexed protein quantification. With the second Spectronaut™ release that is free for academic researchers Biognosys expands its customer base to Q Exactive users facilitating further adoption of HRM technology and supporting open innovation and collaboration between applied and academic research.

## About Biognosys

Biognosys is the leading proteomics company offering services and products for highly multiplexed protein quantification. Founded in 2008 as spin-off from the lab of proteomics pioneer Ruedi Aebersold at ETH Zurich, Biognosys is dedicated to transform life science with superior technology and software.

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