

Biognosys releases Spectronaut™ 6.0

Every researcher with access to high-resolution mass spectrometer can now benefit from the Spectronaut™ software

September 10, 2014 – Zurich-Schlieren (CH) – Biognosys AG, a Swiss Proteomics Company, announced today the next release of its [Spectronaut™](#) software for analysis of Hyper Reaction Monitoring (HRM) data that will now also be available for industry partners upon request. [HRM-MS™](#) is a targeted proteomics technology developed by Biognosys that enables reproducible and accurate quantification of 1000s of proteins in a single instrument run. HRM is based on data-independent acquisition (DIA or SWATH), which can be performed on most state of the art high-resolution mass spectrometric systems.

Since the beginning of 2013 Spectronaut™ has been available to academic community where it is recognized as one of the most advanced solutions for proteome quantification on the market. With the Spectronaut™ 6.0 release Biognosys expands its customer base to industry researchers that have access to high-resolution mass spectrometers.

The new features of Spectronaut™ 6.0 include QC methods for user libraries, normalization report, improved library generation, improved peak picking, 40% speed improvement, increased memory efficiency, and many more. The detailed information on Spectronaut™ and its features can be found in the [software manual](#).

[Spectronaut™](#) software was first launched by Biognosys in January 2013 for analysis of SWATH data. It has been updated in August 2013 with support for DIA data generated on the Thermo Fisher Q Exactive. Further, in April 2014 spectral library generation capability was incorporated into the software. 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 which is crucial for quantitation accuracy and reproducibility.

Industry customers are welcome to submit their Spectronaut™ order inquiry to order@biognosys.ch, while academic researchers can obtain a free Spectronaut™ license in Biognosys' [online shop \(academic e-mail account is required\)](#). Researchers without access to state of the art mass spectrometers can benefit from Biognosys' [Proteome-SEQ™](#) discovery service that is based on the HRM-MS™ technology.

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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