

Biognosys releases Spectronaut™ 7.0

Regulation differences in the samples can now be viewed directly in post-analysis perspective

May 5, 2015 – Zurich-Schlieren (CH) – Biognosys AG, a Swiss Proteomics Company, announced today the next release of its [Spectronaut™](#) software for Hyper Reaction Monitoring (HRM) data that covers a complete workflow from library generation to protein-level expression analysis. [HRM-MS™](#) is a next-generation proteomics technology developed by Biognosys that enables reproducible and accurate quantification of 1,000s of proteins in a single instrument run and is based on data-independent acquisition (DIA) performed on the new generation mass spectrometric systems.

In addition to post-analysis perspective, Spectronaut™ 7.0 also includes support for non-linear gradients, protein grouping support for Proteome Discoverer 1.4, support for Proteome Discoverer 2.0, improved performance and memory efficiency, and more. The detailed information on Spectronaut™ and its features can be found in the [software's manual](#).

[Spectronaut™](#) software was first launched by Biognosys in January 2013 for analysis of SWATH data. It has been updated in August 2013 when a support for DIA data generated on the Thermo Fisher Scientific Q Exactive was introduced. Further releases in April and September 2014 provided multiple important features including library generation capability. With the current release Biognosys provides a comprehensive solution for identifying specific protein expression changes or differences in a large proteome background.

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.

Spectronaut™ Professional remains free for academic researchers and can be obtained directly in the Biognosys' [online shop \(academic e-mail account is required\)](#), while industry customers are welcome to submit their order inquiry for an Enterprise license to [order\[at\]biognosys.ch](#). 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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