

Biognosys releases Spectronaut™ 9.0

The fastest and most precise Spectronaut software yet.

May 16th, 2016 – Zurich-Schlieren (CH) – Biognosys AG, a leading proteomics company, announced today the release of a new [Spectronaut™](#) software for Hyper Reaction Monitoring (HRM). Spectronaut 9.0 is the fastest, most precise proteomics analysis software tool. Designed for high-throughput data analysis, Spectronaut 9.0 cuts analysis time from days to hours and delivers the most confident quantitative proteomics data analysis. Built on the Spectronaut legacy, the new release continues to provide researchers with a complete workflow from library generation to protein-level expression analysis.

The powerful principle behind Spectronaut™ 9.0 software is the integration of its algorithms with Biognosys calibration kits: the [iRT Kit](#) and the [HRM Calibration Kit](#). Both kits are now supported to provide optimal customized parameter calibration that is crucial for quantitation accuracy and reproducibility.

With Spectronaut 9.0, users get protein quantification results in a simpler data format that makes downstream data analysis even easier. Results are exported in a quantitative matrix showing runs vs relative protein quantities. Also, Spectronaut 9.0 will come with ready-to-use spectral libraries for various organisms and tissues. While Spectronaut users will still benefit from sample-specific spectral library generation, these built-in spectral libraries present great references for fast testing of experiments.

Spectronaut was first launched by Biognosys in January 2013 for analysis of SWATH data and has been continually updated since. As Lukas Reiter, Biognosys' CTO, says: "Spectronaut 9 (Collins) is a huge leap towards democratization of high-content, high-throughput proteomics. Experiments comprising 100s to 1000s of samples can now be analyzed on readily available simple computer hardware including post analysis steps such as statistical testing for differential abundance." A more detailed overview over all the new features of Spectronaut™ 9.0 can be found in the release [overview](#) and in the [software manual](#).

[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. HRM-MS™ is based on data-independent acquisition (DIA) performed on new generation mass spectrometric systems.

Spectronaut™ Professional remains free for academic researchers and can be obtained directly at the Biognosys' [online shop](#) while industry customers can obtain their enterprise version [here](#). Researchers without access to state of the art mass spectrometers can benefit from [Biognosys' contract research discovery services](#) that are 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 transforming life sciences with superior proteomics technology.

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