

Biognosys releases Spectronaut™ 8.0

Simpler protein quantification and built-in reference libraries for various organisms and tissues

November 11th, 2015 – Zurich-Schlieren (CH) – Biognosys AG, a leading proteomics company, announced today the next release of its [Spectronaut™](#) software for Hyper Reaction Monitoring (HRM) 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. HRM-MS™ is based on data-independent acquisition (DIA) performed on new generation mass spectrometric systems.

With Spectronaut 8.0, 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, a format that many researchers know from microarrays. Also, Spectronaut 8.0 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 8 (*Cassini*) is one of the most significant Spectronaut releases, laying the ground work for coming Spectronaut versions. *Cassini* comes with its own protein inference closing the gap to the proteins, the biomolecules of interest to us. Proteins and annotation are now under control of the Spectronaut users with more reporting possibilities than ever." A more detailed overview over all the new features of Spectronaut™ 8.0 can be found in the release [overview](#) and in the [software's manual](#).

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](#) while industry customers can obtain their enterprise version [here](#). Researchers without access to state of the art mass spectrometers can benefit from Biognosys' 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 transform life science with superior technology and software.

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