

Biognosys' Spectronaut™ software now supports spectral library generation

The new Spectronaut™ software release offers a comprehensive solution for proteome quantification

April 4, 2014 – Zurich-Schlieren (CH) – Biognosys AG, a Swiss Proteomics Company, announced today the third release of its [Spectronaut™](#) software for analysis of Hyper Reaction Monitoring (HRM) data. [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. It combines the shotgun proteomics' ability to identify large sets of proteins and the quantitation accuracy of MRM/SRM.

HRM is based on data-independent acquisition (DIA) performed on the new generation mass spectrometric systems like the Thermo Scientific™ Q Exactive™ hybrid quadrupole-Orbitrap mass spectrometer or 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™ now also supports the generation of spectral libraries, which has been a bottleneck until now.

The Spectronaut™ software was first launched by Biognosys in January 2013 for analysis of SWATH data and updated in August 2013 when support of DIA data generated on the Q Exactive was introduced. With the current release Biognosys provides the most straightforward solution for proteome quantification currently available on the market.

Other new features of this Spectronaut™ release include a quality control perspective (based on the HRM Kit peptides), interference scoring, fragment ion reporting, and many more. The detailed information on Spectronaut™ and its features can be found in the [software 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 that is crucial for quantitation accuracy and reproducibility.

With the third Spectronaut™ release that is free for academic researchers Biognosys unleashes the full capability of the [HRM-MS™ technology](#), which is also available at Biognosys as a service for discovery applications.

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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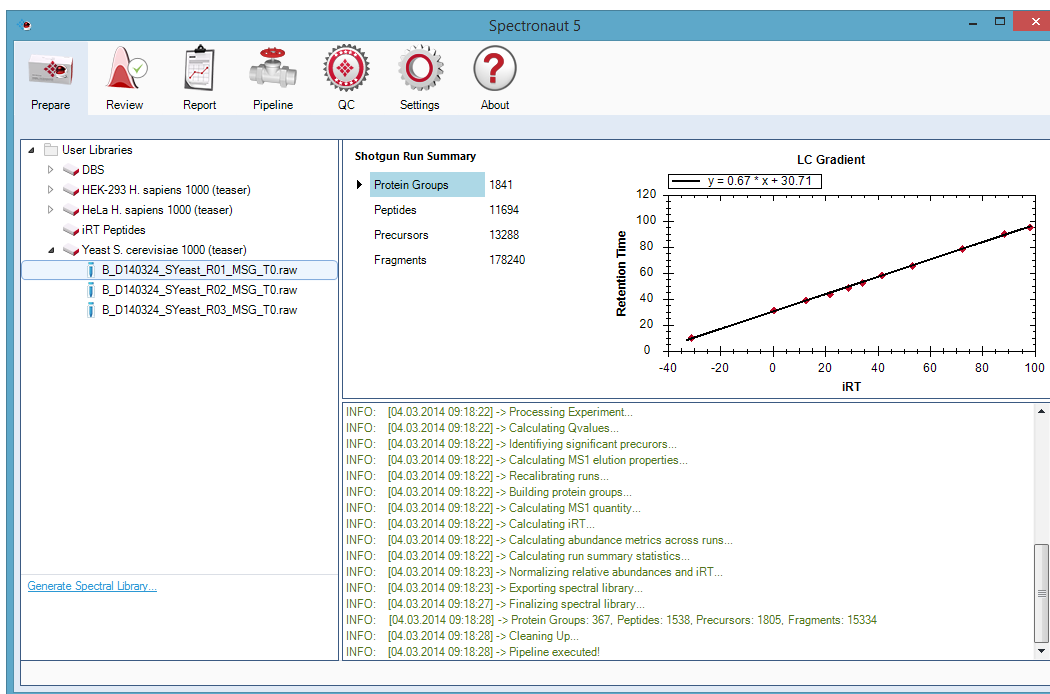


Figure 1: Spectral library generation. Availability of high quality spectral libraries is limiting the adoption of the HRM-MS™. The new Spectronaut™ release provides a one-click option for generating spectral libraries, thus being the easiest and fastest solution currently available on the market.

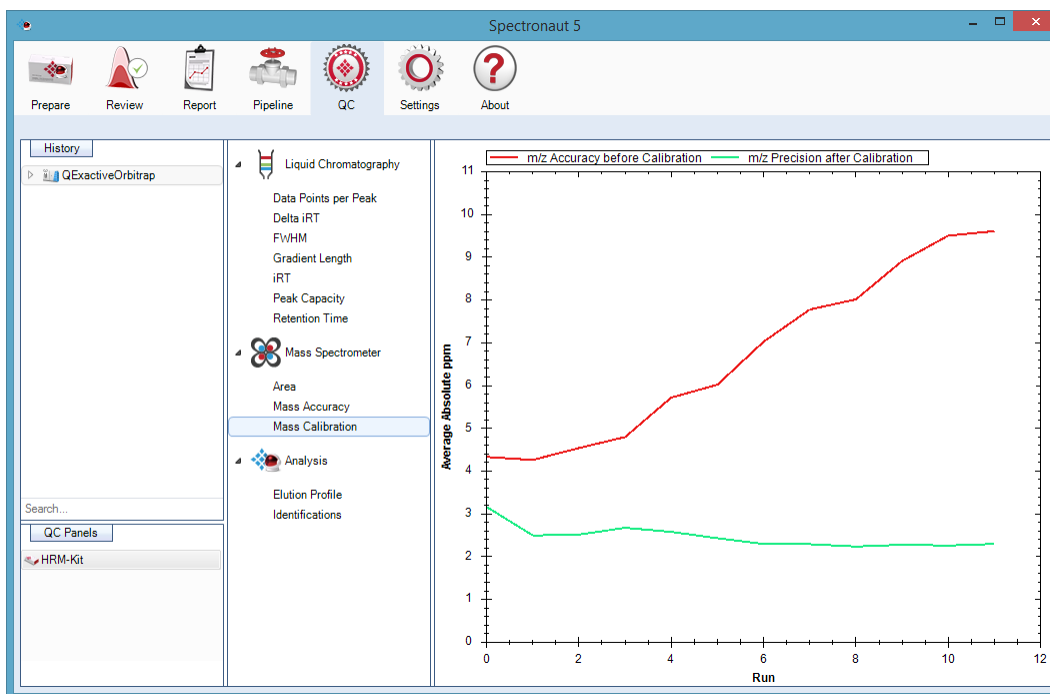


Figure 2: Quality control. Monitoring the quality of system's overall performance is crucial for assuring data consistency and is highly desirable for all experimental workflows. A quality control system is now integrated in the Spectronaut™ Software for setting the highest standards in data analysis.