

Biognosys launches standardized proteome discovery service Proteome-SEQ™

Proteome-SEQ™ enables the quantification of 1000s of proteins using next-generation proteomics HRM technology

September 5, 2014 – Zurich-Schlieren (CH) – Biognosys AG, a Swiss Proteomics Company, announced today the launch of its [Proteome-SEQ™](#) standardized discovery service that enables precise quantification of 1000s of proteins across multiple samples. Proteome-SEQ™ is optimized for different sample types including human tissues and is based on the next generation proteomics [Hyper Reaction Monitoring \(HRM\) technology](#). The service addresses research questions where identification of protein expression differences against the backdrop of the whole measurable proteome is important. Example applications are in drug target discovery, biomarker development, and target deconvolution in phenotypic screens.

HRM-MS™ is a targeted proteomics technology developed by Biognosys that provides reproducible and accurate quantification of 1000s of proteins in a single instrument run and in many aspects resembles next-gen sequencing in the RNA or DNA field. HRM outperforms any other proteomics technique for quantification of large number of proteins and does not require time consuming method development which is a limiting factor with classical affinity based approaches. HRM is based on data-independent acquisition (DIA or SWATH) which collects all detectable ion signals in a single instrument run. These ion maps are then queried with Biognosys powerful signal processing software [Spectronaut™](#) using pre-developed reference assay libraries. The quality of the library determines the quality of data analysis. Biognosys uses a patent protected method for high-content library generation that results in superior specificity and sensitivity compared to public assay repositories.

The palette of quantified proteins can be further extended by combining the reference libraries with assays developed from customer samples. Proteins specifically expressed in the samples which may not have been seen before are thus quantified together with the large number of proteins contained in the reference libraries.

Biognosys currently offers the Proteome-SEQ™ service for human [cell culture](#) and [liver tissue](#) samples with additional reference libraries still in the development. The Proteome-SEQ™ service targets researchers without access to state of the art mass spectrometers or researchers that want to benefit from reference assay libraries optimized for maximum performance of the HRM technology that are available only at Biognosys. For researchers that have access to high-resolution mass spectrometers Biognosys already offers [Spectronaut™](#) software and the [HRM Calibration Kit](#) for assay library generation and data processing.

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 proteomics technology and software.

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