

Biognosys announces a technological breakthrough in the development of its next-generation proteomics workflow

Zurich – November 8, 2017 – Biognosys AG announced today a breakthrough in the development of its next generation proteomics technology that helps scientists to understand complex biological processes. For the first time, Biognosys' data-independent acquisition (DIA) mass spectrometry workflow has identified and quantified more peptides than sequentially possible with data dependent acquisition (DDA) on a Thermo Scientific™ Q Exactive™ HF. The DIA method now provides a clear path to the ultimate life science community goal – to quantify every protein, the complete proteome, in a biological sample of interest. The results of the study have recently been published in the Molecular and Cellular Proteomics journal under the title "[Optimization of Experimental Parameters in Data-Independent Mass Spectrometry Significantly Increases Depth and Reproducibility of Results](#)".

DIA is a mass spectrometric workflow that has been under intense development in recent years by Biognosys and several academic groups including Prof. Ruedi Aebersold's at the ETH Zurich. It overcomes the technical limitation of sampling speed of mass spectrometers by isolating broad ranges of peptide ions in parallel. Using powerful data deconvolution algorithms, DIA technology is only limited by the sensitivity of the detector, not the sequential speed of the mass spectrometer. This enables at the same time deeper and faster analysis of proteins in biological samples. Data acquired on a Thermo Scientific™ Q Exactive™ HF mass spectrometer showed improved quality and depth using DIA as compared to DDA. Contrary to what may be a common misconception, DIA was shown to perform particularly well in ultra-complex samples. In a mixture of four proteomes, more than 12'000 unique proteins could be identified using single shot DIA with excellent quantitation.

"We see great potential in mass spectrometry based proteomics by making it more parallel. DIA is taking a giant leap in the direction of decoding the complete proteome," said Dr. Lukas Reiter, Chief Technology Officer at Biognosys. He adds: "We believe that quality of the data has the highest priority. Hence, we devoted a lot of work towards implementing and validating sound statistical models on peptide and protein level to ensure the data in this work is accurate."

Biognosys' next generation proteomics technology is based on a DIA workflow and represents an ideal platform for unbiased discovery proteomics studies like biomarker discovery, pathway modelling and mechanisms of action studies where deep proteome coverage is required to understand the biology.

About Biognosys

Biognosys is the leading proteomics company offering innovative services and products for highly multiplexed protein quantification. We are dedicated to transforming the life sciences with superior proteomics solutions. Biognosys' next generation technology quantifies proteins with unbeatable precision and depth. Our solution relies on mass spectrometry, which allows simultaneous quantification of thousands of proteins in a single experiment. This new generation protein quantification technology is available to researchers worldwide through our contract research services or our portfolio of innovative reagent and software products. For more information, please visit www.biognosys.com.

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