

Biognosys and Bruker Collaborate to Support Ion Mobility on timsTOF Pro with Spectronaut

Biognosys adds beta support for diaPASEF within Spectronaut, the industry leading data-independent acquisition (DIA) proteomics software.

September 17th, 2019 – SCHLIEREN, (ZH – Switzerland). Researchers will soon be able to directly measure and quantify thousands of proteins using Bruker's (Nasdaq: BRKR) new ion mobility-based mass spectrometer and the corresponding data analysis software Spectronaut, developed by Biognosys; the Swiss next-generation proteomics company.

The performance of mass spectrometric (MS) protein expression analysis has improved dramatically over the last few years. A large part of the expressed proteome can now be quantified in a single tissue sample injection. This has been driven by the invention of the parallel DIA technology, which is rapidly replacing classical sequential, so-called shotgun MS, approaches.

Parallel data acquisition leads to highly convoluted fragment spectra. The complexity can be reduced by upfront chromatography, but there is a tradeoff between better separation and better throughput.

A novel method, published by the group of Matthias Mann at the Max-Planck Institute in Munich, uses ion-mobility as an additional separation step inside the mass spectrometer. This approach promises to reduce data complexity without a reduction in throughput. The method, called Parallel accumulation-serial fragmentation (PASEF), is available on the Bruker timsTOF Pro instrument.

Biognosys, in collaboration with Bruker, have now added beta support for analyzing such data within Spectronaut, making full use of the ion mobility dimension.

Dr. Lukas Reiter, Chief Technology Officer at Biognosys, comments: "We are very interested in, and excited by, the possibilities of enhancing DIA experiments with the 4D capabilities of the timsTOF Pro and diaPASEF. Our initial evaluation of the performance of the diaPASEF method on the timsTOF Pro, based on our newly released diaPASEF data processing in Spectronaut, has already shown industry-leading performance in terms of speed, sensitivity, and quantitative results. We look forward to following Bruker's developments on further applications of the diaPASEF method."

Beta support for PASEF (DDA) and diaPASEF comes with the latest update (version 13.7) of Spectronaut 13. With this update, Spectronaut supports the complete workflow from library generation of PASEF data to the targeted analysis of diaPASEF data.

About Bruker Corporation (Nasdaq: BRKR):

Bruker is enabling scientists to make breakthrough discoveries and develop new applications that improve the quality of human life. Bruker's high-performance scientific instruments and high-value analytical and diagnostic solutions enable scientists to explore life and materials at molecular, cellular and microscopic levels. In close cooperation with our customers, Bruker is enabling innovation, improved productivity and customer success in life science molecular research, in applied and pharma applications, in microscopy and nanoanalysis, and in industrial applications, as well as in cell biology, preclinical imaging, clinical phenomics and proteomics research and clinical microbiology. For more information: www.bruker.com.

Media Contact:

Oliver Rinner, PhD

CEO

Mobile +41 (0) 78 664 47 11

oliver.rinner@biognosys.com

About Biognosys:

Biognosys is a leader in next-generation proteomics, dedicated to transforming life science research by making the most advanced proteomics tools available to researchers. The company offers a suite of products and services to decode the proteome and equip researchers from all fields with a deep view of protein expression in cells, tissues, or body fluids. Biognosys' technology is based on high-resolution mass spectrometry, combined with a novel parallel signal processing approach, for unprecedented quantification of large proteomes in a single experiment. More information at: www.biognosys.com.