NEWS RELEASE

Bruker Announces Release of Breakthrough diaPASEF Workflow for CCS-aware 4D Proteomics on timsTOF™ Pro Platform at HUPO 2019

9/16/2019

- diaPASEF increases protein identifications, sensitivity and data completeness
- CCS-aware diaPASEF processing now supported by Mobi-DIK, PEAKS, Spectronaut, MaxQuant and Skyline proteomics software solutions
- Novel 3D-targeted PRM workflow with additional ion mobility targeting shown as work-in-progress for targeted proteomics with improved sensitivity and quantitation

ADELAIDE, Australia, Sept. 16, 2019 /PRNewswire/ -- At the 18th Human Proteome Organization World Congress (**www.hupo2019.org**), Bruker (Nasdaq: BRKR) today announced the release of the diaPASEF workflow, a novel data-independent acquisition (DIA) method on the timsTOF Pro platform. The timsTOF Pro leverages trapped ion mobility spectrometry (TIMS) and 'parallel accumulation - serial fragmentation' (PASEF), developed in an intensive collaboration over several years with the group of Professor Matthias Mann at the Max Planck Institute in Martinsried1,2, for unmatched duty cycle, sensitivity and speed.

The new diaPASEF3 workflow, shown as work-in-progress at ASMS 2019, uses overlapping windows in the ion mobility domain to trigger MS/MS, efficiently using the quadrupole to transmit precursor ions at high sensitivity. Using the inherent duty-cycle advantage of PASEF, diaPASEF typically results in a further 30% improvement in protein identifications, now with over 7,500 proteins identified in a 120 minute single-shot experiment on 200 ng of HeLa digest. diaPASEF also alleviates the so-called 'missing value problem' in stochastic, data-dependent acquisition (DDA) methods, and thereby improves data completeness and sensitivity.

Data analysis, including 4D feature alignment in retention time, ion mobility, mass and intensity, was originally performed using the new Mobi-DIK software developed in the group of Professor Hannes Röst at the University of Toronto. The breakthrough diaPASEF method is the result of a collaboration with our scientific partners

Professors Matthias Mann (Max Planck Institute, Martinsried), Ruedi Aebersold (IMSB at ETH Zuerich), Ben Collins (Queen's University Belfast), and Hannes Röst (University of Toronto).

Bruker also has worked with several additional partners to develop user-friendly and fast solutions for diaPASEF data analysis. At HUPO 2019, the following beta releases or release versions are available for diaPASEF processing: Mobi-DIK (U. Toronto), PEAKS (Bioinformatics Solutions Inc.), Spectronaut (Biognosys AG), MaxQuant (Max Planck Institute, Martinsried), and Skyline (MacCoss Lab Software). In addition to the much more efficient ion usage in diaPASEF, when compared to traditional DIA methods, the timsTOF Pro provides the additional dimension of ion mobility, or collision cross sections (CCS), which all CCS-aware proteomics software solutions now take advantage of. Besides retention time alignment, the timsTOF Pro also allows simultaneous ion mobility alignment of precursors and fragments in diaPASEF, improving the reliability and specificity of the assignments even further.

More exciting results on the quantitative performance of diaPASEF will be presented at HUPO 2019: Using label-free quantification (LFQ) on a mixture of three proteomes (HeLa, Yeast, E.coli) and Spectronaut software, more than 8,000 proteins could be reliably identified and quantified with at least two peptides at a false discovery rate of 1%.

Dr. Lukas Reiter, Chief Technology Officer at Biognosys, commented: "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."

Dr. Roman Fischer, Principal Investigator at the Nuffield Department of Medicine, Target Discovery Institute at University of Oxford, stated: "The arrival of the timsTOF Pro with PASEF has completely changed the game for clinical proteomics. Suddenly we can scale up clinical studies by a factor of 10x or more, and even improve on robustness, data depth and completeness. We are excited about the prospects for diaPASEF with short gradients for our clinical research."

Work-in-Progress Novel 3D-targeted PRM workflow with additional ion mobility targeting

For targeted quantitative proteomics, Bruker also introduces a novel 3D-targeted Parallel Reaction Monitoring (PRM) method on the timsTOF Pro as work-in-progress at HUPO 2019. In traditional 2D PRM experiments, retention times and masses are used to target and quantify lists of targeted protein biomarkers. A problem in 2D PRM is that interfering peptides that co-elute with similar precursor masses can be co-fragmented, which can

reduce quantitative performance, especially near the lower limits of quantitation in complex matrices, like plasma.

The timsTOF Pro with its unique 4D proteomics capabilities now can target proteins in three dimensions, namely retention time and mass, plus by universal, molecule-specific and precise CCS values. This additional 3D-targeting for PRM in ion mobility, combined with the sensitivity enhancement provided by TIMS/PASEF, and the >100 Hz MS/MS speed at 50,000 mass resolution of the timsTOF Pro, means that more proteins can be '3D-targeted' by PRM with better sensitivity and quantitation.

Dr. Gary Kruppa, Bruker's Vice President of Proteomics, said: "With diaPASEF we expect accelerated development of new applications and more exciting results. The development of fast and user-friendly software for library generation and results analysis also is key to the adoption of diaPASEF. We are very pleased to have such widespread support for diaPASEF software from our collaboration partners. Combined with new developments in 3D-targeted PRM for proteomics, the timsTOF Pro covers ever more CCS-aware 4D proteomics workflows in a unique way."

Bruker has begun collaborating with early adopters on 3D-targeted PRM quantitation for proteomics with new beta-software to evaluate performance and obtain user input:

Dr. Jarrod Marto, Associate Professor at the Dana-Farber Cancer Institute, Harvard Medical Center, and Brigham and Women's Hospital stated: "We are excited to be working with Bruker on combining first-in-class acquisition speed with ion mobility to drive new 3D-targeted PRM workflows on the timsTOF Pro. Our initial results are very promising, and we are very pleased with the collaborative effort to push PRM to new levels of performance."

Please join us at Bruker's booth #37-40 throughout the HUPO conference. Bruker-sponsored lunch seminars will be held on Monday, Sept. 16th, and Tuesday, Sept. 17th, and our breakfast seminar is on Tuesday, Sept. 17th, all at the Adelaide convention center. For a complete list of our seminars with guest speakers and other events, please visit: **https://www.bruker.com/events/2019/hupo.html**

Parallel accumulation – serial fragmentation (PASEF): Multiplying sequencing speed and sensitivity by synchronized scans in a trapped ion mobility device; F. Meier, S. Beck, N. Grassl, M. Lubeck, M. A. Park, O. Raether, and M. Mann; J Proteome Res. 2015 Dec 4;14(12):5378-87.
Online Parallel Accumulation-Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. Meier F, Brunner AD, Koch S, Koch H, Lubeck M, Krause M, Goedecke N, Decker J, Kosinski T, Park MA, Bache N, Hoerning O, Cox J, Räther O, Mann M.; Mol Cell Proteomics. 2018 Dec;17(12):2534-2545.
Parallel accumulation – serial fragmentation combined with data-independent acquisition (diaPASEF): Bottom-up proteomics with near optimal ion usage; F. Meier, A. Brunner, M. Frank, A. Ha, E. Voytik, S. Kaspar-Schoenefeld, M. Lubeck, O. Raether, R. Aebersold, B. C. Collins, H. L. Röst, M. Mann; bioRxiv 656207; doi:

https://doi.org/10.1101/656207.

About the timsTOF Pro with PASEF

The timsTOF Pro system uses PASEF, enabled by Trapped Ion Mobility Spectrometry (TIMS), to provide industry-leading speed for shotgun proteomics. Its unique dual TIMS geometry, combined with the time focusing of the ions in the TIMS device, means that the speed advantage provided by PASEF comes along with simultaneous improvements in sensitivity and quantitation. These gains in speed, sensitivity and quantitation maintain the advantages of Bruker's high-performance QTOF mass spectrometers, including resolving power of 50,000 FWHM even at highest acquisition rates in MS and MS/MS mode, ppm accurate mass, and high isotopic fidelity (True Isotopic Pattern, or TIPTM).

The exceptionally robust timsTOF Pro with PASEF gives scientists the tools to dig deeper into the complex cellular machinery with the potential to discover low-level, biologically significant peptides or proteins, or validate them in translational proteomics research.

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:

Petra Scheffer, Ph.D.

Director Marketing Solutions

Bruker Daltonics

T: +49 (421) 2205–2843

E: **petra.scheffer@bruker.com**

Investor Contact:

Miroslava Minkova

Director, Investor Relations &

Corporate Development

Bruker Corporation

T: +1 (978) 663-3660, ext. 1479

E: **Investor.Relations@bruker.com**

View original content to download multimedia:**http://www.prnewswire.com/news-releases/bruker-announces-release-of-breakthrough-diapasef-workflow-for-ccs-aware-4d-proteomics-on-timstof-pro-platform-at-hupo-2019-300917559.html**

SOURCE Bruker Corporation