



NEWS RELEASE

Bruker Launches the timsTOF™ Pro Mass Spectrometer to Enable the Revolutionary PASEF Method for Next-Generation Proteomics

9/18/2017

Unique Trapped Ion Mobility Spectrometry (TIMS) Adds New Dimension for Robust, Faster Proteome Analysis with Higher Sensitivity

DUBLIN, Sept. 18, 2017 /PRNewswire/ -- **HUPO2017** -- At the 16th Annual World Congress of the Human Proteome Organization (**HUPO**), Bruker introduces the **timsTOF Pro** system for PASEF mass spectrometry, using proprietary trapped ion mobility spectrometry (TIMS) technology for higher-speed, higher-sensitivity and robust shotgun proteomics with outstanding single-shot peptide and protein identification performance.

The novel **timsTOF Pro** is particularly advantageous also for quantitative proteomics workflows, as this innovative TIMS-powered quadrupole time-of-flight mass spectrometer (QTOF-MS) is supported by MaxQuant/Perseus and PEAKS Studio proteome analysis software.

The unique front-end TIMS analyzer is optimized for higher-speed shotgun proteomics from smaller sample amounts with outstanding identification performance. Its unique dual TIMS geometry allows ions to be accumulated in parallel in the first TIMS section, and after an additional TIMS separation step in real time, the ions are released from the second TIMS section for MS/MS fragmentation. This results in nearly 100% duty cycle, giving this parallel accumulation and serial fragmentation (PASEF) technique unprecedented performance for reproducible nanoflow LC-MS analysis of enzymatically digested protein mixtures.

The PASEF capability represents a step-change improvement in performance as it delivers higher-sensitivity and higher-speed shotgun proteomics without loss of mass resolution. Higher scan speeds result in lower mass resolution in FT-based MS technology commonly used for shotgun proteomics. These critical limitations are eliminated by PASEF, allowing for a duty cycle near 100% with high sensitivity while maintaining ultra-high mass

resolution for both the precursor and the product ions. This key PASEF capability leveraging the dual TIMS technology gives scientists the tools to dig deeper into the complex biology of the cellular machinery and the potential to discover low-level, biologically significant proteins, or validate them in translational and clinical proteomics research on large cohort sizes and in longitudinal studies.

Quantitative proteomics is a key area of research in proteomics, and dual TIMS-powered PASEF provides an inherent advantage over the limitations of gated, tandem-in-time, FT-based MS analyzers. The new **timsTOF Pro** delivers over four orders of magnitude of dynamic range with low peptide loads (100-200 ng), which makes it very suitable for proteomics on the small cell populations and low sample amounts often encountered in biological and clinical research.

Matthias Mann, Director of the Department of Proteomics and Signal Transduction at the Max Planck Institute of Biochemistry in Martinsried, Germany, stated: "My lab has collaborated with Bruker in the development of the PASEF technology, and we are delighted to see the **timsTOF Pro** realize the potential for shotgun proteomics that we had originally envisioned. This new technology has the potential to revolutionize several areas in proteomics: clinical research where speed and robustness are key for running large sample cohorts; applications requiring increased sensitivity, for e.g. samples enriched in phosphopeptides or where limited numbers of cells are available for analysis; and for quantitation experiments using isobaric tags, where the additional separation using trapped ion mobility can at least partially remove interference from co-fragmenting species that cause the so-called ratio compression effect that leads to unacceptable errors. We are excited about the potential for further developments of the technology as well."

Gary Kruppa, Vice President for Omics Solutions at Bruker Daltonics, said: "Proteomics researchers always want improvements in speed, sensitivity and quantitative capabilities, while maintaining the advantages of high-resolution, accurate mass and isotopic pattern fidelity so they can go deeper into the proteome. With PASEF, scientists now don't have to trade off resolution for scan speed and sensitivity – they get the triple benefit of high-sensitivity, high-scan speed, and unrivaled specificity through TIMS precursor ion selection. Together, this provides the exciting possibility of discovering low level biologically relevant proteins that currently are beyond the performance envelope of non-TIMS mass spectrometers."

Juergen Cox, Group Leader of the Computational Systems Biochemistry Group at the Max Planck Institute of Biochemistry in Martinsried, commented: "Bruker's decision to adopt an open-file format so that we can directly work with raw data will benefit the community of proteomics researchers using MaxQuant and Perseus. We are impressed with the quality of the data, and look forward to working with Bruker to support mutual customers with state-of-the-art software for the analysis and statistical interrogation of data acquired on the **timsTOF Pro** with PASEF."

About the timsTOF PRO with PASEF

The proprietary **timsTOF Pro** system uses PASEF, enabled by Trapped Ion Mobility Spectrometry (TIMS) to provide industry-leading data acquisition speed for shotgun proteomics. The unique dual TIMS geometry of the **timsTOF Pro**, combined with the time focusing of the ion packets in the TIMS device, means that the speed advantage provided by PASEF comes along with simultaneous improvements in sensitivity and quantitation. All of these gains in speed, sensitivity and quantitation maintain the advantages of Bruker's high-performance QTOF mass spectrometers, including high mass resolution (resolving power of 50,000 FWHM even at highest data acquisition rates), ppm accurate mass, and high isotopic fidelity (True Isotopic Pattern, or TIPTM). The robust **timsTOF Pro** with PASEF gives scientists the tools to dig deeper into the complex biology of the cellular machinery and the potential to discover low-level, biologically significant proteins, or validate them in translational and clinical proteomics research.

About the MaxQuant and Perseus software platforms

MaxQuant is the industry standard in shotgun proteomics data analysis. Developed over the last decade by Juergen Cox, it has become the most used package for the identification and quantification of peptides, proteins and posttranslational modifications. Recently, MaxQuant has been adapted to the analysis of timsTOF data, managing 4D features in the space spanned by retention time, ion mobility, mass and signal intensity. The Perseus software for multi-omics data analysis supports biological and biomedical researchers in interpreting molecular quantification, interaction and protein post-translational modification data. Perseus contains a comprehensive portfolio of statistical tools for high-dimensional data analysis covering normalization, pattern recognition, time-series analysis, cross-omics comparisons and multiple-hypothesis testing. For more information:

<http://www.biochem.mpg.de/5111795/maxquant>.

About PEAKS Studio

PEAKS Studio, the flagship software of Bioinformatics Solutions, Inc., offers an innovative mass spectrometry data analysis workflow to the proteomics research community. Since its debut in the early 2000s, PEAKS Studio has been highly recognized for its benchmarking de novo sequencing algorithm, which was integrated in all other software modules for shotgun proteomics. The combination of de novo sequencing with traditional database searches ensures a complete interpretation of raw spectral data to embrace the complexity and sensitivity of mass spectrometry, and offers advanced solutions for proteomic and therapeutic protein discovery as provided through peptide/protein identification and quantification, peptide mapping, post-translational modifications and sequence variants.

The unique workflow offered by PEAKS Studio together with the compelling data quality derived by fourth-dimension ion mobility of the **timsTOF Pro** has sparked Bioinformatics Solutions, Inc. and Bruker to establish collaborative work. For more information: www.bioinfor.com

About Bruker Corporation (NASDAQ: BRKR)

For more than 55 years, Bruker has enabled 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, productivity and customer success in life science molecular research, in applied and pharma applications, and in microscopy, nano-analysis and industrial applications. In recent years, Bruker has also become a provider of high-performance systems for cell biology, preclinical imaging, clinical phenomics and proteomics research, clinical microbiology, and for molecular pathology research. For more information: www.bruker.com

Media Contact:

Petra Scheffer

Daltonics Division Marketing & Communications

T: +49 (421) 2205-2843

E: petra.scheffer@bruker.com

Investor Contact:

Miroslava Minkova

Bruker Head of Investor Relations

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

E: miroslava.minkova@bruker.com

View original content with multimedia: <http://www.prnewswire.com/news-releases/bruker-launches-the-timstof-pro-mass-spectrometer-to-enable-the-revolutionary-pasef-method-for-next-generation-proteomics-300520791.html>

SOURCE Bruker Corporation