NEWS RELEASE

Bruker Launches Revolutionary timsOmniTM Mass Spectrometer

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Enabling Functional Proteoform Sequencing and Post-Translational Modification (PTM) Identification and Localization with Unprecedented Depth and Speed

Beyond Protein Groups - Ushering in Era of 'Proteoformics' with New Scientific Lamp-Post Shining Light on Functional, Therapeutic and Pathological Protein Isoforms

Integrating timsTOF Speed and Performance with Novel Functionality of Omnitrap

a. timsOmni enables 'Swiss Army Knife' flexibility in electron and collision induced ion fragmentation for next-gen proteoform insights to transform disease research, biologics development and advanced bioprocessing QC
b. Unrivaled structural, sequencing and top-down dissociation flexibility with high speed, high sensitivity and deep sequence coverage, including PTMs, such as phosphorylation or glycosylation, through Omnitrap-powered MS^n functionality
c. Precise control of electron energy for electron capture and electron-induced dissociation modes (eXd), with unmatched sensitivity, delivering up to 100% coverage, e.g., for modified histone proteoforms (H3:1K14ac proteoform)
d. Offering collision-induced unfolding (CIU) to enhance TIMS-derived collisional cross-sections (CCS) for deeper structural insights prior to eXd
e. OmniScape™ top-down sequencing software: machine learning with advanced deisotoping and scoring systems for confident proteoform ID, de novo protein sequencing, PTM mapping, and challenging glycosylation analysis
f. Maintains timsTOF platform high-speed and time-focusing for bottom-up high-sensitivity 4D-

Proteomics performance on low sample amount applications

BALTIMORE--(BUSINESS WIRE)-- For the 73rd Conference on Mass Spectrometry and Allied Topics (ASMS), **Bruker Corporation** (Nasdaq: BRKR) announced the launch of the timsOmni™ system, a transformative new timsTOF-based mass spectrometer designed for scientific, drug discovery, and clinical researchers, as well as for advanced QC on biologics, offering deep structural insights into the functional or pathological proteoforms or oligonucleotides. Multimodal eXd trapping with precise electron energy control, ion accumulation, and reaction time regulation is a cornerstone innovation of the timsOmni™ platform. This also enables CIU, further expanding the value of proteoform CCS information, followed by multiple electron-based (ECD, EID) and collision-based (CID) fragmentation techniques. The timsOmni uniquely enables protein researchers and biologics developers to tailor information-rich dissociation pathways for deeper insights - with high speed and high sensitivity.

timsOmni™ Mass Spectrometer

The ‘Swiss-army knife’ type flexibility of the timsOmni top-down capability enables the identification of low-abundant, aberrant proteoforms, the structurally altered versions of proteins arising from genetic mutations, alternative splicing, or post-translational modifications that deviate from normal physiological forms, disrupting protein function, misfolding, or aggregation, and often play critical roles in the onset and progression of human diseases, including cancer, neurodegeneration, cardiovascular disorders, and autoimmune conditions.

Anders Giessing, PhD, Science Manager at Novonesis in Denmark, said, “We use intact protein mass analysis to ensure performance, stability, and consistency of our diverse protein product portfolio. Introduction of the timsOmni, with its Swiss Army knife versatility, redefines intact mass and top-down analysis with the precision, speed, and confidence needed to provide definitive analytical support in the development and production of industrial enzymes.”

The Omnitrap’s signature high-sensitivity, high-speed, multimodal eXd capability is particularly powerful for mapping PTMs, such as histone proteoforms (H3:1K14ac) that play a crucial role in regulating gene expression by altering chromatin structure and controlling access to the DNA. Other PTMs like glycosylation critically influence protein folding, stability, transport, and cell signaling interactions, and detailed top-down or middle-down sequencing of complementarity-determining regions (CDRs) in humoral and therapeutic antibodies are important in cancer, autoimmunity and biologics development.

Prof. Albert Heck, Professor of Chemistry and Pharmaceutical Sciences at Utrecht University and Scientific Director of the Netherlands Proteomics Center, commented, “Proteomics will finally go ‘protein-centric’ by using the timsOmni. The multimodal eXd capability allows for comprehensive ion sequence ladders that are ideal for de novo sequencing and human plasma antibody repertoire profiling. Analyzing and monitoring circulating antibody levels is

critical for characterizing the progression of a disease, identifying patients with delayed symptom onset, and predicting potential long-term immunity."

Frank H. Laukien, Ph.D., the CEO of Bruker Corporation, added, "The timsOmni is a new lamppost for functional protein science, shining a light on functional and pathological proteoforms and truly enabling a new protein science paradigm for fundamental cell and molecular biology, signal transduction, cancer, neurodegeneration, and other disease research. The timsOmni will also be extremely valuable for biopharma drug discovery and development, as well as for biologics QC analysis, from therapeutic antibodies to antibody-drug conjugates."

The timsOmni is supported by OmniScape™, Bruker's next-generation top-down proteomics software that features state-of-the-art algorithms for de-isotoping complex spectra, automated charge state assignment, de novo protein sequencing support, and sequence confirmation. These key features provide unrivaled benefits for the accurate identification of proteoforms, post-translational modifications, and non-canonical proteins. OmniScape transforms complex eXd fragmentation spectra into actionable biological insights—empowering researchers to navigate the new world of functional proteoformics.

Prof. Ole N. Jensen, Group Leader at the Protein Research Group of the University of Southern Denmark, observed, "The timsOmni technology and OmniScape software already impacted our strategies for intact protein and proteoform analysis. Multimodal MS/MS fragmentation and MS3 afford very high amino acid sequence coverage and accurate localization of post-translational modifications in histones."

The timsOmni comes with the new NEOS off-line nanoESI for the extremely low infusion flow rates required for the study of protein complexes, allowing for extended analysis of scarce samples. The NEOS source works with coated and non-coated emitters. Additionally, the timsOmni retains the high sensitivity of the timsTOF Ultra 2 for nLC dia-PASEF high-throughput bottom-up 4D-proteomics.

The timsOmni ushers in a new era of functional proteomics, setting the stage for landmark discoveries in 'Proteoformics', and advancing a transformative new paradigm in protein research as it illuminates protein function through the deep sequencing of proteoforms, humoral and multi-specific antibodies, and other complex biomolecules.

About Bruker Corporation – Leader of the Post-Genomic Era (Nasdaq: BRKR)

Bruker is enabling scientists and engineers to make breakthrough post-genomic 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 post-genomic life science molecular and cell biology research, in applied and biopharma applications, in microscopy and nanoanalysis, as well as in industrial and cleantech research, and next-gen semiconductor metrology in support of AI. Bruker offers differentiated, high-value life science and diagnostics systems and solutions in preclinical imaging, clinical phenomics research, proteomics and multiomics, spatial and single-cell biology, functional structural and condensate biology, as well as in clinical microbiology and molecular diagnostics. For more information, please visit **www.bruker.com**.

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