NEWS RELEASE

Bruker Advances Functional Proteomics 2.0 with timsOmniTM Mass Spectrometry Proteoform Analysis for Deeper Insights into Disease Biology

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- Novel timsOmni™ workflows enable deeper functional characterization of proteoforms and PTMs, leveraging multi-stage, ultra-sensitive trapped eXd molecular fragmentation
- Bruker ProteoScape™ expands AI-enhanced de novo peptide sequencing for complex samples from metaproteomics to immunopeptidomics
- timsOmni provides a powerful new ‘lamp post’ for illuminating many complex molecular, pathway and mechanism of action dark areas in drug discovery and development

ST. LOUIS--(BUSINESS WIRE)-- **Bruker Corporation** (Nasdaq: BRKR) today announced new advancements to enable Functional Proteomics 2.0 workflows on the timsOmni™ mass spectrometer to enable disease researchers to move beyond canonical protein lists toward biologically or pathologically functional proteoforms and PTM-resolved peptide variants. New releases in Bruker ProteoScape™, OmniScape™, and GlycoScape™ software now support database-independent PTM discovery, confident proteoform characterization, and eXd-enabled glycoproteomics for deeper biological, disease and drug discovery insights.

Annotated timsOmni™ glycopeptide eXd spectrum from GlycoScape™ highlighting both glycan fragment ions as well as peptide fragment ions

Similarly, the now enabled timsOmni deep proteoform methods are equally powerful in interrogating drug targets, as well as biologics, including therapeutic antibodies, ADCs, multispecifics, and their PTM distributions and glyco-heterogeneity.

Confident proteoform characterization and eXd-enabled glycoproteomics on timsOmni

The latest version OmniScape™ 2026b strengthens timsOmni proteoform workflows by integrating the novel

OmniWave™ algorithm, which enables top-down sequencing and proteoform identification at scale with high-confidence annotation of critical PTMs that drive disease signaling. Researchers can now move beyond protein group read-outs to proteoform-centric mechanisms, e.g., distinguishing signaling relevant protein variants that indicate disease states or treatment response. In biotherapeutics research, OmniScape supports verification of expected sequences and non-canonical modifications and can flag sequence variants or heterogeneity that may affect side effects or efficacy.

Bruker is greatly enhancing glycoproteomics with support for trapped electron-based dissociation (eXd) data in GlycoScape software, enabling confident glycopeptide characterization while preserving fragile glycan structures and supporting localization and topology insights. GlycoScape also provides interactive visualization of eXd fragment ions within annotated MS/MS spectra to simplify the validation of results.

“The timsOmni gives scientists access to eXd-enabled fragmentation that can resolve complex PTMs and proteoforms with outstanding fidelity,” said Professor Yehia Mechref, Director of the Texas Tech University Center for Biotechnology & Genomics. “The new software capabilities—especially eXd N-glycopeptide analysis and improved top-down workflows—support deeper understanding of disease biology and provide new avenues for target discovery and translational research.”

Bruker ProteoScape™ adds AI-enhanced de novo peptide sequencing for database-independent discovery in metaproteomics and immunopeptidomics

Bruker is introducing a new de novo peptide sequencing workflow in Bruker ProteoScape v2026b software that pairs an AI-enhanced scoring model—trained on more than seven million MS/MS spectra—with a proven dynamic-programming foundation to deliver accurate de novo sequences from high-resolution timsTOF data. This supports the demand for database-independent proteomics, enabling discovery of peptide variants across complex samples in applications such as metaproteomics and immunopeptidomics, including neoantigen research in immuno-oncology.

“Researchers are increasingly studying biological systems where reference databases alone do not capture the true molecular diversity,” said Bin Ma, founder of Rapid Novor Inc. “Our collaboration with Bruker has enabled Novor.AI to take advantage of large, high-quality timsTOF datasets and combine them with our AI model to deliver the speed, confidence, and precision needed for next-generation de novo peptide sequencing applications.”

About Bruker Corporation – Leader of the Post-Genomic Era

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 specialty diagnostics, 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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