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Bruker advances Functional Proteomics 2.0 with timsOmni Mass Spectrometry Proteoform Analysis

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Bruker ProteoScapeÃ¢â??Â¢ expands AIÃ¢â?¬â??enhanced de novo peptide sequencing for complex samples



US-based Bruker Corporation has 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.

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.

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.

Bruker is introducing a new *de novo* peptide sequencing workflow in *Bruker ProteoScape v2026b* software that pairs an AIÃ¢â?¬â??enhanced scoring model—trained on more than seven million MS/MS spectra—with a proven dynamicÃ¢â?¬â??programming foundation to deliver accurate *de novo* sequences from highÃ¢â?¬â??resolution timsTOF data.

Bruker is greatly enhancing glycoproteomics with support for trapped electronÃ¢â?¬â??based dissociation (eXd) data in *GlycoScape* software, enabling confident glycopeptide characterization while preserving fragile glycan structures and supporting localization and topology insights.