



Untargeted timsTOF Mass Spectrometry Enables Discovery and Mapping of Draft Atlas of the Human Plasma Proteome at Proteoform Resolution

Charité principal investigator Markus Ralser and colleagues discover and map 179,000 plasma proteoforms, revealing a vast molecular landscape for functional proteomics in biomedical research, drug discovery and biomarker discovery

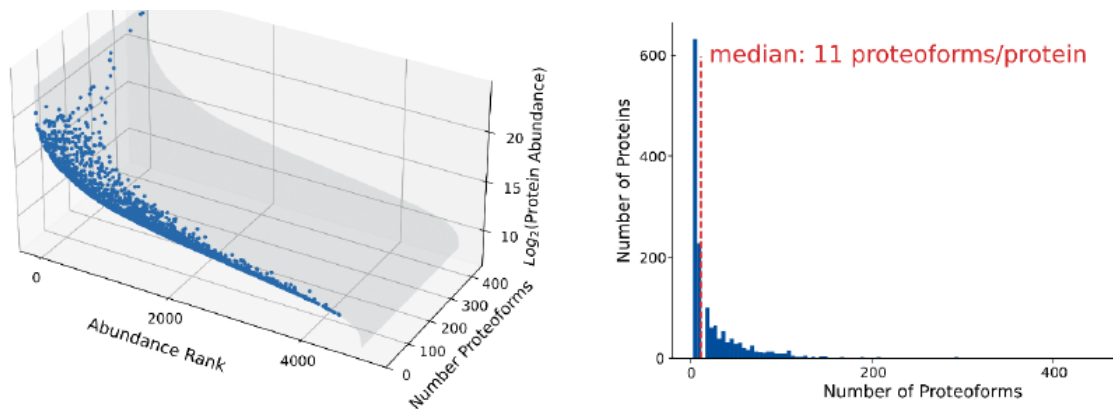
BERLIN, Germany – October 6th, 2026 - [Bruker Corporation](https://www.bruker.com) (Nasdaq: BRKR) announced a seminal bioRxiv preprint, describing a draft atlas of the human plasma proteome at isoform, or proteoform, resolution. The study was conducted by principal investigator Markus Ralser at Charité – Universitätsmedizin Berlin and collaborators. The preprint “A draft atlas of the human plasma proteome at isoform resolution” was posted on September 28, 2026 at <https://doi.org/10.64898/2026.09.26.754256>.

By combining intact protein fractionation with diaPASEF mass spectrometry on Bruker timsTOF mass spectrometry systems, the researchers detected 5,077 plasma protein groups across 179,049 distinct proteoforms. A high-confidence map comprised 44,083 proteoforms, with a median of eleven proteoforms per protein. The study indicates that canonical proteins account only for a fraction of protein diversity in the blood stream, and they may constitute less than half of total protein content.

The atlas reveals extensive proteoform diversity among abundant plasma proteins involved in molecular transport, complement activity and coagulation. It provides a framework for understanding why protein measurements by affinity and mass spec-based proteomics technologies diverge, particularly for low-abundance proteins and for proteins occurring in many molecular isoforms. The workflow did not use nanoparticle-based enrichment, instead combining intact-protein fractionation with sensitive, high-throughput mass spectrometry to resolve and discover plasma proteoform diversity at an unprecedented scale.

“Human plasma contains far more molecular diversity than conventional protein lists suggest,” said Dr. Markus Ralser, Einstein Professor of Biochemistry and Head of the Institute of Biochemistry at Charité – Universitätsmedizin Berlin. *“This first draft of the plasma proteoform atlas shows that proteoforms are not rare exceptions, but a defining feature of plasma biology. Mapping this diversity opens an enormous, largely unexplored molecular space for understanding physiology, disease mechanisms and differentiated biomarkers.”*





“This landmark discovery moves plasma proteomics beyond counting protein groups toward resolving the molecular isoforms that actually carry biological and ultimately biomedical function,” said Dr. Daniel Hornburg, Bruker Vice President, Biomarkers & Precision Medicine. *“The combination of protein separation, diaPASEF and sensitive timsTOF mass spectrometry provides a powerful foundation for studying proteoform-specific biology and for developing the next generation of more specific drug targets and biomarkers.”*

The draft isoform atlas is intended as a starting point for future proteoform in-depth studies across individuals, physiological states and diseases.

“Resolving protein isoforms and their modifications is fundamental to understanding the molecular drivers of disease,” said Dr. Rohan A. Thakur, Bruker Daltonics EVP and President of ToFwerk. *“The breakthrough timsOmni platform now enables deep top-down sequencing with near-complete sequence coverage on many proteoforms, combined with PTM localization and quantitation for in-depth functional proteome studies.”*

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