



## Bruker Launches Ultimate Sensitivity *timsTOF Ultra 2* to Enable New Research Paradigms in Single-Cell and Subcellular Proteomics

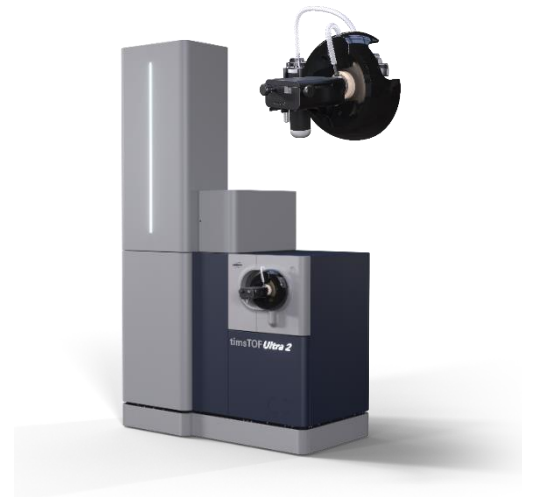
- *timsTOF Ultra 2 enables significant further improvements in deep, high-fidelity 4D-Proteomics™ of mammalian cells, cancer cell lines, or tissue biopsies*
- *With sensitivity to measure >1000 proteins on just 25 pg, the timsTOF Ultra 2 opens new cell and disease biology research windows into PBMCs, small immune cells, bacterial cells, or subcellular organelle proteomics*
- *timsTOF Ultra 2 enables identification and quantitation of ~50% more protein groups and ~100% more peptides at 25 pg of digest sample with 1% FDR*
- *timsTOF Ultra 2 typically yields ~40% more peptides and ~20% more proteins for many other 4D-Proteomics applications with low-medium sample amounts*
- *Improved ion-charge control (ICC 2.0) method makes timsTOF Ultra 2 suitable for a very broad range of sample loading, from low picograms to micrograms*
- *New OmniScape™ top-down proteoform software for automated, near-complete protein sequence coverage from MALDI-ISD and LC-TIMS-MS/MS data*
- *Biognosys launches Spectronaut® 19 (SN19) with optimized AI for further increased depth of protein quantitation and greater peptide sequence coverage*
- *SN19 now specifically trained on timsTOF MS/MS for significant 4D-Proteomics performance improvements; SN19 now fully integrated into timsTOF Ultra 2*
- *PreOmics launches reproducible and affordable deep plasma 4D-Proteomics ENRICHplus kit for 7-fold plasma depth improvement on robust timsTOF HT*
- *Novel capabilities for 4D-glycoprotein analysis: glyco-PASEF® and GlycoScape™*
- *Bruker announces customer shipment of more than 1,000 timsTOF systems*
- *Bruker launches 3 mass spectrometers at ASMS 2024 for 4D-Proteomics, mass-spec multiomics tissue imaging, and for highest-confidence applied analysis*

ANAHEIM, California– June 3<sup>rd</sup>, 2024 – At the 72<sup>nd</sup> ASMS meeting, [Bruker Corporation](#) (Nasdaq: BRKR) launches the new top-of-the-line *timsTOF Ultra 2* system with significantly further enhanced sensitivity for deep profiling of small cells, subcellular organelles, as well as increased sample loading flexibility. Together with new **Spectronaut 19** software and the novel PreOmics **ENRICHplus** kit, Bruker is setting new 4D-Proteomics standards from highest sensitivity to large-scale, deep plasma proteomics. Bruker is also introducing **OmniScape** software for top-down sequence confirmation and *de novo* sequencing for intact, undigested proteoforms, dissociated in the mass spectrometer.



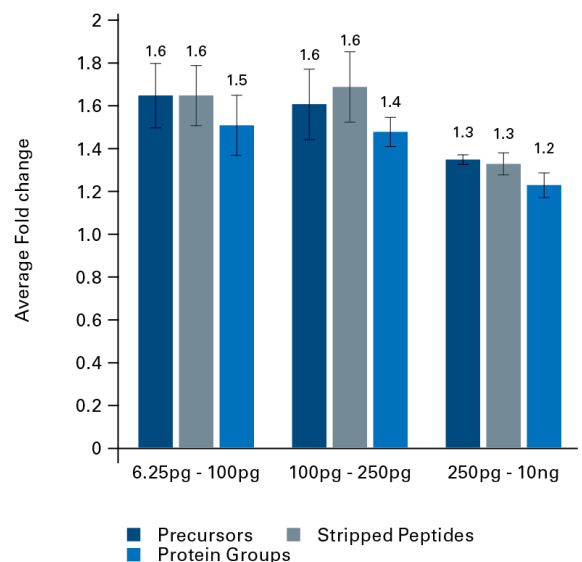
## Bruker Advances Ultimate Sensitivity with new *timsTOF Ultra 2*

The new *timsTOF Ultra 2* delivers ultimate sensitivity of up to 50% more protein groups and up to 100% more peptides on just 25 pg of protein digest, i.e. only 1/10<sup>th</sup> the protein mass of a HeLa cell. This makes *timsTOF Ultra 2* the best choice to investigate immune homeostasis surveying low abundance proteins from small peripheral blood mononuclear cells (PBMCs), or from bacterial cells comprising the microbiome, or for immunopeptidomics to discover cancer neoantigens from fine needle biopsies.



New ion charge control (ICC2.0) software provides sample loading flexibility from low picogram amounts to about a microgram of protein digest.

Bruker *ProteoScape*<sup>™</sup> software now integrates *Spectronaut 19* (SN19) software from Biognosys, the gold-standard for data-independent analysis (DIA). The new SN19 offers significantly improved search engine *AI*, advanced quantification, and allows precise predictions of *timsTOF*'s unique collision cross sections (DeepCCS), retention time (DeepiRT) and fragment ion intensity (DeepFrag), resulting in a 13% average increase in protein group identifications and improvements in quantification precision. See Biognosys [Press Release](#)



Bruker once again intends to offer field upgrades to the *timsTOF Ultra 2* for *timsTOF Ultra/SCP* customers.

## PreOmics launches Reproducible, Affordable ENRICHplus Deep Plasma 4D-Proteomics Solution, Leveraging the Proven Robustness of the *timsTOF HT*

The new single particle PreOmics **ENRICHplus** kit and the *timsTOF HT* now deliver up to 7-fold improvement in protein identification and quantification versus neat plasma. The increased depth of coverage, together with field-proven throughput and robustness of the *timsTOF HT* enables deep plasma proteomics at scale. See PreOmics [Press Release](#)

**Dr. Roman Fischer**, Associate Professor and Head of Discovery, Proteomics Facility, University of Oxford, UK, stated: "timsTOF technology, together with ENRICHplus, is changing the way we do plasma proteomics. On our *timsTOF Pro* we achieve on average



3800 protein identifications per sample with a throughput of 60 samples per day, while only using 20 µl of plasma. We never before achieved such depth with a single run of plasma, now enabling us to detect tissue leakage proteins and other low abundant potential biomarkers for cancer and neurodegenerative diseases. Together with the robust timsTOF system, ENRICHplus is game-changing for deep, affordable plasma proteomics at scale."

### **Bruker Launches *OmniScape* Top-Down Software for Analysis of Intact Proteins**

Bruker is introducing **OmniScape**, the first top-down protein sequence software that covers protein *de novo* sequencing and lead sequence identification through homology searches for detailed proteoform analysis.

**Dr. Boris Krichel**, University of Wisconsin-Madison, summarized: "I am excited about the *de novo* sequencing to discover and annotate proteins in untargeted top-down proteomics. The most impressive function of *OmniScape* is the automatic suggestion of matching proteoforms based on multiple variable modifications."

OmniScape supports different data types from LC-CCS-MS/MS, enabling for example the analysis of multiply phosphorylated proteins. Its ability to integrate different datasets yields very high sequence coverages, providing reliable sequence calls and PTMs. OmniScape can also process MALDI-ISD top-down spectra from the timsTOF fleX and axial MALDI instruments including the new neofleX, as well as data from non-Bruker instruments as a one-for-all top-down protein sequencing and isoform determination software solution.

**Dr. Christian Isak Jørgensen**, Senior Science Manager, Novonosis, Denmark, added: "*OmniScape* addresses a real need in the biotech industry producing recombinant proteins."

### **Novel Acquisition and Computational Capabilities for 4D-Glycoproteomics**

Bruker is introducing **GlycoScape**, the first real-time glycoproteomic software. *GlycoScape* has been developed in collaboration with the Radboud University Medical Center in the public-private partnership project EnFORCE led by Dr. Hans Wessels [1]. The software can identify glycopeptides on-the-fly as data are acquired and without the need to rely on glycan libraries, not only enabling identification of previously unreported glycans, but significantly minimizing false negative results. The unbiased read-out of glycoproteomic data by *GlycoScape* is critical for the advancement of glycobiology in translational and clinical research as these important research fields become accessible in the post-genomic era.



**Dr. Hans Wessels**, Senior Researcher at Radboud University in Nijmegen highlighted key advantages: “GlycoScape opens up the analysis of glycoproteomic mass spectrometry data from the timsTOF platform for on-the-fly processing without glycan database restrictions.”

GlycoScape leverages the **glyco-PASEF** method for ultra-sensitive and rapid glycoprotein data acquisition, using stepped energy CID and oxonium-ion-gated polygon-filtering, that was developed in collaboration with Prof. Albert Heck’s group at Utrecht University.

**Dr. Albert Heck**, Professor of Chemistry and Pharmaceutical Sciences at Utrecht University and Scientific Director of the Netherlands Proteomics Center, noted: “I am pleased with our pioneering work in leveraging the unique strengths of the timsTOF platform for glycoproteomics, now translated to the glyco-PASEF method for research in glycobiology.”

[1] The collaboration project is co-funded by PPP Allowance awarded by Health~Holland, Top Sector Life Sciences & Health, to stimulate public-private partnerships (Grant #LSHM21032).

#### **About Bruker Corporation – the Emerging 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 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](http://www.bruker.com).

#### **Media Contact**

Petra Scheffer  
Bruker Daltonics MarCom Manager  
T: +49 (421) 2205-2843  
E: [Petra.Scheffer@bruker.com](mailto:Petra.Scheffer@bruker.com)

#### **Investor Relations Contact**

Justin Ward  
Sr. Director Investor Relations & Corp Development  
T: +1 (978) 313-5800  
E: [Investor.Relations@bruker.com](mailto:Investor.Relations@bruker.com)