TIMS-MS

timsTOF Ultra

Make the invisible visible

Innovation with Integrity

timsTOF Ultra: Small samples to big discoveries

Unleash 4D-Proteomics™ with the timsTOF Ultra — the ultimate fusion of trapped ion mobility spectrometry (TIMS) with quadrupole time-of-flight (QTOF) technology. Conquer samples, detect low-abundance peptides, and make groundbreaking omics discoveries.

From minute samples to unseen peptides

Introducing the timsTOF Ultra mass spectrometer and CaptiveSpray Ultra ion source—an unstoppable alliance, unleashing unrivaled sensitivity. Discover hidden secrets in low-abundance peptides with the remarkable power of PASEF® acquisition. Unlock the fourth dimension of analysis with ion mobility separation. Say goodbye to chemical tagging with effortless identification of novel peptides. Redefining labs with speed and efficiency, the timsTOF Ultra makes the invisible visible.

Triumph in proteomics with speed and superior resolution

Supercharge your research with PASEF ultra-fast 300 Hz acquisition mode. Experience unrivaled efficiency with near 100% duty cycle. Unleash unparalleled resolution using our state-of-the-art 14-bit digitizer. Identify, characterize, and diagnose with unwavering confidence.

Breaking boundaries

From single-cell proteomics to immunopeptidomics and plasma proteomics, defy the odds with the timsTOF Ultra. With unmatched speed and sensitivity that transcends conventional limitations, embrace scientific possibilities with the exceptional timsTOF Ultra.

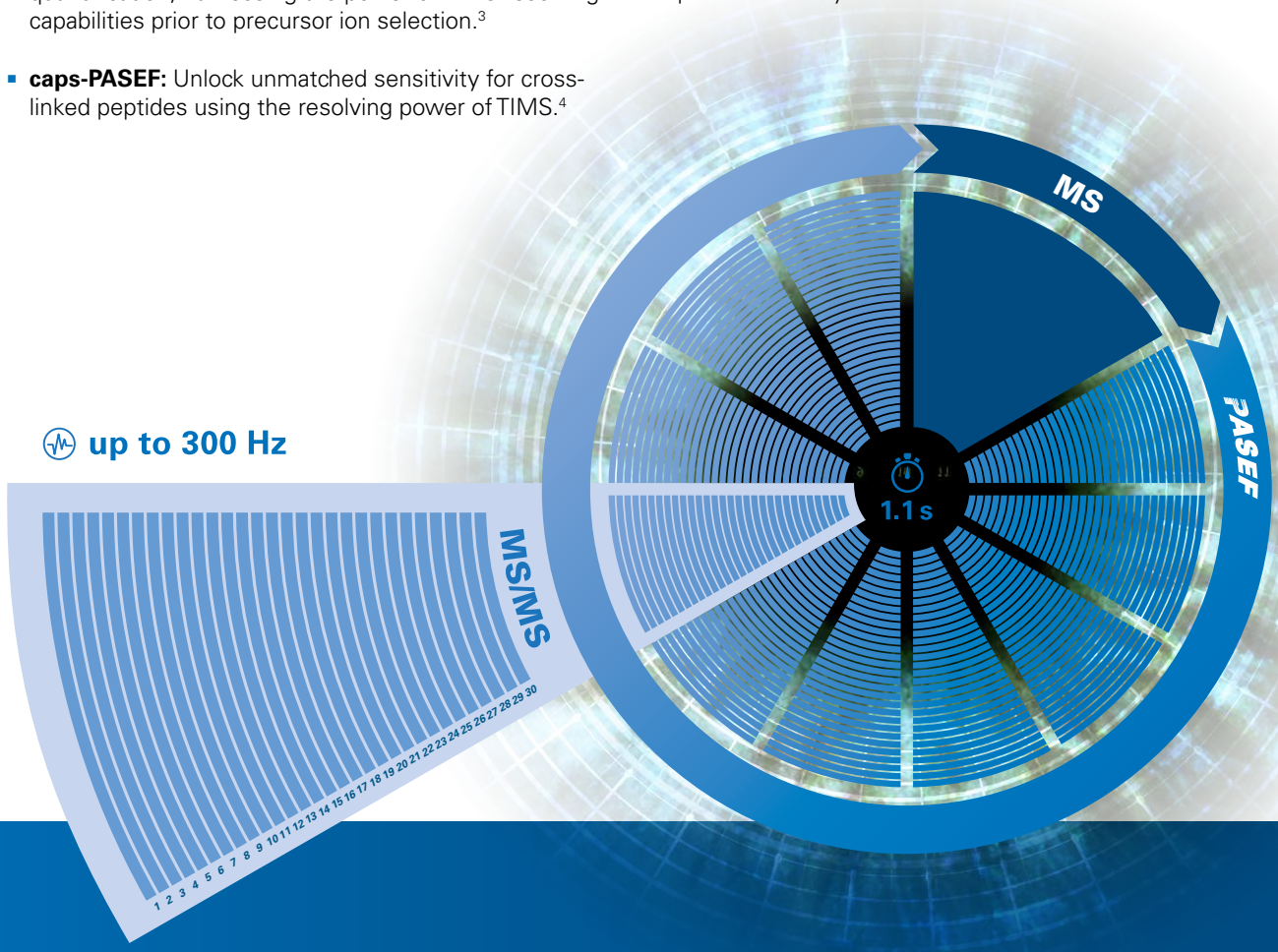
- **Unmatched sensitivity** - TIMS PASEF mode parallelization captures ions with near 100% efficiency, delivering exceptional sensitivity.
- **Enhanced specificity** - MOMA (Mobility Offset, Mass Aligned) allows identification and separation of co-eluting isobaric mass-to-charge ions in the mobility domain, increasing clarity and confidence.
- **Maximum ion transfer** - CaptiveSpray Ultra (CSI Ultra) ionization creates a vortex for optimal ion transfer.
- **Increased confidence** - Higher confidence with low S/N peptide identification using CCS values with CCS-enabled TIMScore™ and TIMS DIA-NN 4D-Proteomics and Spectronaut® software. Identify over 5500 protein groups in 22 mins from 125 pg K562 lysate.
- **Speed and efficiency** - Experience shorter gradients and unparalleled proteome depth thanks to PASEF at 300 Hz speeds.

PASEF speeds: Enabled by TIMS

Experience the fastest and most confident breakthroughs with the fusion of TIMS and quantitative time of flight (QTOF) mass analysis via PASEF. Uncover unprecedented proteome depth while dramatically reducing run times.

The fast track to success

- **dda-PASEF:** Slash run times from 120 minutes to just 30 minutes.[1]
- **dia-PASEF:** Step into the future of label-free bottom-up proteomics as dia-PASEF enhances analysis speed, capturing nearly 100% of peptide precursor ions in m/z and mobility windows.[2]
- **prm-PASEF:** Achieve unrivaled quantitative precision, accuracy, and sensitivity for label-free peptide quantification, harnessing the power of TIMS resolving capabilities prior to precursor ion selection.[3]
- **caps-PASEF:** Unlock unmatched sensitivity for cross-linked peptides using the resolving power of TIMS.[4]
- **midia-PASEF:** Experience the best of both worlds - dda-PASEF-like spectrum quality, enhanced sensitivity, and zero missing values, the ideal choice for immunopeptidomics research.[5]
- **slice-PASEF:** Developed by users like you, amplify sensitivity for the most challenging samples, including single cells and Formalin-Fixed Paraffin-Embedded (FFPE) tissues, through precise precursor ion selection at PASEF speeds, opening new possibilities in proteomic analysis.[6]



1. Meier, Florian. et al. "Online Parallel Accumulation–Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer." Molecular & Cellular Proteomics 17, no. 12 (2018): 2534–45. https://doi.org/10.1074/mcp.tir118.000900 2. Meier, Florian. et al. "Diapasef: Parallel Accumulation–Serial Fragmentation Combined with Data-Independent Acquisition." Nature Methods 17, no. 12 (2020): 1229–36. https://doi.org/10.1038/s41592-020-00998-0 3. Lesur, Antoine. et al. "Highly Multiplexed Targeted Proteomics Acquisition on a Tims-QTOF." Analytical Chemistry 93, no. 3 (2020): 1383–92. https://doi.org/10.1021/acs.analchem.0c03180 4. Steigenberger, Barbara. et al. "Benefits of Collisional Cross Section Assisted Precursor Selection (Caps-PASEF) for Cross-Linking Mass Spectrometry." Molecular & Cellular Proteomics 19, no. 10 (2020): 1677–87. https://doi.org/10.1074/mcp.ra120.002094 5. Distler, Ute, et al. „MIDIAPASEF maximizes information content in data-independent acquisition proteomics." bioRxiv, (2023). https://doi.org/10.1101/2023.01.30.526204 6. Szyrwiel, Lukasz, et al. "Slice-PASEF: Fragmenting All Ions for Maximum Sensitivity in Proteomics." bioRxiv , 2022. https://doi.org/10.1101/2022.10.31.514544

CaptiveSpray Ultra: Ultra-sensitive omics made easy

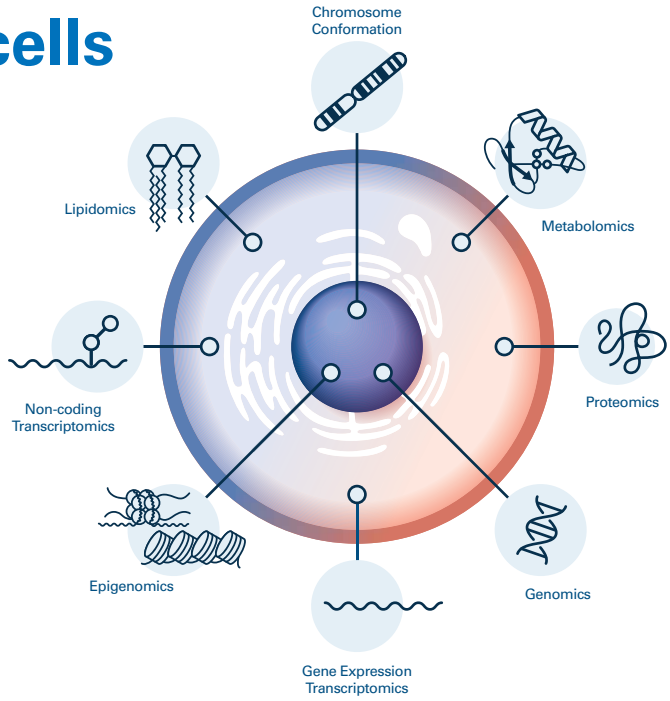
Engineered for the timsTOF Ultra, the CSI Ultra is performance-matched nanospray that boosts ionization efficiency to drive ultra sensitivity. Its unique vortex optimizes ion transfer, delivering high performance across diverse flow conditions. Enhance your mass spectrometry analysis with CSI Ultra precision.

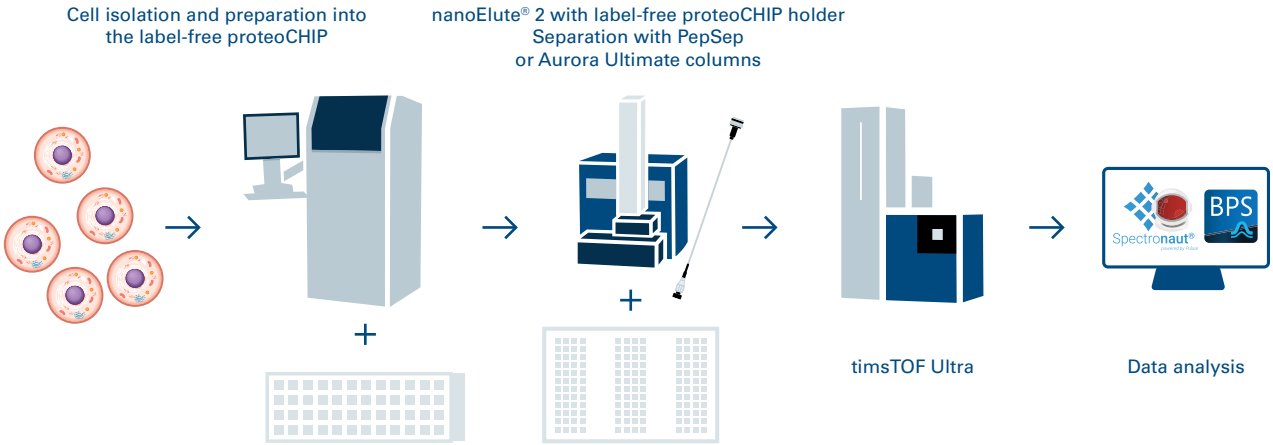
Simplify workflow, eliminate complexity, and achieve exceptional results with minimal maintenance.

Benefits	Features
Exceptional performance	Optimal sensitivity across nanoflow rates and stable spray throughout the liquid chromatographic gradient is made possible by the unique design that maximizes ion transfer.
Simplicity redefined	"On-off" design, installation in just seconds!
The power of compatibility	Wide range of choice of columns which integrate into your existing setup: PepSep, IonOpticks, and even custom self-made columns.
Precision perfected	CaptiveSpray 2 Emitter for unrivaled precision and stability, revolutionizing your chromatographic endeavors.

timsTOF Ultra: See cells in a new light

Discover a new world of single cell proteomics. Explore the intricacies of phenotypes of heterogeneous cells with the robust and highly sensitive mass spectrometry of the timsTOF Ultra. Gain insights into the complexity of diseases, reveal the mysteries of the cell microenvironment, follow the lines of cell-to-cell communication, and pave the way for improved therapeutics.



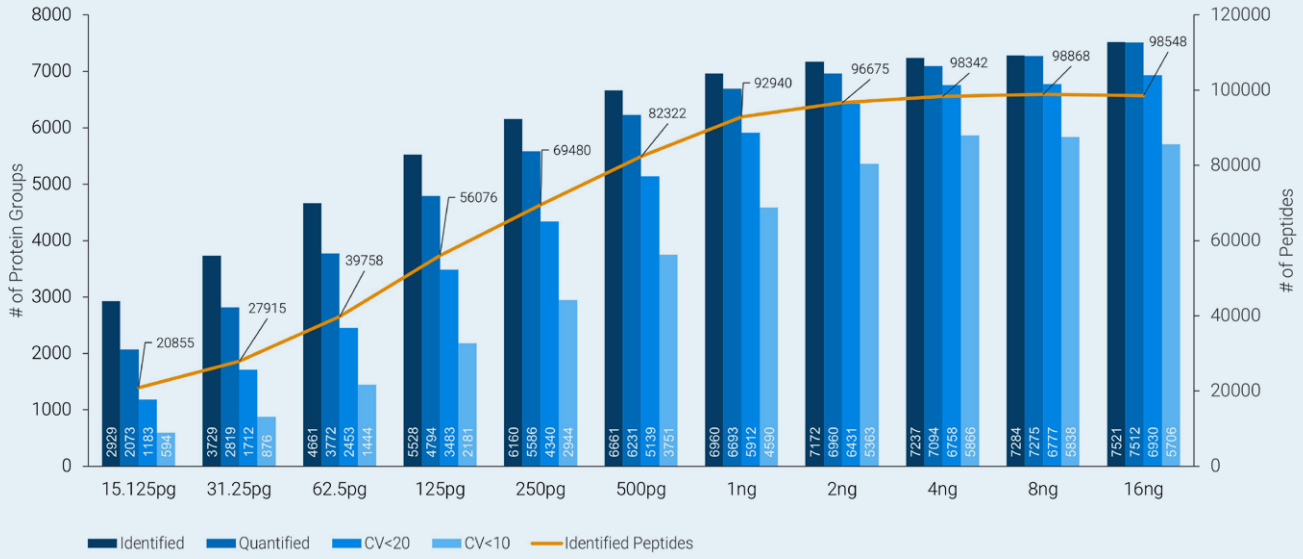


Professor Dr. Karl Mechtler

Head Proteomics Tech Hub, Research Institute of Molecular Pathology, Vienna Biocenter, Vienna, Austria

"I know firsthand the complexities of heterogeneous tissue. To truly understand cellular mechanisms and diseases, it's crucial to differentiate between the various cell types at play. While single-cell analysis has been game-changing, we have faced significant obstacles in maximizing its potential until recently. Our biggest problems at hand are throughput and the number of proteins that can be competitively analyzed compared to RNA sequencing. Therefore, it would make biological sense to detect 6000 or more proteins in a single-cell equivalent experiment. The timsTOF Ultra has successfully overcome these barriers, allowing us to explore the proteome of individual cells at lightning-fast speeds and unparalleled sensitivity, even from minute samples. Thanks to the timsTOF Ultra, single-cell analysis has reached new heights, and I'm excited to see where this breakthrough will lead us next."

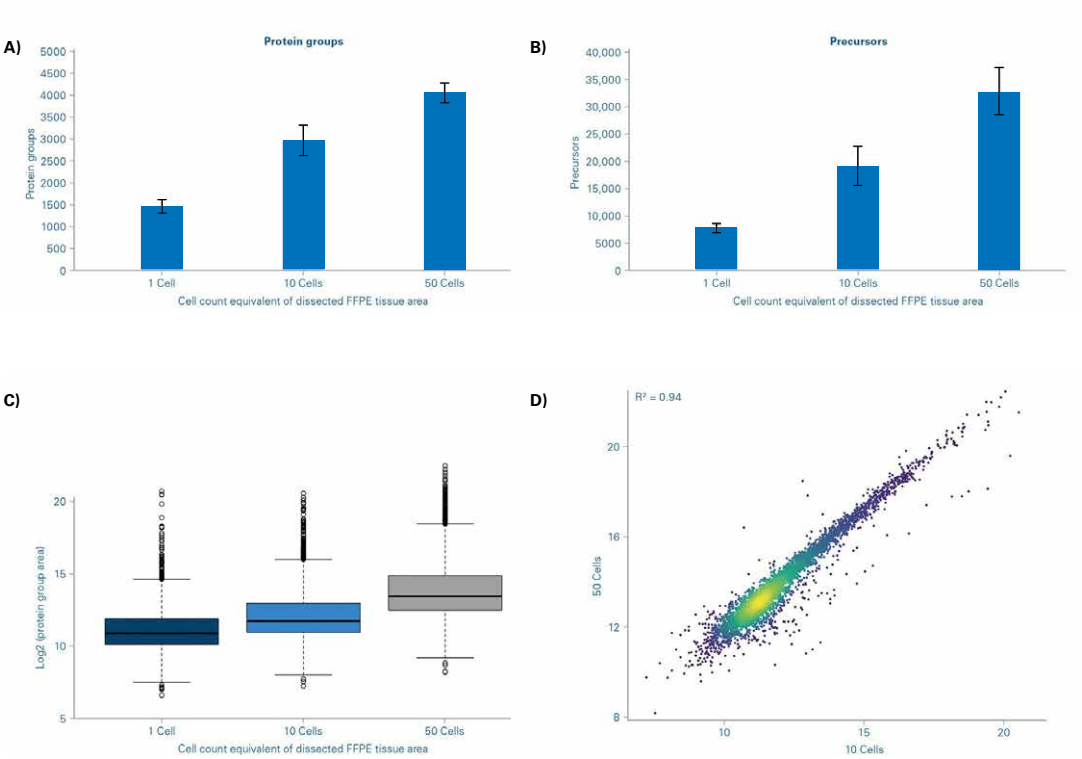
Navigate the unknown with precision and accuracy



Ultra sensitivity at ultra low loads. K562 was digested and loaded onto an IonOpticks Aurora 25 cm column in various concentrations spanning 15.125 pg to 16 ng, and analyzed in triplicate using a 22 minute active gradient on a nanoElute 2 coupled to a timsTOF Ultra. Resulting data was analyzed with Spectronaut 18 in directDIA+. With just 125 pg of material, 5528 proteins and over 55,000 peptides are identified displaying unparalleled depth and sensitivity for precious samples.

A powerhouse for molecular medicine: tackling single cell analysis in FFPE tissue

timsTOF Ultra offers tremendous potential for translational patient treatment by enabling the mapping of FFPE tissue proteins to specific cancer regions, even with minimal sample amounts. With dia-PASEF, timsTOF Ultra takes low-input tissue proteomics to the next level, making it an indispensable solution for molecular medicine labs.



A) Protein group and **B)** precursors identification rates in FFPE Mouse liver tissue dissected by laser capture microdissection (5 µm section) of 600 µm² (~1 cell), 12,500 µm², (~10 cells) and 50,000 µm² (~50 cells) analyzed in dia-PASEF mode using an 11 min active gradient and processing with DIA-NN 1.8.1 using a refined predicted mouse peptide library. **C)** Box plot showing an increase in protein group abundance distribution from 1 cell equivalents to 50 cell equivalents. **D)** correlation of protein abundance (mean per protein per cell equivalent (n = 5)) for the LCM dissected tissues of 10 cells and 50 cells.

Dr. Fabian Coscia

Group Leader Spatial Proteomics at the Max Delbrück Center for Molecular Medicine, Berlin, Germany

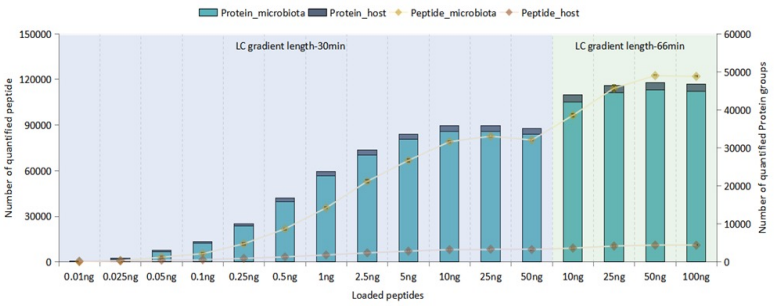
"The single-cell sensitivity dia-PASEF workflow on the timsTOF Ultra has brought our low-input tissue proteomics work to a new level. Using a 20-min nanoflow LC gradient combined with Bruker's optimized dia-PASEF (3x8 window) method, we can reproducibly quantify 1,500-2,000 proteins from laser microdissected mouse liver FFPE tissue of only 1,500 µm², regions of approximately 1-2 hepatocytes. Due to its great sensitivity and robustness, the timsTOF Ultra is our main workhorse in the lab."

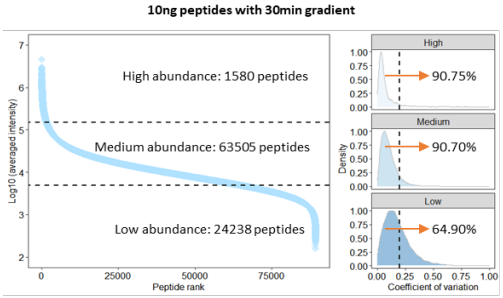
Visualize the microbiome with metaproteomics

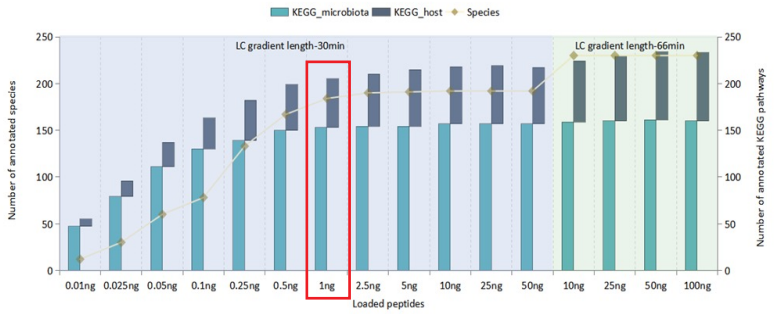
Microbial communities are essential for planetary health and metaproteomics is the key to understanding their functional dynamics. With timsTOF Ultra's ion mobility dimension, taxonomical and functional profiling of microbiome peptides and proteins is more accurate than ever before. Produce astonishing results from samples as small as 1 ng, thanks to shorter gradients and PASEF speeds.

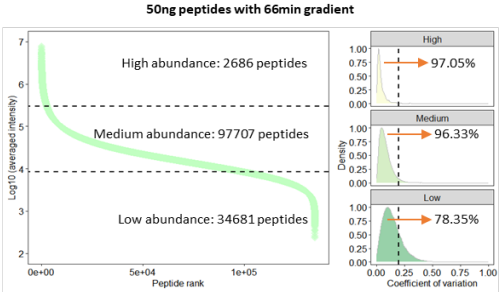
Advantages of TIMS and PASEF-based metaproteomics in microbiome research

- Identify and quantify an unmatched number of peptides and proteins in the mouse gut microbiome and host with remarkable accuracy using the ion mobility dimension.
- Achieve taxonomical and functional profiling depths that rival or surpass commonly used genomic approaches.
- Experience astonishing gains in sensitivity with minimal sample amounts and accelerated analysis with short gradients thanks to "PASEF speeds".









Get ready to complement genomic approaches with sensitivity and accuracy like never before!

5 orders of magnitude sensitivity with very high reproducibility throughout.

Data credit: *Data generated and analyzed by Christoph Krisp, Feng Xian and David Gómez-Varela.*

Pooled mouse gut fecal peptides from 0.01 ng to 100 ng in triplicates with 30 (blue background) or 66 (green background) minutes gradient in dia-PASEF. Number of peptide (lines) and protein (bars) identifications for microbiota and host at different peptide quantities with 30 min gradient (blue area) and 66 min gradient (green area). The dynamic range of quantified peptides from 10 ng (upper) and 50 ng (lower) injection. Density curves show the CV distributions of peptides from corresponding abundance regions (dynamic range equally divided into 3 regions). A number of microbiome species and KEGG functions are annotated from identified peptides and proteins.

Dr. David Gómez-Varela

Systems Biology of Pain, Division of Pharmacology and Toxicology,
University of Vienna, Austria

"Metaproteomics is a new tool in microbiome research with the unique potential to go beyond taxonomical characterization and reach a deep understanding of the functional alterations in microbial ecosystems. The analysis of the immense peptidome landscape of microbial samples is an enormous challenge. The timsTOF Ultra enabled us to reach unprecedented taxonomical identification levels (similar to most genomic approaches) and to improve several fold the quantification, sensitivity, and high-throughput levels of state-of-the-art proteomic technologies. I believe that the use of the timsTOF Ultra will mark a new era in microbiome research, paving the way for exciting findings across biotechnology fields."

When every cell counts for your immunopeptidomics research

Imagine you wouldn't need to grow millions of cells to investigate the immunopeptidome but rather just a few 1000s.

Empower your research with the timsTOF Ultra and Bruker ProteoScape™ Novor, unlocking unparalleled sensitivity, conquering complexity, and propelling breakthrough discoveries in personalized medicine.

Unmatched sensitivity for low abundances

With the power of TIMS and its collisional cross-section (CCS) enabled specificity, the timsTOF Ultra confidently identifies major histocompatibility complex (MHC)-bound peptides, delivering precise results for LC-MS-based immunopeptidomics.

Unparalleled precision

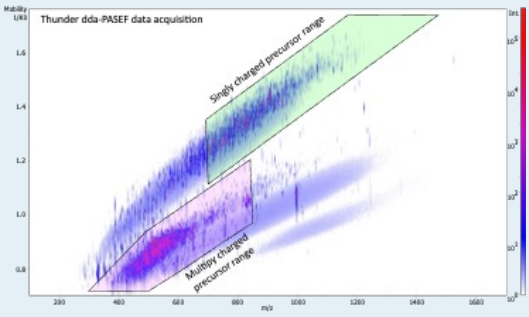
Combined with Bruker ProteoScape Novor, our optimized de novo sequencing engine, the timsTOF Ultra offers real-time sequencing capabilities, outperforming standard Novor and revolutionizing the study of non-canonical proteins.

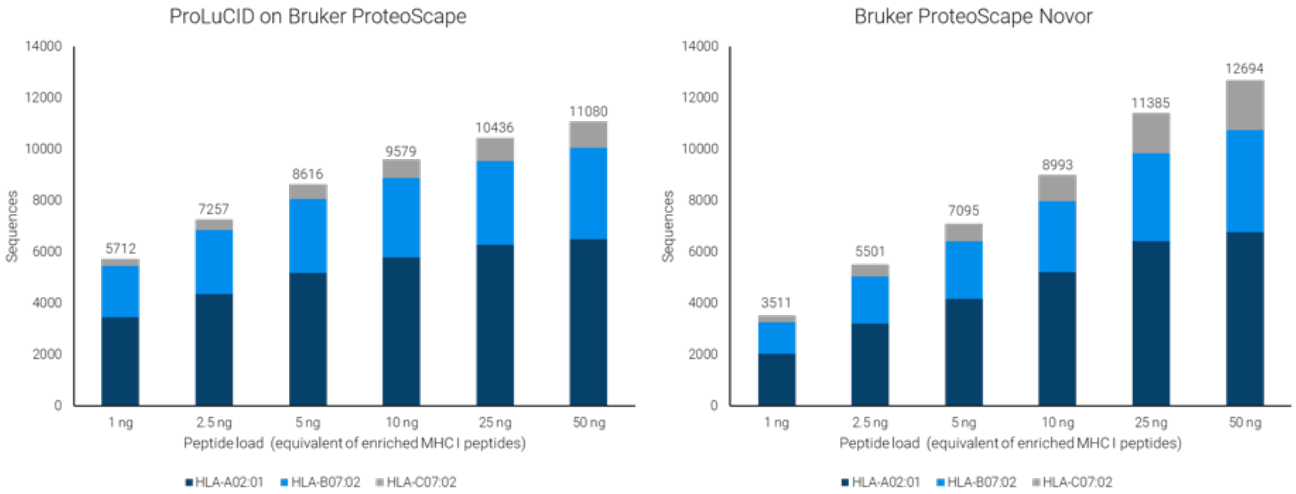
Supercharged performance and unparalleled convenience

- **Unrivaled speed and versatility:** Bruker ProteoScape Novor sets a new benchmark, outpacing competing products by 20x. With no noticeable bias for digestion specificity or species, it delivers rapid results and unparalleled flexibility for your research needs.
- **Run & Done:** Unlock new possibilities for 4D-Proteomics applications with seamless Run & Done capabilities.
- **Enhanced sensitivity in real-time:** Paired with the cutting-edge PASEF technology on the timsTOF platform, Bruker ProteoScape Novor integrates a fast, accurate, and precise peptide de novo sequencing algorithm for diverse applications.

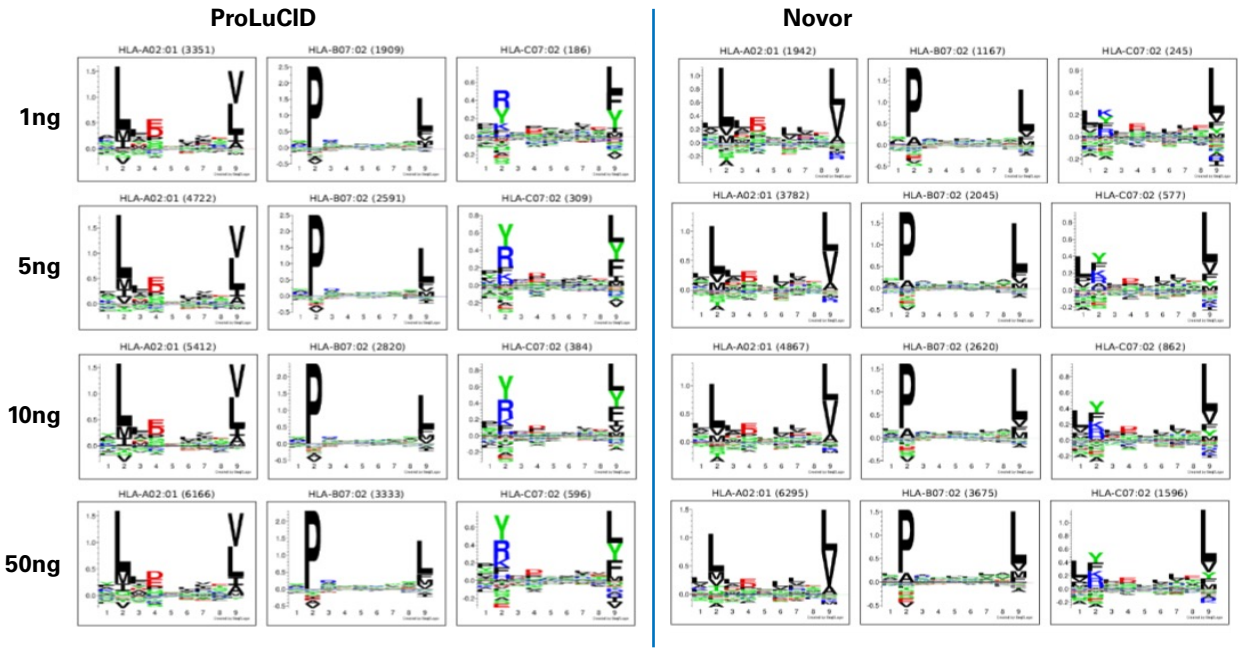
Make use of the mobility dimension for selecting only ions of interest

The gas phase separation of singly charged peptides due to TIMS during a PASEF cycle enhances the specificity of precursor ion selection, and becomes a special advantage for LC-MS-based immunopeptidomics, as ~20% of neoantigens are only found as +1 precursors*





Ultra sensitivity for your rare precious samples. Enriched immunopeptides from JY cells were run on a 25 cm IonOpticks column coupled to a timsTOF Ultra in various concentrations and searched with Bruker ProteoScape either with the ProLuCID search engine or the BPS Novor Package. A multitude of singly-charged and double-charged immunopeptides are observed even at sub-nanogram loads. Motif analysis shows the excellent correlation of immunopeptides at various human leukocyte antigens (HLA) alleles.



An example HLA Class 1 peptide from an immunopeptidomic dataset, de novo sequenced by BPS Novor (top) or ProLuCID database search (bottom) and corresponding Gibbs clustering of all 9-mer peptides in the dataset (Feola, S. et al. PeptiCHIP: A Microfluidic Platform for Tumor Antigen Landscape Identification. ACS Nano 15, 15992–16010 (2021). Processing of the entire dataset (93,158 MS2 spectra) was fully de novo sequenced in under 1 minute with BPS Novor.

Data credit: *Enriched JY Cells (provided by Prof. Stefan Tenzer and Dr. David Gomez-Zepeda), dda-PASEF, 38 min active gradient, 250 nL/min (nanoElute 2)*

Going beyond blood: high-flow plasma proteomics

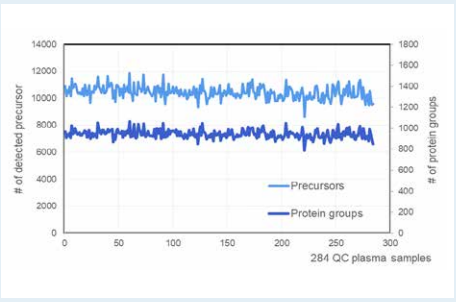
Achieving accurate identification and monitoring of biomarkers in plasma's proteome composition requires comprehensive population screening. Experience the power of the timsTOF Ultra and VIP-HESI, combined with µ-flow and normal flow chromatography. Conduct large cohort studies with unmatched sensitivity and sample throughput. Redefine the future of healthcare with precision medicine today.

"In plasma proteome research we face large inherent variability due to biological variation between individuals and pre-analytical variation. Thus, the ability to measure large cohorts with high-system robustness is key. The TIMS technology addresses the needs of our plasma proteome research by improving specificity and providing ultra-high sensitivity." - a leading diagnostics company.

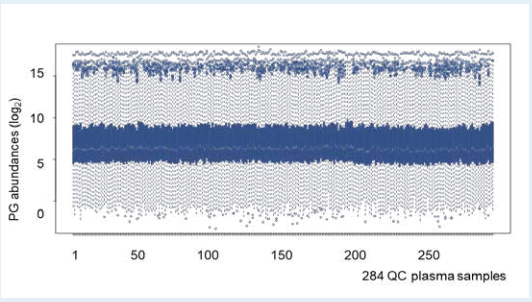
- Robust electrospray technology enables up to 5000 LC/MS runs, providing exceptional longevity.
- Achieve 3x signal gain at a flow rate of 50 µL/min with the 50 µm sprayer, ensuring optimal sensitivity.
- Effortlessly replace the standard VIP-HESI sprayer with a convenient drop-in replacement for seamless integration.
- Experience efficient peptide detection and quantitation in under 10 minutes per sample with our 4D-Proteomics approach.
- Benefit from increased column lifetime, reducing maintenance and replacement costs.

A)

B)



C)



A) VIP-HESI ionization source. **B)** Precursor and protein identifications monitored over 284 injections of 20 µg tryptic digest of depleted mouse plasma on µ-flow HPLC at 40 µL/min (acquired on timsTOF Pro) **C)** Protein abundance distribution monitored over 284 injections of depleted mouse plasma analyzed in Spectronaut 17 Software (acquired on timsTOF Pro, with permission of Dr. Mukul K. Midha, Research Scientist, Moritz Group Institute for Systems Biology, Seattle, USA)

Extending the advantages of ultra sensitivity: lipidomics

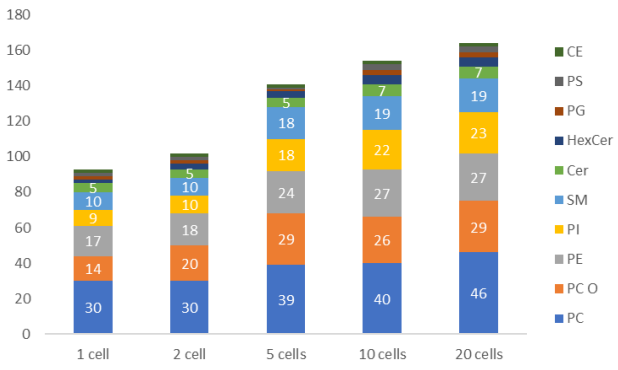
Break free from sequencing limitations and start identifying and characterize lipids with precision that lead to groundbreaking discoveries in single-cell biology, cancer pathology and clinical research.

Discover analytical depth and superior sensitivity by combining the timsTOF Ultra, the nanoElute 2, and CSI Ultra source for complete characterization. Explore new frontiers of discovery today.

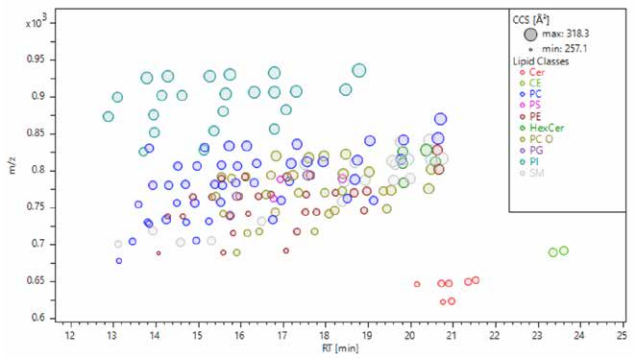
Tap into the unknown

With the timsTOF Ultra single cell lipidomics becomes even more accessible than on the timsTOF SCP.

A)



B)



A) *A549* lung cancer cells isolated with cellenONE platform (Cellenion) analyzed on the timsTOF Ultra coupled with nanoElute 2 via CSI Ultra source. **B)** Two-dimensional map of automated lipid annotations as illustrated in MetaboScape®.

Dr. Seul Kee Byeon

Assistant Professor, Mayo Clinic, Minnesota, USA

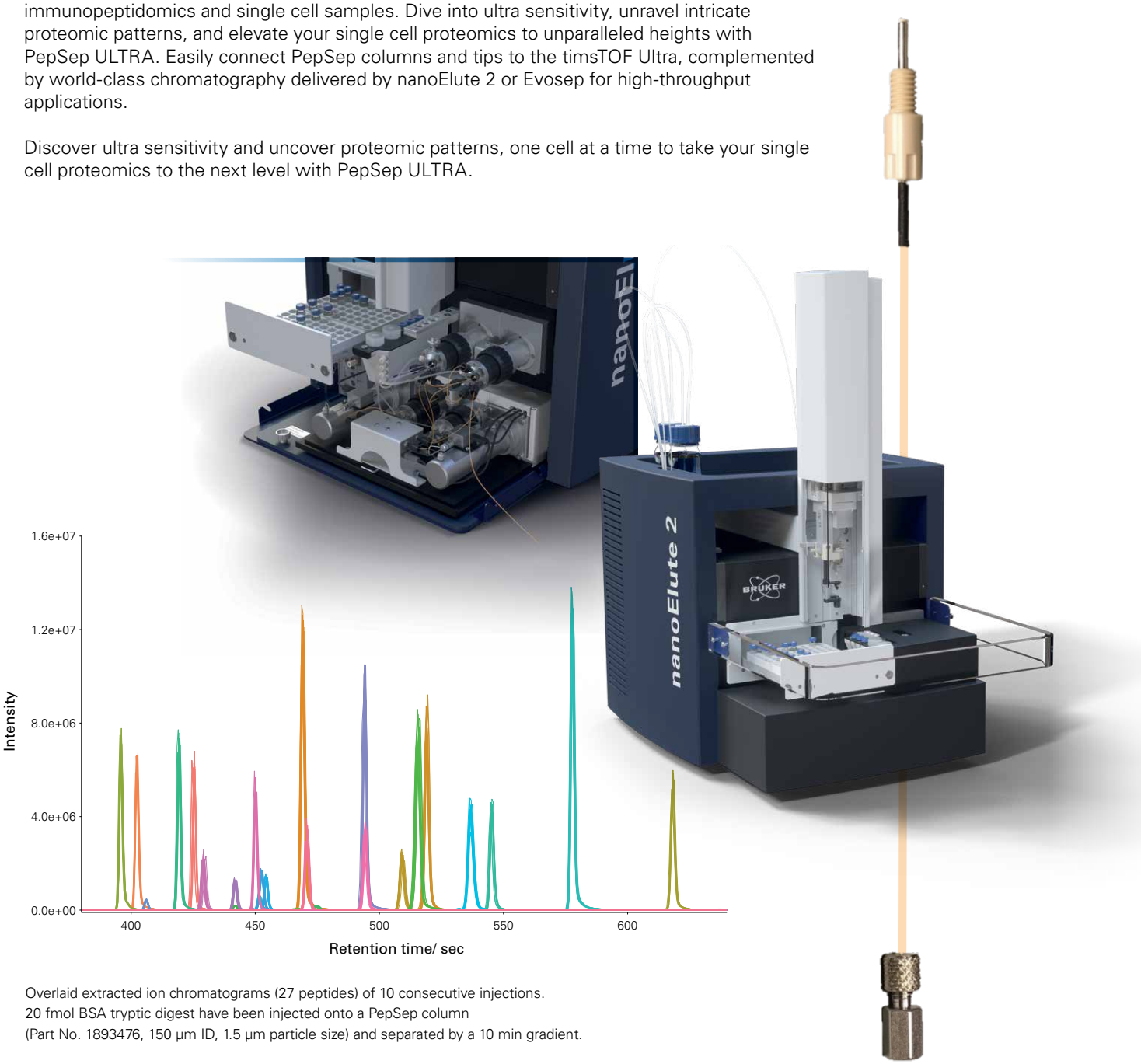
"I am excited that Bruker's timsTOF SCP allows me to do single cell lipidomics. I have been able to detect more than 100 species of lipids from an isolated single cell in positive ion mode alone. My next steps include studying heterogeneity at the single cell level, which has not been possible before at this scale. Bruker's application development team has helped me set up the methods and data analysis for these specialized experiments."

Ultra separation delivered at PASEF speed

Ultra sensitivity and reproducibility at PASEF speeds. Detect and quantify thousands of proteins in one single cell. Achieve unrivaled speed, exceptional performance, and unwavering robustness for all your proteomics applications. With PepSep columns seamlessly integrate into the CSI Ultra source, fitted with no-fuss static tips available in either 10 or 20 µm, you'll have ultimate control.

PepSep ULTRA columns redefine ultra sensitivity at PASEF speed for greater IDs on immunopeptidomics and single cell samples. Dive into ultra sensitivity, unravel intricate proteomic patterns, and elevate your single cell proteomics to unparalleled heights with PepSep ULTRA. Easily connect PepSep columns and tips to the timsTOF Ultra, complemented by world-class chromatography delivered by nanoElute 2 or Evosep for high-throughput applications.

Discover ultra sensitivity and uncover proteomic patterns, one cell at a time to take your single cell proteomics to the next level with PepSep ULTRA.



Overlaid extracted ion chromatograms (27 peptides) of 10 consecutive injections.
20 fmol BSA tryptic digest have been injected onto a PepSep column
(Part No. 1893476, 150 µm ID, 1.5 µm particle size) and separated by a 10 min gradient.

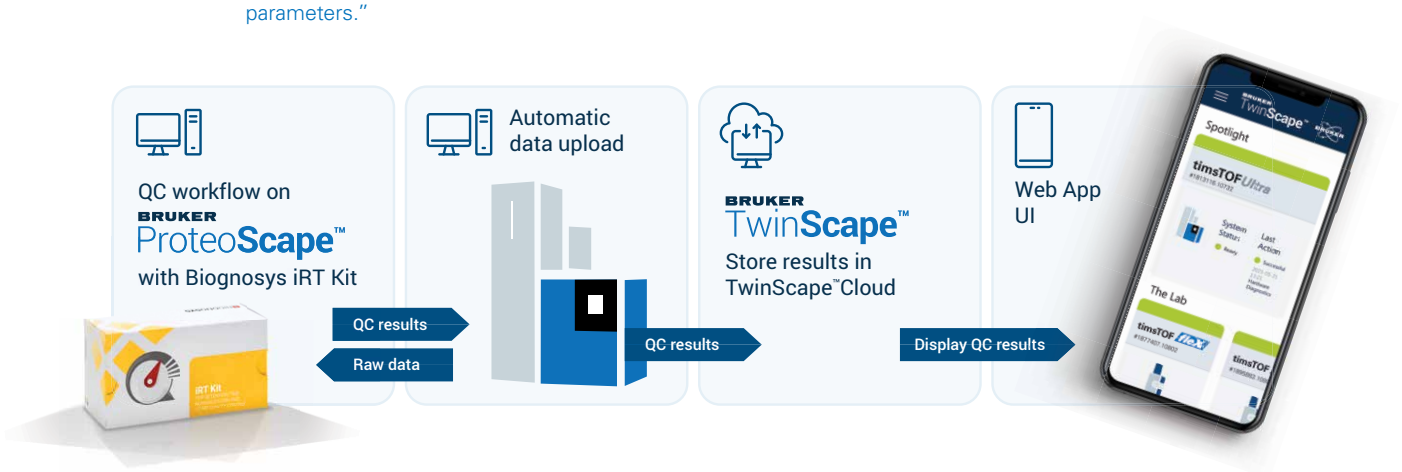
Uninterrupted 24/7 predictive monitoring safeguards your samples

Automate lab operations by harnessing the power of TwinScape. This innovative solution creates virtual replicas of your instruments and assays, enabling you to simulate and predict their behavior and safeguard the quality of your precious samples.

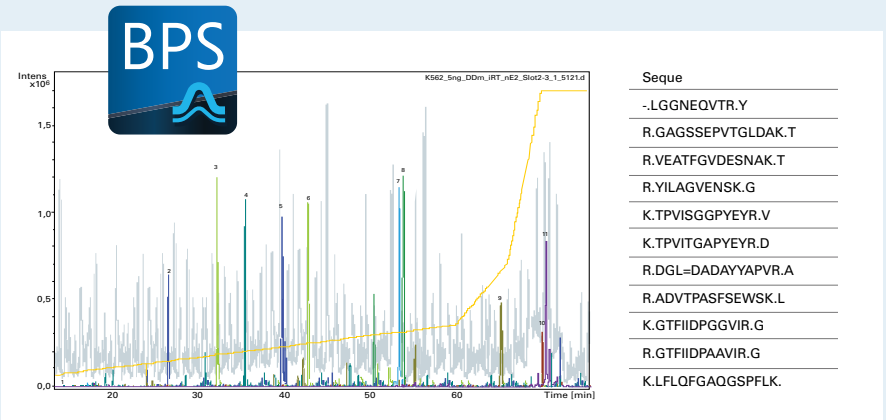
Dr. Eduardo Chicano-Gálvez

Head of IMIBIC Mass Spectrometry and Molecular Imaging Unit, Cordoba, Spain

"The system Quality Control (QC) module in Bruker ProteoScape in combination with the Biognosys iRT kit and TwinScape allows us to monitor both our liquid chromatography and mass spectrometry in real time, enabling us to ensure that our entire platform is running smoothly and precious clinical samples are not lost. Combined with the complete Bruker Ecosystem, from sample prep to data analysis, we are able to go from sample to results on large cohort clinical proteomics analysis projects in a short amount of time helping us to maintain our requirements in sensitivity, robustness, traceability and analytical quality parameters."



- Precursor intensity/area
- Precursor mass accuracy
- Retention time
- Peak shape metrics: FWHM
- MS/MS quality, similarity
- CCS (collisional cross section)



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R.DGL=DADAYYAPVR.A
R.ADVTPASFSEWSK.L
K.GTFIIDPGGVIR.G
R.GTFIIDPAAVIR.G
K.LFLQFGAQGSPFLK.

Benefits	Features
Unmatched sensitivity	Near 100% ion capture efficiency for ultra sensitivity in TIMS PASEF mode.
Enhanced specificity	MOMA identification and separation of co-eluting isobaric mass-to-charge ions in the mobility domain.
Maximum ion transfer	CaptiveSpray Ultra ionization optimizes ion transfer through vortex formation.
Increased confidence	Identify over 5500 protein groups from 125 pg K562 lysate in 22 mins via CCS-enabled TIMScore and TIMS DIA-NN 4D-Proteomics or Spectronaut 18 Software.

For Research Use Only. Not for use in clinical diagnostic procedures.

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