TIMS-MS

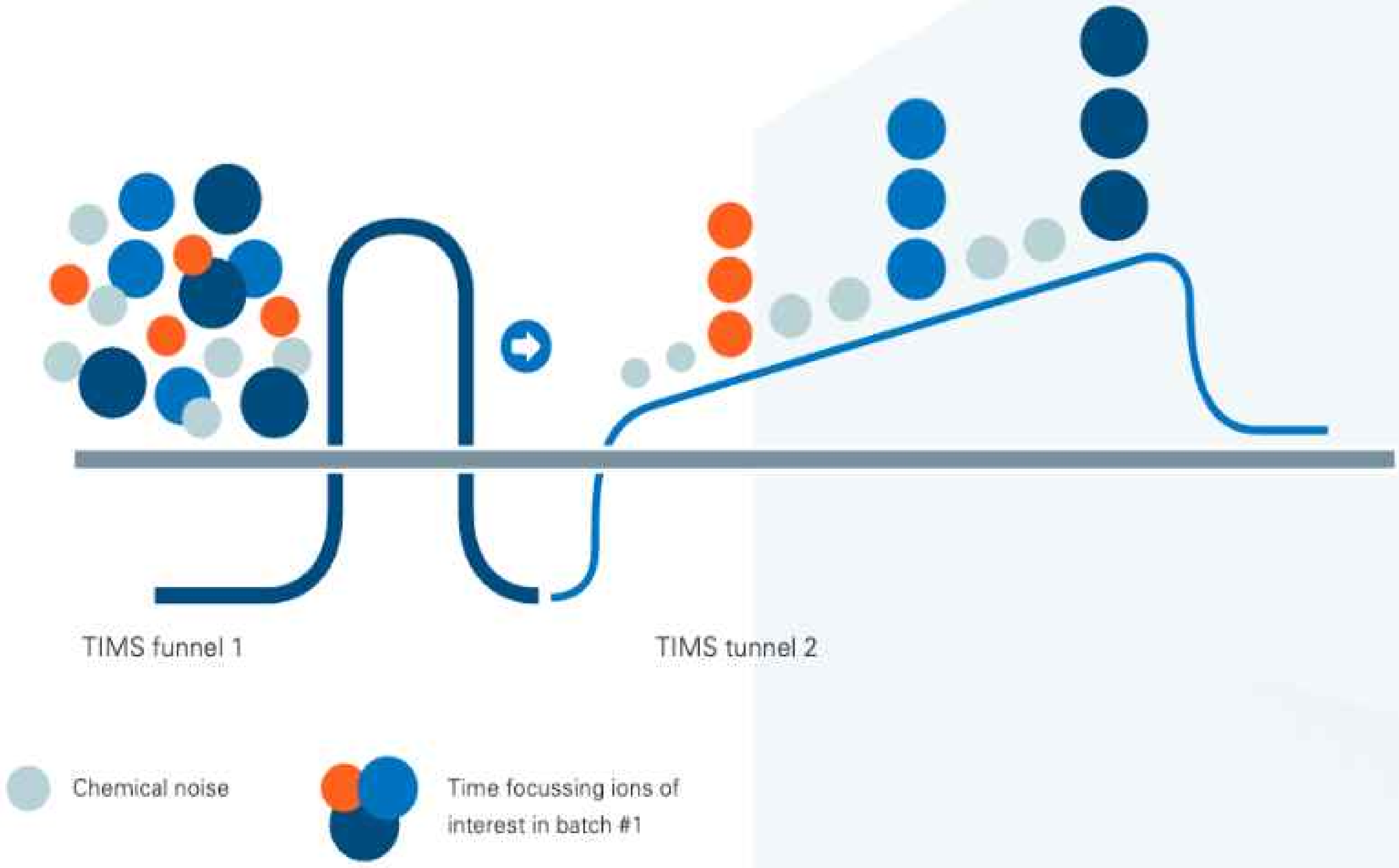
timsUltra AIP

Redefining sensitivity

Innovation with Integrity

A Legacy of Innovation: Trapped Ion Mobility Mass Spectrometry

Trapped Ion Mobility Spectrometry (TIMS) has been transforming the trajectory of life-changing research from the very moment it launched. By adding a new fourth dimension of separation power and analytical depth, the timsTOF empowers researchers to tackle previously challenging questions and achieve breakthroughs that improve human health. Join us as we continue to defy the odds with TIMS. **The possibilities are endless.**



Dual-TIMS and CCS-enabled analysis

Trapped ion mobility spectrometry (TIMS) resolves sample complexity through an added dimension of gas phase separation on top of LC-MS. TIMS accumulates and concentrates ions (time-focusing effect) of a given mass-to-charge and mobility (based on cross sectional attributes). This allows for higher fidelity separation of noise from signal, which enables an increase in sensitivity with speed (> 100 Hz TIMS duty cycle). The 4th generation dual TIMS-XRTIMS achieves a near 100% duty cycle by accumulating ions in TIMS funnel 1, while ions in TIMS tunnel 2 are released sequentially (> 150 Hz). This process of parallel accumulation serial fragmentation (PASEF®) enables high speed collisional cross section (CCS) analysis.

Did you know?

Stay on top of your research and upgrade your System.

- From **timsTOF Pro** → **timsTOF Pro 2** → **timsTOF HT**

Elevate your system to the most reliable and potent proteomics workhorse. **Or...**

- From **timsTOF SCP/timsTOF Ultra/timsTOF Ultra 2** → **timsUltra AIP**

Upgrade your 2021 system to today's highest sensitivity standards.

2023

timsTOF *Ultra*

2024

timsTOF *Ultra 2*

2025

tims*Ultra AIP*

Next generation ultra-sensitive instrument for cutting-edge research with uncompromised performance.

The timsUltra AIP:
Down to Subcellular Sensitivity Analysis

The timsUltra AIP (Athena Ion Processor) features a novel ion processor that delivers over 2x signal improvements, enhancing sensitivity and enabling deep-proteome analysis from even minimal sample input. The programmable AIP allows tailored transfer-mass ranges, focusing on information-rich areas for limited sample amounts, or broad ranges for top-down or glycoproteomics experiments, further reinforcing the system's versatility, powered by the combination of TIMS and ICC2.

Nikolai Slavov

Professor, Bioengineering, Director, Single-Cell Proteomics Center, Northeastern University
Founding Director, Parallel Squared Technology Institute

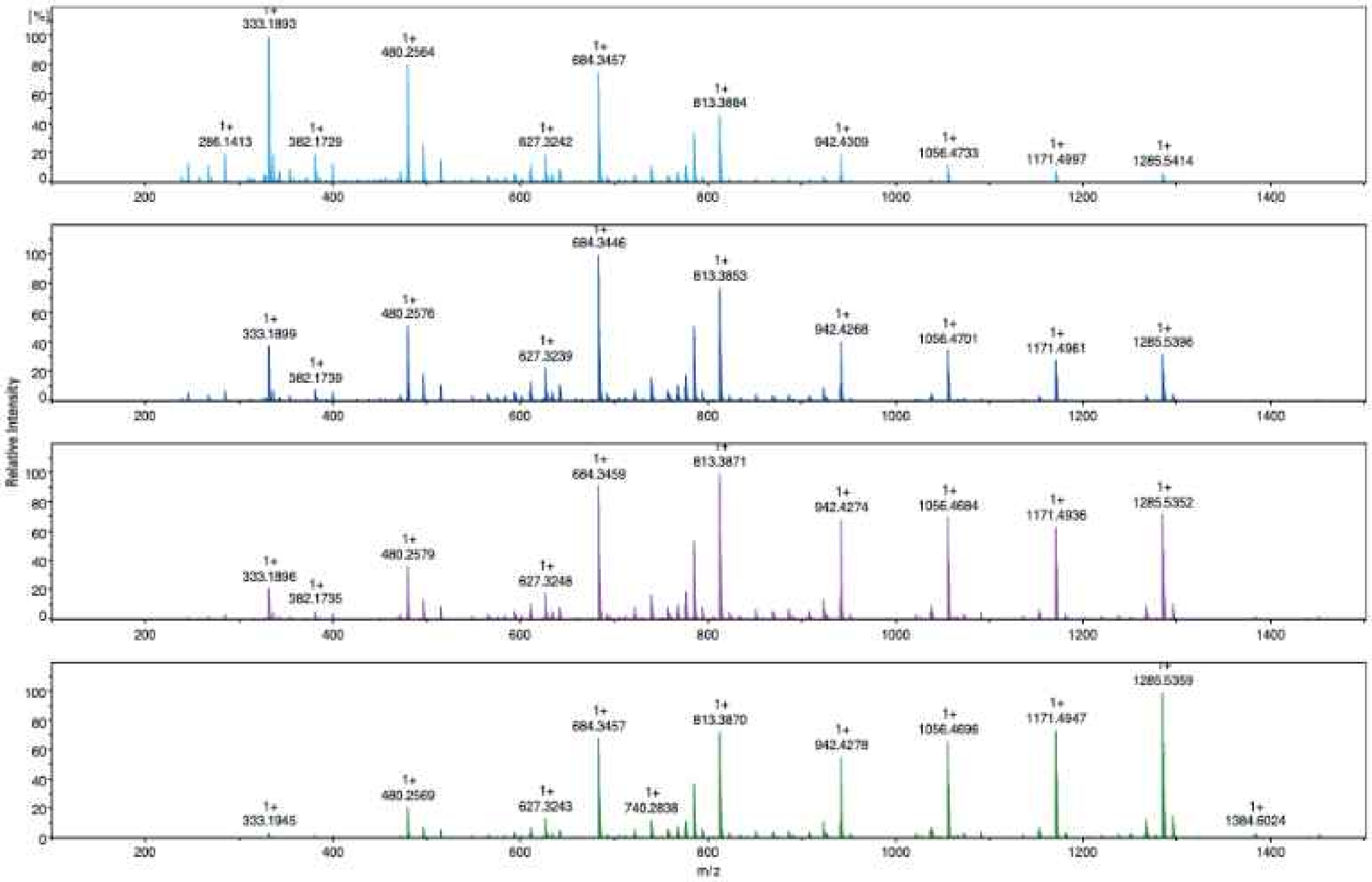
" The AIP upgrade delivers a 3-fold sensitivity gain for peptide fragment ions, which bolsters peptide sequence identification and enables proteomic analysis at a new level of sensitivity."

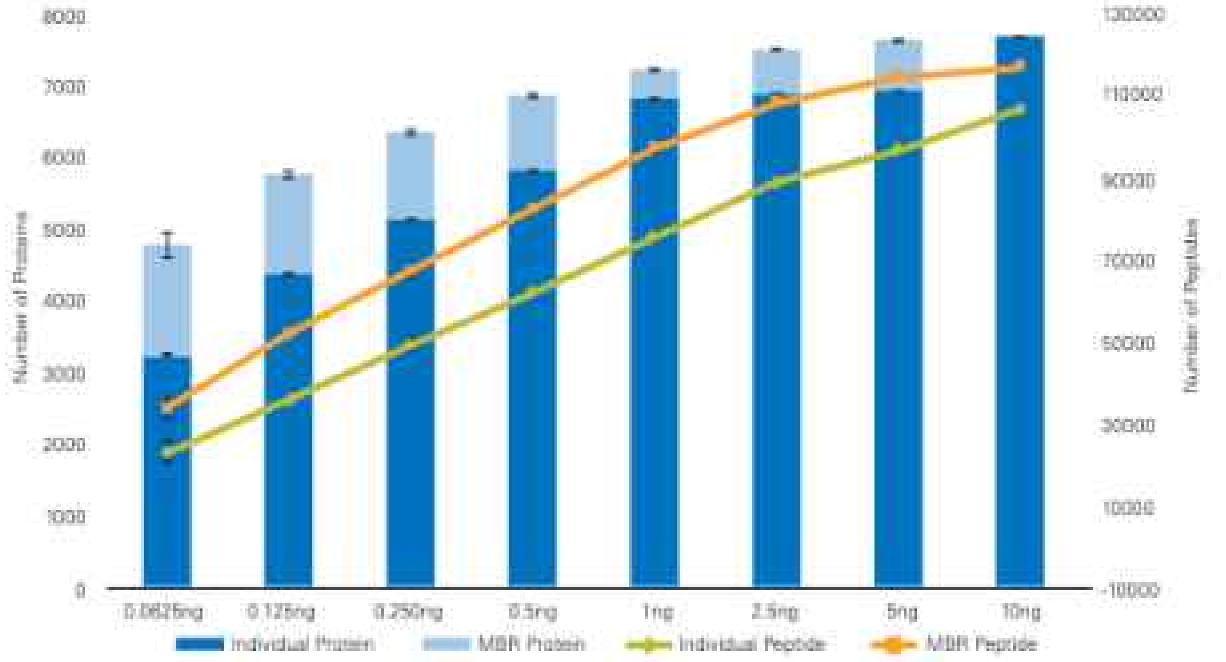
Instrument Feature/Capability

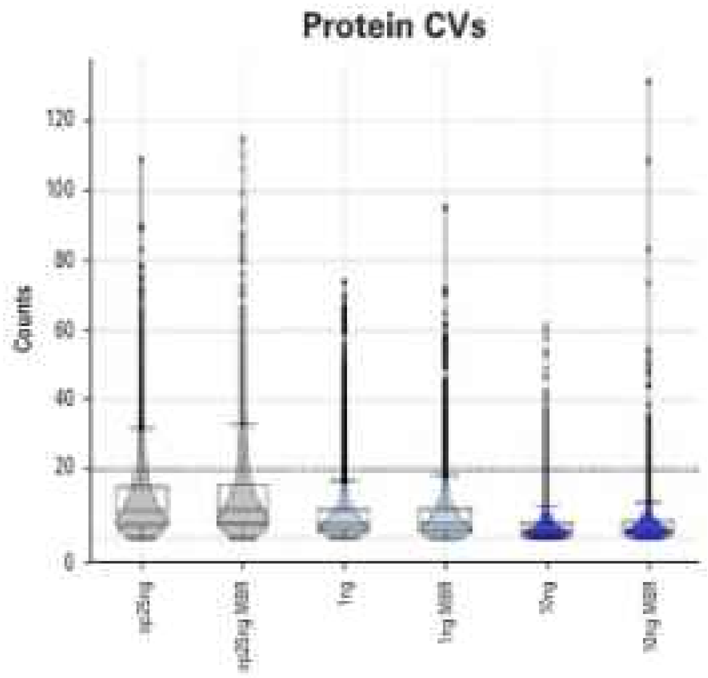
- **Controlled release of ions** from collision cell, optimizing spatial distribution of fragments
  - Significant fragment ion signal improvement
  - Flexible and tailored transfer-mass range for every application
- **CaptiveSpray Ionization Source (CSI)** with optimized gas flow for higher ion current and sensitivity
- **PASEF Melodies:** Full support of all PASEF modes including diagonal-PASEF® exclusive on the TIMS platform
- **ICC 2.0 (Ion charge control 2.0)** allowing for more leniency in sample loadings and a more user-friendly experience
- Latest **Spectronaut® 20 integrated** into Bruker ProteoScape™ (BPS)
- **Upgradeable** from the timsTOF SCP, timsTOF Ultra, and timsTOF Ultra 2
- **PASEF** – for ultra-speed at 300 Hz

Depth, Sensitivity And Flexibility Without Limits: Discover More from Precious Samples

With advancements in timsTOF technology, the new AIP continuous to enhance sensitivity and allows ultimate flexibility with adjustable fragment ion transfer. From bulk proteomics applications with highest robustness, depth, and scale to restricted sample amounts like smallest individual immune cells, subcellular compartments, or immunopeptides from fine needle biopsies, timsUltra AIP offers limitless research opportunities.







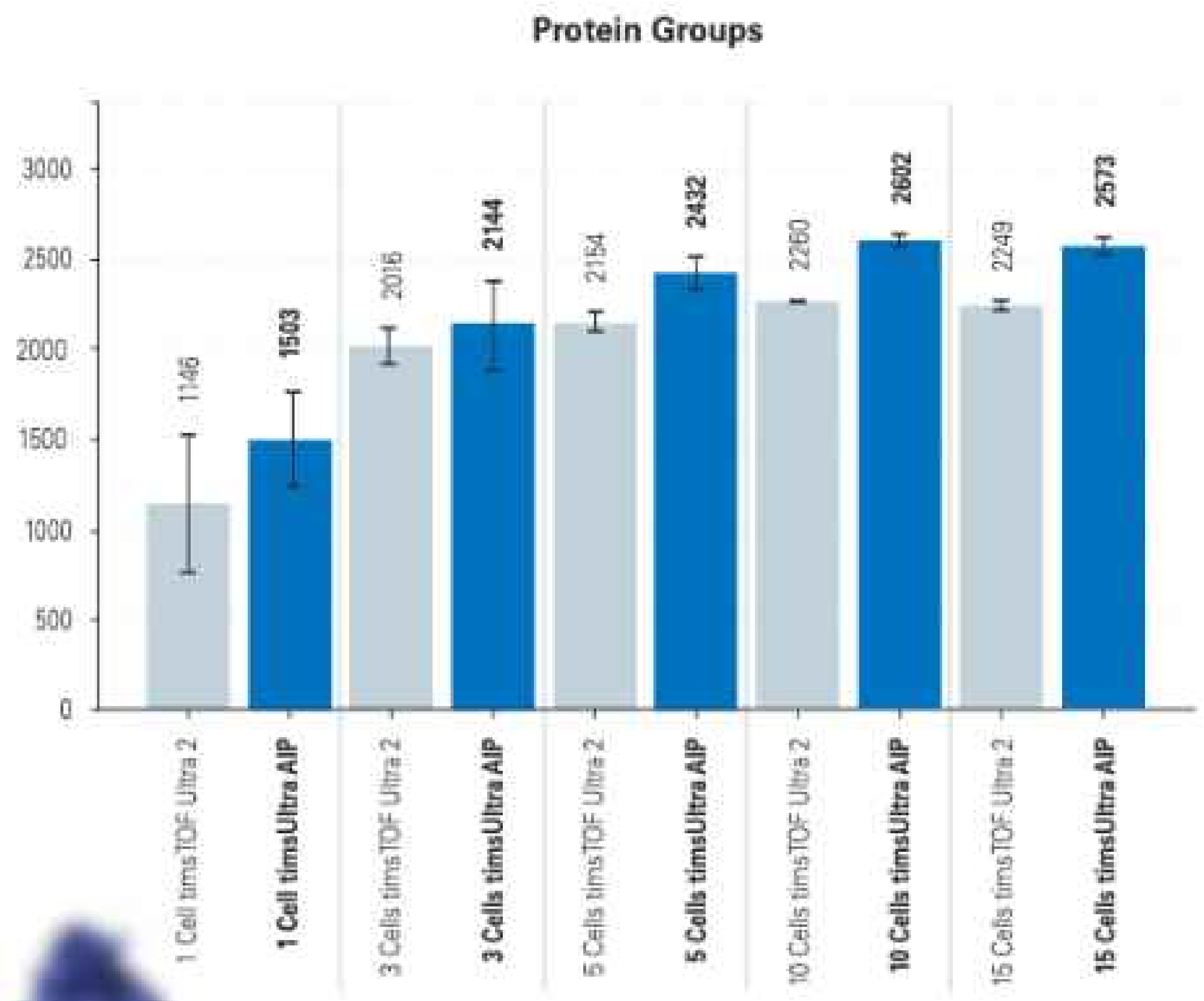
Study Cellular Heterogeneity Without Limits: New Insights from most Challenging Single Cell Samples

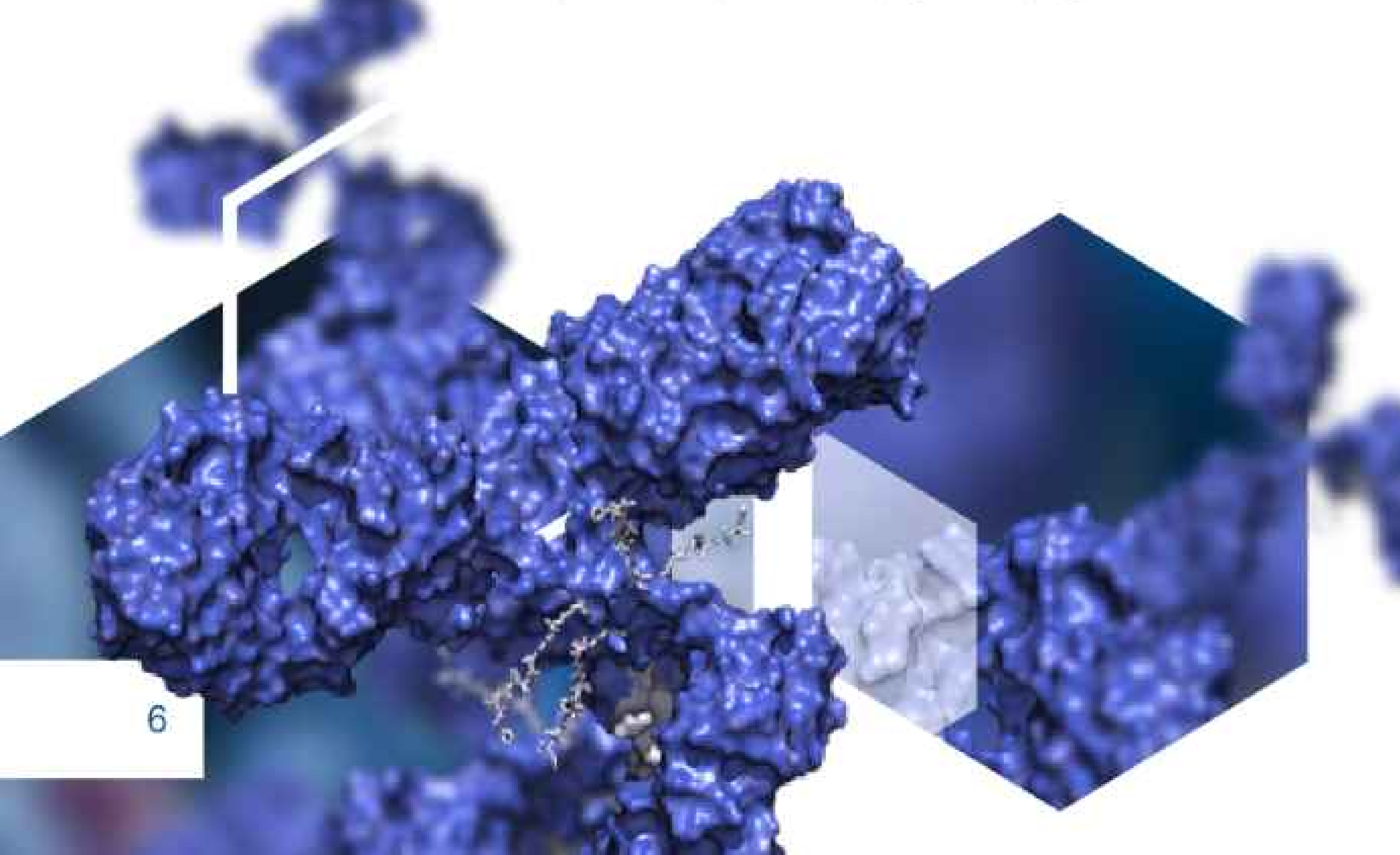
The timsUltra AIP builds on the legacy of the timsTOF platform, offering all the advantages of 4D-Proteomics - uncompromised speed, selectivity, sensitivity, and robustness - this platform is ideal for researchers needing to analyze even the most challenging samples like single cardiomyocytes. Its robustness ensures true high throughput, making it perfect for cutting edge research environments.

Jennifer Van Eyk

Director of Basic Science Research in the Barbra Streisand Women's Heart Center & Professor at Cedars-Sinai, Cardiology

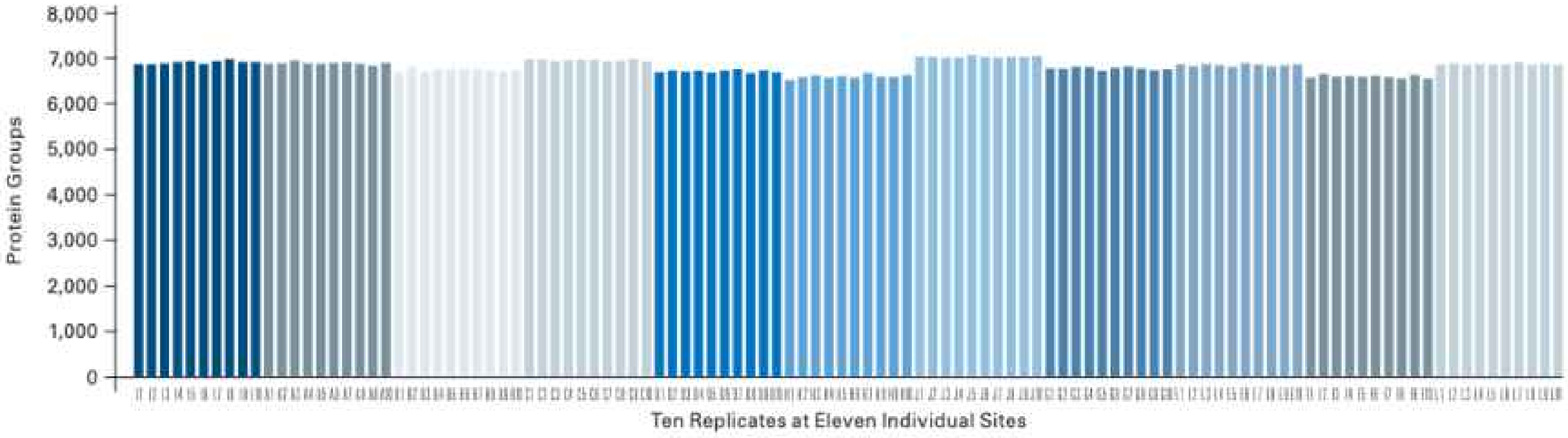
"With the new timsUltra AIP, we are able to gain much deeper proteomics insights into particularly challenging to study single cardiomyocytes. The sensitivity, throughput, and robustness of timsTOF enables us to gain novel insights into cardiovascular diseases."

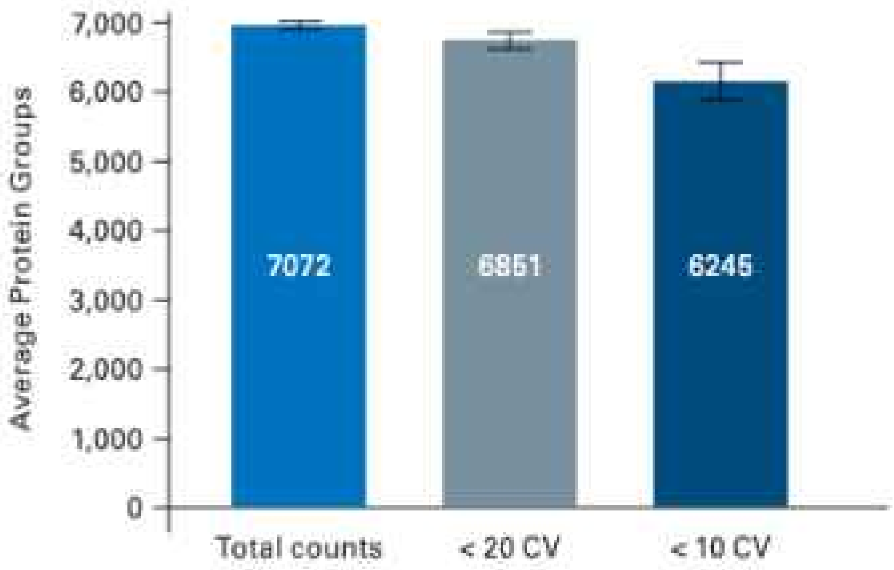

Protein Groups

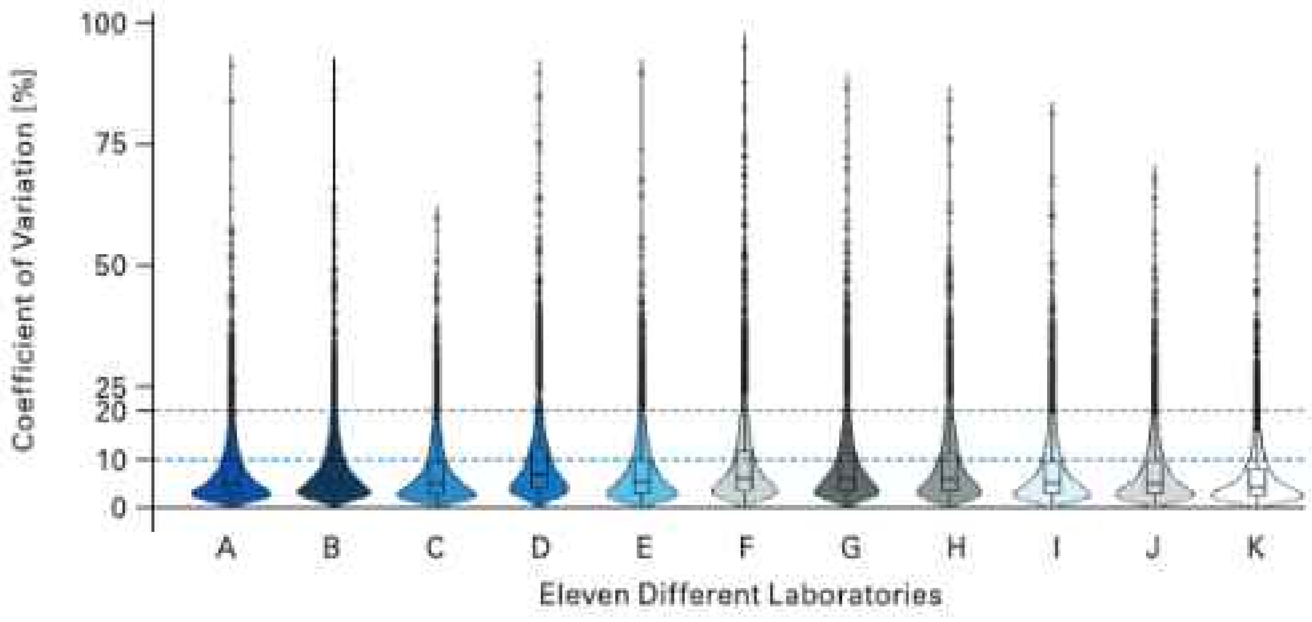


Engineered for Maximum Robustness and Performance, Your Daily Companion for all Omics Applications

The timsTOF platform stands out for its exceptional reliability and minimal maintenance needs, making it ideally suited for seamless integration into everyday laboratory workflows with maximum uptime and fast turnarounds. More than >7000 protein groups can be identified on average in only 5-minute gradient time with ease and across sites. Achieve top edge reproducibility over time without manual interference.







Read the Application Note to Learn More:

Discover the Potential of Immunopeptidomics with TIMS and PASEF

Trapped ion mobility separation (TIMS)-based mass spectrometry is a game-changer in research. It swiftly identifies neo antigens, allowing the development of personalized therapies tailored to each patient's immune profile. This accelerated discovery process, even with minimal samples, speeds up research and enhances our understanding of cancer progression and our immune system. Ultimately, it offers hope and tangible progress in the fight against cancer, translating into real-world impact.

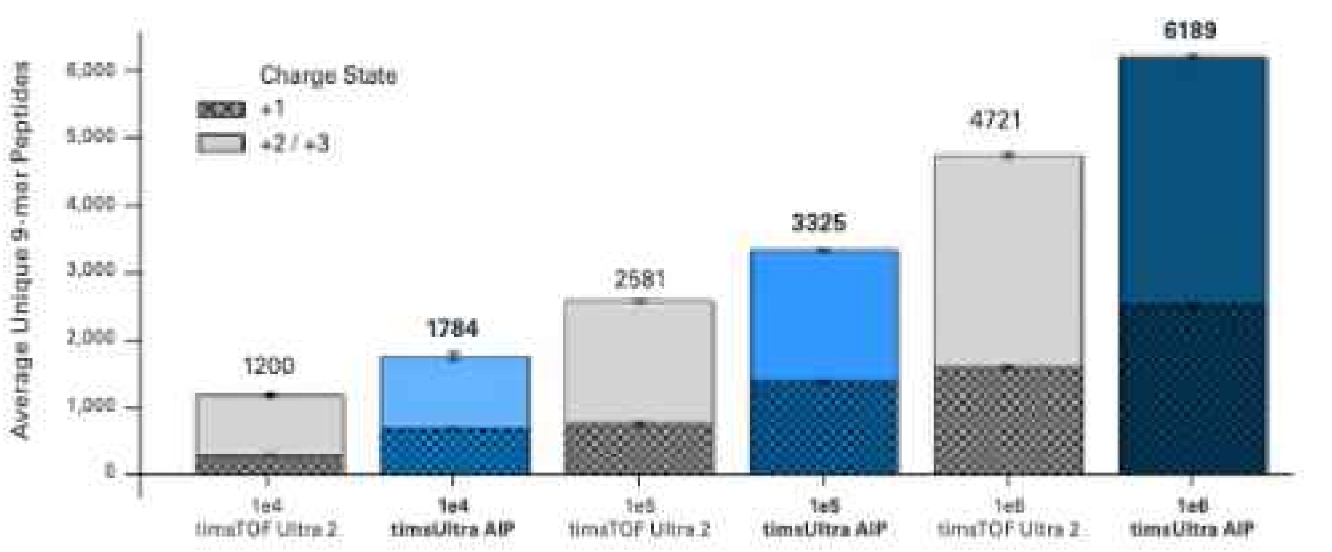
- **Minimizing off-target effects** and maximizing immunotherapy treatment efficacy.
- **Deeper insight** into mechanisms underlying cancer progression.
- **Personalized treatment strategies** based on individual patient's immune profile.
- **Identify and characterize** potential therapeutic targets swift and robust across many samples.

» Robert R. Salzler

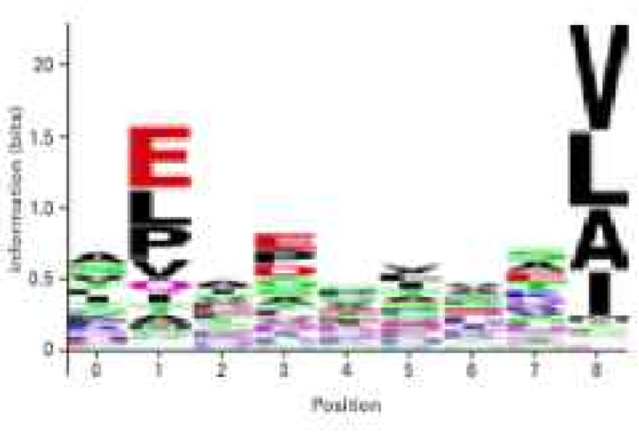
Senior Principal Scientist, Regeneron

> "TIMS-based mass spectrometry has revolutionized our research by swiftly identifying neo antigens from smallest sample amounts. The ability to capture singly charged immunopeptides using TIMS polygon filtering is particularly impressive. It offers hope in the fight against cancer by enabling personalized treatment strategies and robust identification of therapeutic targets."

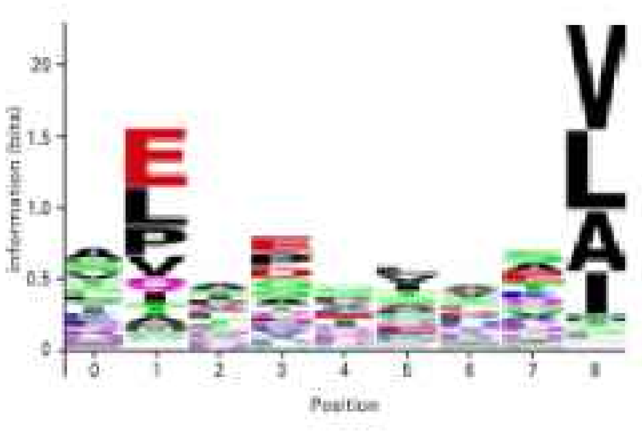
Unique 9-mer identifications from indicated starting material with timsTOF Ultra 2 or timsUltra AIP Collision Cell



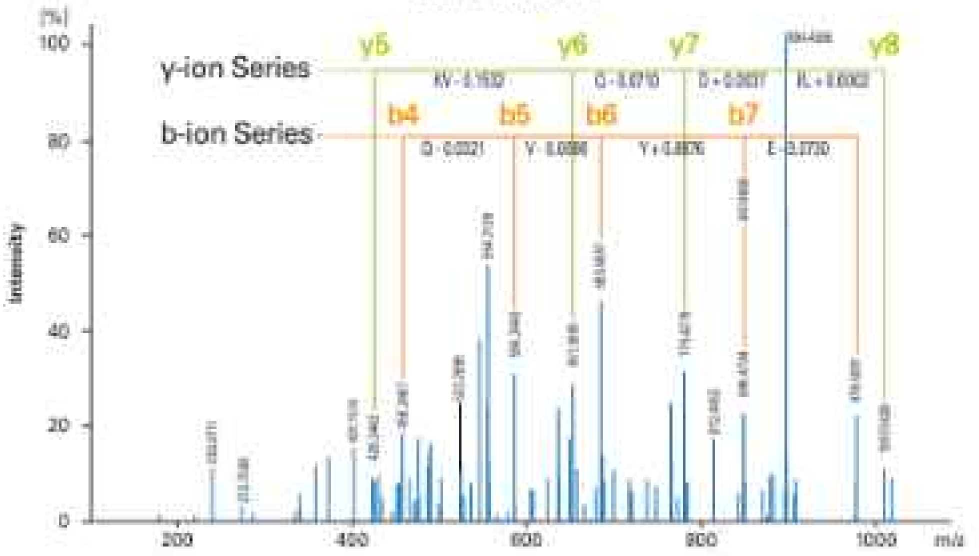
timsTOF Ultra 2



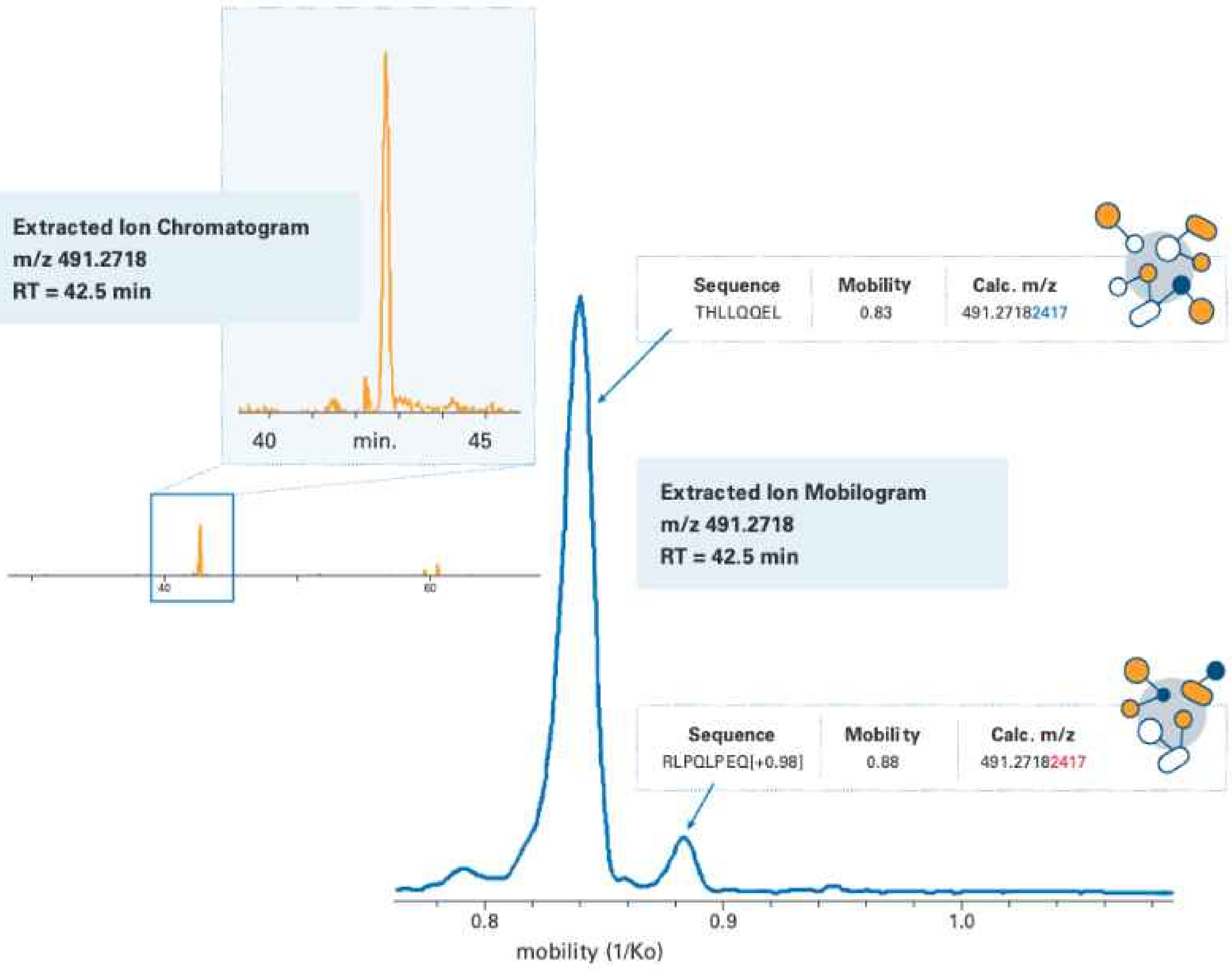
timsUltra AIP



timsUltra AIP



Shed Light onto Co-eluting Shadows with MOMA



The Bruker Solution for Immunopeptidomics

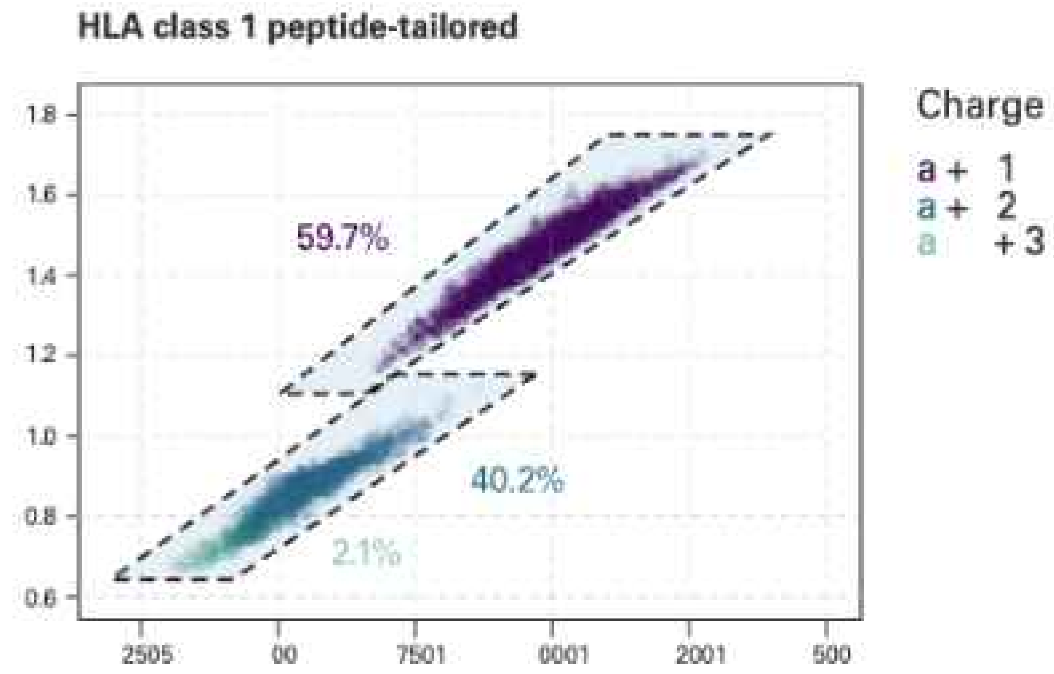
Bruker offers a comprehensive solution for immunopeptidomics research, combining the high-performance of timsTOF mass spectrometry with powerful bioinformatic tools.

- **Exclusive sensitivity:** timsTOF's unique separation power reveals hidden low-abundance peptides, allowing researchers to identify neoantigens from even the smallest samples. This addresses the need for less tissue, more data.
- **Sharper focus:** Accurate targeting of MHC peptide properties makes sure no ions are missed, ensuring comprehensive identification of potential therapeutic targets.
- **No more isobaric shadows:** TIMS combined with advanced data analysis unveils hidden gems, separating true hits from imposter ions that might otherwise be missed.
- **Precision single charge targeting:** Unique polygon filtering only includes singly charged peptide masses of interest, not unwanted noise, resulting in cleaner data and more confident identification of neoantigens.
- **Bioinformatics powerhouse:** Bruker ProteoScape with its integrated BPS Novor module unleashes the power of advanced de novo sequencing, rapidly deciphering unknown peptides (~2 minutes for 1-hour acquisition, >1000 spectra/second). Newly trained in MHC data for improved identification of neoantigens.

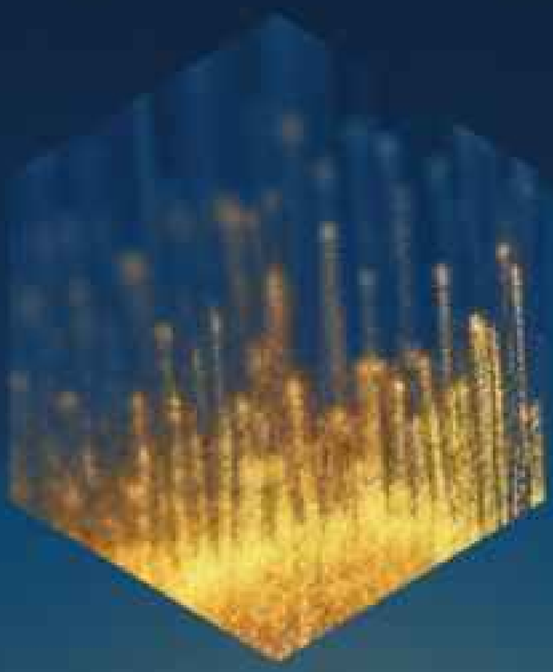
Learn More about Immunopeptidomics:

The Power of TIMS and PASEF

- **Unparalleled neoantigen accuracy:** MOMA technology uses ion mobility to resolve complex mixtures, minimizing chimeric spectra, and separating isobaric peptides. This ensures precise neoantigen identification and quantification for reliable immunopeptidomics data.
- **CCS molecular fingerprints – decoding peptide structure:** timsTOF technology provides CCS measurements for each peptide, acting as unique molecular fingerprints that reveal peptide size and shape. Analyzing CCS data offers valuable insights into peptide conformation, aiding in confident identification and characterization."
- **BPS Novor 2.0: Streamlined neoantigen discovery software** empowers you to discover cancer neoantigens without needing next-generation sequencing. This powerful tool streamlines your workflow and accelerates neoantigen identification, paving the way for personalized cancer therapies.



Immunopeptidomics polygon filtering: Exemplary heatmaps of ions of specific charge state distribution and masses are targeted.[1]



Anthony W. Purcell

Professor and Head of Immunoproteomics Laboratory, Monash University

"Machine learning based de novo cataloging of the neoantigen landscape fuels cancer immunotherapy research."

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[1] *Gomez-Zepeda, D., Arnold-Schild, D., Beyrle, J. et al. Thunder-DDA-PASEF enables high-coverage immunopeptidomics and is boosted by MS2Rescore with MS2PIP timsTOF fragmentation prediction model. Nat Commun 15, 2288 (2024). https://doi.org/10.1038/s41467-024-46380-y*

Did you know?

timsTOF technology offers a unique set of features that empower your research in immunopeptidomics:

- **Defining your Search Space:** The timsTOF platform utilizes a unique **TIMS polygon filter**. This filter allows you to define a specific region of interest within the mass-to-mobility space (m/z vs CCS). This targeted approach, in combination with PASEF acquisition modes like **glyco-PASEF** and **diagonal acquisition**, significantly enhances sensitivity for specific classes of peptides, such as glycopeptides, further streamlining your analysis.

Juliane Walz

Professor at the Department of Peptide-based Immunotherapy,
University and University Hospital Tübingen, Germany

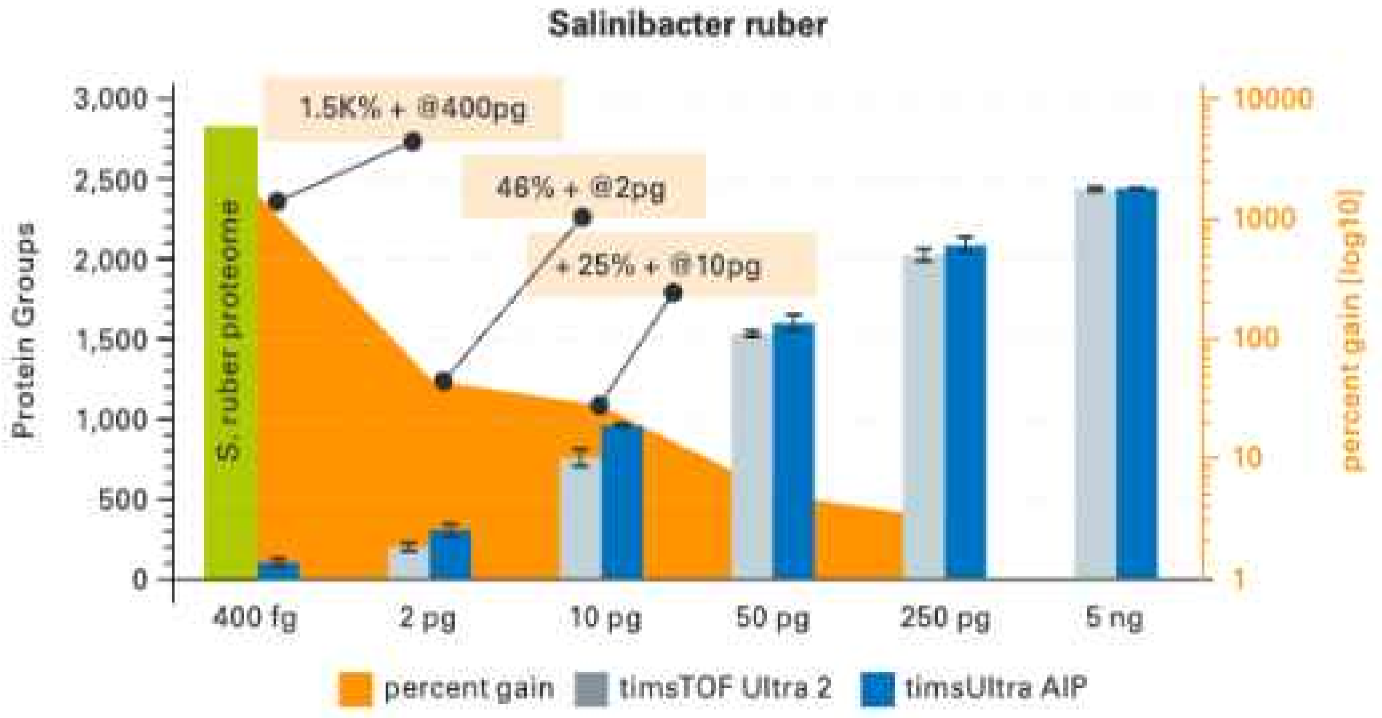
"Using timsTOF, we created a large-scale benign reference data set, which enabled the refinement of previsouly described tumor antigens, as well as the de novo identification of broadly off the shelf antigens and mutation-derived neoepitopes as targets for future peptide-based cancer immunotherapy development."

Hoenisch Gravel, N., Nelde, A., Bauer, J. et al. TOFIMS mass spectrometry-based immunopeptidomics refines tumor antigen identification. Nat Commun 14, 7472 (2023). https://doi.org/10.1038/s41467-023-42692-7

Revealing the Microbiome-Host Conversation with uMetaP

The human body hosts trillions of microbes within intricate ecosystems known as microbiomes. Understanding not just which microbes are present, but how they function, is essential for advancing health and preventing disease. Metaproteomics — the large-scale study of proteins from microbial communities — has emerged as a transformative tool, revealing the functional interactions between the microbiome and the host.

To further this effort, a new **Center of Excellence for Metaproteomics** has been launched at the **University of Vienna** in partnership with **Bruker**, combining leading research with advanced technology to pioneer next-generation microbiome analysis.



by Feng Xian PhD and David Gomez-Varela PhD

Dr. David Gómez-Varela's team is pioneering metaproteomic methods that are advancing microbiome science:

- **5,000x Sensitivity Boost**
  Detects one bacterium in a million using DIA-PASEF on timsTOF Ultra.
- **NovoMP for De Novo Discovery**
  Novel FDR validated workflow improves taxonomic coverage by 200%.
- **Function Beyond Genes**
  Quantifies low-abundance microbial proteins.
- **Looking Ahead with timsUltra AIP**
  Our new AIP-equipped instrument delivers enhanced spectra quality — set to further boost de novo performance.

David Gómez-Varela

Director of the Center of Excellence for Metaproteomics, Division of Pharmacology and Toxicology, University of Vienna

"We live in a microbial world, where trillions of microorganisms shape the health of every ecosystem. Yet the protein-level signatures that reflect bacterial activity remain largely elusive due to sensitivity limitations. With the new AIP system, we can now detect bacterial peptides in the sub-picogram range, reflecting the level of a single bacterium's proteome — a major leap in sensitivity. This enables to explore microbial life in unprecedented detail, unlocking new possibilities for understanding functional diversity of microorganisms."

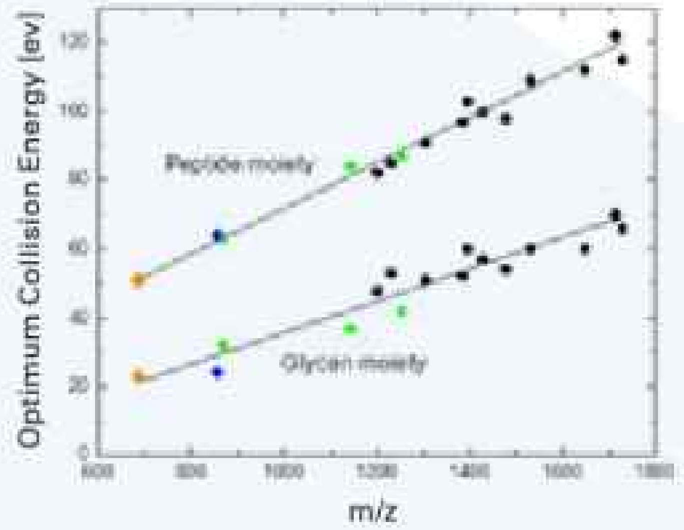
Ultra-sensitivity metaproteomics redefines the gut "dark metaproteome", uncovering host-microbiome interactions and drug targets in intestinal inflammatory diseases | bioRxiv

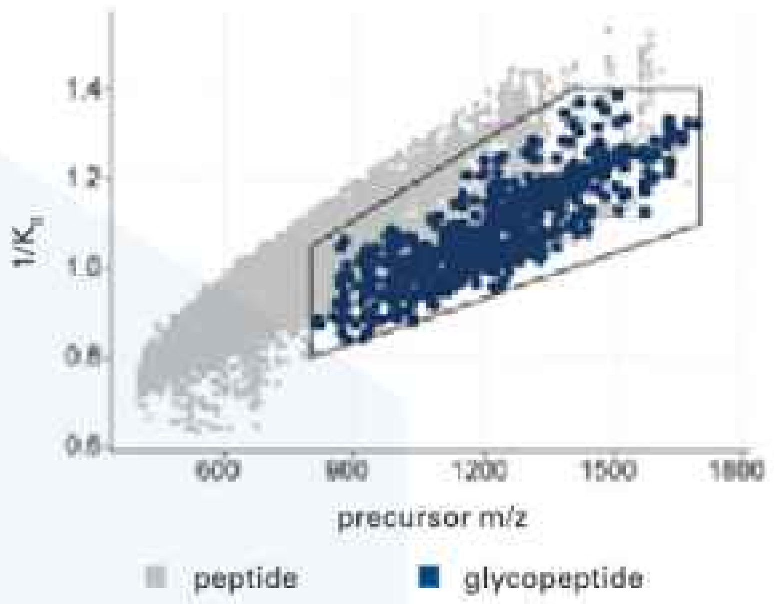
glyco-PASEF:
Explore Glycosylation with Confidence

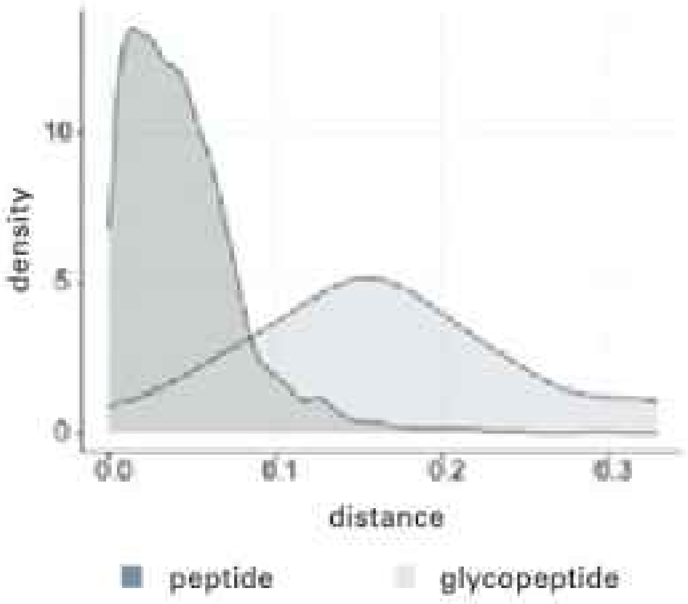
Glycosylation is one of the most intricate type of PTMs that plays a critical role in many biological processes. Glyco-PASEF, a fragmentation technique specifically designed for glycopeptides, offers unparalleled sensitivity and resolution for in-depth analysis of these intricate sugar structures. By combining advanced separation techniques and fragmentation strategies, glyco-PASEF facilitates the comprehensive characterization of glycans, providing researchers with in-depth information about glycosylation patterns and their functional significance.

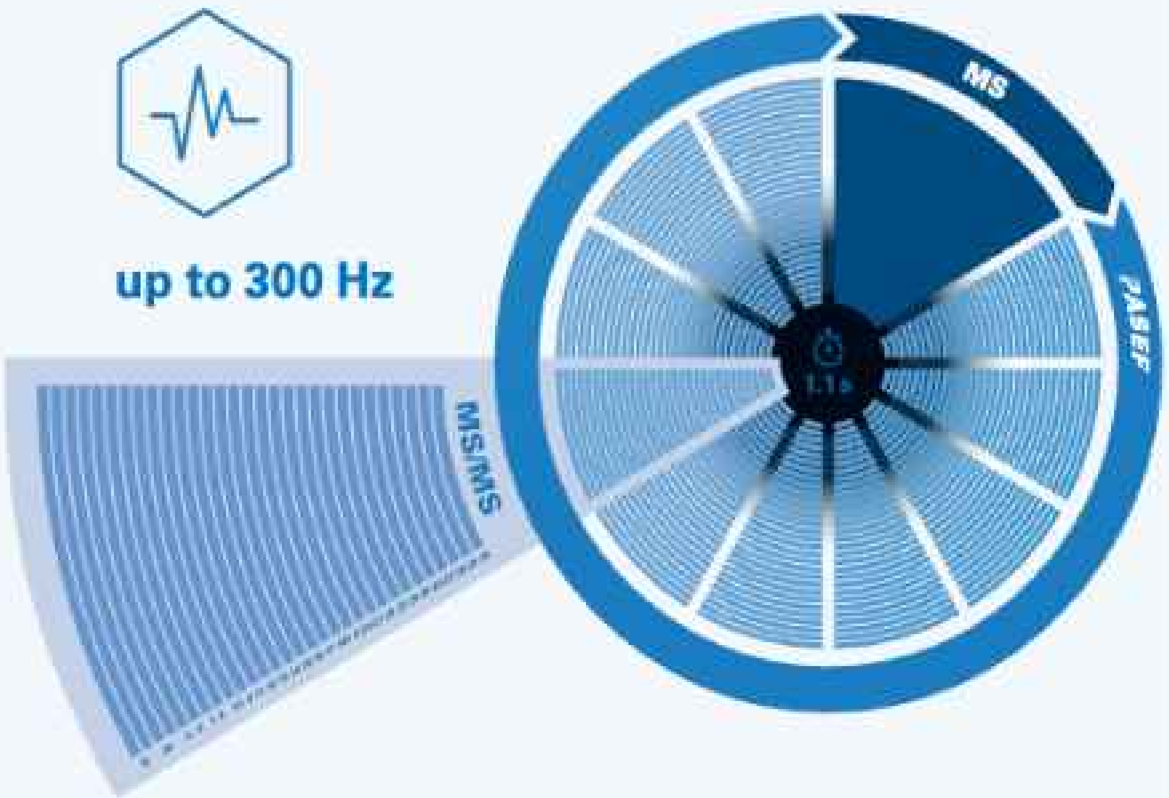
BRUKER
GlycoScape™

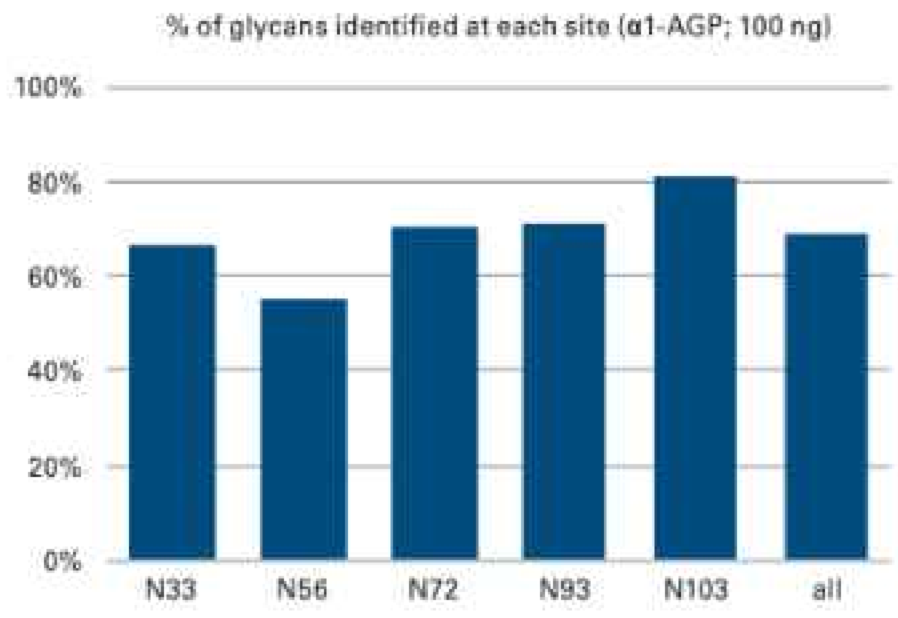
- **glyco-PASEF:** stepped energy-CID and oxonium ion gating for superior results
- **Combine the speed** of PASEF and the specificity of ion-mobility-clustering for glycoproteome analysis
- **Run & Done with GlycoScape™:** a platform for real-time 4D-Glycoproteomics results











Tin Long Wong, Brian P. Mooney, Gustavo J. Cavallero, Minhui Guan, Lei Li, Joseph Zaia, and Xiu-Feng Wan
Journal of Proteome Research 2023 22 (1), 62-77 DOI: 10.1021/acs.jproteome.2c00469

» Albert Heck

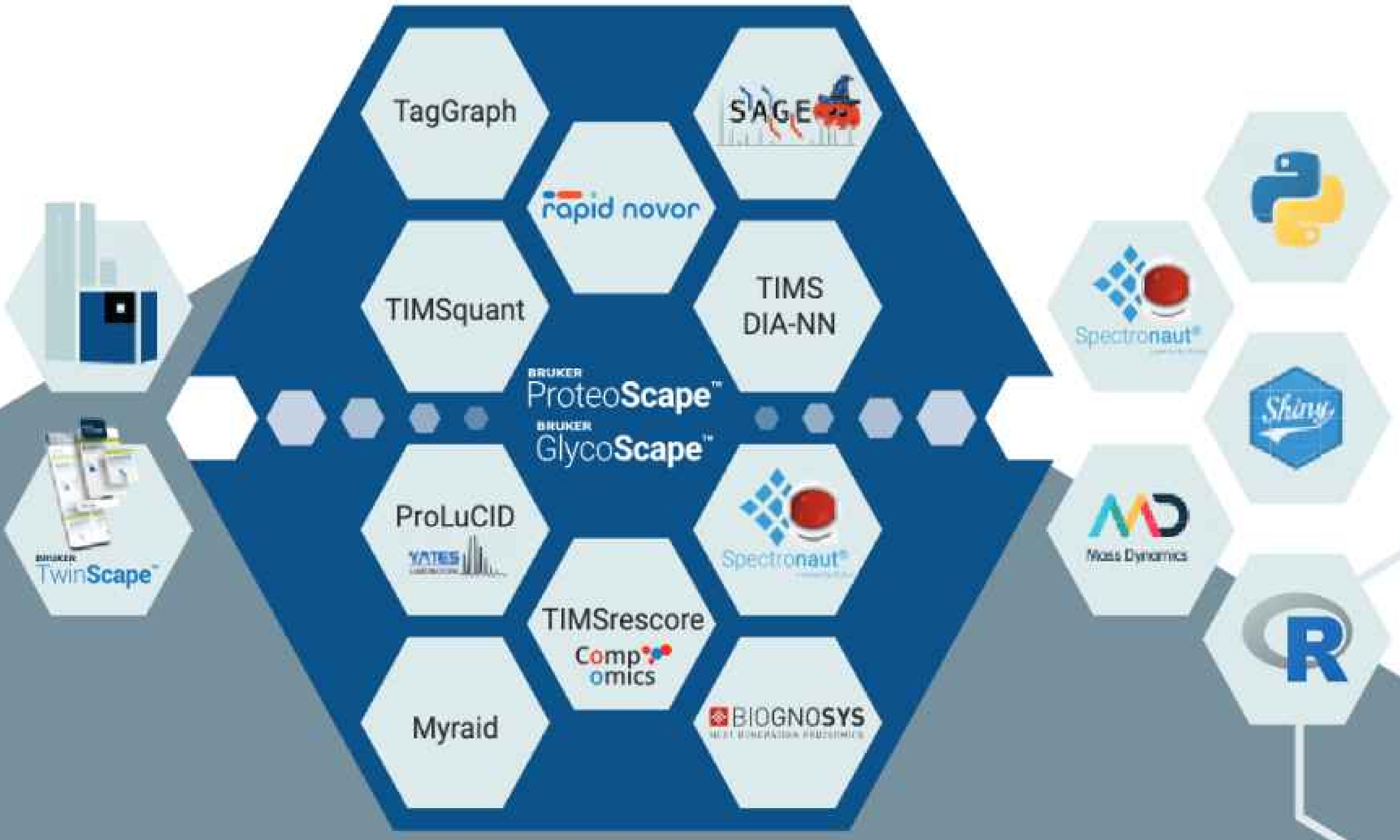
Professor of Chemistry and Pharmaceutical Sciences, Utrecht University and Scientific Director of the Netherlands Proteomics Center

"Leveraging the unique strengths of the timsTOF for glycoproteomics, glyco-PASEF® accelerates glycobiology research."

Learn More about 4D-Glycoproteomics:

Bruker ProteoScape – Seamless Processing of your Data to Access Insights

- **Run & Done** – real-time GPU powered database search or de novo sequenceing results for dda-PASEF acquisition.
- **Analysis automation** – Integrated acquisition and analysis workflow, so you can start an acquisition, walk away and come back to results ready for evaluation.
- **ProteoScape acquistion control (PAC)** – Define minimum or maximum thresholds for data quality and automatically stop acquisition if these thresholds are not met. Worry-less about your precious samples.
- **Integrated software packages** include the latest version of Spectronaut and TwinScape and more.



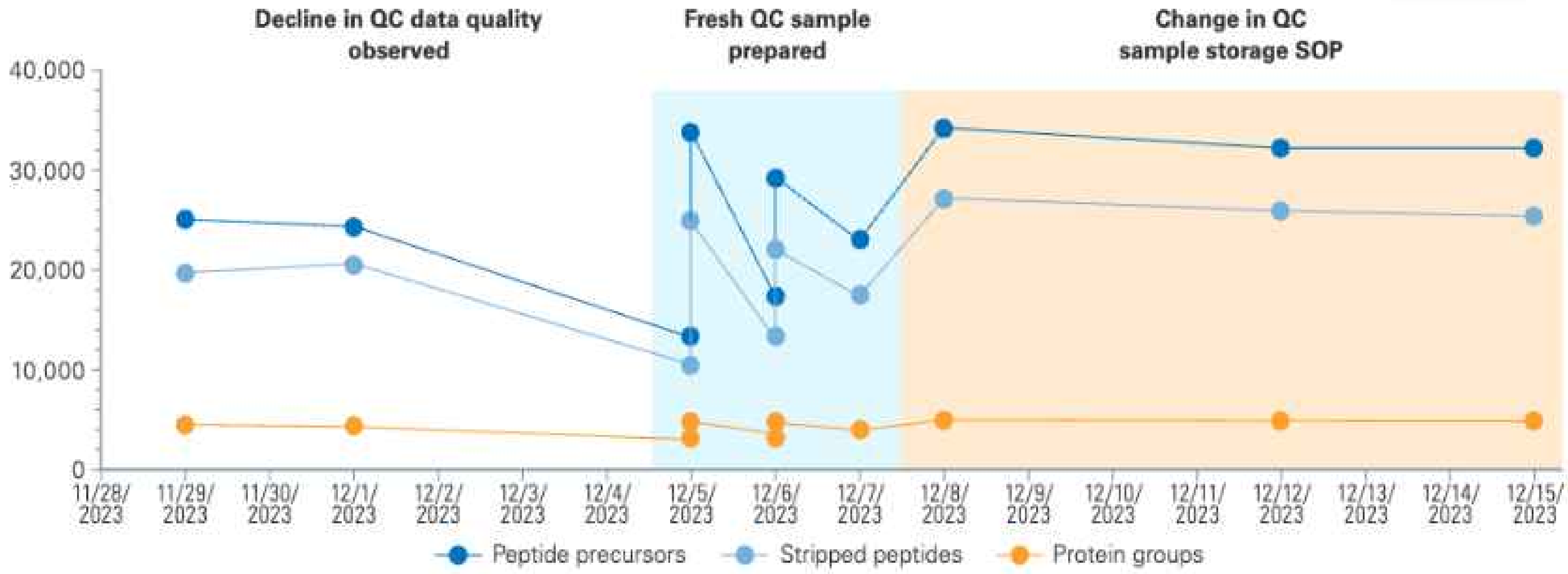
timsTOF-optimized algorithms –
BPS integrates CCS-enabled algorithms for timsTOF data through collaboration with partners:

- **BPS Novor** Machine learning-based de novo sequencing engine trained on millions of spectra for efficient peptide sequencing.
- **TagGraph:** Extends BPS Novor results to enable routine discovery of amino acid modifications, sequence alterations, and proteolytic processing.
- **Spectronaut:** DIA analysis platform integrated with BPS for directDIA+ workflows, enhancing timsTOF prediction models for up to 40% improved sensitivity and accuracy, supporting 20+ PTMs.
- **TIMSrescore:** Optimized MS2Rescore version with machine learning models for improved prediction of peak intensities, retention times, and ion mobility. Developed in collaboration with University of Ghent's Compomics Team.
- **Myriad:** Real-time glycopeptide identification for glyco-PASEF acquisitions, enabling novel glycan discovery. A collaborative tool with Dr. Wessels' group at RadboudUMC.

TwinScape – Shaping Quality, Virtually

TwinScape™ is a digital twin-driven solution designed to elevate quality management in modern proteomics laboratories. It bridges physical systems with virtual models to help monitor performance, spot deviations, and ensure measurement platforms meet the highest research standards — empowering teams to trust their data and accelerate discovery.

Advanced Quality Management with TwinScape



Complete workflow with Bruker ProteoScape and iRT standards from Biognosys

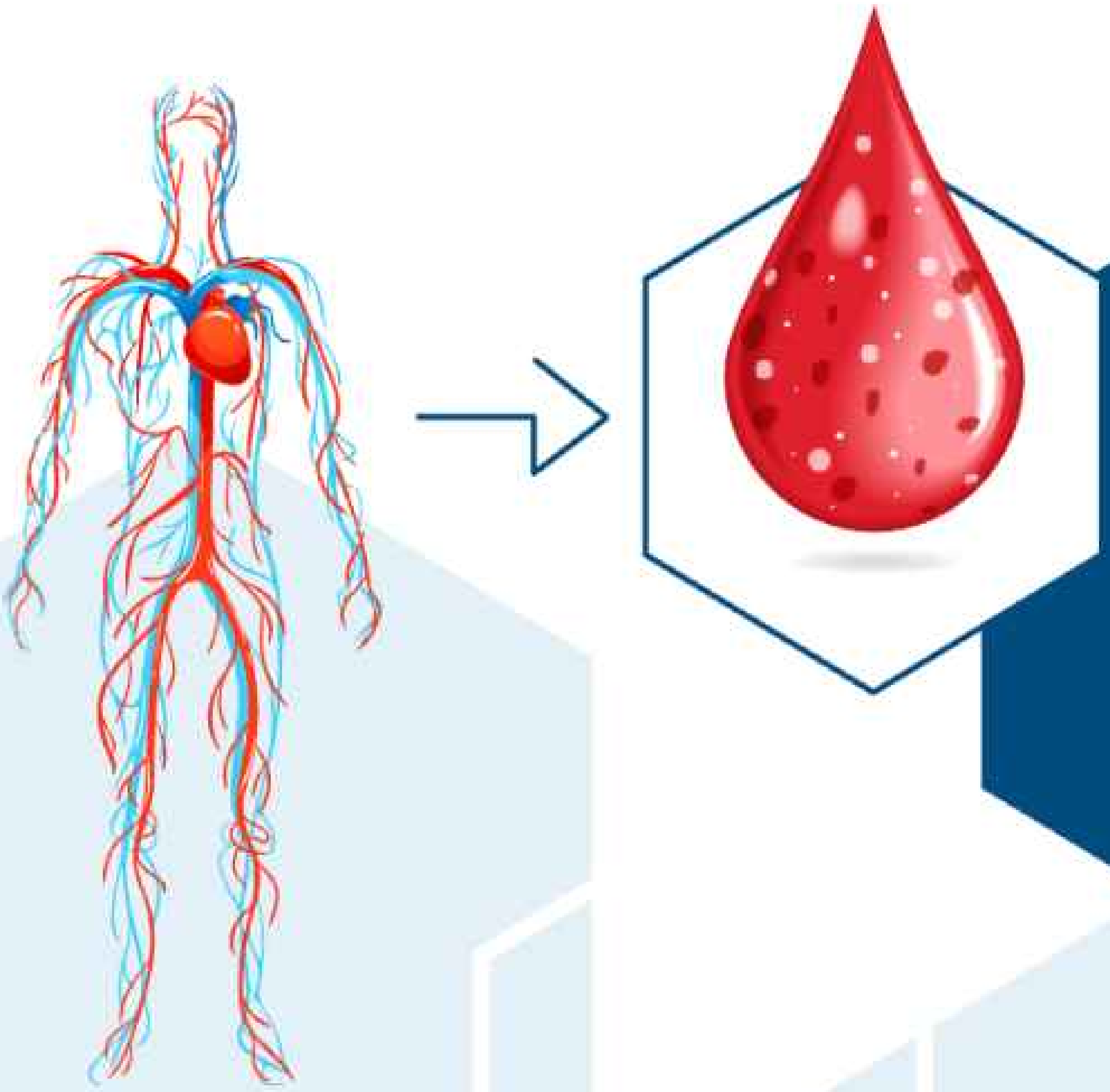
Julian Langer

Head of the shared Mass Spectrometry Lab, Max Planck Institutes of Biophysics and Brain Research, Frankfurt, Germany

"TwinScape™ has been a great addition to our standard HeLa/iRT-based quality control pipeline and has quickly become part of our routine QC checks. The level of insight and constant monitoring that TwinScape™ provides has dramatically improved our workflow efficiency and not only allowed us to address potential problems before they escalate but also enabled proactive technical customer support."

Bruker Ecosystem: Next-Gen Liquid Biopsies and Plasma Analysis

Blood plasma and other high dynamic range samples offer a rich but historically hard to access source of diagnostic and prognostic biomarkers. The Bruker ecosystem offers the unique and required combination of depths of coverage, robustness, throughput, and reproducibility to access proteomics information from small to large cohorts at a price point that allows you to scale. From platelet rich to clean plasma, in humans and model systems, don't miss bioinsights and benefit from up to 10x improved coverage.



Tissue leakage proteins:

- **Extracellular vesicles**
- **Secreted proteins**
- **Immune complexes**

Dr. Stefanie Hauck

Head of Core Facility Metabolomics and Proteomics, Helmholtz Munich, Germany

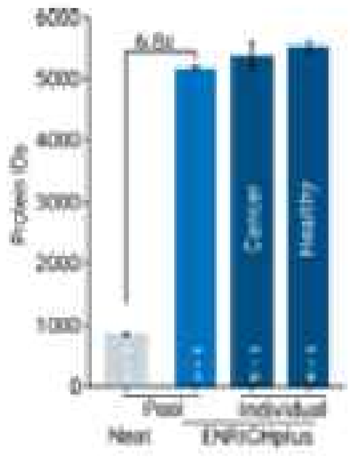
> "In our Core, we always aim to stay ahead of advancements, which is why gaining access to ENRICH technology has been a game-changer. With ENRICH-iST, we doubled our plasma protein identification capabilities. Then came ENRICHplus, which took things even further. On average, we now identify around 3,600 plasma protein groups in single shot experiments, a 5.3-fold increase compared to our standard workflow using iST-BCT for neat plasma."

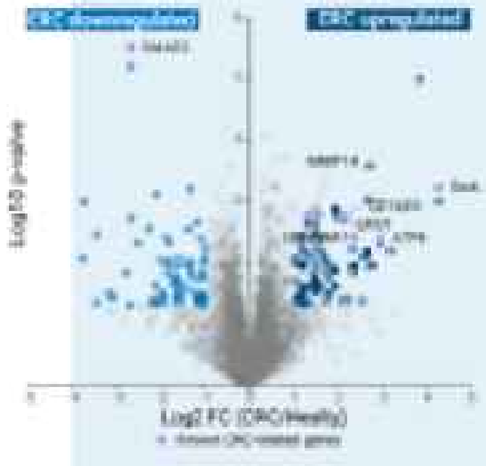
Powering Breakthroughs in Plasma Proteomics with timsTOF

Deep, affordable, automatable, and quantitative:
Scalable ENRICH technology unlocking the power of plasma, serum, and CSF proteomics on timsTOF with proprietary single-particle precision

PREOMICS

- **ENRICH technology** enables **high-performance biomarker discovery through excellent reproducibility, streamlined automation**, and broad sample compatibility with deep proteome coverage.
- **ENRICH-iST** is an easy, flexible, all-in-one solution for human and preclinical mammalian samples, delivering clean peptides from **plasma, serum, or CSF** in under 5 hours.
- **ENRICHplus** achieves maximum depth for **human EDTA plasma**, increasing identifications by up to 7-fold versus neat plasma, with robust quantification and high-throughput compatibility.





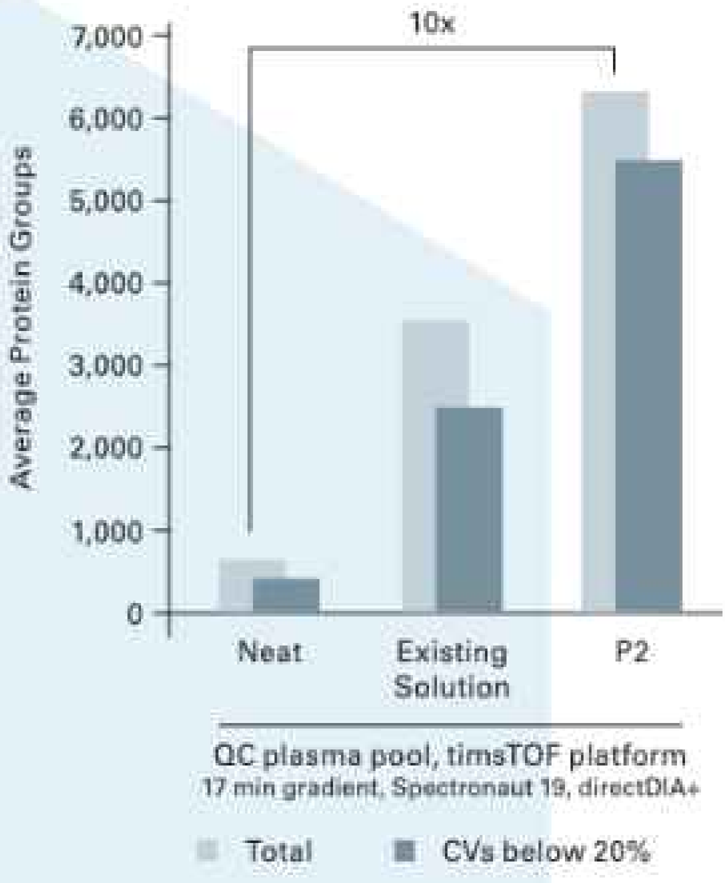
More information about ENRICH Technology:

timsTOF Empowers Biognosys' P2 Enrichment System: Leading Depth, Robustness, and Throughput for Plasma Proteomics

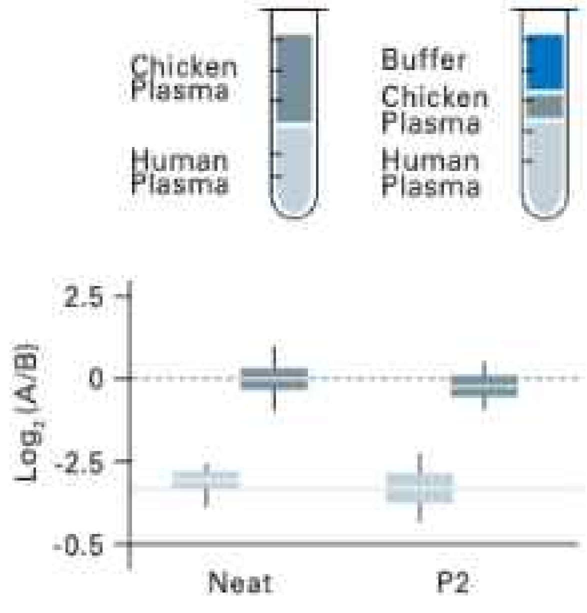
BIOGNOSYS
NEXT GENERATION PROTEOMICS

Biognosys' **TrueDiscovery Plasma Biomarker Discovery** service, powered by the proprietary **P2 Enrichment System** for single-well, particle-based plasma enrichment and timsTOF, offers researchers unmatched proteome depth and quantitative precision with record throughput.

P2 Enrichment System



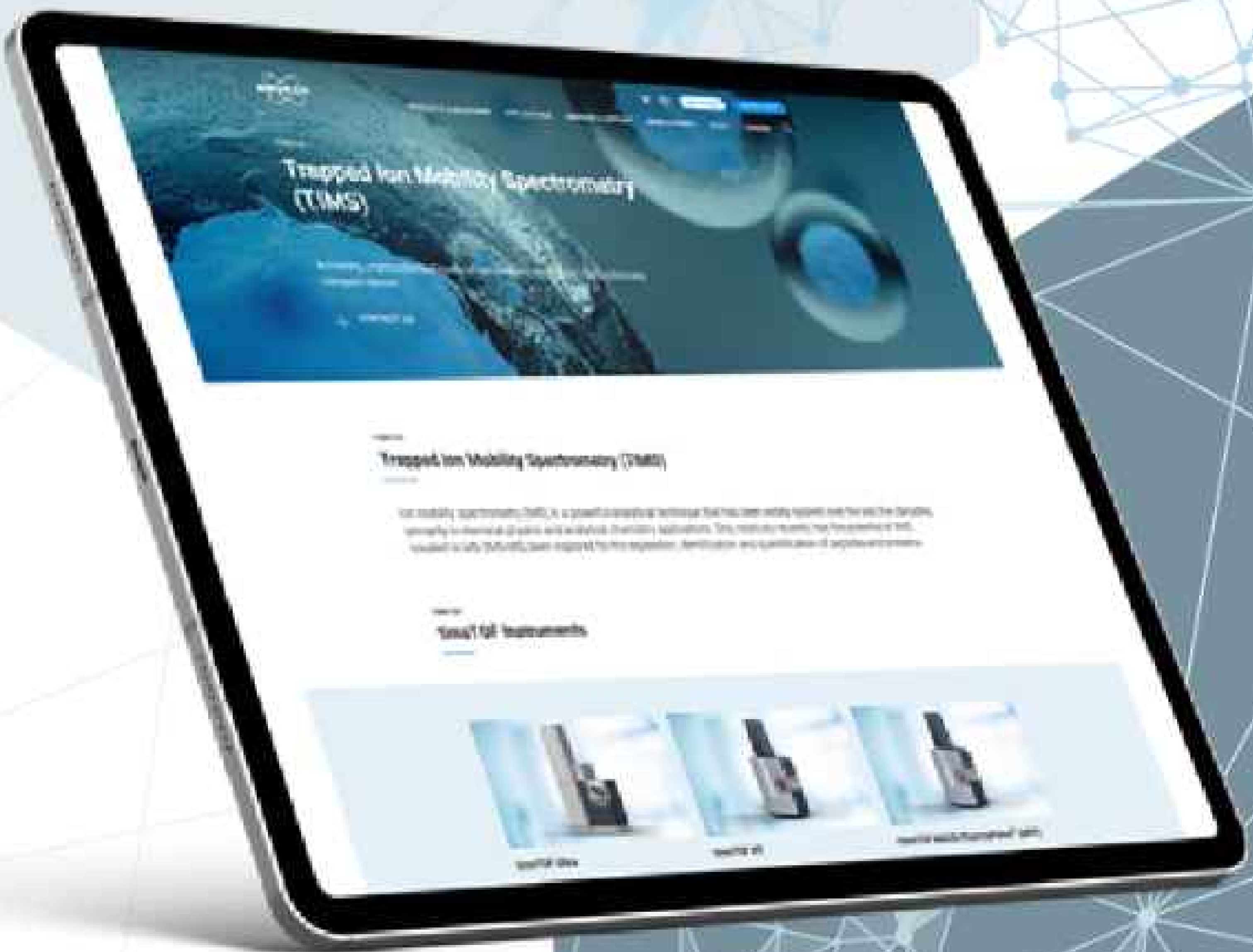
QC plasma pool, timsTOF platform
17 min gradient, Spectronaut 19, directDIA+



More information about P2 Enrichment System:

- **Highest reported enrichment in plasma** with up to 10-fold increase compared to neat plasma and a depth of coverage of more than 6000 proteins.
- **Attractive project turnaround times** and cost-efficiency thanks to unparalleled throughput.
- **Unrivaled quantitative accuracy**, proven by controlled quantitative experiments from the diverse matrix of plasma samples.
- **Available as a CRO service or via multi-year licensing** for in-house use for labs equipped with timsTOF instruments.

Further Reading and References



Trapped Ion Mobility Spectrometry (TIMS)

Trapped Ion Mobility Spectrometry (TIMS)

timsTOF Instruments

Explore More: Recommended Reads and Resources

1. **Introducing the timsUltra AIP:**
   www.bruker.com/timstof-ultra
2. **PASEF: Discover the Advantage of SPEED with Confidence**
   www.bruker.com/de/products-and-solutions/mass-spectrometry/timstof/pasef.html
3. **Immerse into the Capabilities of 4D-Proteomics**
   www.bruker.com/en/applications/academia-life-science/proteomics/4d-proteomics.html
4. **Immediately dive into Results of your Experiment**
   www.bruker.com/en/products-and-solutions/mass-spectrometry/ms-software/proteoscape.html
5. **TwinScape: Streamlined Quality Control and Monitoring**
   www.bruker.com/en/products-and-solutions/mass-spectrometry/ms-solutions/twinscape.html
6. **timsOmni**
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Bruker – Innovation and Integrity:
Building an Ecosystem for the Community

Benefit	**Feature**
Controlled release of ions	from collision cell, optimizing spatial distribution of fragments • Significant fragment ion signal improvement • Flexible and tailor transfer-mass range for every application.
CaptiveSpray Ionization Source (CSI)	with optimized gas flow for higher ion current and sensitivity
PASEF Melodies	full support of all PASEF modes including diagonal-PASEF® exclusive on the TIMS platform
ICC 2.0 (Ion charge control 2.0)	allowing for more leniency in sample loadings and a more user-friendly experience
Spectronaut® 20 integrated	in Bruker ProteoScape™ (BPS).
Upgradeable	from the timsTOF SCP, timsTOF Ultra, and timsTOF Ultra 2
PASEF	for ultra-speed at 300 Hz

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