TIMS-MS

timsTOF Ultra 2

Redefining sensitivity

Innovation with Integrity

A Legacy of Innovation: The timsTOF (2016-2024)

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 timsTOF. **The possibilities are endless.**

timsTOF *Pro*

2017

2019

MALDI with TIMS

timsTOF *flex*

2020

IP2

MALDI 2 TECHNOLOGY

Broader compound classes with MALDI

timsTOF SCP

timsTOF *Pro 2*

Entry-level OMICS workhorse supporting all PASEF workflows

2021

2022

timsTOF *HT*

High-volume instrument, combining speed and performance for routine, large-scale analyses.

Did you know?

Stay on top of your research and upgrade your System.

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

or

- From **timsTOF SCP** → **timsTOF Ultra** → **timsTOF Ultra 2**

2024

timsTOF *Ultra 2*

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

2023

piolab
Instruments GmbH

Partnership
PREOMICS

Partnership
BIOGNOSYS
NEXT GENERATION PROTEOMICS

FasmaTECH

The timsTOF Ultra 2:
Down to Subcellular Sensitivity Analysis

The timsTOF Ultra 2 features the exclusive CSI Ultra 2 ion source, which provides a more than 30% higher ion current, resulting in increased sensitivity and allowing for even less sample input. This instrument is perfect for researchers who need to perform deep proteome analysis on complex samples, such as those from immunopeptidomics studies or sub-cellular fractionation experiments.

》

Nikolai Slavov

Professor, Bioengineering, Director, Single-Cell Proteomics Center, Northeastern University

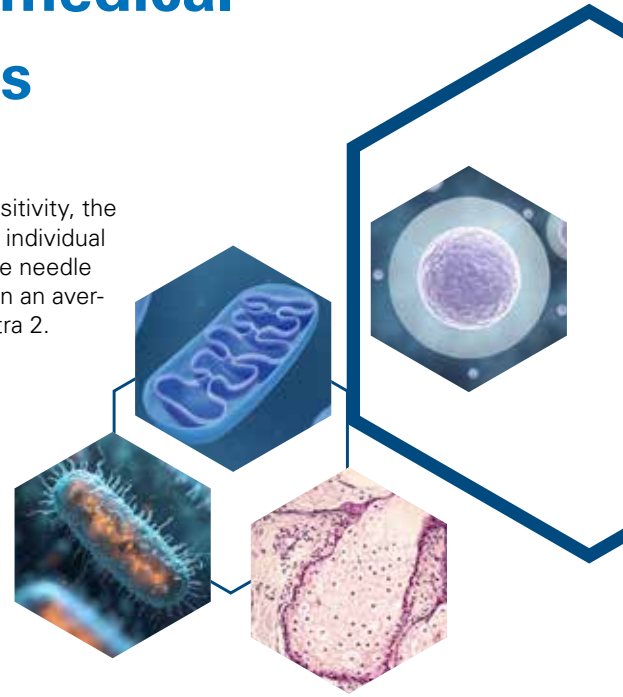Founding Director, Parallel Squared Technology Institute

" The high efficiency of ions utilization by timsTOF systems is well complemented by the new CSI increasing the efficiency of ion delivery. It is a combination that maximizes not just protein detection but also quantification for the most sensitive applications, including proteomics of subcellular organelles."

- **Exclusive CSI Ultra 2** with optimized gas flow for more than 30% higher ion current increasing sensitivity.

- **diagonal-PASEF®** exclusive on the timsTOF platform

- **ICC 2.0** (Ion charge control 2.0) allowing for more leniency in sample loadings and a more user-friendly experience.

- Gain **access to the new ENRICHplus** for your dedicated plasma workflows

- Latest **Spectronaut® 19 integrated** in Bruker ProteoScape™ (BPS)

- **Upgradeable** from the timsTOF SCP and timsTOF Ultra
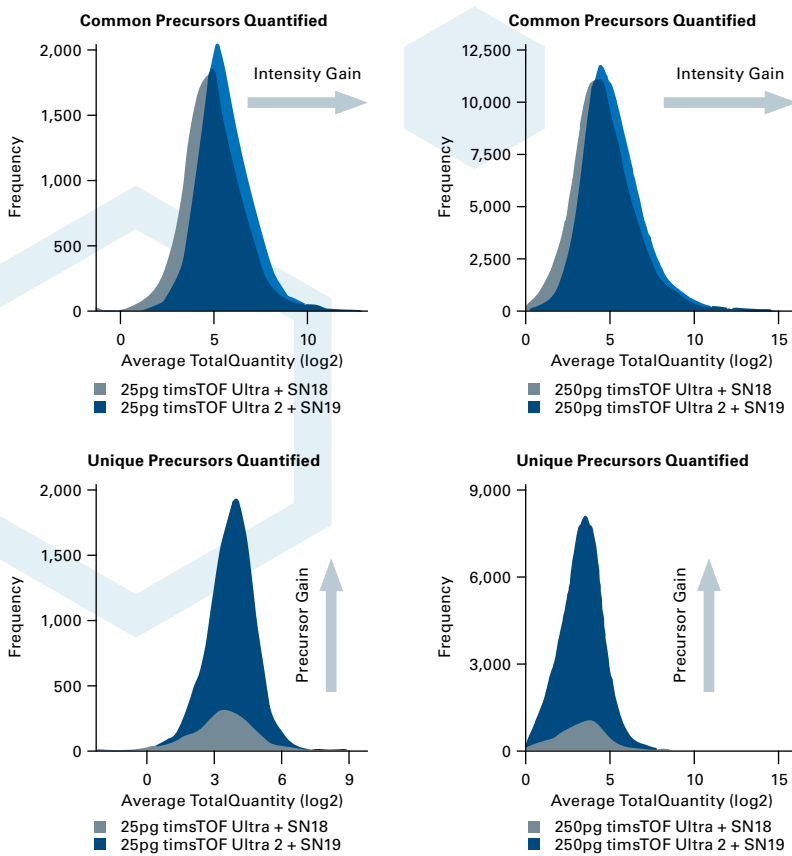
- **PASEF** – for ultra-speed at 300 Hz

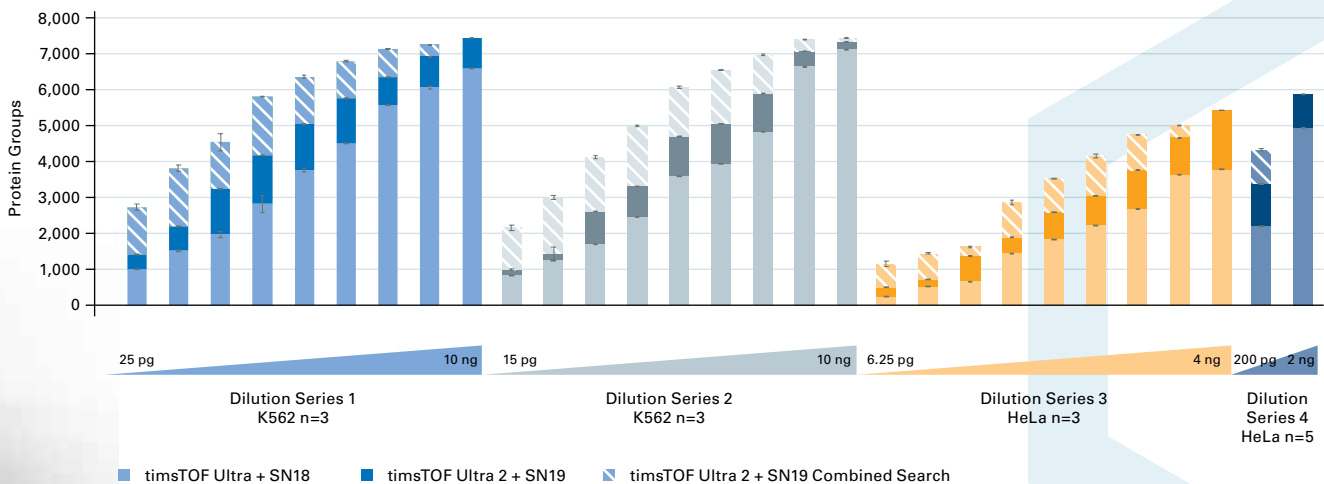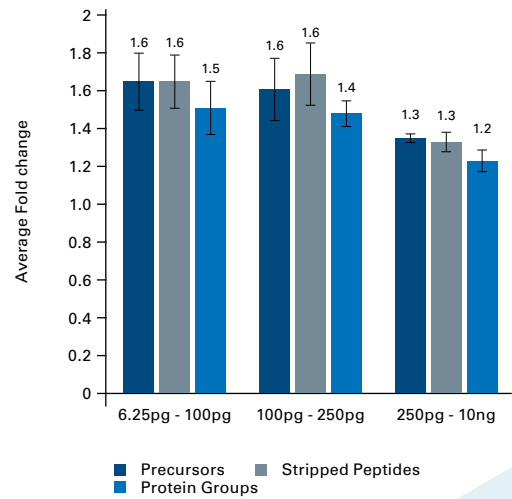# Ultimate Sensitivity for Biomedical Insights Beyond Single Cells

With advancements in timsTOF technology and continuously enhancing sensitivity, the potential expands to address questions from restricted sample amounts like individual small immune cells, subcellular compartments, or immunopeptides from fine needle biopsies. Individual Peripheral blood mononuclear cells (PBMCs) smaller than an average cell become accessible with the improved sensitivity of the timsTOF Ultra 2.

What will be your Next Discovery?

Common Precursors Quantified

Intensity Gain

- 25pg timsTOF Ultra + SN18
- 25pg timsTOF Ultra 2 + SN19

Common Precursors Quantified

Intensity Gain

- 250pg timsTOF Ultra + SN18
- 250pg timsTOF Ultra 2 + SN19

Unique Precursors Quantified

Precursor Gain

- 25pg timsTOF Ultra + SN18
- 25pg timsTOF Ultra 2 + SN19

Unique Precursors Quantified

Precursor Gain

- 250pg timsTOF Ultra + SN18
- 250pg timsTOF Ultra 2 + SN19

Mean Fold Change by Load Amount across Multiple LC Conditions and Cell Types timsTOF Ultra + SN18 : timsTOF Ultra 2 + SN19

- Precursors
- Protein Groups
- Stripped Peptides

Dilution Series 1
K562 n=3

Dilution Series 2
K562 n=3

Dilution Series 3
HeLa n=3

Dilution Series 4
HeLa n=5

- timsTOF Ultra + SN18
- timsTOF Ultra 2 + SN19
- timsTOF Ultra 2 + SN19 Combined Search

timsTOF HT: Daily Companion for all Omics Applications

The timsTOF HT 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 a wide range of samples with ease. Its robustness ensures true high throughput, making it perfect for demanding research environments

» Jenny van Eyk

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

"I appreciate that timsTOFs are field-upgradable, allowing my team to access the next gen MS performance without replacing the entire system"

- **diagonal-PASEF** enabled for best-in-class DIA performance exclusive on the timsTOF platform.

- For **deep, robust, and accurate** cell, tissue, and plasma analysis

- Gain **access to the new ENRICHplus** for your dedicated plasma workflows

- Latest **Spectronaut 19 integrated** in Bruker ProteoScape (BPS)

- **Upgradeable** from timsTOF Pro or timsTOF Pro 2

- **PASEF** – for ultra-speed at 300 Hz

Engineered for Maximum Robustness and Performance

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.


Ten Replicates at Eleven Individual Sites

Eleven Different Laboratories
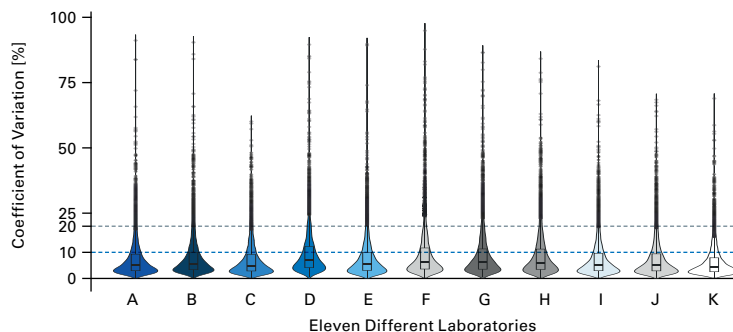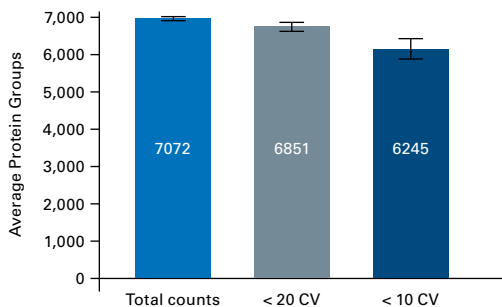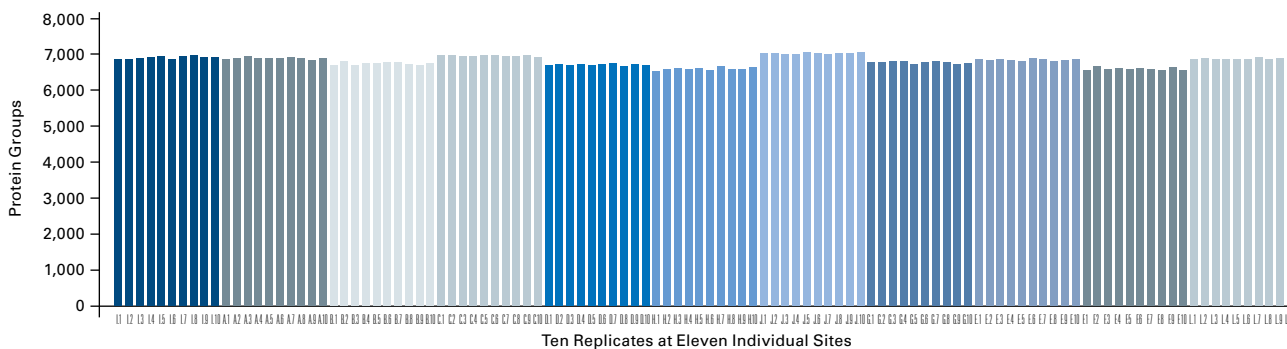
Read the Application Note to Learn More:

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.
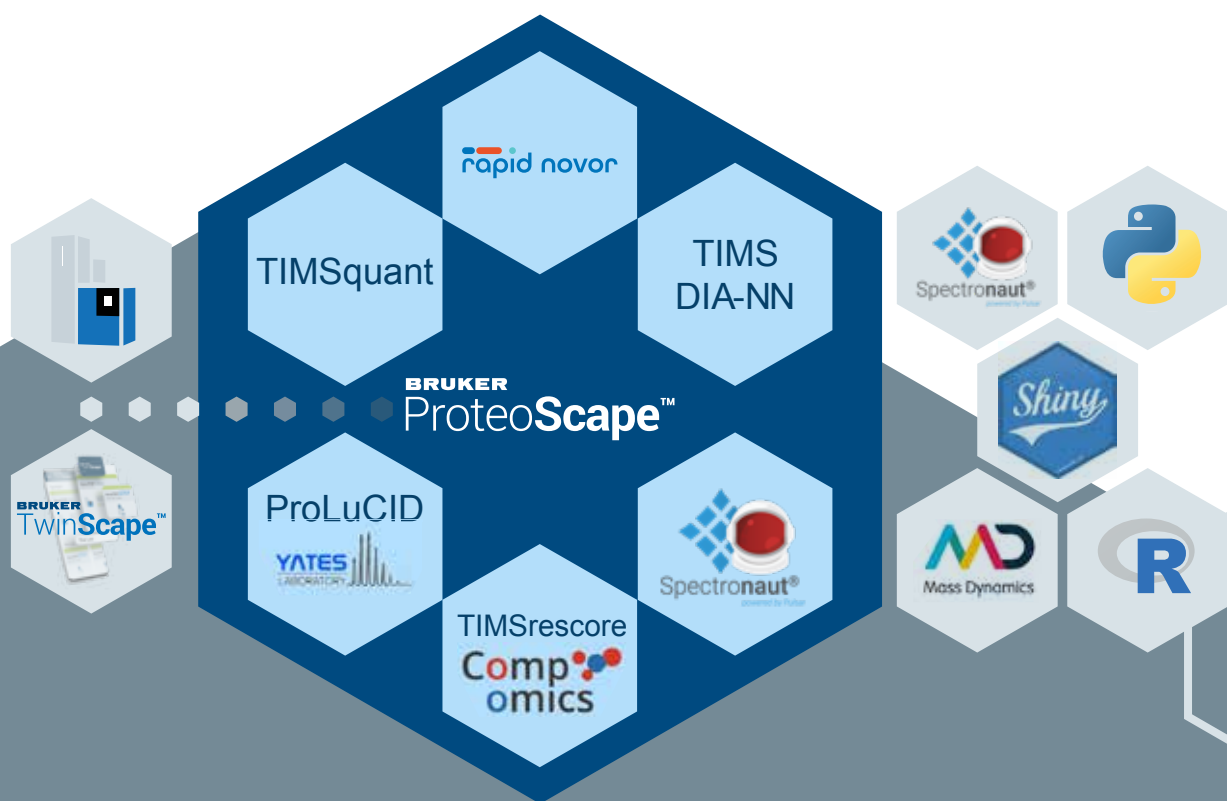
timsTOF-optimized algorithms – BPS integrates a suite of CCS-enabled algorithms, optimized for timsTOF data through collaboration with our partners

- **BPS Novor** is a machine learning-based de novo sequencing engine trained on millions of spectra for efficient and accurate peptide sequencing

- **Spectronaut** – Leading DIA analysis integrated with BPS for direct workflows. Enhanced prediction models for timsTOF data boost sensitivity and accuracy by up to 40% with support for >20 PTMs.

- **TIMSrescore** – a timsTOF optimized version of MS2Rescore, including machine learning models for enhanced prediction of Fragment Peak Intensities, Retention Time, and Ion Mobility, to ensure Accurate PTM Identification. A collaboration with University of Ghent's Compomics Team.

# TwinScape – a Digital Twin-Driven Solution for Quality Management

TwinScape™: a digital twin-driven solution for quality management in the modern proteomics laboratory. Data quality management is an emerging topic in proteomics laboratories aimed at ensuring that measurement platforms meet the standards and expectations of researchers who use them.

Advanced Quality Management with TwinScape
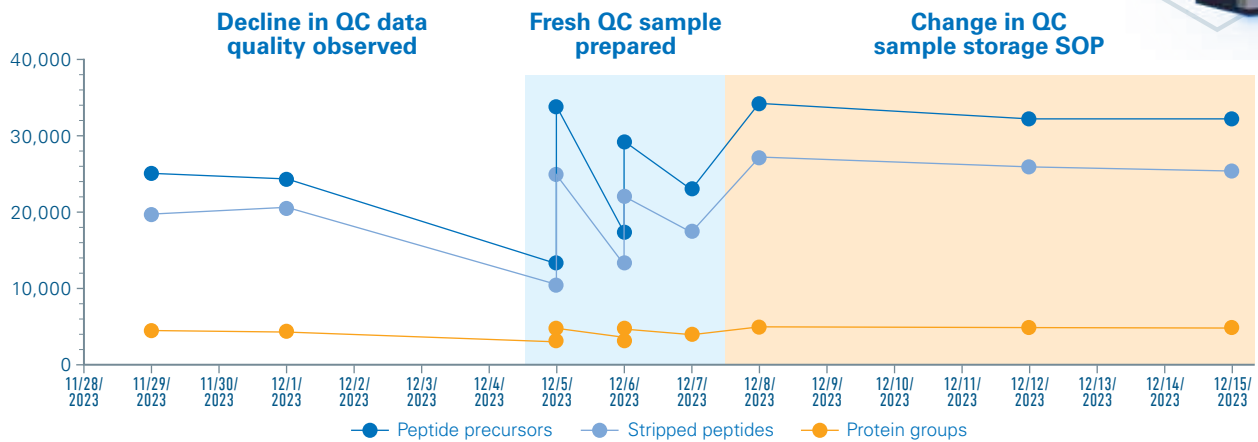
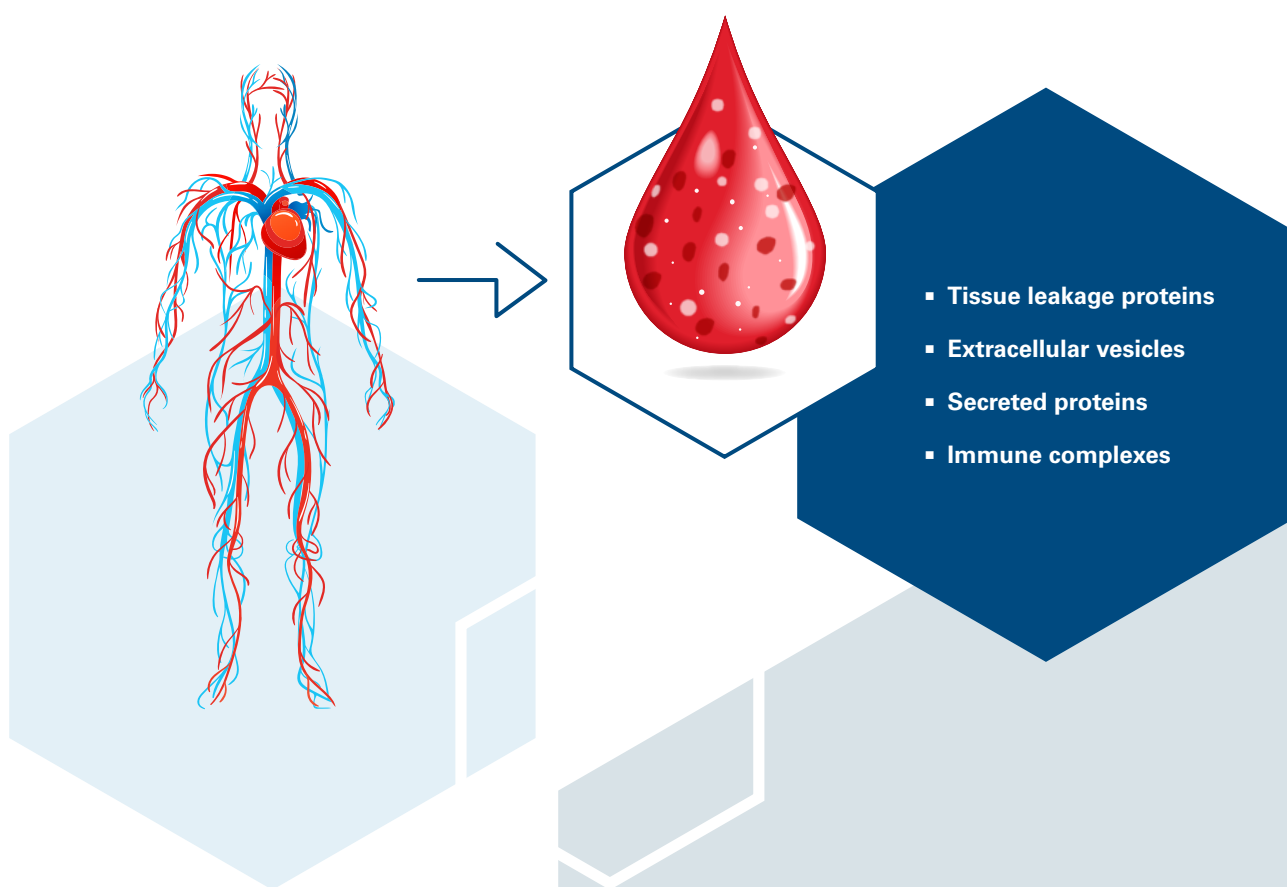**Complete workflow with Bruker ProteoScape and iRT standards from Biognosys**
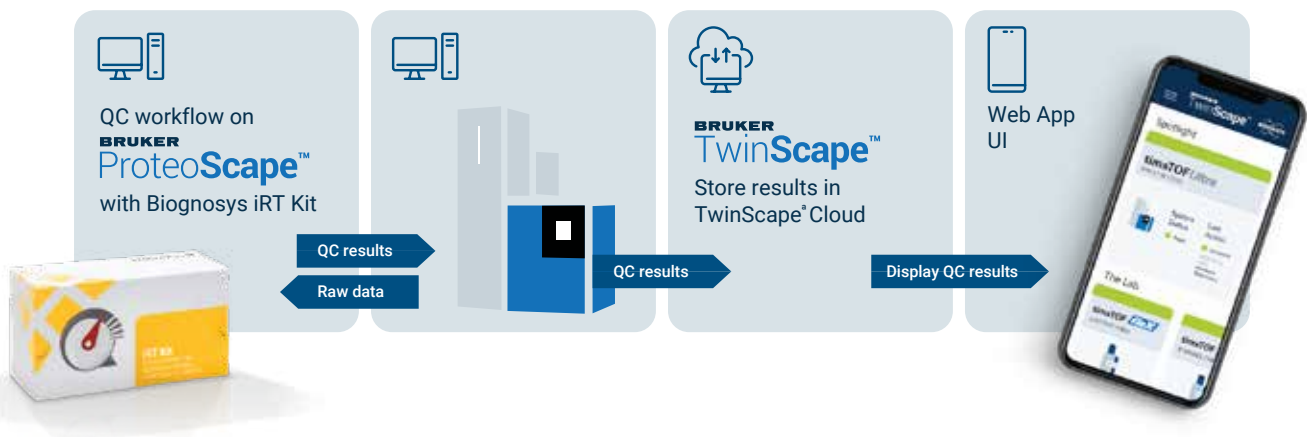
Anne-Claude Gingras

Ph.D., Senior Investigator, Director Lunenfeld-Tanenbaum Research Institute, Professor in the Department of Molecular Genetics, University of Toronto, Vice President Research, Sinai Health, Toronto, Canada

"BPS, Biognosys iRT kit and TwinScape seamlessly provide an overhead, over-time view of QC and system performance in simple plots"

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**

» Roman Fischer

Associate Professor and Head of Discovery Proteomics Facility, University of Oxford

"timsTOF technology together with ENRICHplus is changing the way we do plasma proteomics. On Bruker's timsTOF Pro we could 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 a high-throughput and robust timsTOF system ENRICHplus is a complete, efficient and game changing platform for deep plasma proteomics."
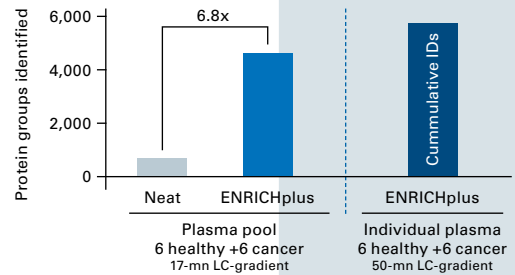
Accelerate Deep Discoveries in your Lab with the timsTOF Platform and ENRICHplus

Deep, robust, effortless and affordable: Single proprietary particle enabling high throughput studies with retained quantitative precision

PREOMICS

- **ENRICHplus enables deepest access to the plasma proteome by up to 7-fold increase** in comparison to neat plasma with superior reproducibility.

- In a small clinical study (6 healthy donors, 6 colorectal cancer patients) **a cumulative number of 5800 protein groups is identified.**

- ENRICHplus utilizes a propriety single particle solution **supporting automated workflows and retaining quantitative precision.**


**Get Exclusive Early Access to the New ENRICHplus Technology**

timsTOF empowers TrueDiscovery®, a specialty CRO service with leading depth, robustness, and throughput in plasma from Biognosys

Biognosys' TrueDiscovery plasma biomarker discovery service, powered by the novel, proprietary P2 Particle System for single-well, particle-based plasma enrichment and timsTOF, offers researchers unmatched proteome depth and quantitative precision with record throughput.

Spectronaut®
powered by Pulsar
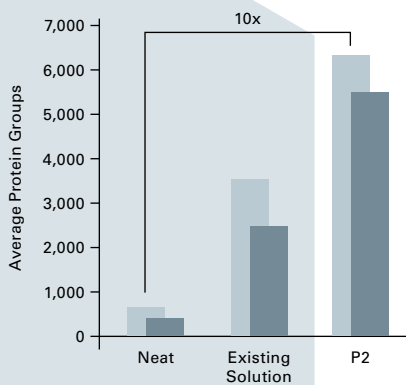
QC plasma pool, timsTOF platform
17 min gradient, Spectronaut 19, directDIA+

Total   CVs below 20%
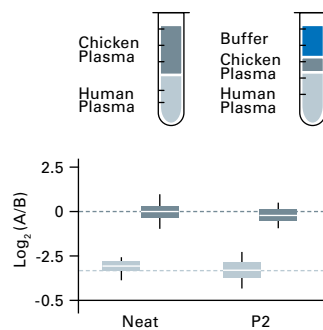
- **Highest reported enrichment in plasma** with up to 10-fold increase compared to neat plasma and a depth of coverage of more than 6000 proteins in a single plasma pool.

- **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.

- **Rich biological insights** and easy transferability to clinical assays.

Learn More at biognosys.com/plasma:

Streamlining Drug Discovery with Precision

- **De-risking drug development:** Chemoproteomics empowers researchers to identify and validate drug targets with unparalleled precision, improving the success rate in later stages of development. Innovative proteomics approaches translate to significant advantages and streamlined workflows.

- **Minimizing adverse effects:** By enabling the design of highly targeted therapies, chemoproteomics paves the way for drugs with fewer off-target effects, ultimately improving patient outcomes.

Unveiling the Potential of Targeted Protein Degradation (TPD) using timsTOF

Targeted protein degradation, using small molecules like molecular glues and PROTACs, revolutionizes drug discovery by eliminating disease-causing proteins with high precision and minimal off-target effects, promising breakthroughs in understanding diseases, developing new therapies, and targeting the previously undruggable proteome.

» Uli Ohmayer

Head of Mass Spectrometry and co-founder
NEOsphere Biotechnologies

"The timsTOF's robustness facilitates high-throughput screening of entire degrader libraries with rapid turnaround, maximum coverage, and unparalleled accuracy and precision "

☼ Did you know?

Despite continuous breakthroughs, around 85% of the human proteome remains classified as "undruggable". timsTOF-powered workflows unlock this vast resource of potential drug targets.

- **High-throughput, proteome-wide analysis:** Accurately assess cell-wide effects through comprehensive quantitative proteomic readouts.

- **Early off-target assessment:** Proteomics offers a complete view during novel degrader screens, prioritizing safety in drug development.

**Tune in to
Learn More:**
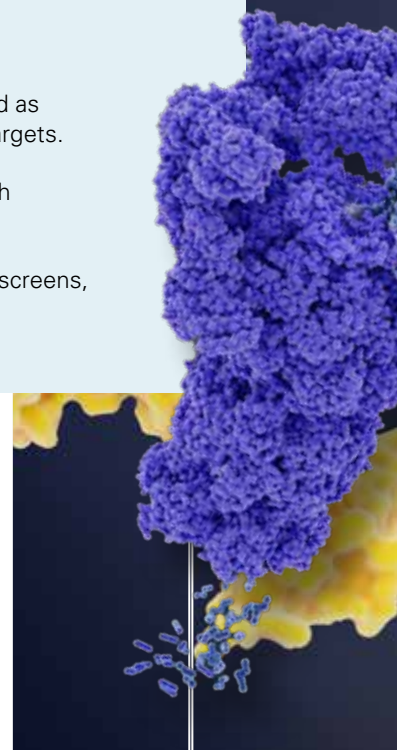
Unlocking Insights with Ubiquitinomics: Validating TPD Assays

Ubiquitinomics has emerged as a vital tool for validating targeted protein degradation (TPD) assays, offering a window into the intricate mechanisms of protein breakdown pathways. By meticulously probing the ubiquitin landscape within cells, researchers gain crucial insights into the efficiency and specificity of degrader molecules. This approach sheds light on the dynamics of protein ubiquitination and degradation, ultimately validating the precision of TPD strategies.

timsTOF Ultra 2: Empowering Ubiquitinomics Research

The timsTOF Ultra 2 mass spectrometer plays a pivotal role in Ubiquitinomics research, offering unparalleled capabilities:

- **Validating degrader-drug targets:** Ubiquitinomics enables rigorous validation of degrader molecules' efficacy in targeting specific proteins for ubiquitination and degradation.

- **Sensitivity vs costly enrichment:** The exceptional sensitivity of timsTOF Ultra 2 maximizes the value of costly ubiquitin-(K-GG) peptide enrichment, ensuring reliable detection of low-abundance modified peptides.

- **Scalability for diverse workflows:** timsTOF HT seamlessly integrates with TPD workflows, offering high-throughput analysis for large-scale studies. Downscale your enrichment protocols and reduce costs without compromising data quality.

Learn More about TPD:

Discover the Potential of Immuno-peptidomics with TIMS and PASEF

Trapped ion mobility separation (TIMS)-based mass spectrometry is a game-changer in research. It swiftly identifies neoantigens, 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.

- **Personalized treatment strategies** based on individual patient's immune profile.

- **Identify and characterize** potential therapeutic targets swift and robust across many samples.

- **Minimizing** off-target effects and maximizing immunotherapy treatment efficacy.

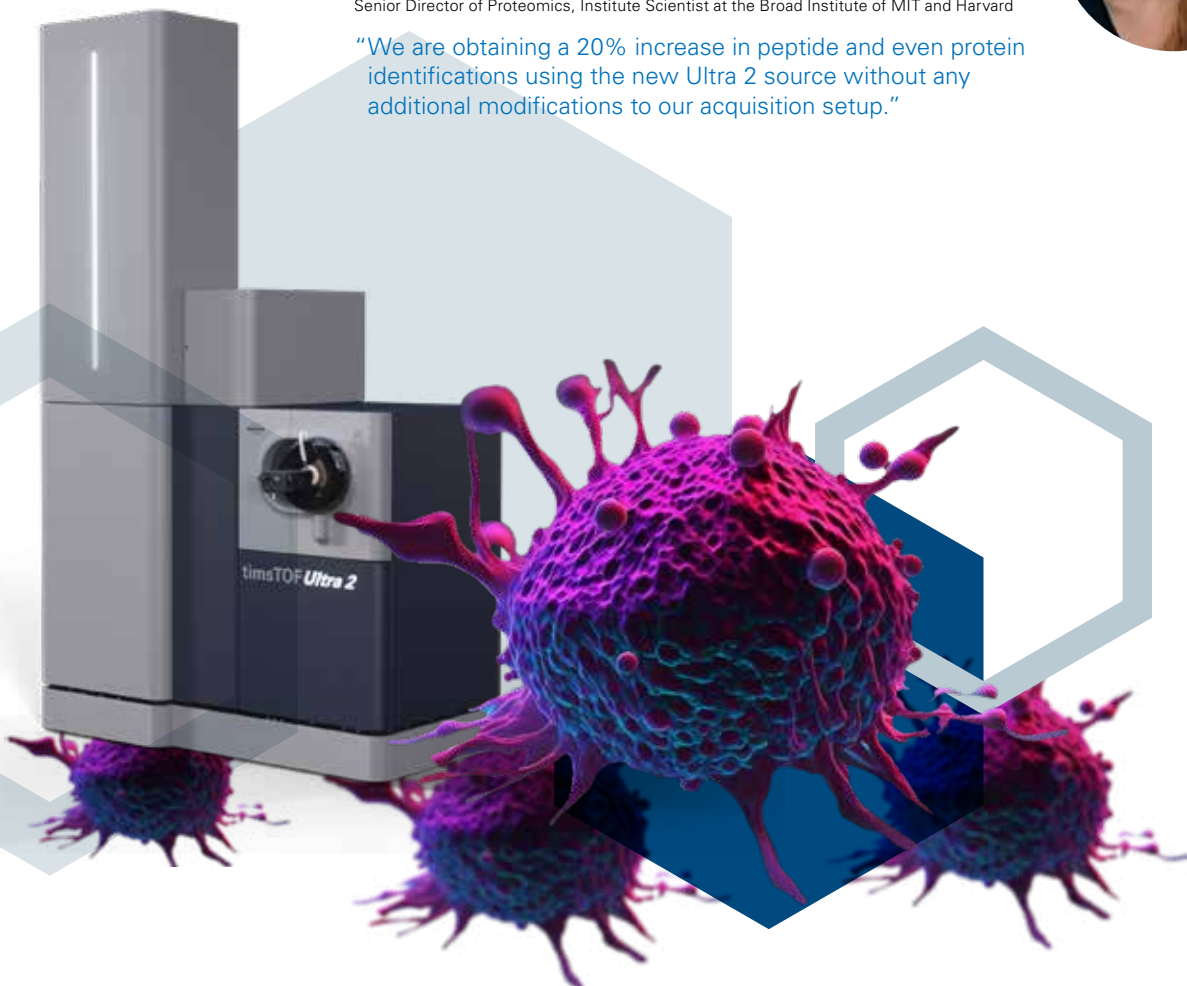- **Deeper insight** into mechanisms underlying cancer progression.

❱❱ Claudia Ctortecka
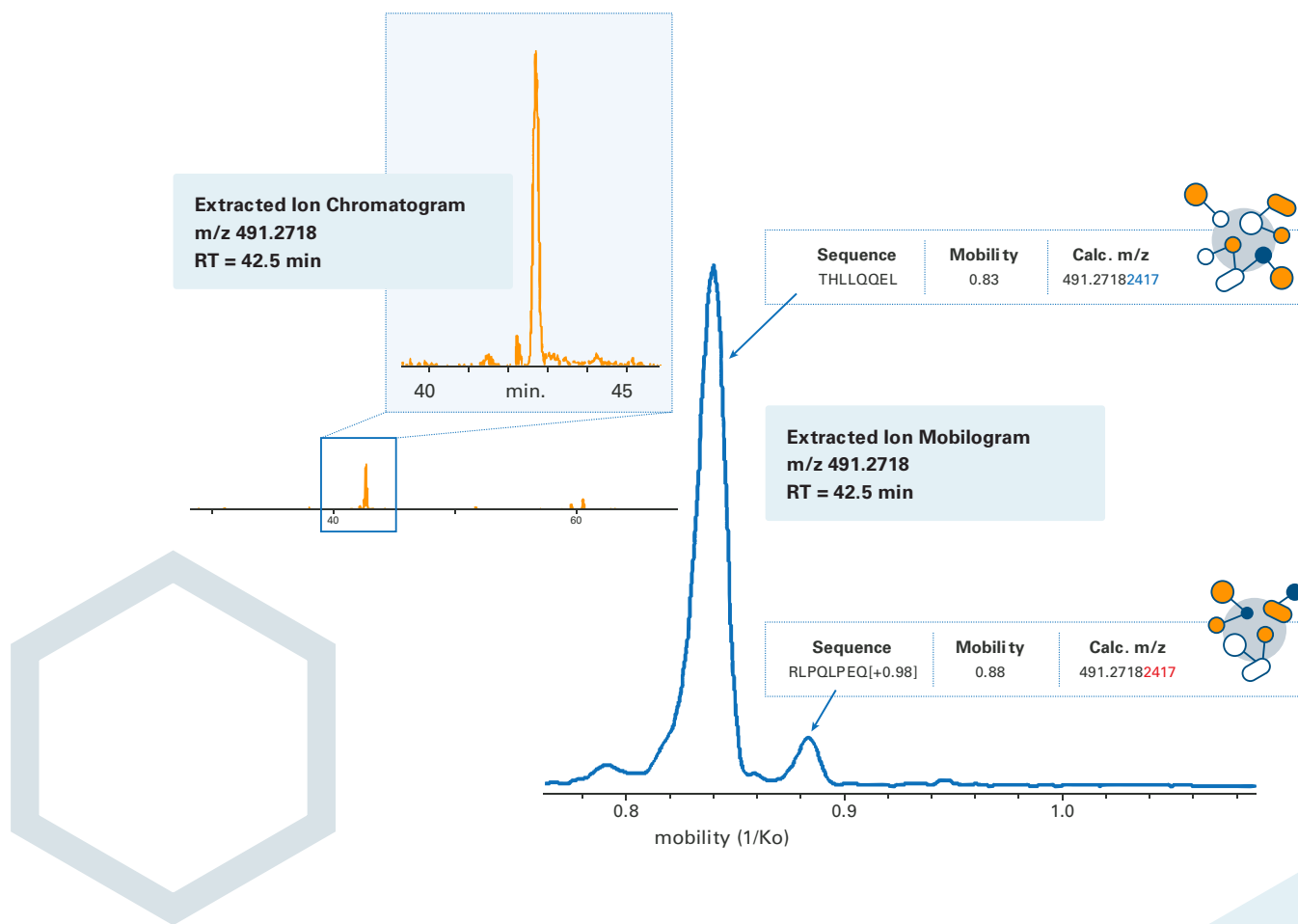Postdoctoral Fellow

& Steven A. Carr
Senior Director of Proteomics, Institute Scientist at the Broad Institute of MIT and Harvard

"We are obtaining a 20% increase in peptide and even protein identifications using the new Ultra 2 source without any additional modifications to our acquisition setup."

timsTOF *Ultra 2*

Shed Light onto Co-eluting Shadows with MOMA

Extracted Ion Chromatogram
m/z 491.2718
RT = 42.5 min

Sequence	Mobility	Calc. m/z
THLLQQEL	0.83	491.27182417

Extracted Ion Mobilogram
m/z 491.2718
RT = 42.5 min

Sequence	Mobility	Calc. m/z
RLPQLPEQ[+0.98]	0.88	491.27182417

mobility (1/Ko)

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.

HLA class I peptide-tailored
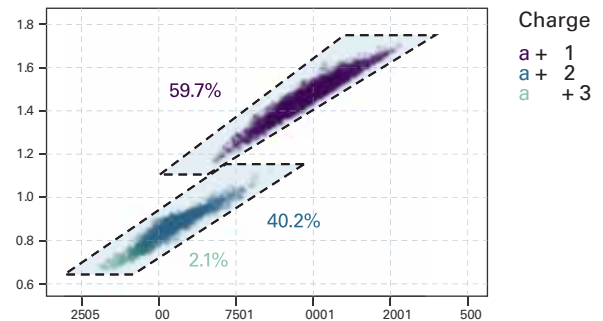
Immunopeptidomics polygon filtering: Exemplary heatmaps of ions of specific charge state distribution and masses are targeted.[1]

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."

[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

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: A Metaproteomic Journey

The human body harbors trillions of microbes in complex ecosystems known as microbiomes. Understanding how these microbes function is crucial for maintaining health and preventing disease. Metaproteomics has emerged as a revolutionary tool, offering a deeper look into the bidirectional workings between the microbiome and the host.

Going Beyond Species Identification

Traditionally, microbiome research has been focused on identifying the types of microbes present. Metaproteomics takes this several steps further by analyzing the proteins of these microbes and the host express. This unveils their functional activities, providing a more complete picture of the microbiome's role in health and disease.

- **Beyond taxonomy:** Metaproteomics goes beyond simply identifying the microbes present, revealing their functional roles within the ecosystem and the host's response.

- **Understanding functional alterations:** By analyzing protein expression, researchers can understand how the microbiome and the host's cells change in response to diet, drugs, or disease.

- **Microbiome profiling:** Analyze microbial samples and detect antimicrobial proteins and proteins of unknown function never encountered before.

- **Diagnostic and therapeutic possibilities:** Quantification of changes in the bacterial's physiology at unprecedented sensitivity.

David Gómez-Varela

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

"The timsTOF Ultra is a quantum leap in Metaproteomics by reaching unprecedented taxonomical and functional profiling, improving the limit of detection and quantification more than 5000 times, at higher throughput compared to state-of-the-art proteomics technologies in Metaproteomics."

On Demand Webinar with David Varela: Ultra-sensitive Mass Spectrometry Sheds Light on the Microbiome

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

peptide · glycopeptide   peptide · glycopeptide
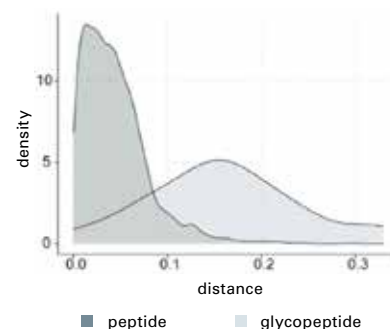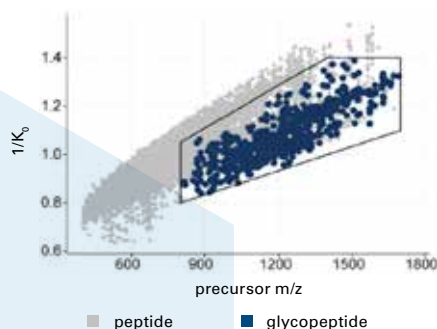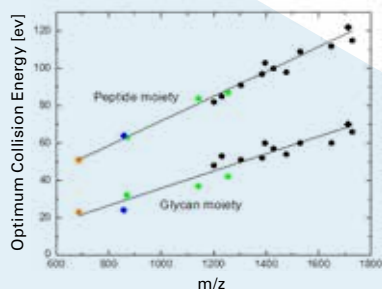
up to 300 Hz
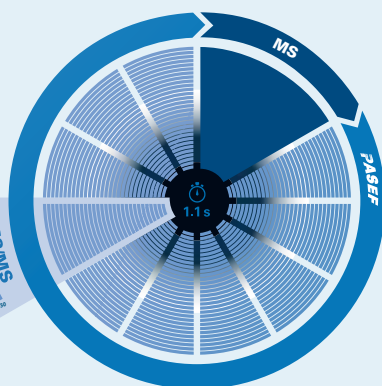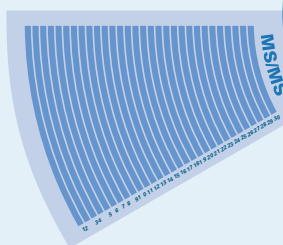
% of glycans identified at each site (α1-AGP; 100 ng)
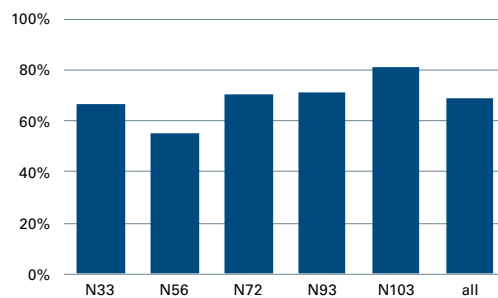
Tin Long Wong, Brian P. Mooney, Gustavo J. Cavallero, Minhui Guan, Lei Li, Joseph Zaia, and Xiu-Feng Wan Journal of Proteome Research 2023 22 (1), 62-77 DOI: 10.1021/acs.jproteome.2c00469

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:

Every Cell Counts:
Single Cell Proteomics with timsTOF

The field of proteomics is undergoing a revolution, with single-cell analysis emerging as a powerful tool to unlock the mysteries of individual cells. Deep visual proteomics takes center stage, seamlessly integrating microscopy with low-input proteomics. This innovative approach allows researchers to pinpoint specific regions of interest within a cell and delve deeper into cellular dynamics with unprecedented precision and resolution.

Transformative Insights for Biomedical Research

Single-cell proteomics offers a wealth of benefits, empowering researchers to gain deeper biological insights and make informed decisions:

- **Cell type specificity:** Gain a comprehensive understanding of protein expression within distinct cell types.

- **Low-abundance protein discovery:** Identify critical regulatory mechanisms, including transcription factors, that were previously undetectable.

- **Precise regional analysis:** Illuminate localized protein dynamics within specific areas of interest, facilitated by deep visual proteomics.

- **Deciphering cellular heterogeneity:** Resolve the complexities of cellular variations, including those observed in tumors.

- **Subcellular exploration:** Explore the uncharted territories within a cell, uncovering the proteome of subcellular compartments.

Christine Carapito
LSMBO Co-Director, & CNRS Research Director

& Jeewan-babu Rijal
Postdoctoral Fellow

"After obtaining very encouraging results on a timsTOF Pro 2 instrument on both single cells and immunopeptidomics samples, the setup of the timsTOF Ultra in our lab felt as another real game changer.

Single cell proteome coverage is more than doubled and fine DIA-PASEF methods optimizations for singular immunopeptides allowed us to reach unprecedented sensitivity to identify populations of peptides presented as extremely low.

Thanks to these improvements, we have confidently started addressing clinical research challenges with our biologists and clinicians collaborators."
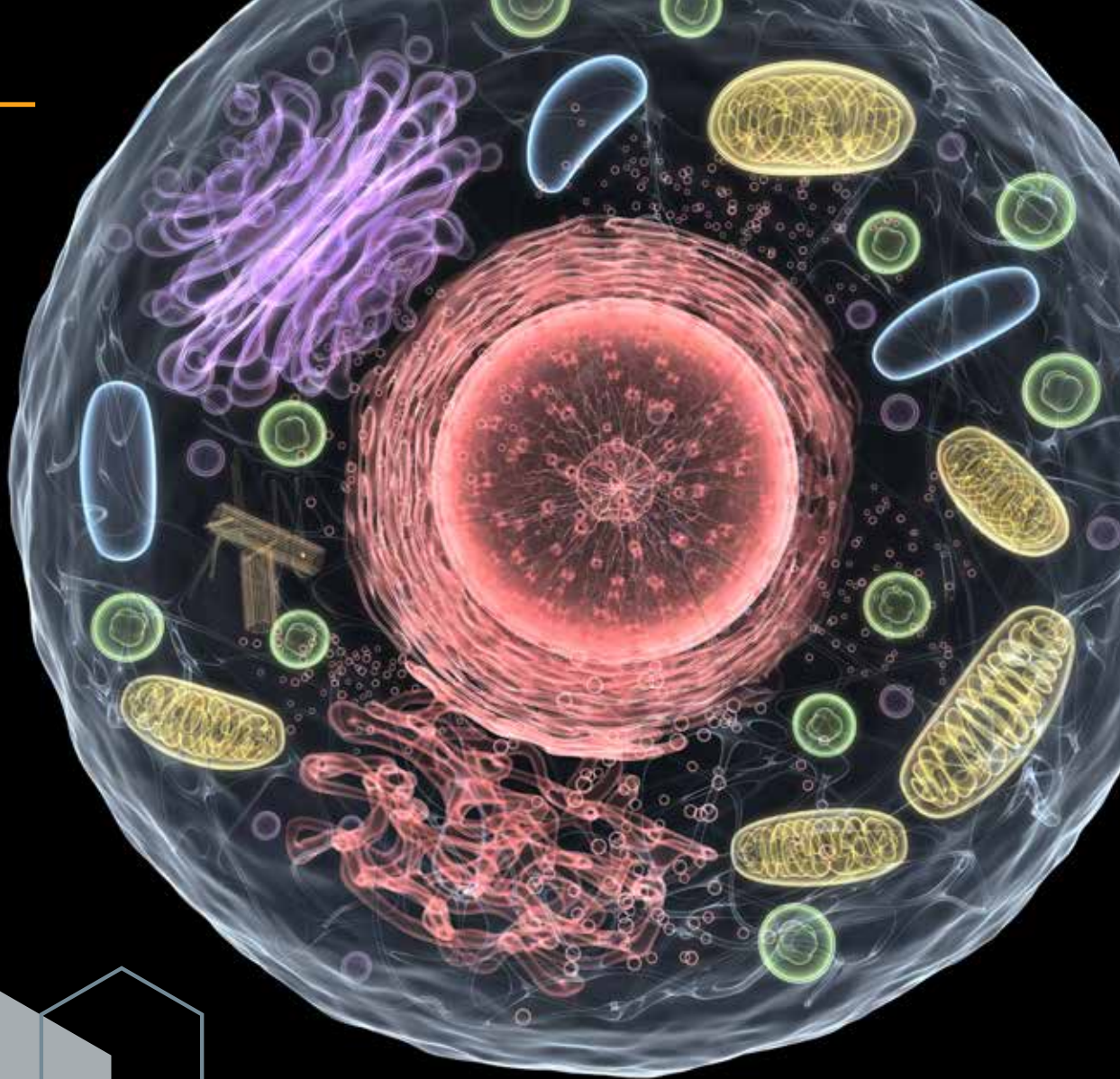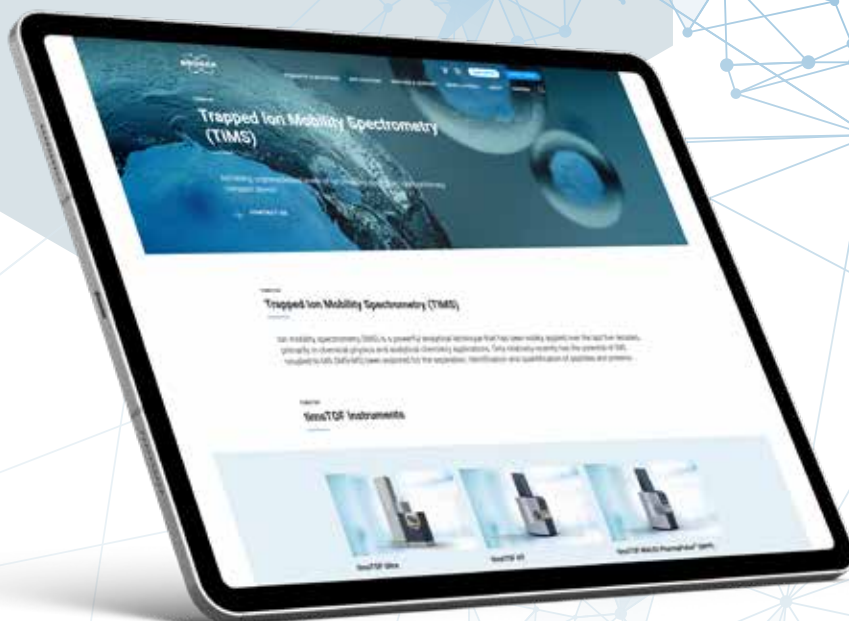
Ryan Kelly

Professor at Brigham Young University, Dept of Chemistry and Biochemistry

"The excellent sensitivity of the timsTOF Ultra has opened up new possibilities for our single-cell and low-input tissue proteomics work."

timsTOF *Ultra 2*

Further Reading and References

Explore More: Recommended Reads and Resources

1. Introducing the timsTOF Ultra 2:
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/academ-
ia-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/proteos-
cape.html*

**5. TwinScape: Streamlined Quality Control
and Monitoring**
*www.bruker.com/en/products-and-solutions/
mass-spectrometry/ms-solutions/twinscape.
html*

6. 4D-Proteomics Content Collection:
*www.bruker.com/en/landingpages/bdal/
proteomics-content-collection.html*

7. Pharma Content Collection:
*www.bruker.com/en/landingpages/bdal/
pharma-content-collection.html*

**8. Everything you need. Maximum
Sensitivity, Speed, and Robustness**
*www.bruker.com/en/products-and-solutions/
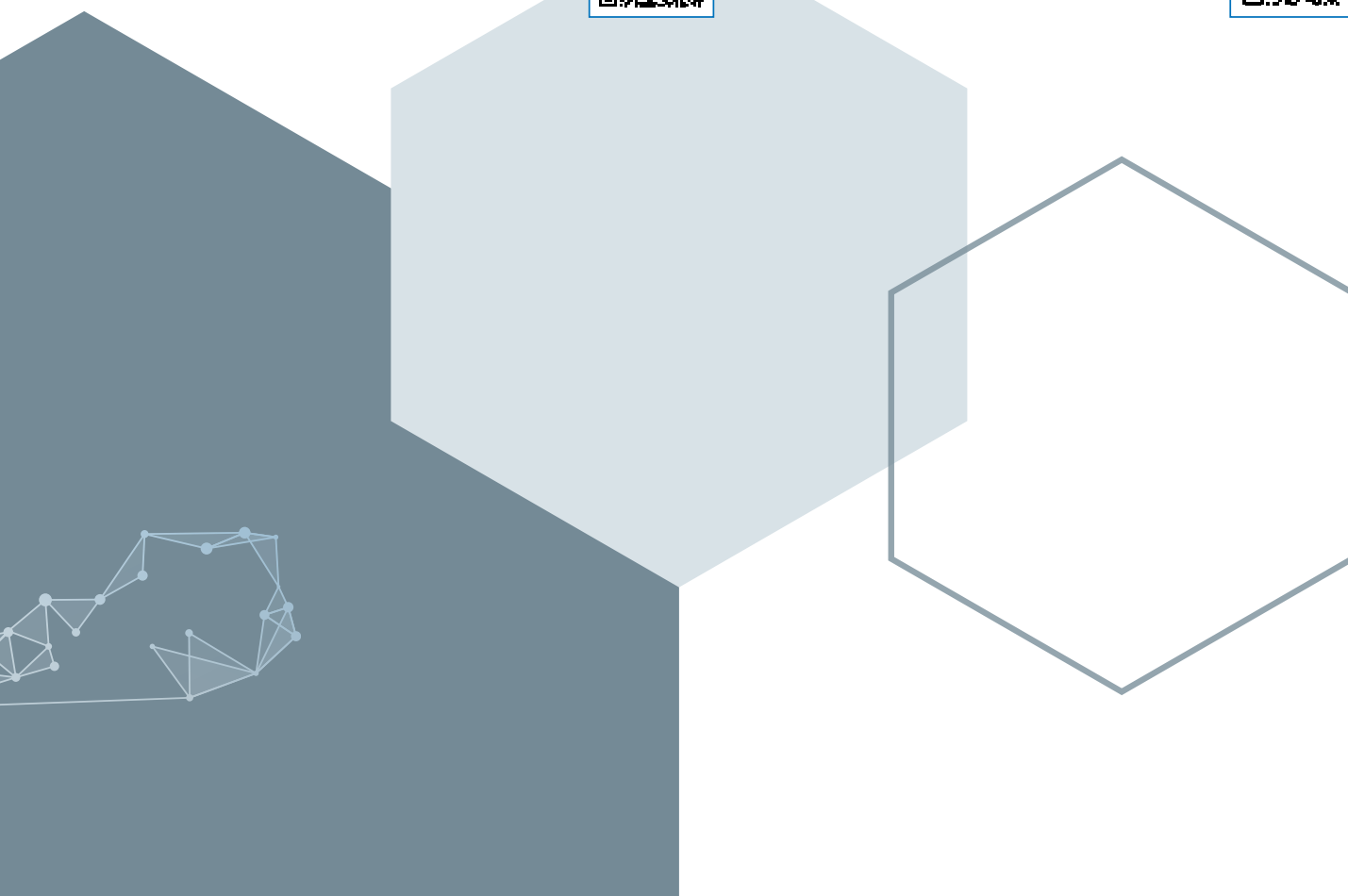mass-spectrometry/lc-ms/pepsep-columns.
html*

**9. Setting the Standard for Protein Analysis
with PreOmics**
https://www.preomics.com

**10. The Gold Standard for DIA Proteomics
Analysis: Spectronaut**
https://biognosys.com/software/spectronaut/

Bruker – Innovation and Integrity:
Building an Ecosystem for the Community

Benefit	Feature
Increased sensitivity	Meaningful upgrades to increase sensitivity
Increased dynamic sample input range	ICC 2.0 enabled for timsTOF Ultra 2 – Stable identification and quantification at high sample loads
Upgradeability	Upgrade paths for the timsTOF Pro → timsTOF Pro 2 → timsTOF HT as well as timsTOF SCP → timsTOF Ultra → timsTOF Ultra 2
Expanding PASEF possibilities	diagonal-PASEF enabled and optimized – the newest development in acquisition modes
ENRICHplus	Democratization of deep plasma proteomics for true scale for high throughput studies with quantitative precision. Reliable, standardized and fully automatable end-to-end solution with ENRICHplus
Bruker ProteoScape	Seamless and with integration of Spectronaut 19 for parallel processing, fast and comprehensive data insights
TwinScape	Digital Twin-Driven Quality Management

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