Revolutionizing Biomedical Research with a Novel DIA Strategy

ZT Scan DIA

What is ZT Scan DIA?

ZT Scan DIA is a novel mass spectrometry data-independent acquisition method developed by SCIEX. It is designed to provide comprehensive proteomic and biomarker analysis, enabling researchers to gain detailed insights into complex biological systems.

How Does ZT Scan DIA Work?

ZT Scan DIA employs a continuously scanning quadrupole coupled to a time-of-flight analyzer to achieve more selective MS/MS data with high quantitative precision and accuracy to analyze complex biological systems, ideally with high sample throughput.

Achieving Superior Sensitivity and Specificity

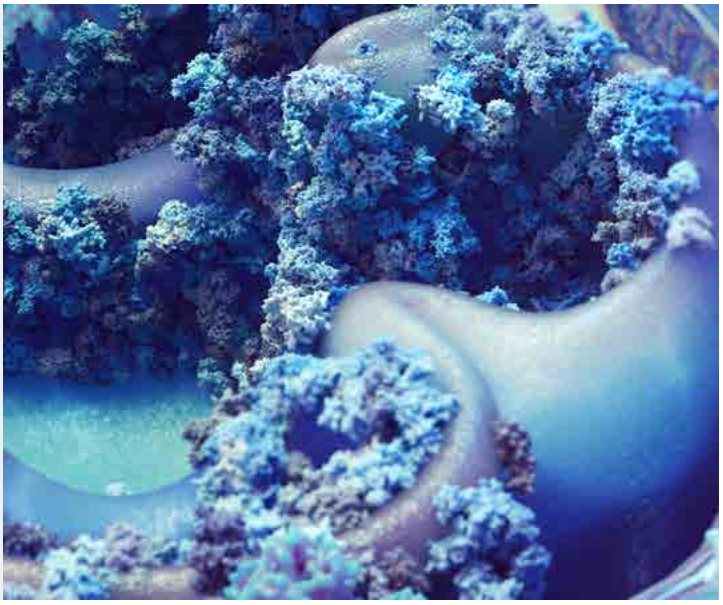
One of the standout features of ZT Scan DIA is its exceptional sensitivity, allowing for the detection of low-abundance molecules that are often overlooked by other techniques. This high sensitivity is crucial for identifying key biomarkers and understanding subtle changes in biological systems.

Delivering Comprehensive Analytical Data

ZT Scan DIA provides detailed and comprehensive data on proteins, peptides, and biomarkers, facilitating deeper insights into biological processes and disease mechanisms.

The Main Advantages of ZT Scan DIA

- Identifies significantly more proteins, peptides, and biomarkers than discrete-window DIA methods.
- Excels in detecting low-abundance molecules with high sensitivity and minimizes interferences through its high specificity, ensuring accurate and reliable quantification.
- Delivers precise and accurate quantification with high-quality MS/MS spectra, supporting efficient high-throughput analysis, ideal for large-scale studies.
- Reduces interferences from co-eluting isobaric analytes, improving specificity and accuracy.



The Role of SCIEX Technology

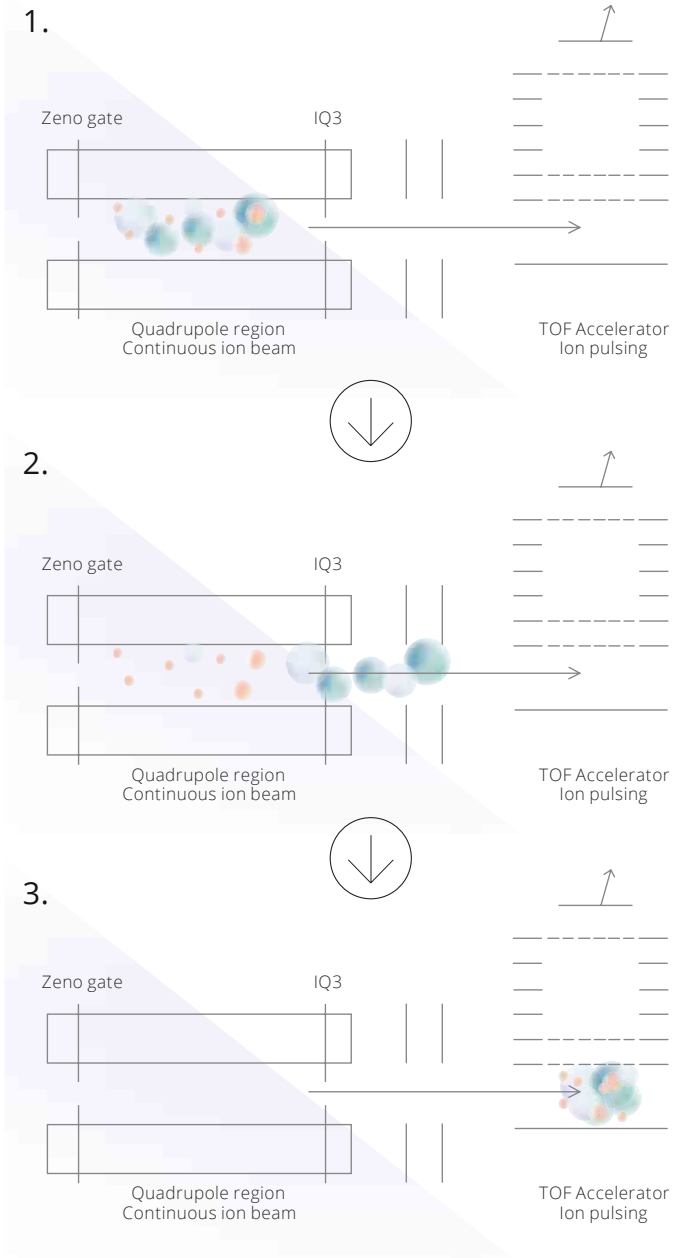
- SCIEX technology, particularly the ZenoTOF 7600+ system featuring ZT Scan DIA (Zeno trap-enabled scanning data-independent acquisition), plays a crucial role in advancing biomedical research by providing high-throughput and high-sensitivity analytical capabilities.
- Enables comprehensive proteomic and biomarker analysis, facilitating the discovery of novel biomarkers and therapeutic targets.
- Supports the study of complex biological processes by delivering detailed and accurate data on protein modifications and interactions.
- Enhances the characterization of low-abundance molecules, which are often critical in understanding disease mechanisms and developing targeted therapies.
- Integrates seamlessly with existing workflows, improving efficiency and throughput in research laboratories.
- Provides robust and reproducible results, ensuring reliability and confidence.
- Supports data-driven decision making in clinical and translational research by providing comprehensive and high-quality analytical data.
- This high-resolution, precise, and accurate analysis is applicable across various research fields, including aging, inflammation, neurodegenerative diseases, cardiovascular diseases, cancer research, and beyond.
- By combining the depth of data independent acquisition (DIA) methods with the precision of targeted approaches, ZT Scan DIA enhances the identification and quantitation of analytes, making it a powerful tool for advanced scientific studies.

Case Studies

Enhancing Phosphopeptide Discovery with ZT Scan DIA

This study investigates the application of ZT Scan DIA technology in enhancing phosphopeptide discovery, a critical aspect of understanding cellular signaling pathways. By leveraging the advanced capabilities of ZT Scan DIA, the aim is to improve the identification and quantification of phosphopeptides, providing deeper insights into cellular processes.

Zeno trap enabled QTOF

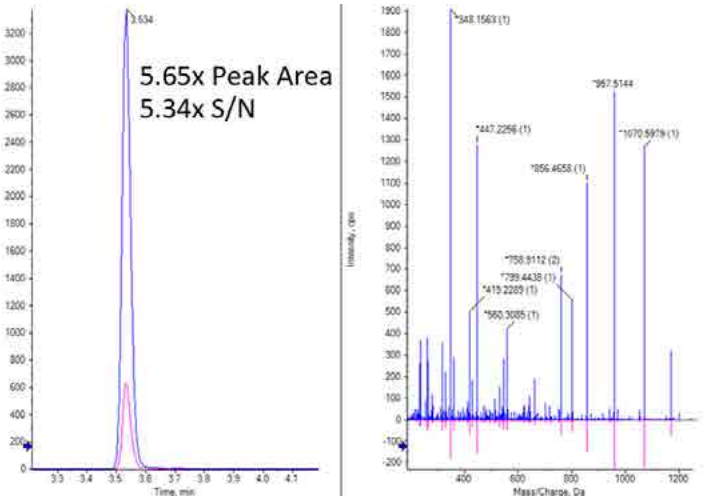


All ions enter the TOF at the same time, achieving

>90%

duty cycle

ZenoTOF 7600+ system



Key Findings from the Study

- ZT Scan DIA identified up to three times more phosphopeptides compared to traditional discrete-window DIA techniques.
- Detected previously unseen low-abundance phosphopeptides.
- Improved accuracy of phosphopeptide characterization.

Conclusions

ZT Scan DIA significantly enhances phosphopeptide discovery, offering a more comprehensive understanding of cellular signaling pathways. This advancement holds the potential to provide better insights into disease mechanisms and aid in the development of targeted therapies.

Throughput (samples-per-day, SPD)	Sample input	Protein Group gain (CV < 20%)
60 SPD	250 ng	7% (8%)
	50 ng	2% (4%)
	5 ng	33% (41%)
	1 ng	46% (51%)
200 SPD	250 ng	18% (17%)
300 SPD	250 ng	21% (21%)
500 SPD	250 ng	55% (55%)

ZT Scan DIA boosts performance overall and particularly for shorter gradients/faster sample throughputs and low sample inputs.

Study Methodology

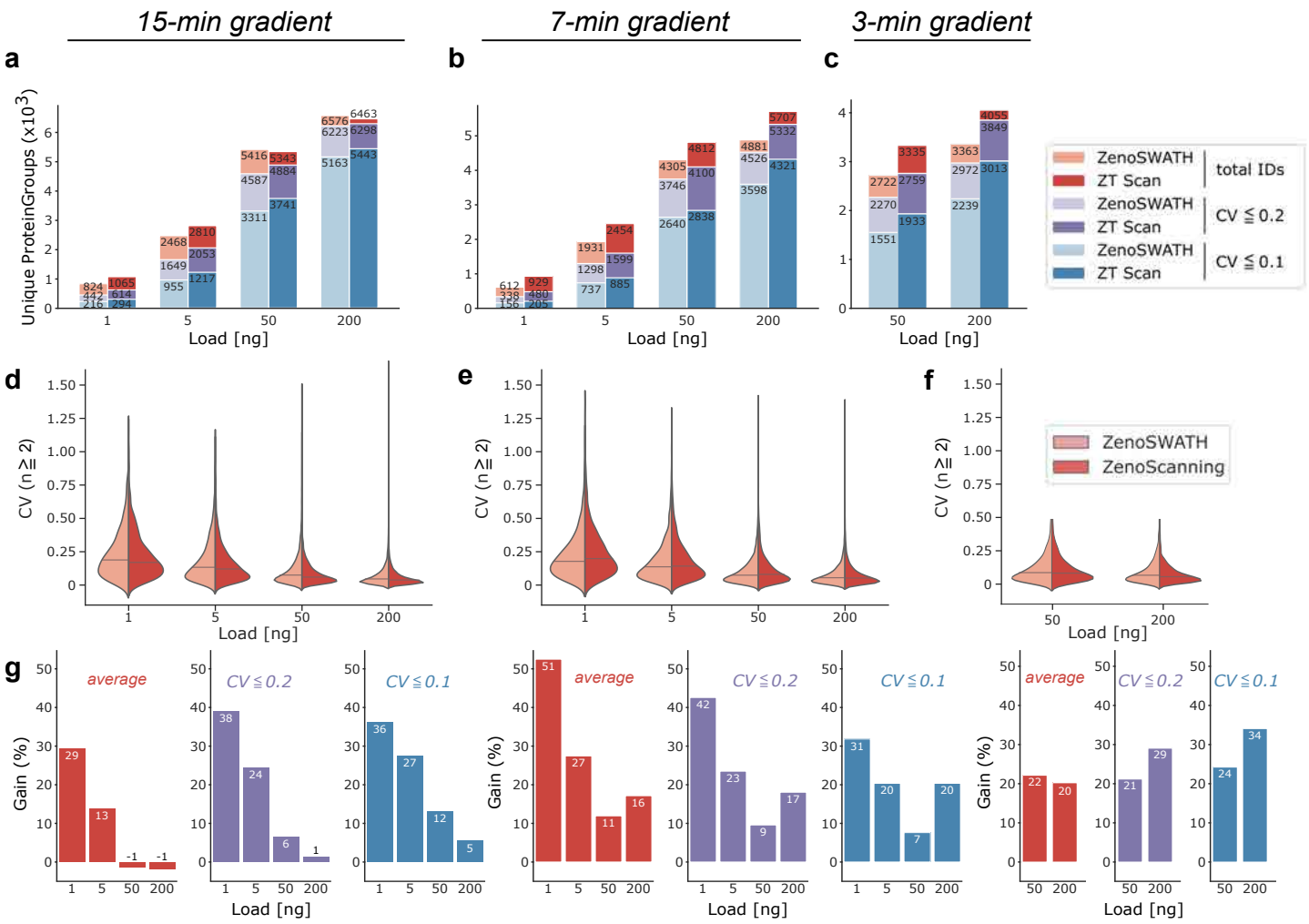
Phosphopeptide samples were collected and analyzed using ZT Scan DIA on a Zeno Trap-enabled QTOF system. The study implemented a high-throughput workflow with shorter liquid chromatography (LC) run times and higher duty cycles to maximize efficiency. High-quality MS/MS spectra were generated for precise quantification and data were analyzed using advanced statistical methods to ensure accuracy and reliability.

Implications

The success of ZT Scan DIA in phosphopeptide discovery suggests its potential for widespread adoption in proteomic research, particularly in studies focused on cellular signaling. This could lead to advancements in understanding and treating diseases related to signaling pathway dysregulation.

Advancing Glycoproteomics with ZT Scan DIA

This study explores the use of ZT Scan DIA in advancing glycoproteomics, focusing on the identification and characterization of glycopeptides. The technology aims to provide a broader and more accurate understanding of glycoprotein functions and their roles in diseases.

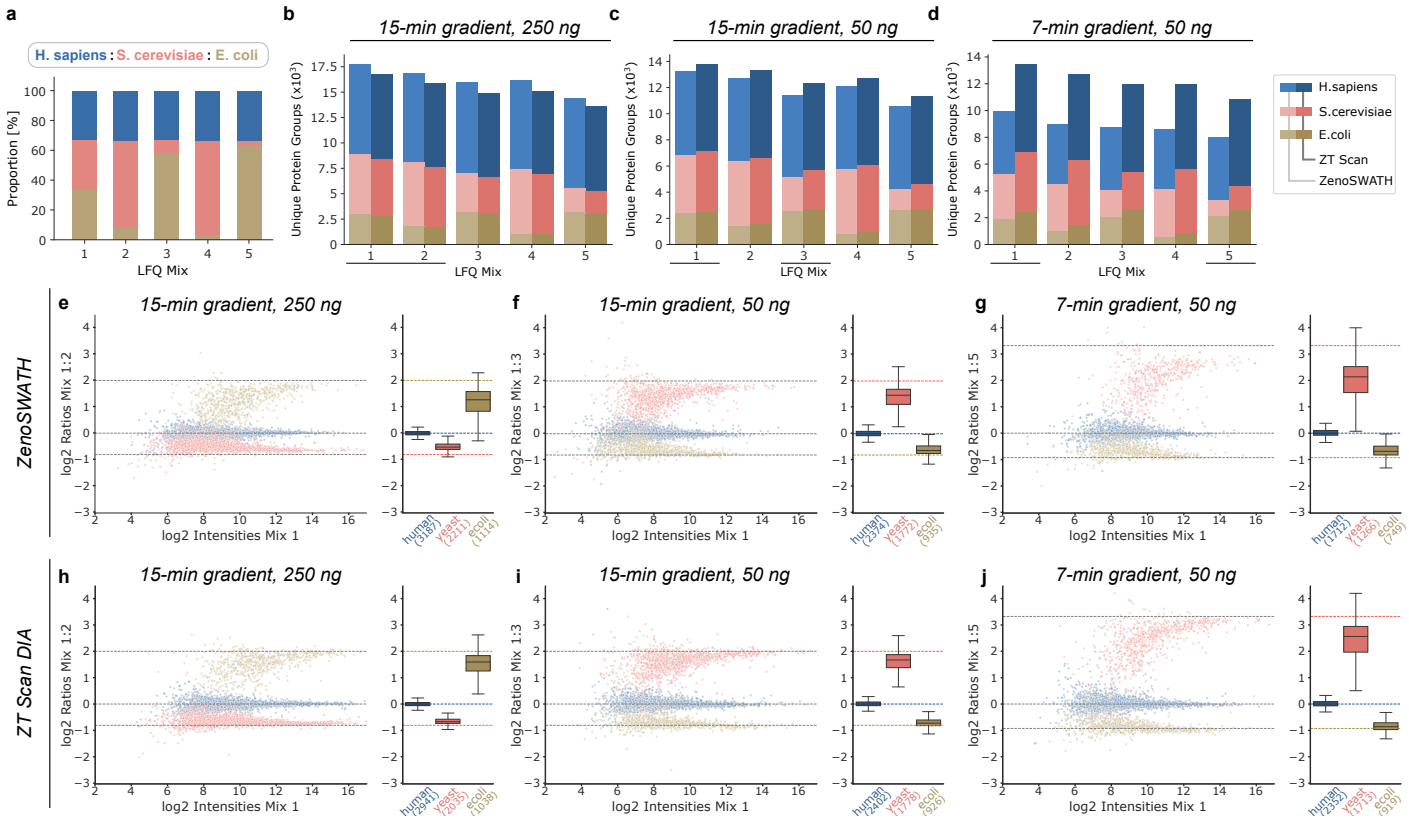


Study Methodology

Glycoprotein samples were analyzed using ZT Scan DIA, which utilized high sensitivity and specificity for accurate mapping of glycopeptide fragments. High-quality MS/MS spectra were generated to ensure precise quantification.

Key Findings from the Study

- ZT Scan DIA identified a broader range of glycopeptides.
- Detected previously unseen low-abundance glycopeptides.
- Improved the accuracy of glycopeptide characterization, providing comprehensive data for glycoproteomics research.



Conclusions

ZT Scan DIA significantly enhances glycoproteomics research by delivering more comprehensive and accurate data. This advancement improves our understanding of glycoprotein functions and their implications in diseases.

Implications

The enhanced capabilities of ZT Scan DIA in glycoproteomics suggest its potential to revolutionize research in this field and could lead to better diagnostics and treatments for diseases where glycoproteins play a crucial role, facilitating advancements in personalized medicine.

ZT Scan DIA in Pancreatic Cancer Biomarker Discovery

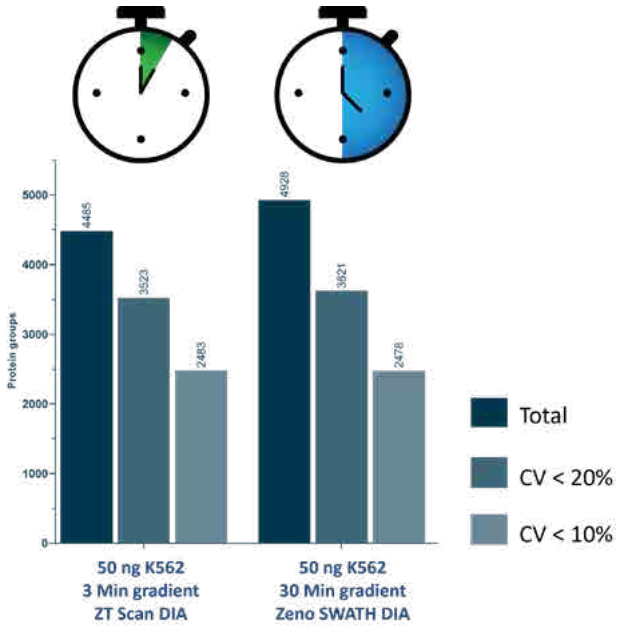
This study focuses on the application of ZT Scan DIA in discovering novel biomarkers for pancreatic cancer. By providing deeper insights into the disease's molecular mechanisms, ZT Scan DIA helps advance pancreatic cancer research, leading to improved diagnostic and therapeutic strategies.

Study Methodology

Pancreatic cancer tissue samples were analyzed using ZT Scan DIA, employing a high-throughput workflow with shorter LC run times and high sensitivity. High-quality MS/MS spectra were generated for precise quantification. The study utilized sophisticated data analysis methods to ensure the reliability of biomarker identification.

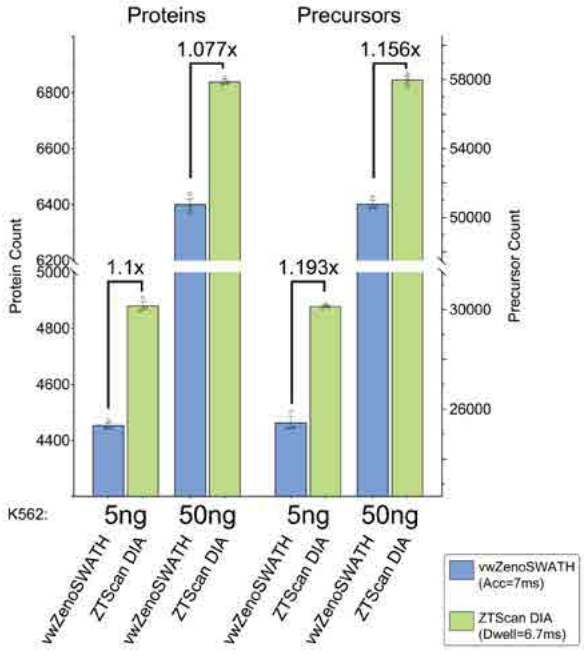
Key Findings from the Study

- ZT Scan DIA has the capacity to identify novel biomarkers for pancreatic cancer.
- Provided deeper insights into the molecular mechanisms of pancreatic cancer.
- Improved accuracy of biomarker identification and quantification.



Conclusions

ZT Scan DIA significantly advances pancreatic cancer research with the potential to uncover novel biomarkers. This advancement has the potential to inform better diagnostics and targeted treatments for pancreatic cancer.



Implications

The successful application of ZT Scan DIA in pancreatic cancer biomarker discovery highlights its potential for broader use in cancer research. SCIEX technology could help facilitate the development of more effective diagnostic tools and treatments, ultimately improving patient outcomes in pancreatic cancer and other malignancies.

Conclusion

Revolutionizing Biomedical Research

The introduction of SCIEX ZT Scan DIA technology has significantly transformed the landscape of proteomic and biomarker analysis. It has demonstrated exceptional sensitivity, specificity and quantitative performance, providing comprehensive and accurate data across various research domains.

ZT Scan DIA method versatility is evident in its successful application across multiple research fields, including glycoproteomics and cancer biomarker research. This has led to a deeper understanding of complex biological processes and disease mechanisms.

Key Findings from the Study

- Across all studies, ZT Scan DIA consistently identified a greater number of biomarkers and low-abundance molecules that were previously undetectable using traditional methods.
- Provided high-quality MS/MS spectra, ensuring precise quantification and characterization of proteins, peptides, and glycopeptides.
- Novel biomarker discoveries for research in various diseases, including cancer, neurodegenerative and cardiovascular diseases, informing potential future diagnostic and therapeutic strategies.
- ZT Scan DIA enabled a more detailed and accurate proteomic profile, offering deeper insights into the molecular mechanisms underlying complex biological processes.

Future Directions

- Explore the use of ZT Scan DIA in additional research areas such as rare diseases, metabolic disorders, and personalized medicine, to further harness its potential.
- The comprehensive data provided by ZT Scan DIA will be instrumental in developing more accurate and reliable diagnostic strategies for various diseases, enhancing early detection and patient outcomes.
- Leveraging the novel biomarkers and molecular insights gained from ZT Scan DIA, researchers can investigate more effective and targeted therapeutic development, ultimately leading to improved treatment efficacy and patient care.
- Ongoing refinement and development of ZT Scan DIA technology will focus on further enhancing its sensitivity, specificity, and throughput capabilities, maintaining its position at the forefront of proteomics research and expanding further to metabolomics and lipidomics studies.

Final Remarks

- ZT Scan DIA stands out for its ability to detect low-abundance molecules with high quantitative precision and accuracy, setting a new benchmark in proteomic analysis.
- This innovative approach ensures comprehensive and detailed data acquisition, providing researchers with invaluable insights into complex biological systems.
- ZT Scan DIA's successful application in diverse research areas underscores its versatility and potential to drive advancements in various biomedical fields.
- By enabling the discovery of novel biomarkers and offering deeper molecular insights, ZT Scan DIA is at the forefront of driving innovation and discovery in biomedical research.

Further Reading and Resources

ZenoTOF 7600+ system

Video: First impressions of ZT Scan DIA, Tim Heymann – Mann Lab, Max Planck Institute of Biochemistry.

Video: Enhancing quantitative proteomics: EAD and ZT Scan DIA - Ludwig Roman Sinn, Ralser and Demichev Labs, Charité – Universitätsmedizin Berlin.

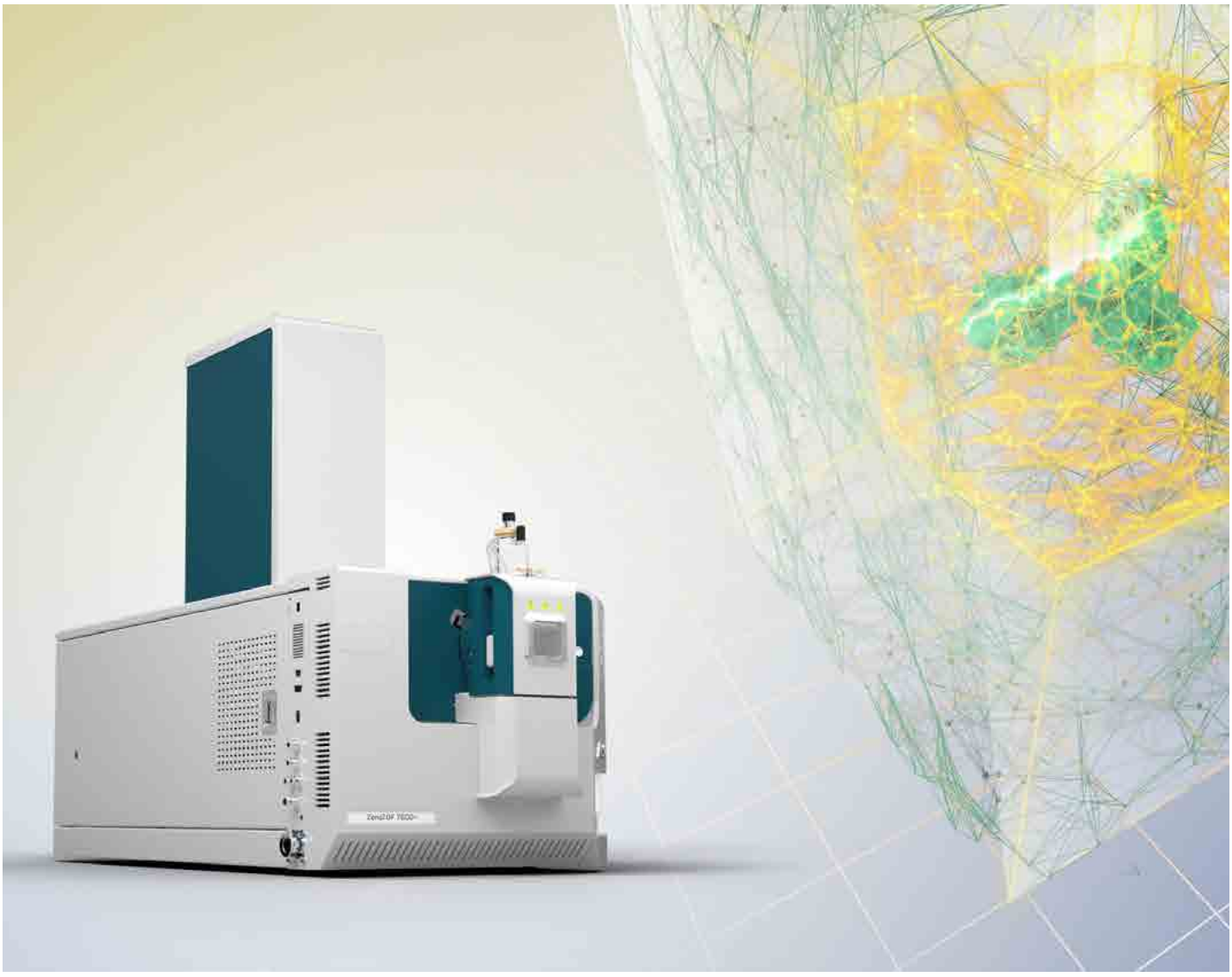
Technical overview: Continuing the data-independent acquisition (r)evolution: Introducing ZT Scan DIA for quantitative proteomics.

Technical note: Improved proteomics performance at high throughput using ZT Scan DIA on the ZenoTOF 7600+ system.

Technical note: Improved proteomics performance for low sample loadings using ZT Scan DIA on the ZenoTOF 7600+ system.

Technical note: Selecting optimal ZT Scan DIA acquisition methods on the ZenoTOF 7600+ system for quantitative proteomics.

Product brochure: ZenoTOF 7600+ system.



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