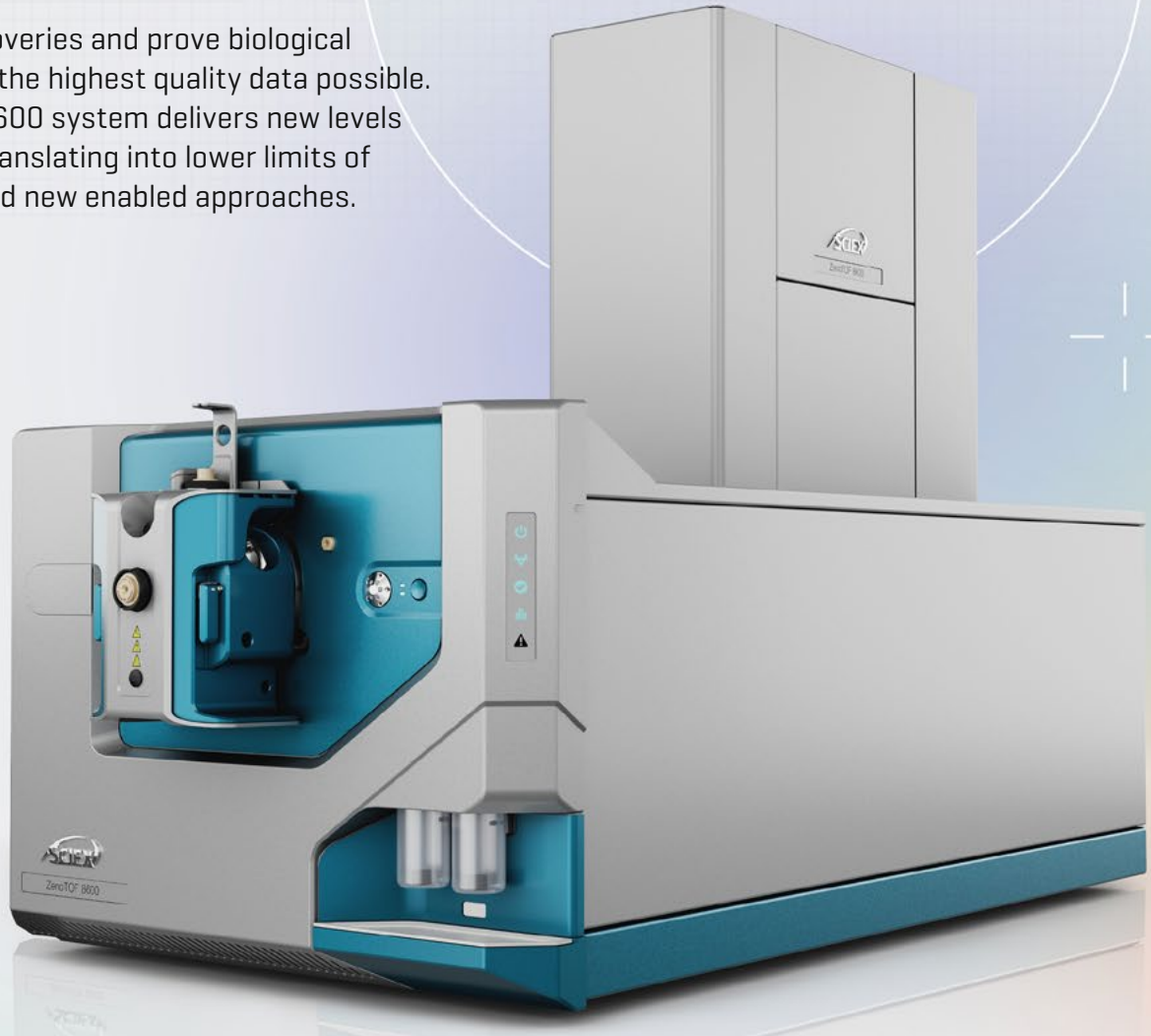
SCIEX ZenoTOF 8600 system

Extraordinary discoveries **demand** extraordinary proof

Drive new discoveries and prove biological relevance with the highest quality data possible. The ZenoTOF 8600 system delivers new levels of sensitivity translating into lower limits of quantitation and new enabled approaches.



danaher

The power of precision

Introduction

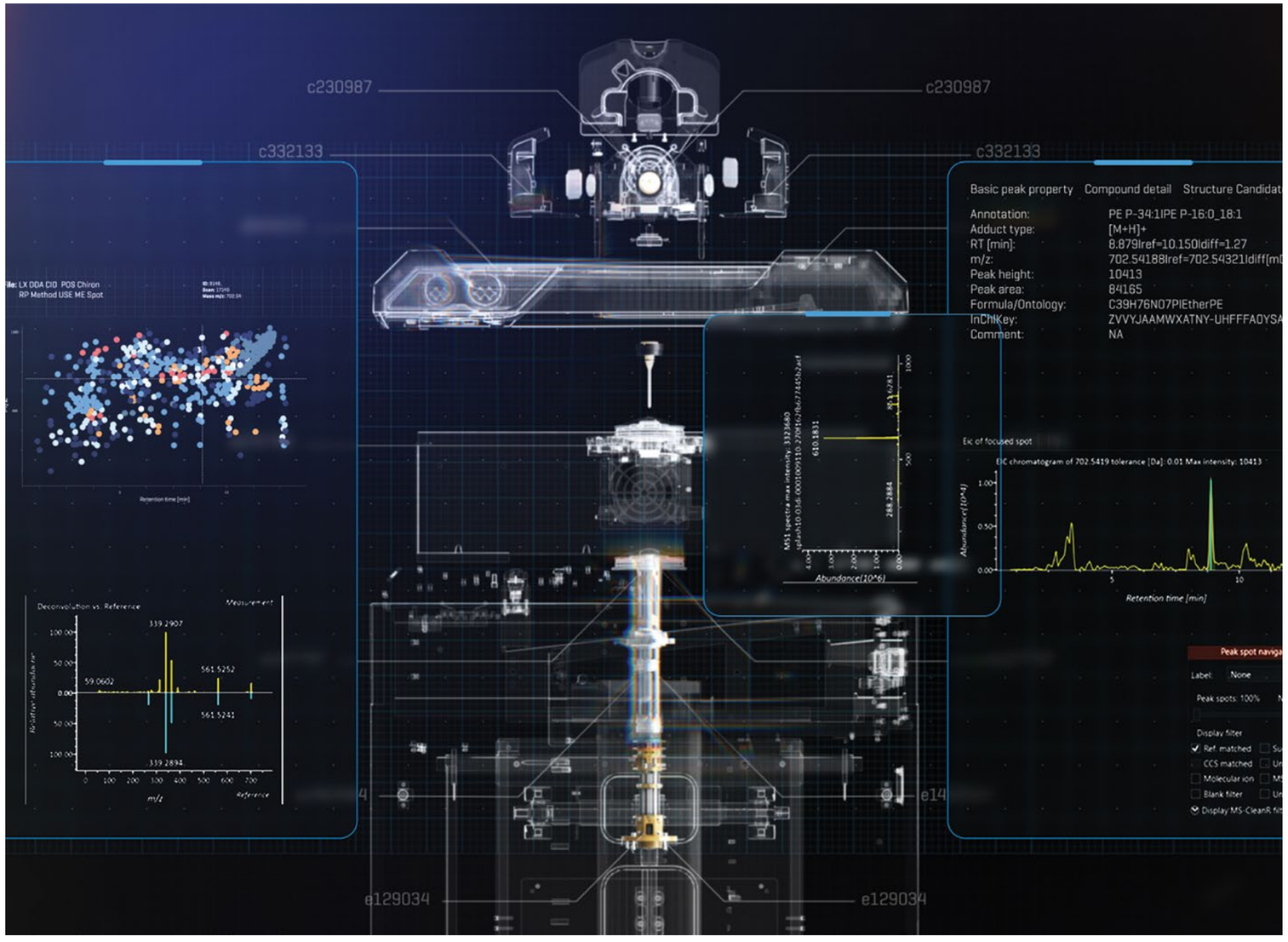
Welcome to the forefront of scientific innovation. In the quest to make groundbreaking biological discoveries, the quality of data and the technology used are paramount.

The **ZenoTOF 8600 system** combines proven technology from our most sensitive triple quad with that of our most versatile accurate mass innovations. This new platform delivers 10x improvement in sensitivity* and the speed to unlock enhanced performance across a multitude of accurate mass workflows.

- The discovery of low-abundance protein or metabolite biomarkers requires high quantitative precision so that they can be translated into clinical research.
- Precise characterization of drug metabolites and disease-associated lipids requires rich and sensitive MS/MS data generated using versatile fragmentation techniques.
- Quantitation of a wide variety of low-abundant compounds requires simultaneous sensitivity, precision, and speed—usually a challenge for ordinary, accurate mass technology.

The **ZenoTOF 8600 system** represents a leap forward in mass spectrometry, offering noteworthy sensitivity and precision.

This brochure will guide you through the capabilities of the **ZenoTOF 8600 system**, showcasing how it can transform your research by enabling the detection and quantitation of low-abundance biomarkers with extraordinary accuracy. Discover how this advanced system can help elevate your research, providing the robust data you need to drive new discoveries and prove biological significance.



10x

better sensitivity across scan modes compared to SCIEX previous instrument

You're understandably skeptical. You're supposed to be. That's why we're giving you access to the technical data as a part of our launch.

Access the data driving our claims

Learn more

*Compared to the ZenoTOF 7600+ system

Features of the SCIEX ZenoTOF 8600 system

Ionization source

The OptiFlow Pro ion source incorporates the reliability and efficiency of the Turbo V ion source while providing flexibility for quickly switching flow rates.

Mass Guard technology with optical detector

The novel combination of Mass Guard technology and a new optical detection system allows the instrument to operate effectively at higher ion currents while protecting it from contamination.

ZenoTOF versatility

Zeno trap can be enabled to deliver enhanced sensitivity. Ions are accumulated in the Zeno trap before being pulsed rapidly into the TOF, meaning we can detect up to 20x more ions than a classical QTOF design.

Scan speeds of up to 858 Hz

The fastest SCIEX QTOF yet! When using ZT Scan DIA 2.0, the isolation window for MS/MS slides along the m/z range of interest during each cycle. With a quadrupole scan speed of up to 4000 Da/s, the system can operate at a MS/MS scan rate of up to 858 Hz, dependent on the pre-defined mass range, (not accounting for multiple precursors in a single isolation encoded window).

ZT Scan DIA 2.0 for all molecule types

The flexibility in mass range and compound parameters extends functionality across diverse workflows, including small molecule analysis. Methods are easy to set up and require minimal user optimization, facilitating the analysis of large sample cohorts.

High-energy EAD

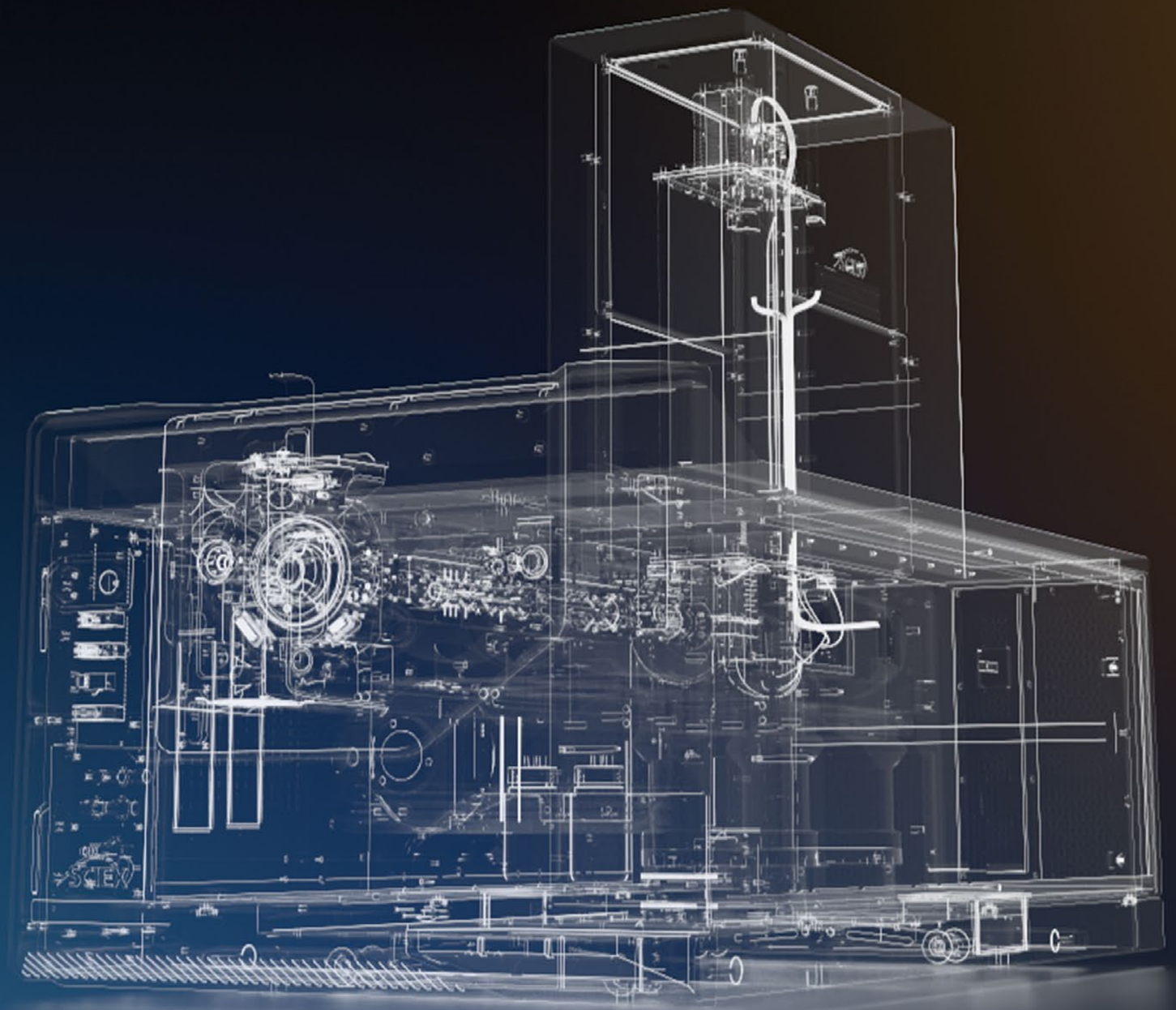
Acquire higher-quality EAD spectra faster across all molecule types*. Perform CID or EAD profiling on equivalent timescales, gaining deeper insights into lipid biology, protein modifications, and metabolite structures. Extend electron-based fragmentation capabilities into negative ionization with up to 50 eV.

Integrated innovation

SCIEX OS 4.0 software enables users to track instrument performance, instrument health and enhanced automated system tuning, helping to ensure that users can easily attain and maintain optimum performance from their system.

More energy efficient

The **ZenoTOF 8600 system** uses dry roughing pumps, which can reduce electricity consumption by up to 24% relative to oil-sealed pumps.



*Compared to the ZenoTOF 7600+ system

An accurate mass platform evolved from SCIEX leadership in fast, sensitive, and resilient quantitation

Ion generation

- The OptiFlow Pro ion source incorporates the reliability and efficiency of the legendary Turbo V ion source while providing flexibility for quickly switching flow rates
- A versatile ion source with wide compound coverage with interchangeable ESI and APCI towers and a dedicated nano module
- All flow rate calibration probes to remove the complexity of maintaining mass accuracy

Ion transmission

- The tapered dodecapole geometry of the DJet ion guide focuses the ions into the second stage QJet ion guide
- By prefocusing the larger ion flux through the wider orifice, the D Jet ion guide increases system sensitivity and improves the signal-to-noise ratio
- Dual-frequency modes for QJet operation improve transmission of high m/z (>4000 Th)

Optical detection

- The novel combination of Mass Guard technology and a new optical detection system allows the system to operate effectively at higher ion currents while protecting it from contamination
- Robust scintillators and photon multipliers in the optical detector extend lifetime and together with enhanced algorithms improve LDR and maintain mass accuracy

Zeno trap and EAD cell

- Highly tunable electron activated dissociation (EAD) allows for a range of free electron- based fragmentation mechanisms within one device
- Zeno trap delivers improved MS/MS duty cycle gain with 5-20X gain in MS/MS sensitivity coupled with either EAD or CID fragmentation when compared to the classical QTOF design

Mass guard technology

- Integration of our innovative ion filtering technology from the 7500+ QTRAP system
- Mass Guard technology is incorporated in Q0 and creates a high m/z cut-off above the target mass range, which removes unwanted high m/z species and narrows the m/z range of ions transmitted past Q0

Key benefits of the ZenoTOF 8600 system

A new accurate mass platform evolved from SCIEX leadership in fast, sensitive and resilient quantitation. Performance that lets you do more with a single system; sensitivity and functional speed improvements in MS1 and MS2 enhance data quality across many workflows.

10x sensitivity

- 10x more sensitivity in MS1 and MS2* allows for the high-precision identification of low-abundance proteins, lipids, and metabolites using targeted, DIA, and DDA methods.
- The incorporation of proven SCIEX triple quad technology enables fast and sensitive quantitation, with up to 10-fold lower LOQs and a linear dynamic range of up to 5 orders*.

Deliver on important timelines

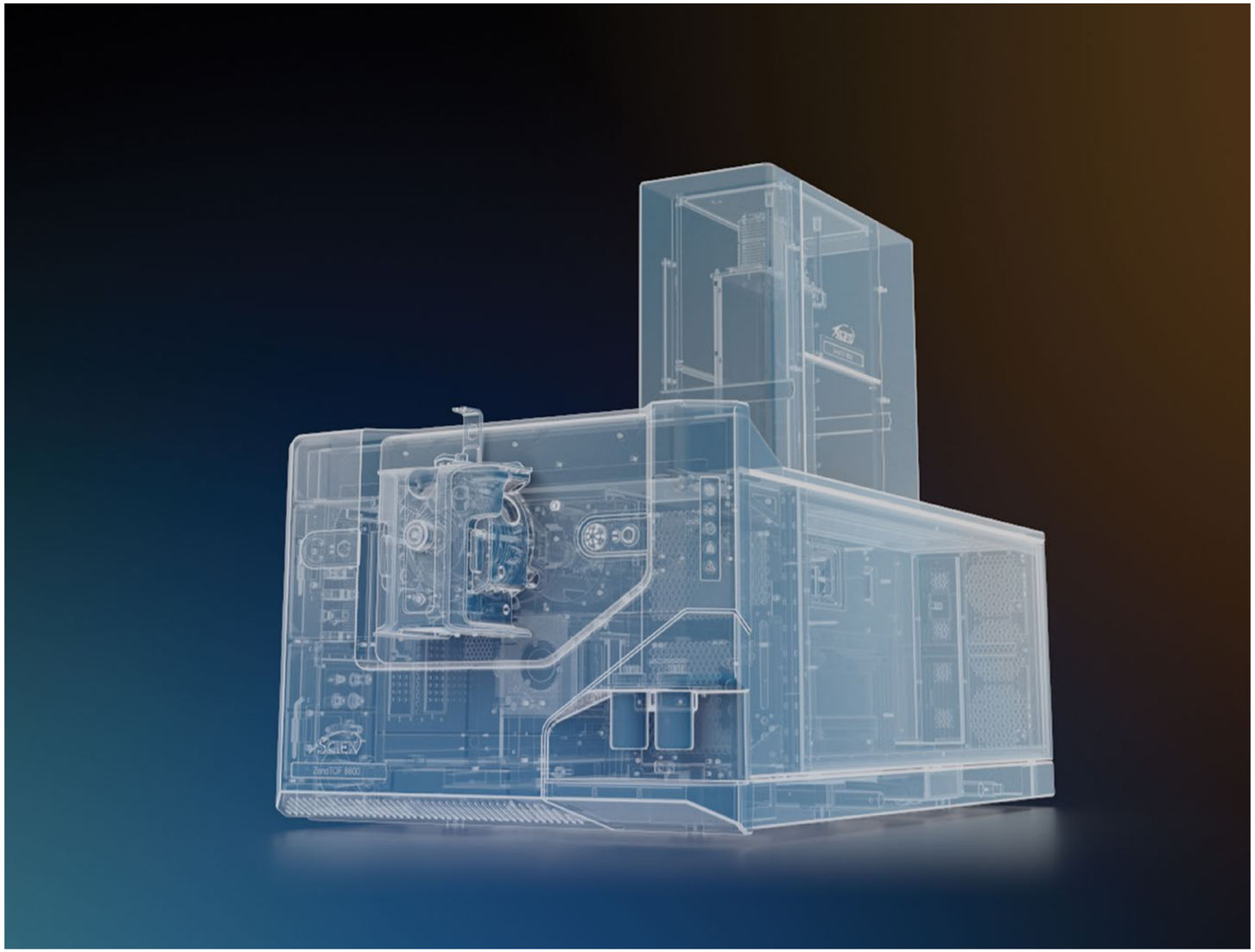
- Sensitivity and performance-driven functional speed improvements* maximise throughput.
- The ability to acquire higher-quality EAD spectra faster unlocks new approaches such as rapid data-dependent acquisition, gaining deeper insights into lipid biology, protein modifications, and metabolite structures.

Discover more with comprehensive data analysis

- ZT Scan DIA 2.0 unlocks broader molecule support with higher speeds*.
- Tailored Q1 window selectivity helps maximize the quantitative accuracy and boost annotated identifications.
- With an extended mass range that enables all molecule workflows, ZT Scan DIA 2.0 is the most comprehensive SWATH DIA approach and a powerful high-throughput discovery tool for omics research.

Transforming data into actionable insights

- Simplify, streamline and optimize workflows using SCIEX OS 4.0 software. The latest developments encompass a comprehensive portfolio of innovative features to maximize the capabilities of the ZenoTOF 8600 system, from method development to real-time QC and data acquisition.
- Strategic software collaboration to deliver optimized data insights and drive discovery, including PEAKS software and DIA-NN for proteomics and MS-DIAL for metabolomics and lipidomics data processing.



*Compared to the ZenoTOF 7600+ system

Demand more than protein identification

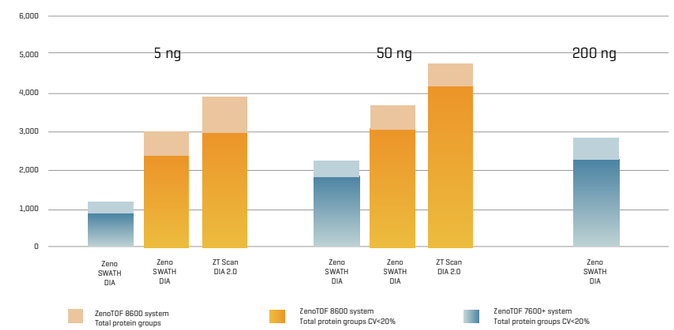
Quantify everything you identify with precision using ZT Scan DIA 2.0, and with 10x more sensitivity*, extend your capacity into low cell number research. Now even small fold changes to be discovered and verified credibly.

Up to

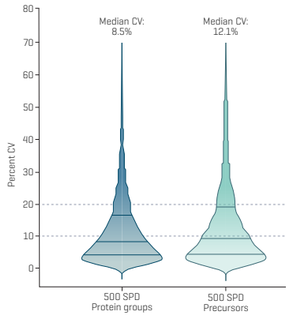
3x

more protein groups identified using HT 500 SPD compared to the previous generation QTOF system

High-throughput proteomics powered by Zeno trap enabled DIA



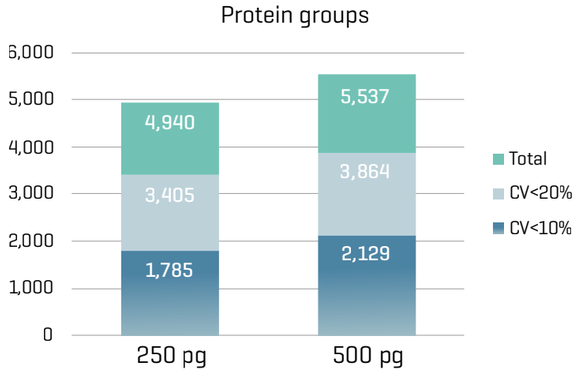
More protein groups and precursors were identified at 5 ng loadings on the ZenoTOF 8600 system than at 200 ng loadings on the ZenoTOF 7600+ system. Using ZT Scan DIA 2.0 resulted in further gains in identifications compared to using Zeno SWATH DIA. ZT Scan DIA 2.0 enables gains in quantitative identifications for precursors and protein groups of >5-fold and >3-fold, respectively.



Quantify everything you identify with an average %CV of 8.5 using ZT Scan DIA 2.0.

Read technical note

Working towards low cell number



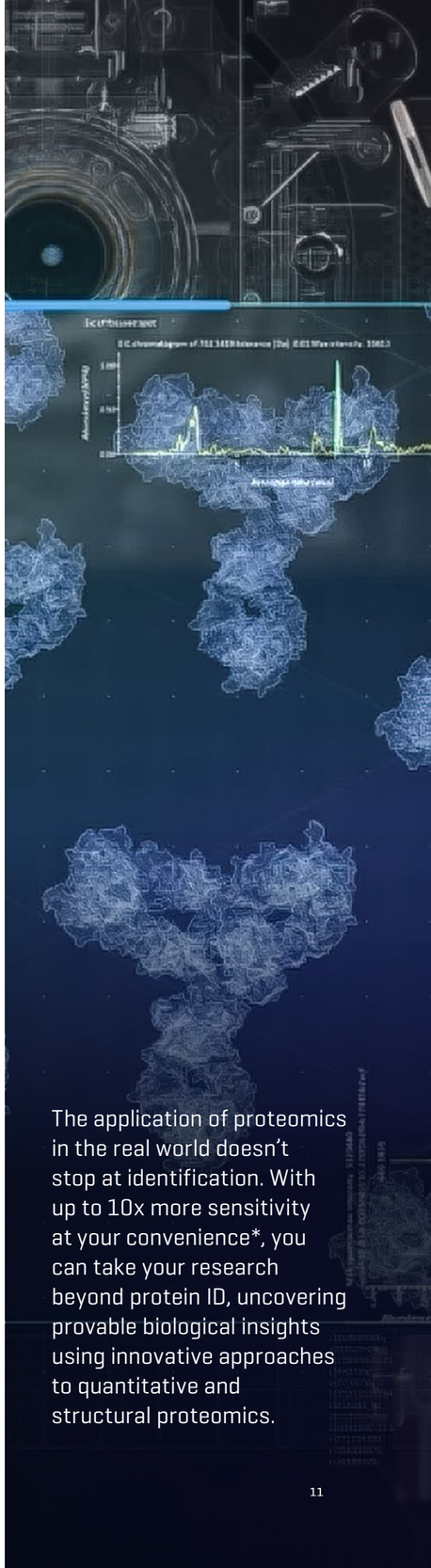
Identify up to 2.5x more proteins at low loads of just 250pg* with Zeno SWATH DIA. The ability to identify and reliably quantify over 4900 proteins from 250pg of K562 cell lysate opens the door for low cell number research that can uncover nuanced biological insight

Read technical note

"The ZenoTOF 8600's performance in our hands has been excellent—fast, sensitive, and remarkably stable. It opens up new workflows in both discovery and targeted proteomics without compromising throughput."

Matthias Mann
Professor, Max Planck
Institute of Biochemistry

*Compared to the ZenoTOF 7600+ system

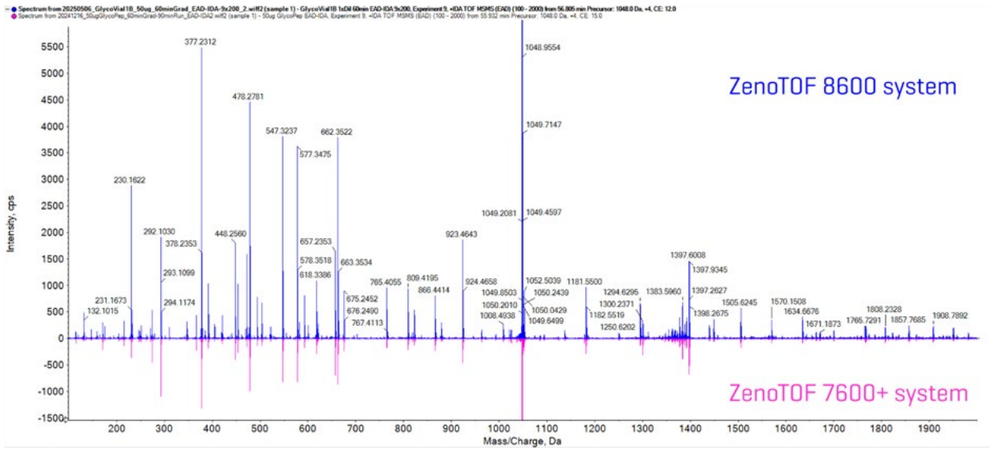


The application of proteomics in the real world doesn't stop at identification. With up to 10x more sensitivity at your convenience*, you can take your research beyond protein ID, uncovering provable biological insights using innovative approaches to quantitative and structural proteomics.

Performance that lets you do more with a single system

The increased sensitivity and functional speed improvements unlock a multitude of new approaches*, such as fast, precursor resolution DIA and discovery EAD using DDA. Generate rich, reproducible data that stands up to peer review, enhancing your understanding of cellular processes and their role in disease.

Comprehensive structural characterization and site localization of PTMs

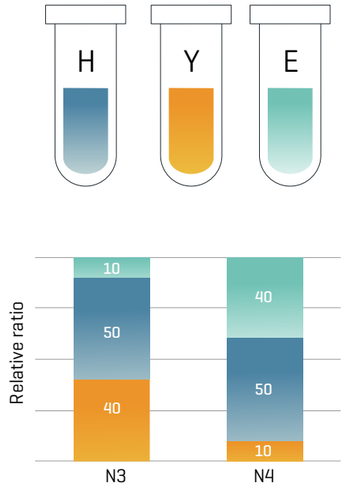


Characterize low-abundance protein and peptides that were previously undetectable*. Identify and localize crucial, sitespecific post-translational modifications (PTMs) to understand their functional diversity.

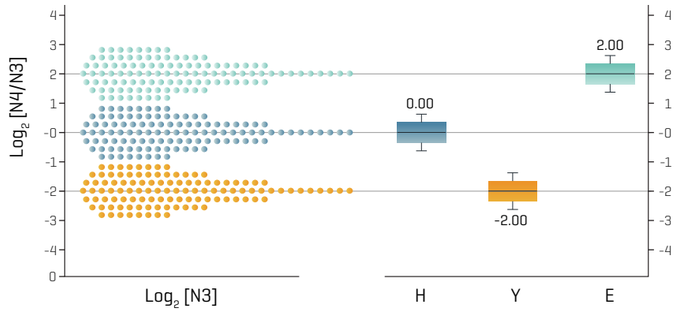
EAD MS/MS spectrum of glycopeptide IYPGVDFGGEELN(HexNAc)4(Hex)5(NeuAc)2VTFVK (P03952|KLKB1_HUMAN), precursor mass 1047.954 Da

*Compared to the ZenoTOF 7600+ system

Accurate quantitation



	Human	Yeast	E.coli
Expected Ratio	0.00	-2.00	2.00
Observed Ratio	-0.08	-2.11	1.85
Difference	-8%	-6%	-8%



Accurate LFQ across three species is essential to ensure reliable cross-species comparisons of protein expression. It also validates the robustness of the quantitation method across different proteomes. The ZenoTOF 8600 system enables accurate quantitation of 3 individual proteomes in a 3 species mix, with values measure to within 8% of the expected.

Software is the vital connector between technology and insights that will drive discovery.

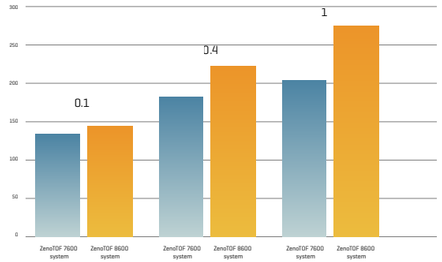
Whether characterizing potentially complex proteins, routinely screening or quantifying modalities in complex matrices, each of these workflows requires advanced data processing technologies to interrogate data and deliver actionable insight. To help you make these discoveries with your existing data pipeline, the ZenoTOF 8600 system is compatible with various third-party software tools.

The proof to confidently assign biological significance across the metabolome

Improved lipid and metabolite identification

Detect, differentiate, and quantify low-abundance metabolites and lipids with up to a 10x sensitivity increase in MS1 and MS2 compared to existing SCIEX accurate mass technology.

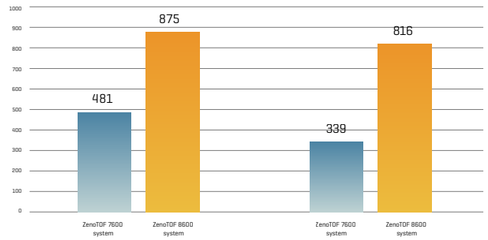
Untargeted metabolomics (DDA)
data processed using MS-DIAL 5.5 software



Plasma equivalents

Poor quality, irreproducible data can jeopardize your discoveries. Using traditional CID-based DDA approaches, reference-matched metabolite IDs are boosted by up to 1.4x and lipids by up to 1.8x, with significantly higher signal-to-noise ratios

Untargeted lipidomics (DDA)
data processed using MS-DIAL 5.5 software



DDA with CID DDA with EAD

EAD on the ZenoTOF 8600 further enhances DDA profiling, offering 15x more fragments at up to 10x greater sensitivity. With up to 2.4x as many lipid structural annotations*, you can identify and annotate lipids at the fatty acid, positional isomer, double bond position, and stereochemistry levels.

Read technical note

Read technical note

Up to

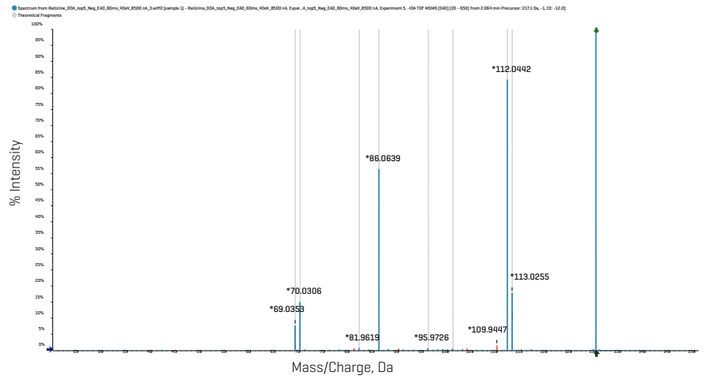
2.4x

more structural lipid annotations compared to SCIEX previous instrument

"The ZenoTOF 8600 enhances significantly our capacity to detect and identify metabolites, to find things that matter, and to understand mechanisms."

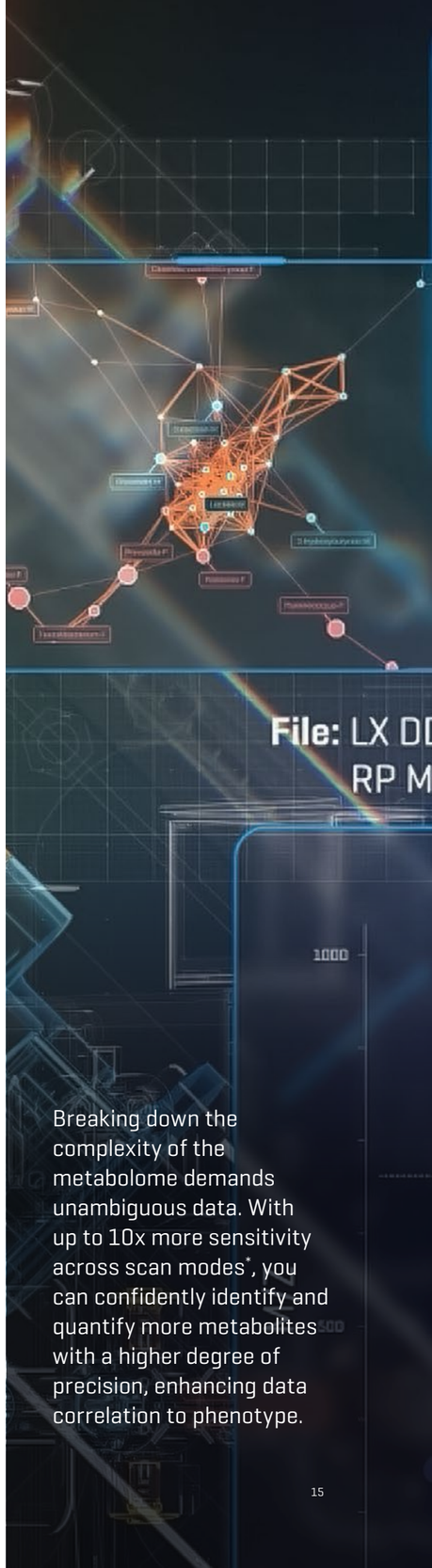
Nicola Zamboni
Adjunct Professor, Inst. of Molecular Systems Biology, ETH Zurich

Introducing higher electron energies up to 50eV



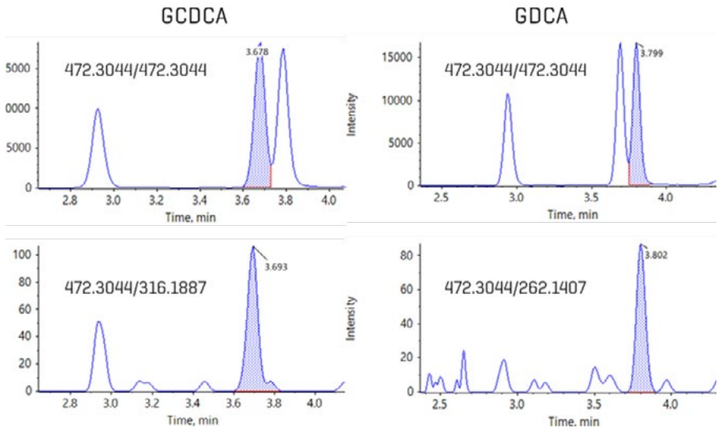
Electron-based fragmentation capabilities can now be extended into negative ionisation mode with a Kinetic energy of up to 50 keV available. A powerful tool for lipidomics, and other metabolites, where some ionize more efficiently in negative mode. This can not only improve sensitivity and selectivity but also lead to better differentiation and characterization of complex mixtures. An example is shown for Isoleucine, data collected at 40 eV.

*Compared to the ZenoTOF 7600+ system



Breaking down the complexity of the metabolome demands unambiguous data. With up to 10x more sensitivity across scan modes*, you can confidently identify and quantify more metabolites with a higher degree of precision, enhancing data correlation to phenotype.

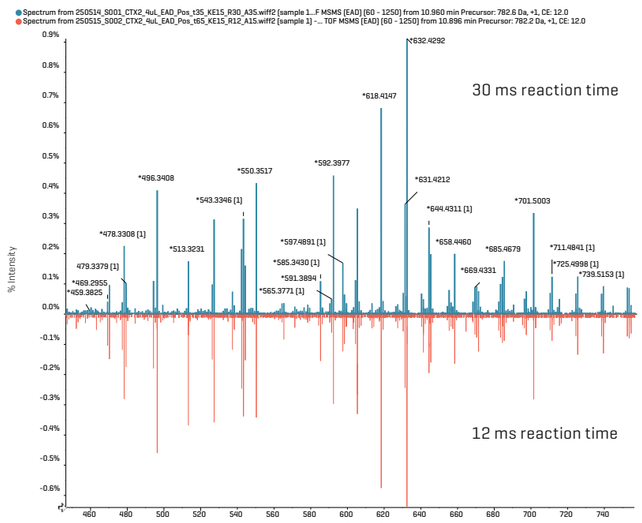
Analytical versatility opens new perspectives, paving the way for extraordinary discoveries



Transforming routine quantitative analysis with EAD-based fragmentation

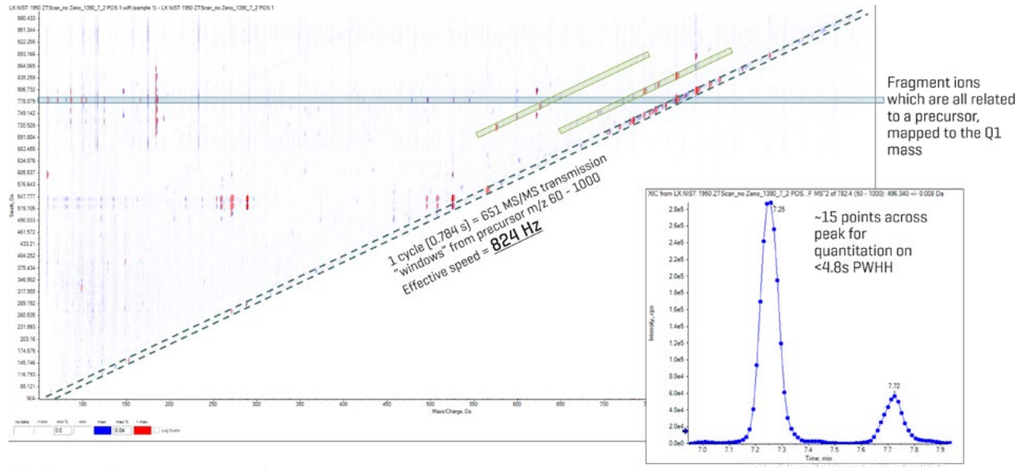
The analysis of isomers that have identical CID-based product ion spectra requires chromatographic method development to ensure quantitative specificity and accuracy. The use of EAD-based fragmentation may mitigate the need for lengthy chromatographic separations and save on method development time. For example, bile acid isomers can be resolved using EAD-based fragmentation. GCDCA and GDCA, which are indistinguishable by CID-based fragmentation, have unique, diagnostic fragments using EAD. These fragments can be used to specifically quantitate each isomer, regardless of their chromatographic separation

Read technical note



Faster, high-energy EAD

Increased sensitivity translates into faster acquisition of high-quality EAD spectra, giving more experimental flexibility for deeper insights into lipid biology and metabolite structures, enabling the identification of more lipids with increased structural information through annotation acyl chains and localisation of double bond position. For singly charged molecules, a 30 ms reaction time was previously required, but now almost identical results can be achieved at 12 ms. This affords EAD to be run at CID rates, collecting more MS/MS per cycle.



ZT Scan DIA potential for lipidomics

Approach large cohort analysis confidently and help ensure high quantitative accuracy across your datasets. With ZT Scan DIA 2.0, high selectivity DIA with encoded window, precursor isolation approaching unit resolution (1 Da), offering a paradigm shift in untargeted metabolomics and discovery lipidomics, allowing you to quantify previously elusive metabolites and lipids

Unlock the full potential of your metabolomics and lipidomics data

SCIEX works with leading researchers and third-party vendors to enable the processing and integration of metabolomics and lipidomics data. This ensures that as we continue to develop our acquisition strategies, you get the most from your data with cutting edge solutions that enhance data accuracy, scalability, and analytical capabilities.

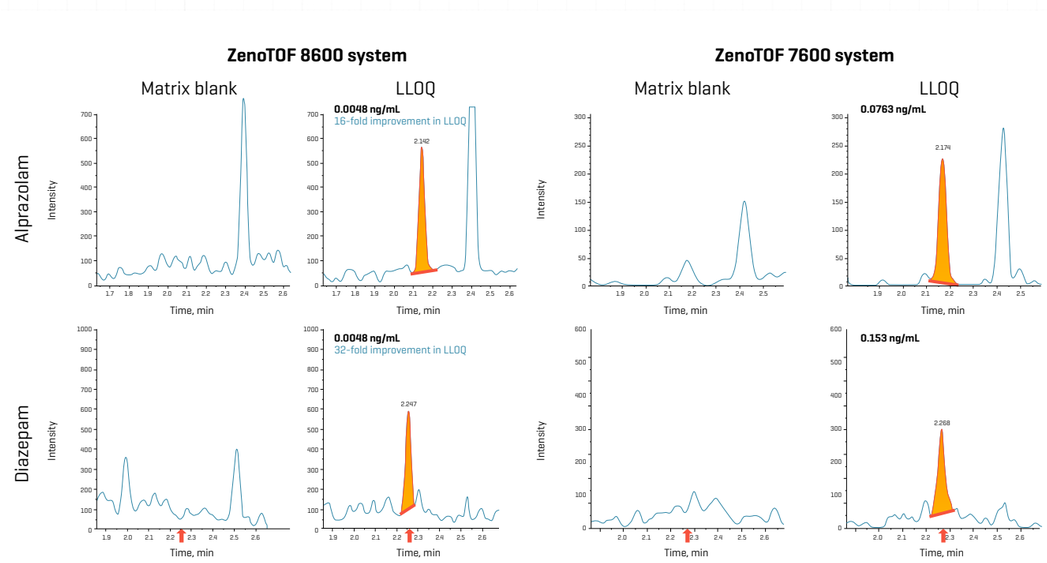
Sensitive quantitation that stands up to scrutiny

Incorporation of proven SCIEX triple quad technology enables fast and sensitive quantitation, with up to 10-fold lower LOQs and a linear dynamic range of up to 5 orders.*

Significantly lower LLOQs can be achieved using the ZenoTOF 8600 system compared to the ZenoTOF 7600 system

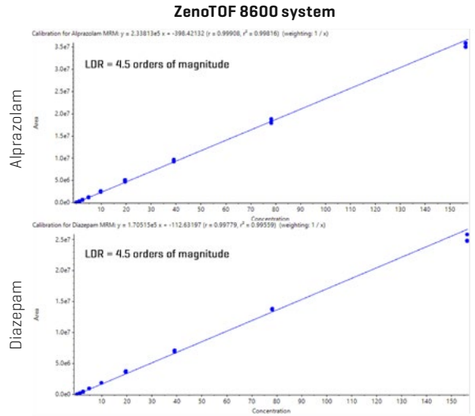
Targeted quantitation

Quantify with single digit-pg/ mL sensitivity for small molecules and up to 5 orders of linear dynamic range in complex biological matrix



Alprazolam, diazepam and trimethoprim showed a 16-, 32- and 8-fold improvement in LLOQ, respectively, compared to the ZenoTOF 7600 system.

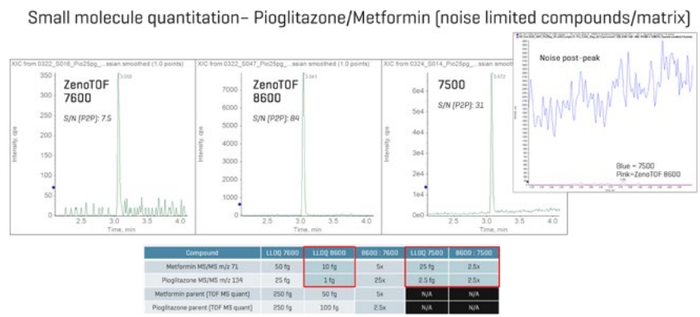
Read technical note



Accurate quantitative performance was achieved with %CV <13% at all concentration levels across a wide linear dynamic range (LDR) of up to 4.5 orders of magnitude.

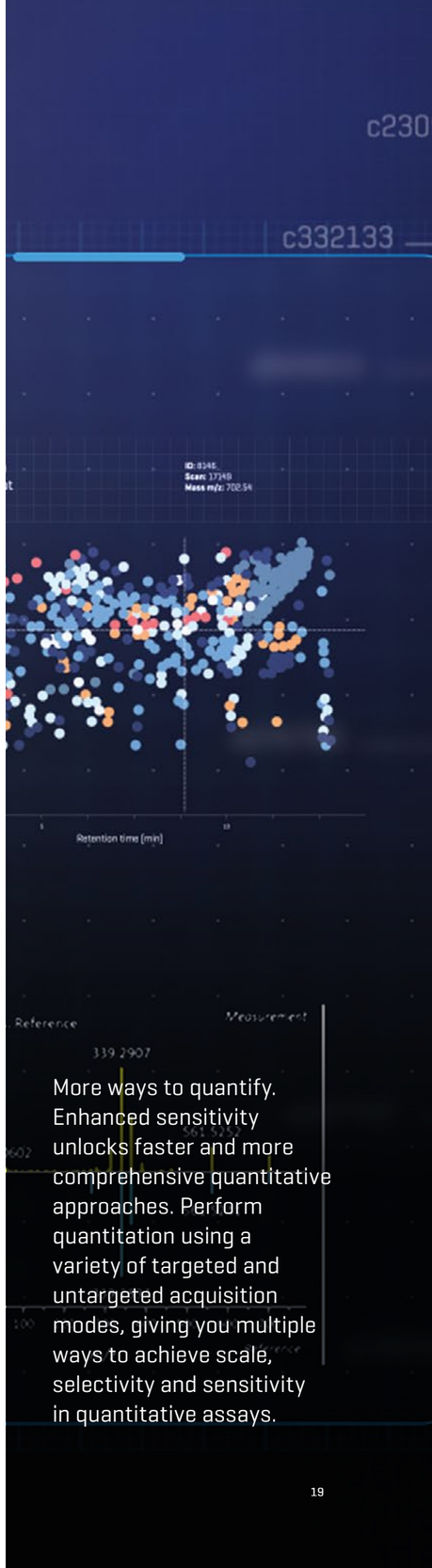
Quantitation without compromise

Tackle quantitation with the added benefits of HRMS to deliver comparable results to a high-end QQQ. Quantify thousands of species from complex samples in short acquisition times and with high precision.



Compound	LLOQ 7600	LLOQ 8600	8600 : 7600	LLOQ 7500	8600 : 7500
Metformin MS/MS m/z 71	50 fg	10 fg	5x	25 fg	2.5x
Pioglitazone MS/MS m/z 134	25 fg	1 fg	25x	2.5 fg	2.5x
Metformin parent (TOF MS quant)	250 fg	50 fg	5x	N/A	N/A
Pioglitazone parent (TOF MS quant)	250 fg	100 fg	2.5x	N/A	N/A

*Compared to the ZenoTOF 7600+ system

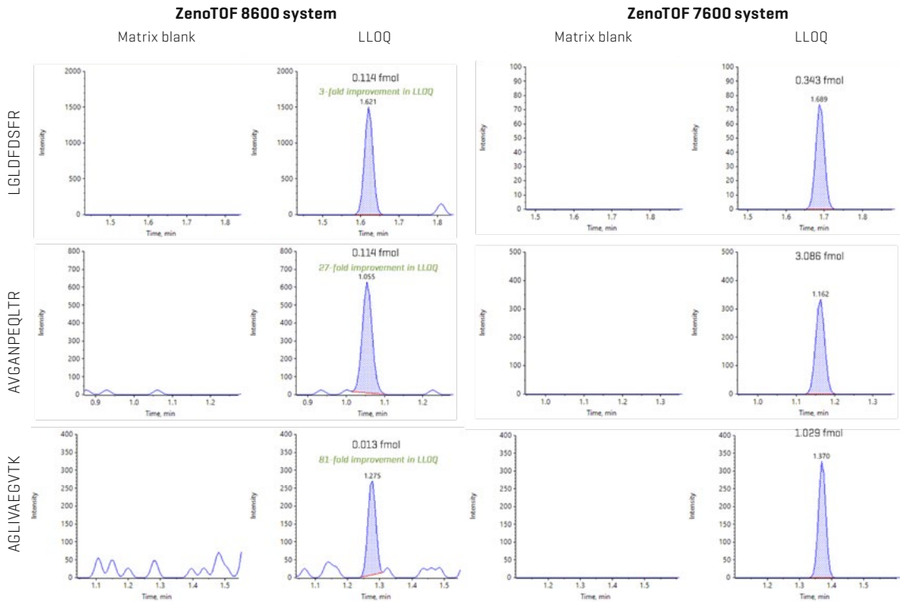


More ways to quantify. Enhanced sensitivity unlocks faster and more comprehensive quantitative approaches. Perform quantitation using a variety of targeted and untargeted acquisition modes, giving you multiple ways to achieve scale, selectivity and sensitivity in quantitative assays.

Sensitive quantitation that stands up to scrutiny (continued)

Accurate mass quantitation is no longer a compromise. With the ZenoTOF 8600 system, expect extraordinary performance across versatile quantitation approaches.

Significantly lower LLOQs can be achieved using the ZenoTOF 8600 system compared to the ZenoTOF 7600 system

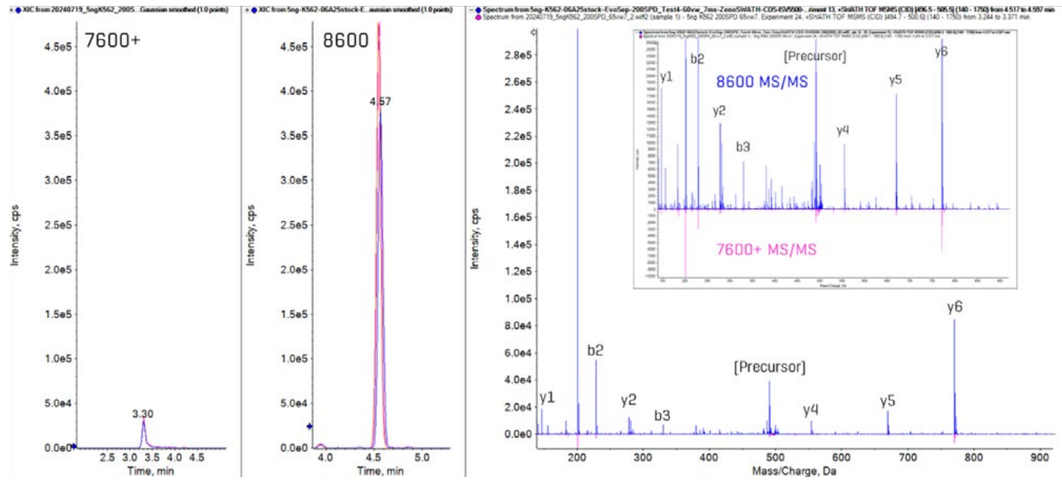


LGLDFDSFR, AVGANPEQLTR and AGLIVAEGVTK showed a 3-, 27- and 81-fold improvement in LLOQ compared to results from the ZenoTOF 7600 system. A sum of 3 fragment ions was applied for quantitation for all peptides.

Accurate quantitative performance was achieved with %CV <13% at all concentration levels across an LDR of up to 4.3 orders of magnitude

Read technical note

Sensitivity gains with the ZenoTOF 8600 system



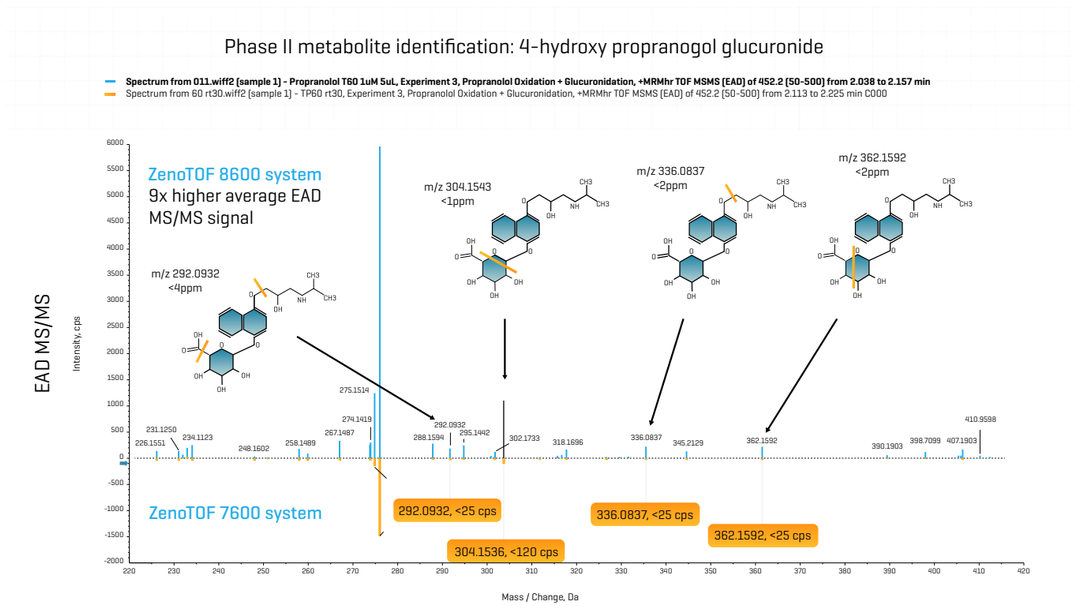
The XIC peak areas increase 10-fold on the ZenoTOF 8600 system. The right panel shows the MS/MS spectrum for this peptide on the ZenoTOF 8600 system (blue trace) and the inverted MS/MS spectrum from the ZenoTOF 7600+ system (pink), demonstrating the difference in signal intensities.

For regulatory quantitative solutions, SCIEX OS software features enhanced user access monitoring and audit trail evaluation. Audit Trail View filters high-risk events for compliance. The Central Administrator Console (CAC) manages users, roles, and projects across systems, supporting all compliance standards. The Configuration Module sets up roles and access levels quickly.

AI Quantitation software streamlines non-regulated sample analysis by leveraging AI and machine learning to reduce fragment selection and data processing time. It automates key calculations like half-life, clearance, IC50, and recovery, helping accelerate access to biologically relevant answers.

Compelling evidence that eliminates uncertainty in metabolite ID

Enhanced EAD MS/MS sensitivity for phase II metabolite identification



Confidently differentiate the sites of metabolism and precisely track minor biotransformations in circulating metabolites. Identify more biotransformations and increase structural certainty with the localization of more sites of metabolism*.

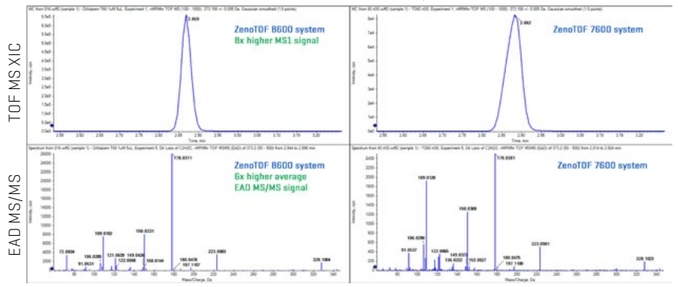
Read technical note

"The enhanced sensitivity of the instrument has helped elevate data quality for drug metabolite characterization and maximize sample efficiency, streamlining clinical and preclinical research processes"

Rahul Baghla
Senior Manager, Pharma and Biopharma Quant SCIEX

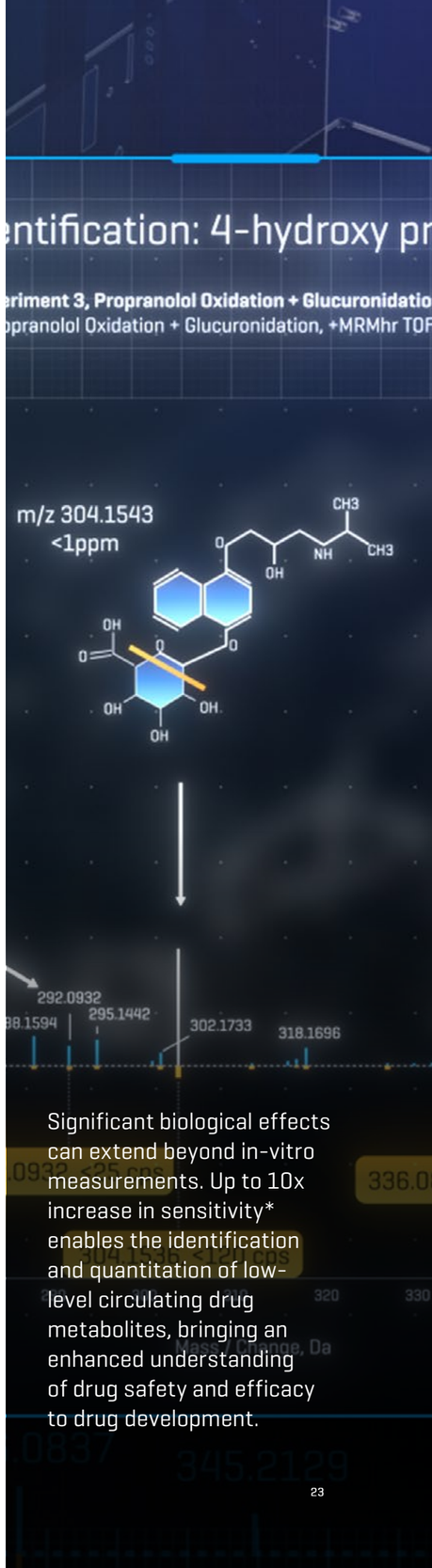
Ultra-sensitive MS1 and EAD MS/MS for phase I and II metabolite identification and characterization

Reduce the risk that critical drug metabolites are undetected. 10x sensitivity across MS1 and MS2* allows you to detect challenging low-abundance phase II metabolites, like glucuronides, in complex biological matrices. This accurate in-vivo data supports the drug's safety profile and efficacy claims, streamlining regulatory submissions.



Molecule Profiler streamlines molecular analysis, uncovering peptide biotransformations and impurities. Boost confidence with MS/MS data using CID and EAD. Efficiently analyze linear and cyclic peptide therapeutic samples with enhanced sensitivity and precision through automated processing software, ensuring compliance and productivity.

*Compared to the ZenoTOF 7600+ system



Significant biological effects can extend beyond in-vitro measurements. Up to 10x increase in sensitivity* enables the identification and quantitation of low-level circulating drug metabolites, bringing an enhanced understanding of drug safety and efficacy to drug development.

"The ZenoTOF 8600 has completely transformed how we approach biomarker discovery. With its incredible sensitivity and the power of ZT Scan DIA 2.0 technology, it won't just improve your research—it will redefine what's possible. For us, it's not just a tool; it's the future of high-resolution mass spectrometry."

Tatjana Talamantes,
Senior Product Manager,
High Resolution Accurate
Mass SCIEX

Software that powers discoveries

The SCIEX ZenoTOF 8600 system is powered by the fully integrated SCIEX OS software, which acquires, processes and reports your accurate mass data.

Bringing integration, integrity and accessibility to large-scale data studies, SCIEX OS is built on a foundation of powerful algorithms and automation that enable efficient data interpretation, at scale, to the level needed for clinical research relevance.

Its remarkable quantitative useability facilitates collaboration, enabling researchers across labs, countries and continents to share insights and produce meaningful impact.

SCIEX OS 4.0 software enables users to track instrument performance, instrument health and enhanced automated system tuning, ensuring users can easily attain and maintain optimum performance from their system.

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Learn more

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Unlock the potential of your SCIEX instruments and operational capabilities with the support of an expert team of engineers, technicians and instrument specialists, helping you to optimize instrument performance, maximize uptime and streamline your laboratory workflows. Nobody knows your system technology and cares about your workflows better than SCIEX.

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SCIEX Now

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- Access online training courses and articles.
- Manage software licenses linked to your registered instruments.
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SCIEX Now learning hub

- SCIEX Now learning hub success programs provide LC-MS and CE training customized to meet your exact needs.
- With a selection of training methods and certifications available, you can build a mass spectrometry program that is most suited to your lab and users.
- Starting with a clear understanding of your desired learning outcomes, we aim to help you improve lab productivity and consistency by designing and delivering a program that is focused on knowledge advancement and retention.

Find out more

Headquarters
250 Forest Street in Marlborough, MA 01752
Phone 508-383-7700
sciex.com

International Sales
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