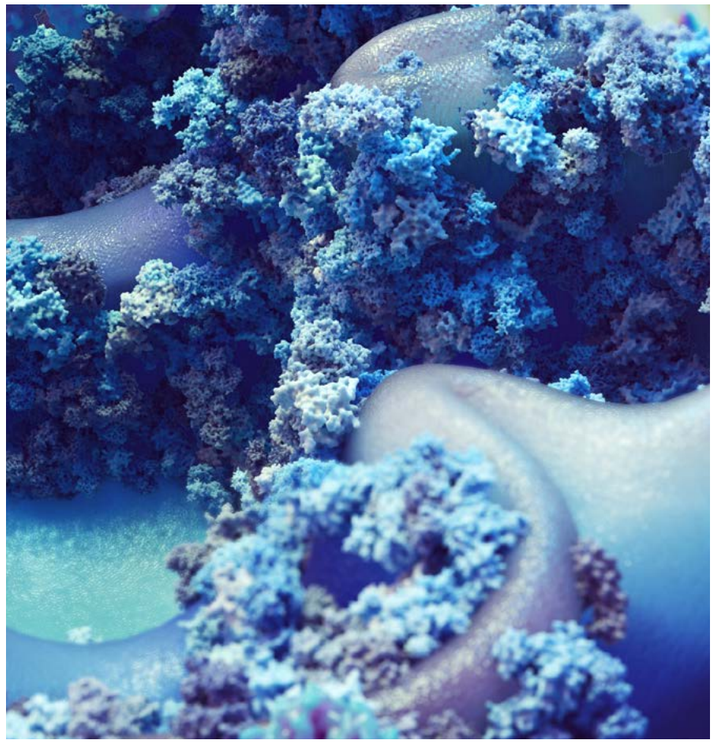
ZenoTOF 7600+ system

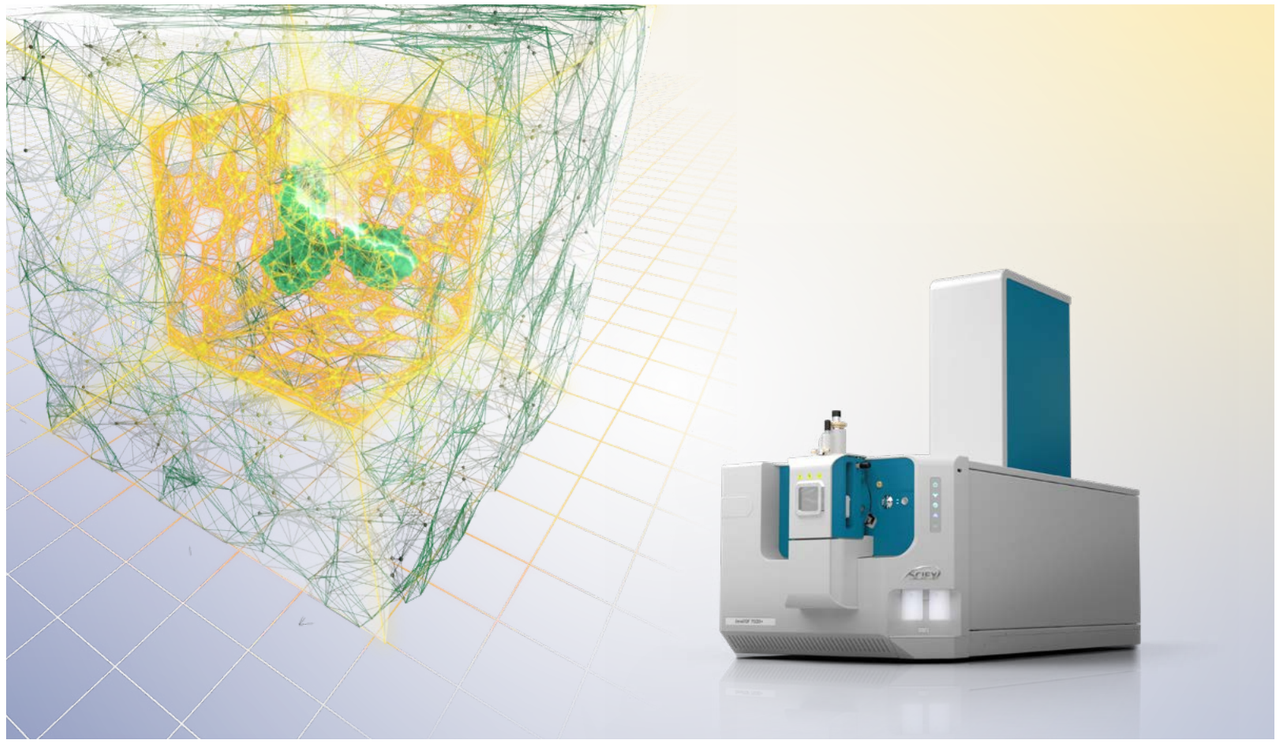
Taking biology beyond ID numbers

A Zeno trap-enabled QTOF equipped with ZT Scan DIA, adding the specificity of the scanning quadrupole dimension to enhance speed, depth and certainty in quantitative measurements.

danaher

The power of precision





Welcome to the future of proteomics

When crucial therapeutic pathway decisions are needed, protein and peptide quantitation with multidimensional, multi-acquisition certainty is essential.

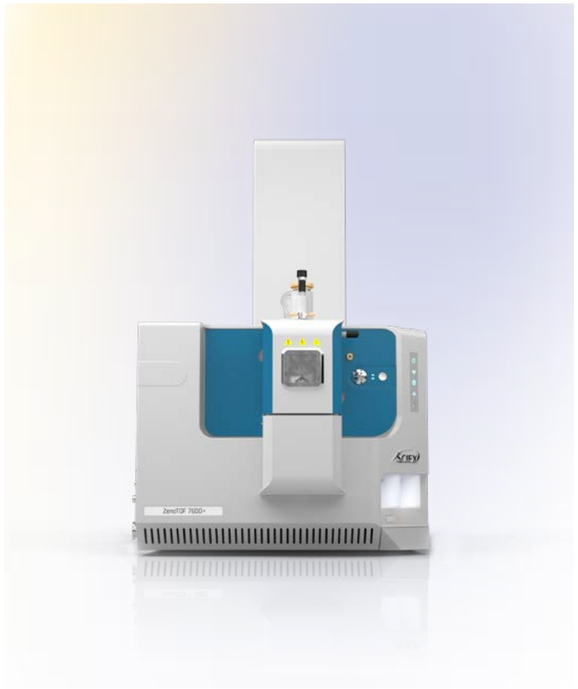
The decisions you make count. Whether confirming a biomarker as the right target or validating a new translational biomarker for drug discovery, determining the pathway for biotherapeutic efficacy demands timely and precise decisions.

Welcome to the future of proteomics, where the numbers that count are the proteins quantified, and the precision of their measurement is calculated at the speed of life.

Over

125%

improvement in the detection of quantifiable protein groups at sub-nanogram levels



Identify and quantify significantly more analytes in a shorter time, with less sample and higher precision.

Ionization source

The **Optiflow Turbo V ion source** incorporates the reliability and efficiency of the Turbo V ion source while providing flexibility for quickly switching flow rates, including nanoflow regimes for the highest sensitivity.

Detection

Performance gains with fast LC gradients, using the **ZenoTOF 7600+ system**, increase as sample loading and complexity increase when using **ZT Scan DIA** with added specificity of the scanning quadrupole dimension.

ZT Scan DIA

The powerful combination of DIA, Zeno trap and added specificity of the scanning quadrupole dimension enhances depth and certainty in quantitative measurements.

Simplified workflows

ZT Scan DIA methods are easy to set up with minimal user optimization needed, making the **ZenoTOF 7600+ system** ideally suited to the analysis of large sample cohorts.

Tunable electron fragmentation of all molecule types

Exclusive to SCIEX, the ability to tune electron kinetic energy to employ electron activated dissociation (EAD) extends the utility of the approach to all molecule types.

Scan speeds of up to 640 Hz

The fastest SCIEX QTOF yet! When using **ZT Scan DIA**, the isolation window for MS/MS slides along the m/z range of interest during each cycle. Based on a defined m/z range, scanning at 750 Da/s with a sliding isolation window of 5 Da would equate to a scan rate of 640 Hz.

Overcome QTOF MS/MS duty cycle deficiencies

Ions are accumulated in the Zeno trap before being pulsed rapidly into the TOF, meaning we can detect up to 20x more ions.

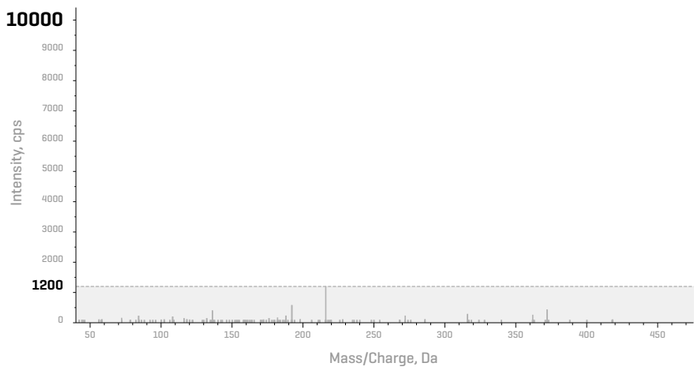
Deliver on important timelines

With up to 10-fold improvement in throughput for protein quantitation, the **ZenoTOF 7600+ system** enables 1-minute gradient analyses using **ZT Scan DIA** for low to moderate protein loads.

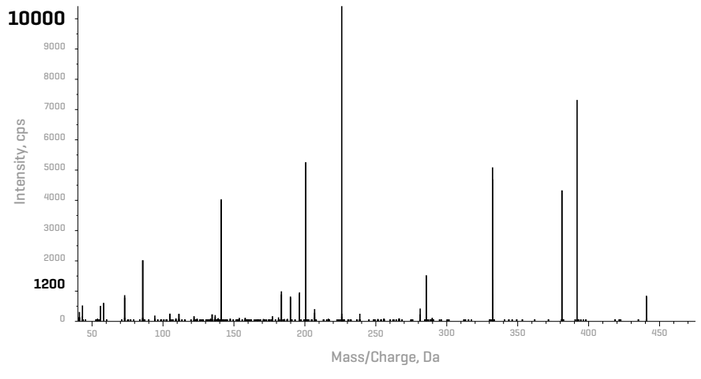
Unlock sensitivity for quantitative proteomics

Enabled by Zeno trap pulsing, the **ZenoTOF 7600+ system** unlocks sensitivity gains to uncover new proteomics information. Ions are accumulated in the Zeno trap before being pulsed rapidly into the TOF, meaning up to 20x more fragment ions can be detected.

Without the Zeno trap pulsing



With the Zeno trap

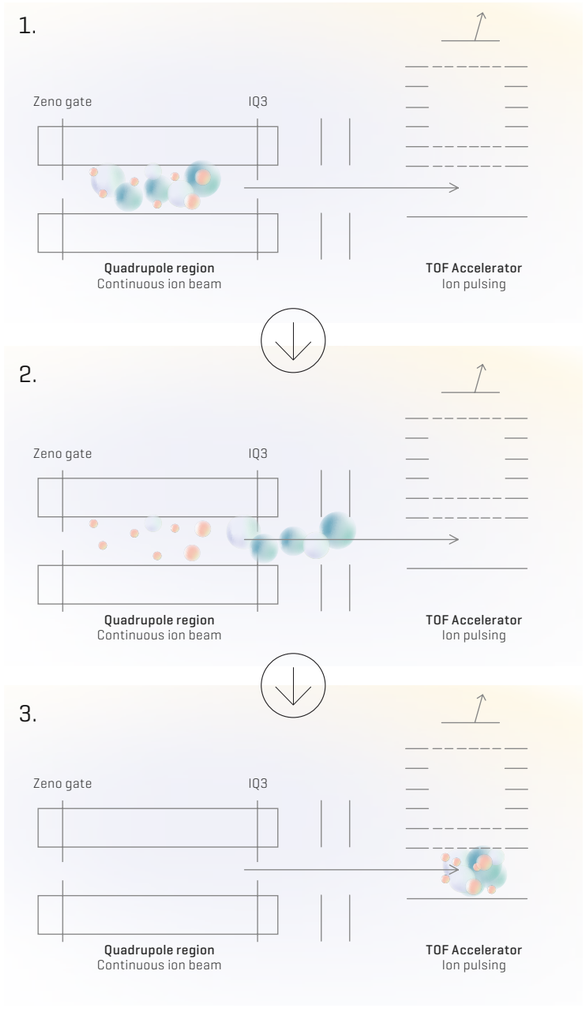


Achieve sensitivity gains of

5–20x

with Zeno trap

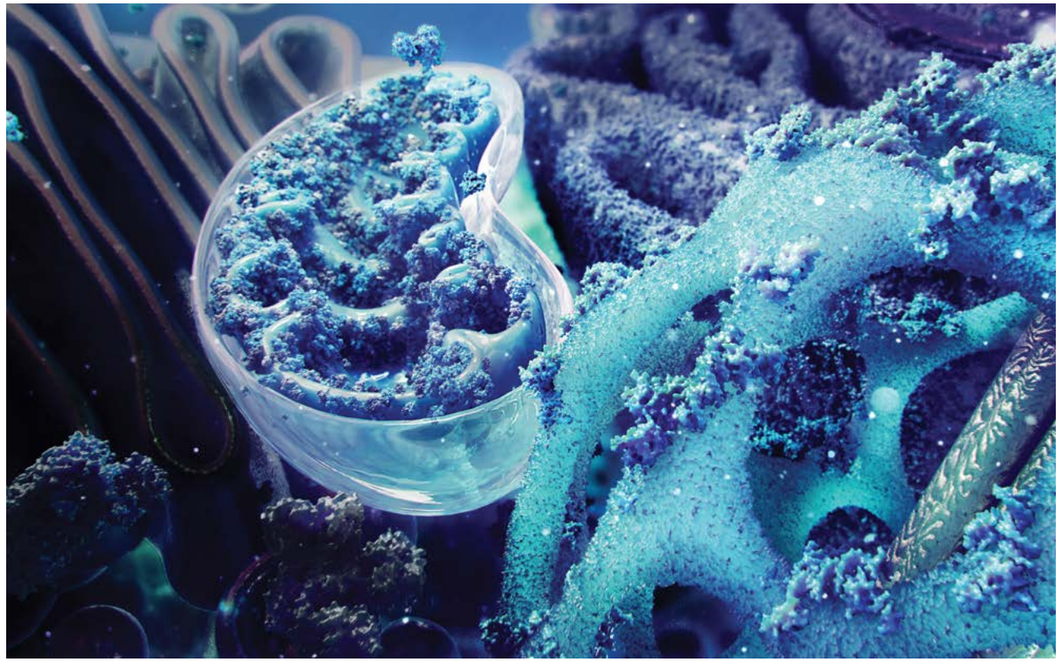
Zeno trap enabled QTOF

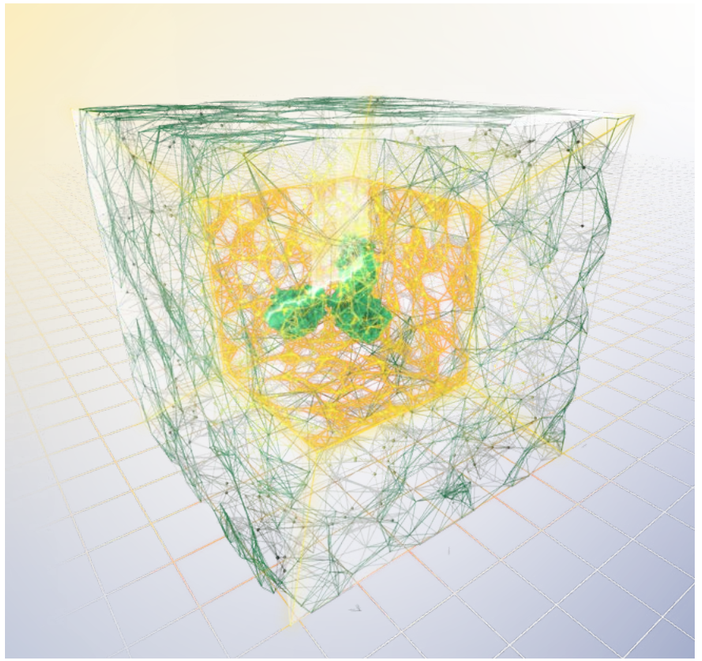


All ions enter the TOF at the same time, achieving

>90%

duty cycle





Quantitative proteomics: the numbers that count

Translating insights into actionable data in biomarker research is challenging due to the need for both data depth and measurement quality. In proteomics, quickly quantifying numerous proteins is essential for large-scale clinical research studies. However, detecting low-abundance proteins in small samples requires sensitive techniques.

Traditionally, researchers had to choose between sensitivity for a few proteins or broad quantitation with reduced precision. The **ZT Scan DIA** on the **ZenoTOF 7600+ system** resolves this dilemma by combining the depth of data-independent acquisition (DIA) methods with the specificity of data-dependent acquisition (DDA) and the precision of targeted approaches. This innovative method enables precise, fast and sensitive quantitation of entire proteomes, overcoming previous limitations.

Precise

Fast

Sensitive quantitation

Target, validate and translate with ZT Scan DIA

The **SCIEX ZenoTOF 7600+ system** takes quantitative accuracy to the next level. This high-resolution mass spectrometry solution combines powerful MS/MS sensitivity, fragmentation-centric technology and innovative developments in data-independent acquisition (DIA) approaches.

Whether confirming a biomarker as the right target or validating a new translational biomarker for drug discovery, determining the pathway for biotherapeutic efficacy demands timely and precise decisions.

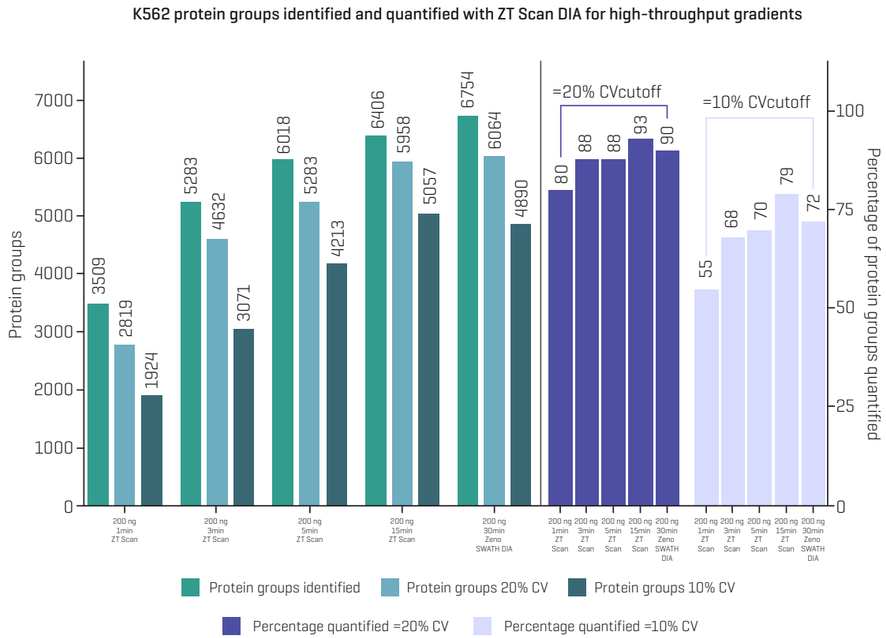
The **ZenoTOF 7600+ system** offers the selectivity of the scanning quadrupole dimension, high sensitivity MS/MS enabled by Zeno trap pulsing and fast time-of-flight acquisition rates to improve the detection of quantifiable protein groups by over 125% at sub-nanogram levels when using **ZT Scan DIA** relative to conventional sequential-window DIA. This innovative method offers precise quantitation of entire proteomes with exceptional speed and sensitivity, overcoming previous limitations.

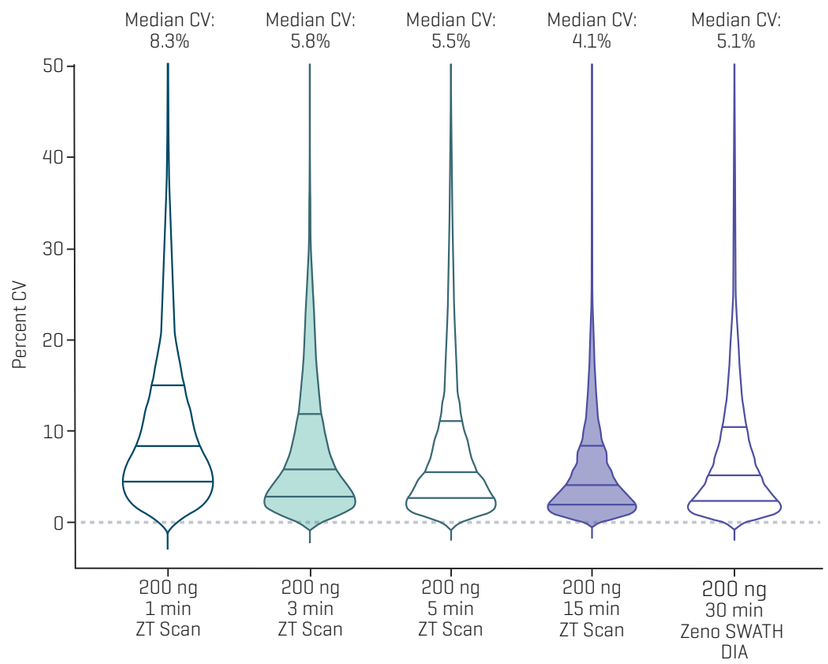
Find out more about the ZenoTOF 7600+ system

Learn more

Biology beyond protein ID

ZT Scan DIA revolutionizes quantitative proteomics by bridging protein identification and translation with quantitation at unmatched speed, accuracy and precision. Enhanced by quadrupole scanning, it provides the certainty needed to validate protein biomarkers and choose therapeutic pathways with confidence.





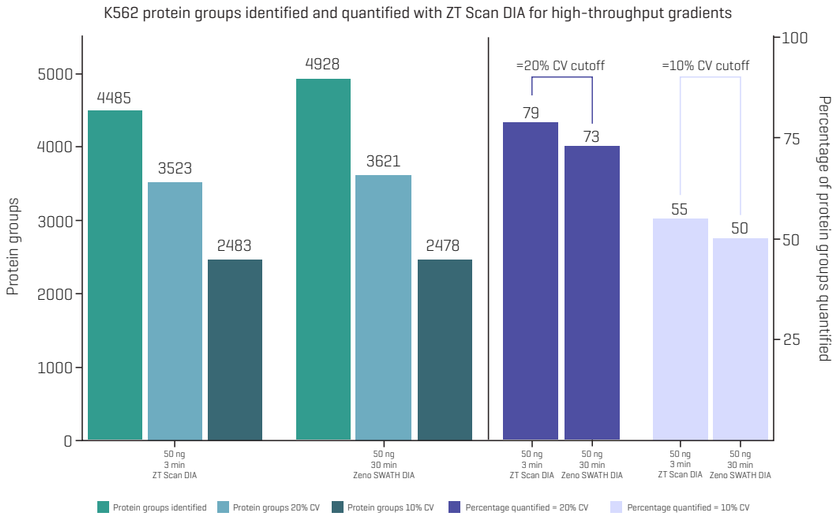
Precise quantitation of entire proteomes with exceptional speed and sensitivity

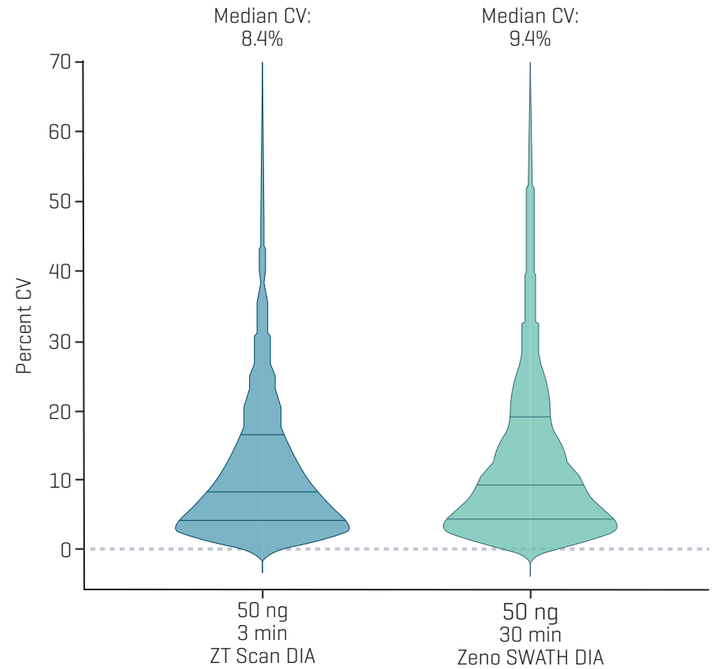
Data processed with DIA-NN (p.g.matrix.tsv file used for ID reporting).
Human cell lines pH spectral library: 11,269 protein groups and 169,395 precursors.

Biological relevance at speed

Translational certainty requires comprehensive proteome coverage that can be validated at scale. **ZT Scan DIA** enables precise protein quantitation with no compromise in depth or coverage. With up to 10-fold increased throughput, it allows for 1-minute analyses of low to moderate protein loads.

10x
throughput improvement





1 min
active gradients

ZT Scan DIA enables precise protein quantitation with no compromise in depth or coverage

Data processed with DIA-NN (p.g.matrix.tsv file used for ID reporting).
Human cell lines pH spectral library: 11,269 protein groups and 169,395 precursors.

Biological nuances unlocked

In biomarker discovery, analyzing low protein loads requires high precision and minimal error margins. **ZT Scan DI**A offers up to 9-fold increased protein coverage at low loads, enhancing certainty and enabling precise decision-making.

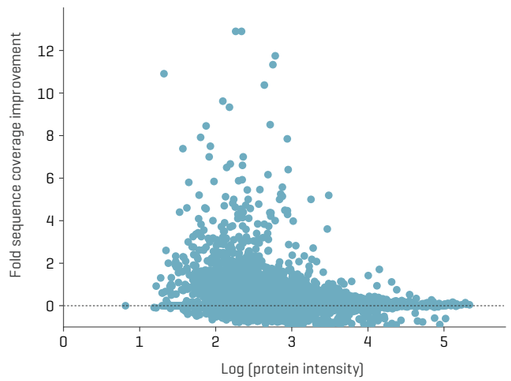
The data shows the improvements in protein coverage depth with **ZT Scan DIA**, represented by the fold-change gain in overall sequence coverage per protein (A), the differential in actual sequence coverage per protein (B), and the change in number of amino acid residues identified per protein (C) using **ZT Scan DIA** relative to **Zeno SWATH DIA**. **ZT Scan DIA** extends protein characterization depth through higher-confidence identifications of peptides, particularly those from lower-abundance proteins.

(Mixed species sample: human (HEK 293 + MCF7) + yeast + mouse + drosophila extract tryptic digest, acquired either with ZT Scan DIA method (750 Da/sec, 5 Da window) or Zeno SWATH DIA (65 variable-width windows))

9x

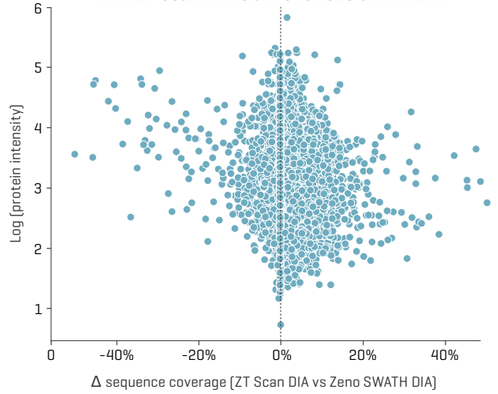
protein coverage increase

Fold change in sequence coverage per protein with ZT Scan DIA relative to Zeno SWATH DIA



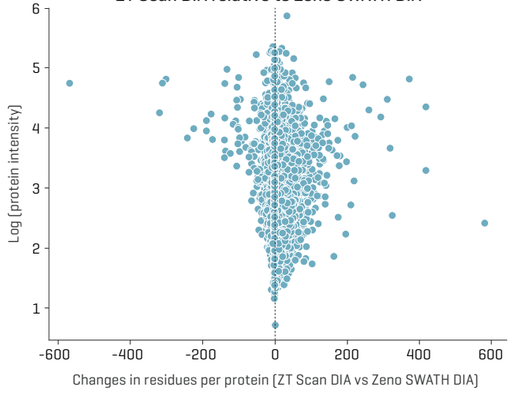
High precision and minimal error margins

Sequence coverage difference per protein with ZT Scan DIA relative to Zeno SWATH DIA



ZT Scan DIA extends protein characterization depth through higher-confidence identifications of peptides

Amino acid residues identified per protein with ZT Scan DIA relative to Zeno SWATH DIA



Expand data insight with complementary and tunable fragmentation

Electron-activated dissociation (EAD) provides fast, reagent-free, and easy-to-use fragmentation, enhancing analytical capabilities.

EAD offers a variety of electron-based fragmentation mechanisms and can fragment peptides while preserving critical MS/MS information for identifying and localizing PTMs. Unlike other techniques, EAD delivers reproducible and consistent data at fast scan speeds and is compatible with UHPLC time frames. Coupling EAD with the Zeno trap in the **ZenoTOF 7600+ system** allows the detection of low-abundance diagnostic fragment ions, improving sequence coverage.

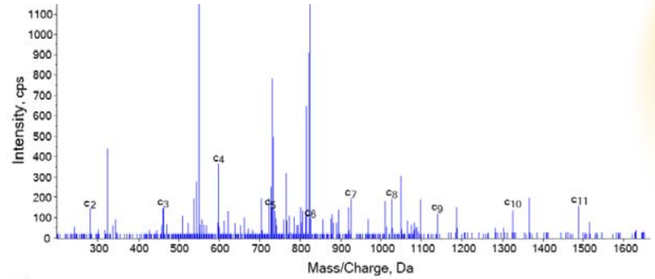
Improved bottom-up characterization performance to meet challenges of complex next generation therapeutics

- Confirmation of PTMs (glycosylation, disulfide-bonds, phosphorylation, sulfation, ...)
- Detailed determination of aa isomers
- Fragmentation of singularly, doubly and multiply charged ions
- Comprehensive sequence coverage

Sequence information **directly from the intact molecule** (top/middle down)

Tunable: Wide range of electron energy (up to 25 eV) allows high degree of selectivity for backbone fragmentation and maintenance of side chain, in particular EAD-CID hybrid

Fast (electron reaction capture time ~10-30ms), **reagent free**, and **easy to use** (similar to CID, set and forget)

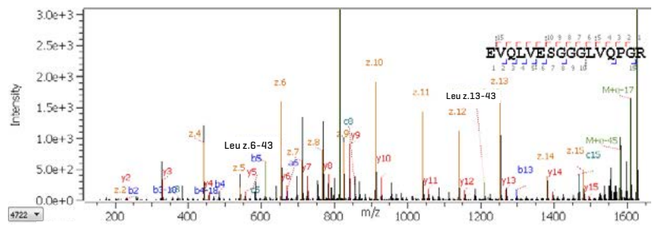


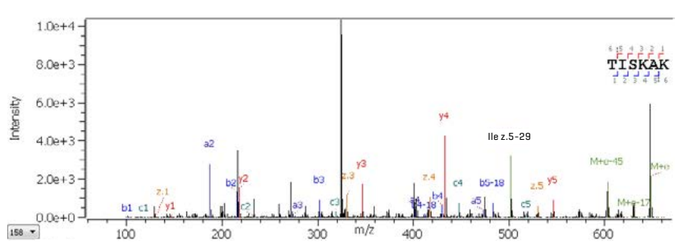
	Symbol	Res. Mass	# (N)	b	c	y	z	z + 1	z + 2	# (C)
▸	V	99.06841	1	100.07569	117.10224	*1645.77742*	*1628.79087*	***1629.75870***	***1630.76652***	12
	Y	163.06333	2	263.13902	**280.16557**	*1546.70901*	*1529.68246*	*1530.69029*	*1531.69811*	11
	T[Pho]	181.01401	3	444.15303	**461.17958**	1383.64568	1366.61913	**1367.62696**	1368.63478	10
	H	137.05891	4	581.21194	**598.23849**	1202.63167	1185.60512	**1186.61295**	**1187.62077**	9
	E	129.04259	5	710.25454	**727.28108**	**1065.57276**	1048.54621	**1049.55403**	**1050.56186**	8
	V	99.06841	6	809.32295	**826.34950**	936.53016	919.50362	**920.51144**	***921.51927***	7
	V	99.06841	7	908.39136	**925.41791**	837.46175	820.43520	**821.44303**	**822.45085**	6
	T	101.04768	8	1009.43904	**1026.46559**	**738.39334**	721.36679	**722.37461**	**723.38244**	5
	L	113.08406	9	1122.52311	**1139.54965**	**637.34566**	620.31911	**621.32693**	**622.33476**	4
	W	186.07931	10	1308.60242	**1325.62897**	**524.26159**	507.23504	**508.24287**	**509.25069**	3
	Y	163.06333	11	1471.66575	**1488.69230**	**338.18228**	321.15573	**322.16356**	323.17138	2
	R	156.10111	12	*1627.78936*		175.11895	158.09240	159.10023	160.10805	1

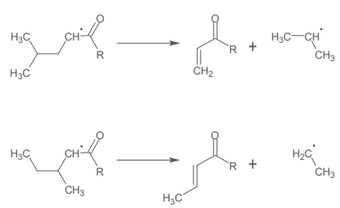
A step change in fragmentation technology

Localization of a phosphorylation site near the N-terminus of a peptide with tyrosine and threonine. The c' fragment ion series enables localization of a phosphorylated threonine adjacent to a tyrosine. The c' ion series is shown in the spectrum and the modification site was located with 99.98% probability in Mascot software. Both the c' and z·(z+1) ion series are hig hlighted in the table below the EAD spectrum and the detected fragments (+1 charge state) are highlighted in bold red.

Differentiation of leucine and isoleucine using EAD







EAD clearly indicates the identity of two leucine residues within this peptide sequence through the loss of 43 Da from the z6 and z13 ions. At the bottom, loss of 29 Da from the z5 ion identifies an isoleucine within this peptide sequence.

Software solutions that power discoveries

The SCIEX **ZenoTOF 7600+ 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.

Find out more
SCIEX OS software

Learn more

Delivering insight

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, they each require advanced data processing technologies to interrogate data and deliver actionable insight. The **ZenoTOF 7600+ system** is compatible with various third party software tools that will help you make these discoveries within your existing data pipeline.

DIA-NN is a universal software suite for data-independent acquisition (DIA) proteomics data processing. Conceived at the University of Cambridge, UK, in the laboratory of Kathryn Lilley (Cambridge Centre for Proteomics), DIA-NN is currently being further developed in the laboratory of Vadim Demichev at the Charité (University Medicine Berlin, Germany).

DIA-NN uses deep neural networks (DNNs) to distinguish real signals from noise, as well as new quantification and interference-correction strategies. DIA-NN 1.9 fully supports the ZenoTOF 7600+ system.

PEAKS Studio is a comprehensive, vendor-neutral, proteomics software platform that provides systematic identification and quantification of peptides/proteins in a complex protein mixture using tandem mass spectrometry (LC-MS/MS). Developed by Bioinformatics Solutions Inc., in Waterloo, ON, Canada, PEAKS uses a unique de novo-assisted database search algorithm to maximise the peptide identification efficiency for in-depth analyses of complex proteomes.

With PEAKS Studio 12.5, fully take advantage of the ZenoTOF 7600+ system by utilizing the data extracted from the Q1 dimension The interactive interface also provides a detailed, easy-to-use, user interface for data visualisation, result validation and reporting.

Learn more

Additional third party proteomics software compatibility:

Spectronaut™ Pulsar

The power of precision

SCIEX Now support network

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- 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

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