SCIEX

The power of precision

ZT Scan DIA: the smart hybrid

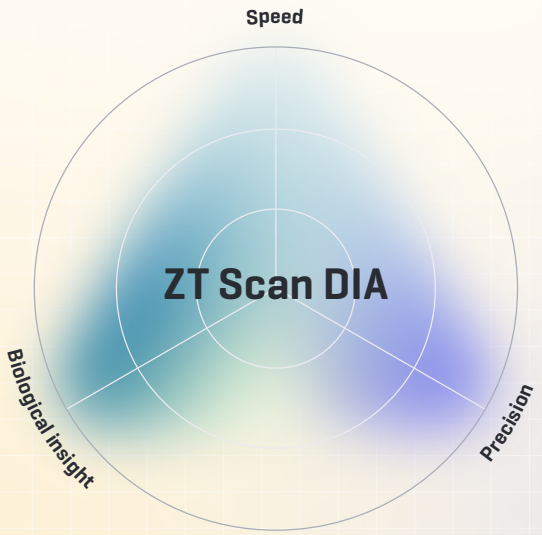
Why compromise when you can have it all?

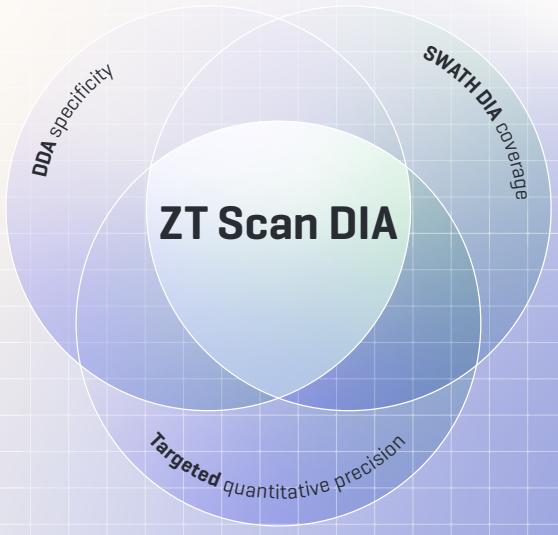
Large sample cohorts? Highly complex samples? Unclear outcomes?

Omics research at the cellular level is full of promise—but also prone to error, due to its highly complex nature. Conventional analytical methods often force a trade-off between speed of analysis, depth of information, or reproducibility of results. ZT Scan DIA changes that.

ZT Scan DIA combines the precision of data-dependent acquisition (DDA), the simplicity of SWATH data-independent acquisition (DIA), and the quantitative accuracy of a targeted acquisition strategy into a single, streamlined method. This multi-acquisition approach resolves the complexity of chimeric spectra while enabling deeper and more precise molecular quantitation.

This isn't a new tweak. It's a new approach that leverages scanning logic with Zeno trap-enhanced MS/MS to deliver faster, deeper, more reproducible outcomes.





Why ZT Scan DIA matters

High throughput

Up to 10x faster analyses, ideal for large cohort biomarker studies

Precision & reproductibility

Accurate quantitation with no compromise in depth of coverage

Quantitation

up to 50% gains

Delivers 40–50% gains in protein identification and quantitation, even at >200 samples/day

Biological relevance

Uncovers low-abundance peptides with confidence, enabling biomarker validation

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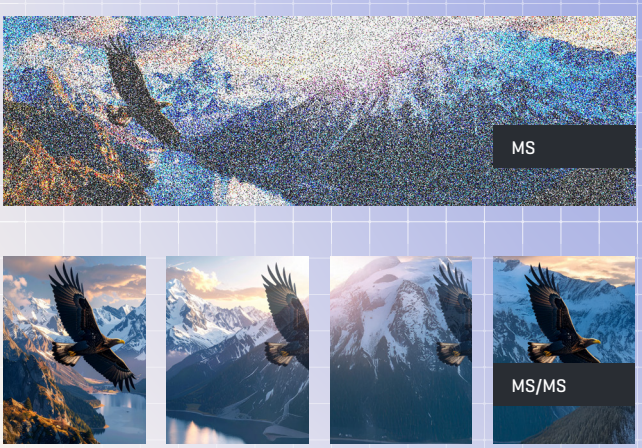
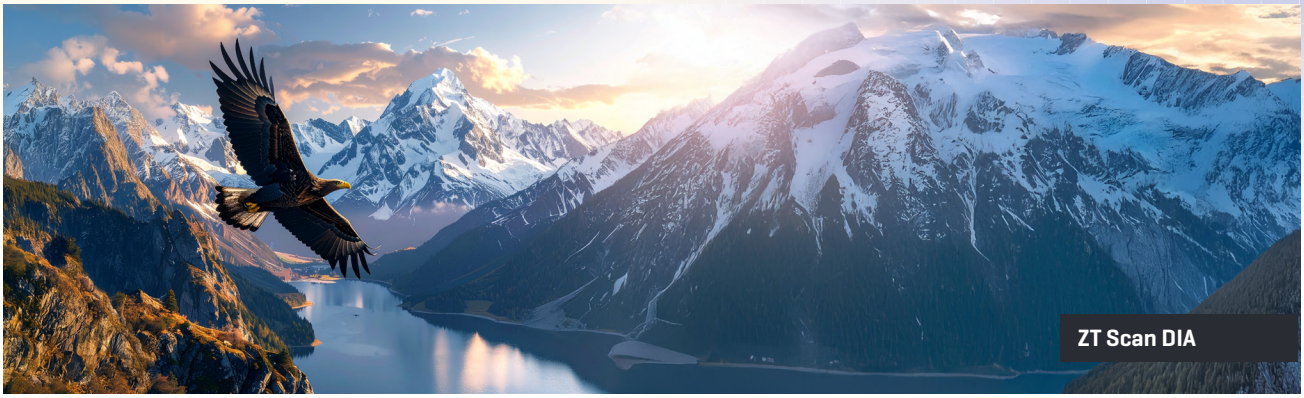
Coverage. Speed. Precision.

ZT Scan DIA captures MS/MS spectra through continuous sweeps across the m/z range, like panning a camera over a scene, linking MS1 information to each MS/MS scan. Enhanced with Zeno trap, every "sweep" delivers high-resolution data at unprecedented speeds. Rather than using fixed or variable windows—or choosing between depth and speed—ZT Scan DIA unifies best-in-class acquisition strategies into one seamless scan, ultimately capturing the true, whole picture.

MS:
Lower definition overall view, great for the "big piture" but lacks detail.

MS/MS:
Multiple high resolution close ups that give greater specificity, but doesn't capture a single moment, resulting in false readings when data overlaps.





How it's different

Capability score: ●●●● High ●●●○ Medium ●●○○ Low	ZT Scan DIA	Zeno SWATH DIA	SWATH DIA	DDA
Acquisition speed	●●●●	●●●○	●●○○	●○○○
Acquisition	Zeno trap + Scanning DIA	Zeno trap + variable window DIA	Variable window DIA	Data-dependent acquisition
Data reproductibility	●●●●	●●●○	●●○○	●○○○
Quantitative precision	●●●●	●●●○	●●○○	●○○○
Depth of coverage	●●●●	●●●●	●●●○	●○○○
Chimeric deconvolution	●●●●	●○○○	●○○○	●●○○

Bring the power of ZT Scan DIA to your omics research

Learn more →

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