



See more,
much more
clearly

NEXT-GENERATION PROTEOMICS PLATFORM



Every peak. Every run. Every time.

The Next-generation Proteomics Platform is here:

The new **AB SCIEX TripleTOF® 6600 System** with **SWATH™ Acquisition 2.0**.

Now you can capture every detectable peptide and protein in every run, with MRM-quality quantitation and sample-to-sample reproducibility that accelerate your research.

SWATH™ Acquisition 2.0 data independent acquisition with variable windows and enhanced processing enables maximum quantitation from each precious sample. Thousands of proteins can be examined at once with almost no method development. Plus, the results of every run are archived so you can analyze new protein biology anytime in the future. **Nothing hides from SWATH™.**

Only the **TripleTOF® 6600** can deliver the speed, sensitivity and dynamic range that turn data into meaningful conclusions faster than ever.

Next-generation proteomics platform

AB SCIEX TripleTOF® 6600 System + SWATH™ Acquisition 2.0

Quantify thousands of proteins across large sample sets with greater accuracy and reproducibility than ever before.

As your lab needs shift from small discovery experiments to quantitative work on larger sample sets, your need for comprehensive quantitation will grow.

Now there's a proteomics platform with the features and performance that deliver real biological insights to power your research in the years ahead.

- **Empower your biological research through comprehensive quantitation**

SWATH™ 2.0 delivers the combination of low variability and comprehensive coverage with coefficients of variation previously achievable only by targeted techniques – increasing capacity 30X vs. conventional targeted proteomics.

- **Attain better data with greater precision, accuracy and completeness**

Providing an additional full order of linear dynamic range in MS and MS/MS, the TripleTOF® 6600 lets you dig deeper to quantify low-abundant analytes from high resolution accurate mass data.

- **Achieve faster time-to-results**

Experience 10X faster sample-to-answers than conventional targeted proteomic methods with higher multiplexing.

Spend more time
on biology
less on technology.



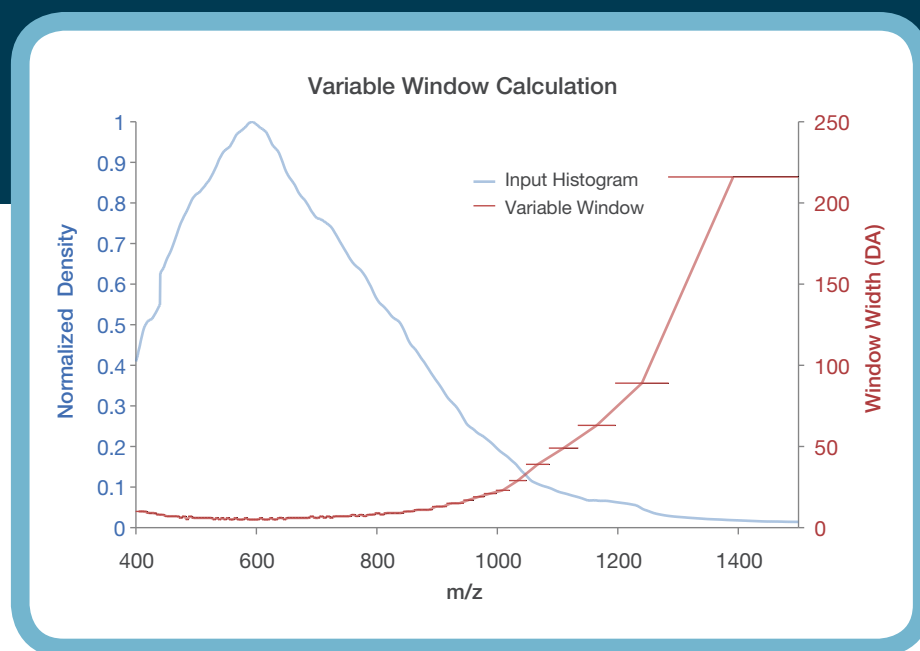
Enhanced SWATH™ 2.0 with variable windows...

delivers greater specificity and reproducibility on lower abundance peptides so you can examine the proteome more completely, as well as observe complex relationships with greater ease. Plus, each run becomes a permanent digital archive that can be mined again, and again.

Variable windows provide more visibility so you can be confident in your results, with up to 200 windows per cycle generated on the TripleTOF® 6600.

SWATH™ captures nearly every detectable peptide, using:

- Narrow m/z windows where precursor density is high for the most selectivity – as low as 2 Da
- Wider windows where density is lower to ensure broader precursor mass range for wider compound coverage



Overall, a broader
mass range, so
proteins
simply can't hide

Nothing hides from

SWATH

Analyze your results **more easily,** **with confidence**

SWATH™ 2.0 Data Processing

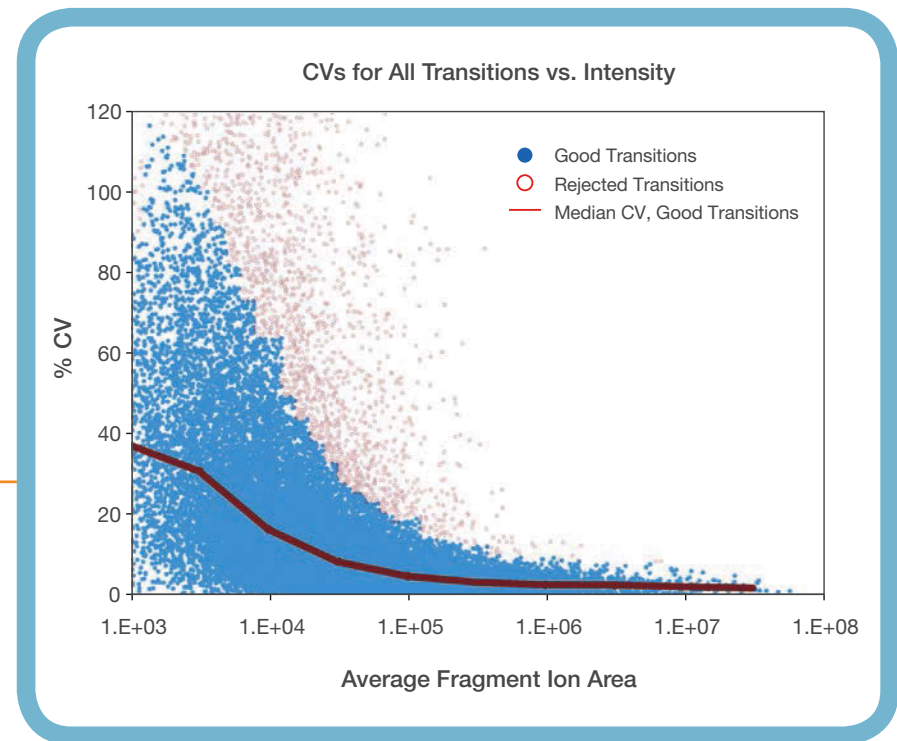
Not only can you collect more data with greater specificity than ever before, the SWATH™ 2.0 data processing application generates results faster and with greater confidence to increase your productivity.

- Retention time calibration expands ion library options
- Improved scoring with false discovery analysis ensures higher confidence in your results
- Increased speed and scale accommodate larger studies

CVs for Transitions vs Intensity

A typical SWATH™ analysis on a TripleTOF® 6600 System generates:

- Quantitative data for 3000 proteins [15,300 peptides] with CV's less than 20% – 30X more proteins than conventional targeted proteomics
- Greater than 4 orders biological dynamic range and >90% more peptides than previous instruments



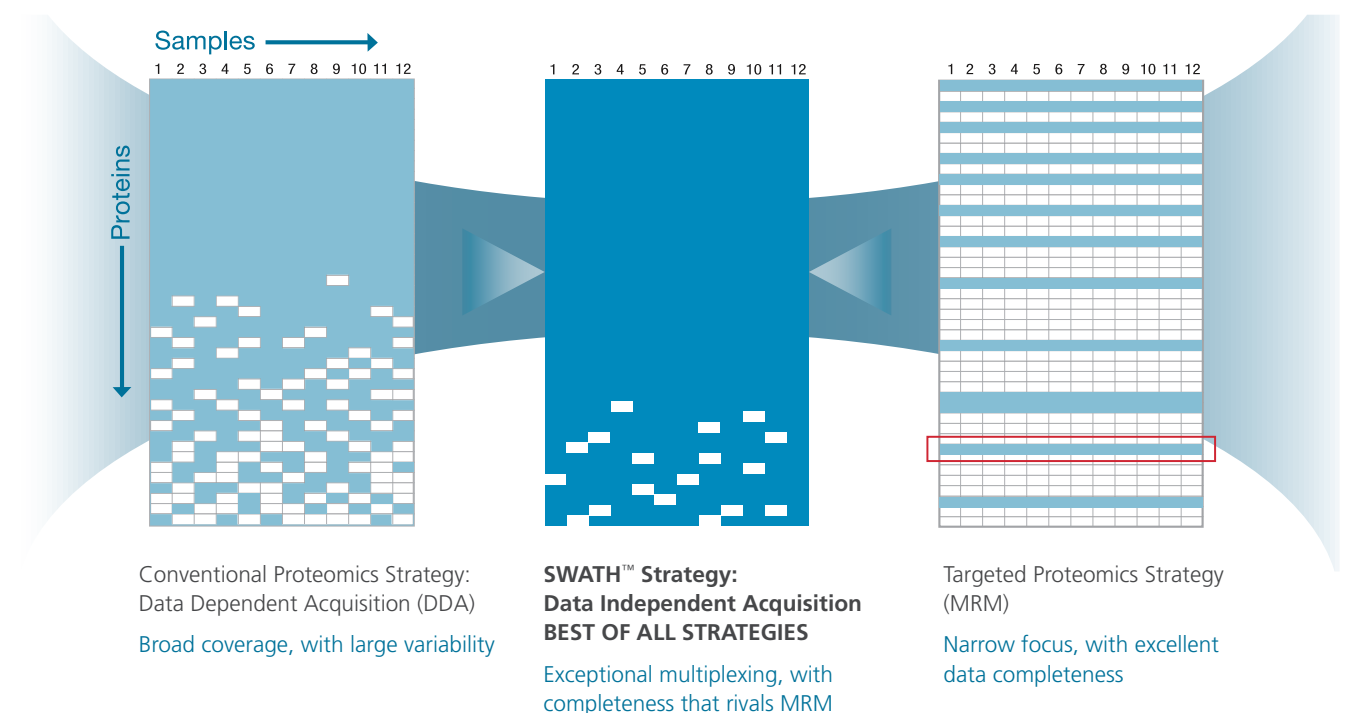
TripleTOF® 6600 + SWATH™ 2.0

Maximizing productivity in **targeted proteomics**

SWATH™ 2.0 data completeness

Capture more critical data faster, so you can uncover new protein relationships.

The TripleTOF® 6600 enables unrivaled coverage of your proteome in a single analysis with greater dynamic range and enhanced data quality.



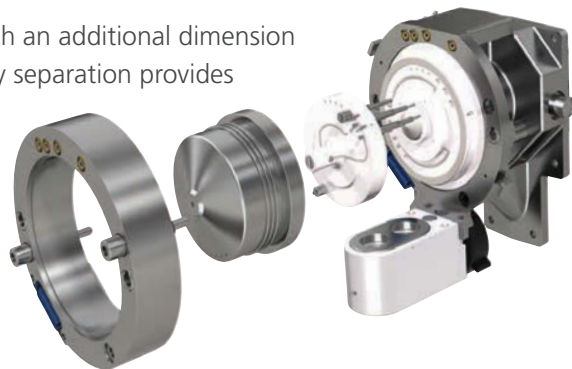
Taking TripleTOF[®] to new heights

The TripleTOF[®] 6600 extends the power and features of AB SCIEX TripleTOF technology, delivering high performance to drive a wide range of powerful applications – 90% more peptides than previous systems:

- Broader linear dynamic range: greater than 5 orders
- Wider Q1 mass range: isolation for ions up to 2250 m/z
- Enhanced mass accuracy stability: <2 ppm RMS
- Higher quality MS/MS with superior mass resolution and speed:
 - 35,000 TOF MS mode
 - 20,000 high-sensitivity MS/MS mode
 - 30,000 high-resolution TOF MS/MS mode
- Better quantitation quality
 - Up to 100 MS/MS per second

SelexION[™] Gas Phase Fractionation: greater precision for complex samples

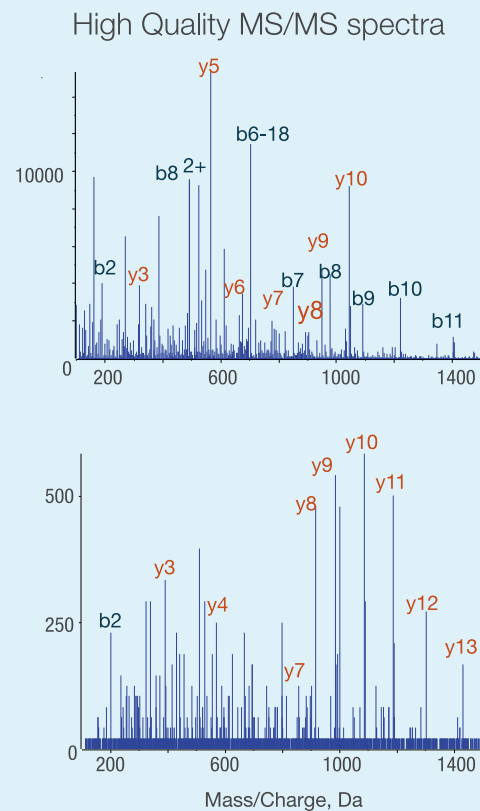
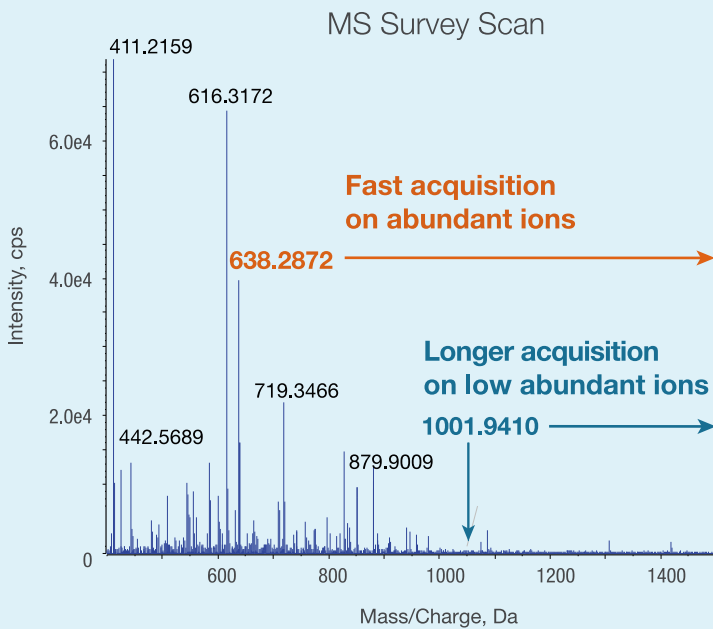
Get more out of every sample with an additional dimension of separation. Differential mobility separation provides a simplified and flexible strategy to dig deeper into complex biological samples.



Dynamic Accumulation improves results

For traditional discovery experiments, we've improved **data-dependent acquisition with Dynamic Accumulation** to deliver higher quality MS/MS for even the lowest abundant peptides.

Smarter MS/MS for Higher Spectral Quality



The TripleTOF 6600® maximizes productivity with its **realtime** management of MS/MS acquisition time, based on the intensity of selected precursors, **resulting in more identified proteins.**

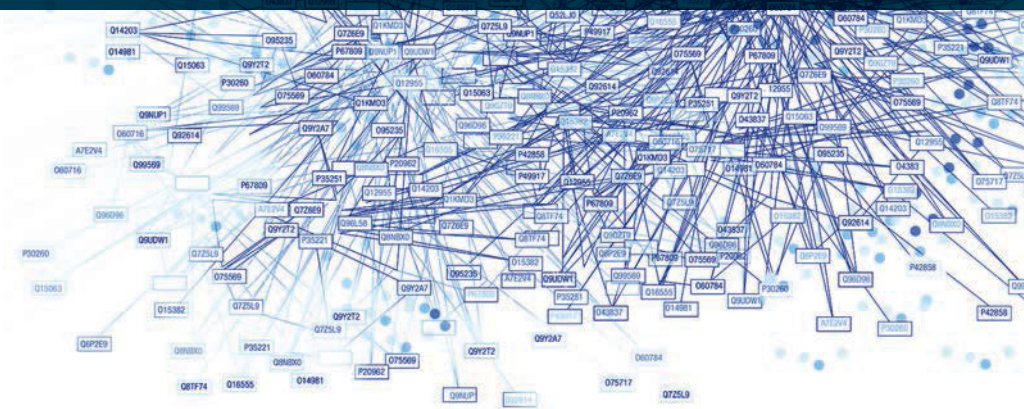
Less time is spent on more intense ions...

while more time is devoted to less intense ions

The power of **proven software productivity** and analytics

AB SCIEX provides a comprehensive portfolio of mass spectrometry software that is intuitive and versatile to match your specific application requirements.

Products are designed for flexible integration with many open standards, maximizing data utility for a complete application solution.



SWATH™ Software

The SWATH™ Acquisition micro application enables fast and easy data processing of large SWATH™ data sets.



PeakView® Software

offers a qualitative review of LC/MS and MS/MS data for enabling users to explore and interpret mass spectral data with special tools for processing accurate mass data, structural interpretation and batch analysis.



Bio Tool Kit Software

provides a range of tools for manual spectral interpretation of protein and peptide MS and MS/MS.



MultiQuant™ Software

enables the processing of high-resolution MS and MS/MS data quickly and easily, for absolute and relative quantitative information.



ProteinPilot™ Software

provides powerful algorithms that let you derive more identifications and quantification information from every proteomic sample.

Delivering everything you need to build successful solutions for your application

Resource/Application	Proteomics	Biologics	Metabolomics / Lipodomics	Drug Metabolism	Unknown screening in food, environmental, or tox research
Mass Spectrometer	TripleTOF® 6600 with Analyst® Software				
Ion Source	NanoSpray® III	DuoSpray™ for routine accurate mass		– OR –	Ion Drive™ Turbo V for maximum signal
Performance Option	SelexION™ differential mobility technology for gas-phase fractionation to reduce sample complexity, or to separate challenging mixtures				
SCIEX Separation Technology	nanoLC 400 with cHiPLC® Systems Single- or Multi-Dimensional nanoflow Liquid Chromatography	microLC 200 System — or — ultraLC 100 Systems	microLC 200 System — or — ultraLC 100 Systems		
Software	ProteinPilot™ PeakView® SWATH™ Bio Tool Kit MarkerView™ MultiQuant™	BioPharmaView™ ProteinPilot™ PeakView® MarkerView™ MultiQuant™	PeakView® MasterView™ MarkerView™ LipidView™ MultiQuant™	PeakView® MetabolitePilot™ MultiQuant™	PeakView® MasterView™ MarkerView™ MultiQuant™
Services	Choose from a range of world-class service offerings to suit the needs of your lab				





The Next-generation Proteomics Platform is here.

Our AB SCIEX application specialists are available to help you configure everything you need for your specific applications.

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We take it personally

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Headquarters

500 Old Connecticut Path
Framingham, MA 01701 USA
Phone 508-383-7700
www.absciex.com

International Sales

For our office locations please call the division headquarters or refer to our website at www.absciex.com/offices

