Extending the limits of high resolution quantitative and qualitative analysis
AB SCIEX has been a leader in the field of mass spectrometry for more than 25 years. With each generation of our system solutions, we have raised the bar for quantitative and qualitative analysis in pharmaceutical drug development, life science research, food and environmental safety, forensic toxicology, and clinical research.

The original TripleTOF™ 5600 system was the first system to combine comprehensive qualitative exploration, rapid profiling, and high-resolution quantitation on a single accurate mass platform. The next generation, TripleTOF™ 5600+ system adds innovative acquisition strategies, tools for regulatory compliance, and compatibility with ion mobility separation to enable research that was previously impossible.

FOR RESEARCH USE ONLY. NOT FOR USE IN DIAGNOSTIC PROCEDURES.
The AB SCIEX TripleTOF™ 5600+ System

High resolution quantitative and qualitative analysis

The AB SCIEX TripleTOF 5600+ extends the market-leading capabilities of the TripleTOF family, by providing broader applicability in the pharmaceutical industry and enabling a new paradigm in proteomics research. No other accurate mass MS/MS instrument has the speed and sensitivity to deliver comprehensive qualitative exploration, rapid profiling, and high-resolution quantitation in complex matrices – all in a single injection, on a single platform.
One system, flexible workflows

For the first time, pharma, academic and analytical testing scientists can integrate comprehensive qualitative exploration, rapid profiling, and high-resolution quantitation workflows on a single platform providing faster and more accurate answers to “what is in the sample, how much is there, and does it change?”

Speed and resolution for definitive identification

- Select up to 100 precursors and get high resolution MS/MS in a second for fast LC conditions
- Identify precursors with confidence with high mass accuracy in MS and MS/MS mode
- Target analyte classes with advanced IDA (information-dependent acquisition) workflows
  > Multiple mass defect scanning
  > Neutral loss scanning
  > Exclusion / inclusion lists / isotope pattern matching
- Identify unknowns with robust, intelligent multiple collision energy workflows
Quantitative and qualitative information in a single run

- Combine high-resolution MS quantification with high-resolution MS/MS ID confirmation
- Quantify every compound—even under fast LC conditions
- Re-visit data for further interrogation
- Powerful new MS/MS acquisition workflow with SWATH™ Acquisition provides additional specificity and robustness to the profile workflow

Relative and absolute quantitation with high resolution Scheduled MRM<sup>®</sup>

- Maximize specificity with MRM quantitation using high resolution fragment ions
- Multiplex functions for many analytes with triple quadrupole MRM acquisition rates and collect full scan MS/MS spectra for each precursor with no additional cycle time
- Maintain fast cycle time for superior peak definition, even in fast LC separations
- Linear dynamic range of 4 orders or greater for quantitative accuracy
Innovative technology

Beginning with the best-in-class quantitative performance of the Triple Quad™ 5500 system, AB SCIEX researchers developed the AcceleratorTOF™ Analyzer to deliver high resolution at the speed and sensitivity required to maintain the precision and limits-of-quantitation associated with MRM. The result is the breakthrough AB SCIEX TripleTOF™ 5600+ System—the next generation in quadrupole TOF technology.

- 15kV acceleration voltage for higher sensitivity and resolution
- High transparency grids throughout for minimal ion loss
- Two-stage ion reflector compensates for energy dispersion to maximize resolution
- 40 GHz four channel TDC and detector provide highest sampling speeds and maintains high resolution – even at low mass
- 30kHz accelerator for highest acquisition rate
- New entrance optics improves ion beam focusing post LINAC
Intelligent implementation

Improve productivity and specificity by acquiring information instead of just data.

- **Dynamic background subtraction** (DBS) minimizes collection of MS/MS on background ions to increase identification of low-level analytes in the presence of background noise.

- **Multiple mass defect triggered IDA** (Information Dependent Acquisition) improves efficiency and reduces the need for multiple injections to get comprehensive information. Mass defect can be applied for specific mass ranges, and multiple mass defects can be applied.

- **MS/MS ALL** is a powerful workflow enabled by the speed and sensitivity of the Triple TOF™ 5600+ system, where high quality MS/MS spectra are generated for all masses. This is the foundation of the ground-breaking SWATH™ Acquisition that is changing the landscape of quantitative proteomics.

Ion mobility enabled, for a new dimension in selectivity

On the TripleTOF 5600+, SelexION™ technology adds a new dimension to accurate mass selectivity for enhanced quantitative and qualitative performance.

AB SCIEX SelexION Technology compliments and extends the power of accurate mass and the **Scheduled MRM®** workflow, by removing interferences at the structural level.

The 5600+ system with SelexION technology is the ultimate accurate mass tool for the separation of isobaric species, isolation of challenging co-eluting contaminants and reduction of high background noise, improving data quality and enhancing selectivity for challenging samples requiring advanced analytical separations.
Performance delivered

Scientists have come to expect industry-leading performance from AB SCIEX mass spectrometers. The TripleTOF™ 5600+ system delivers with high-resolution, high-sensitivity data, excellent mass accuracy stability, and fast acquisition rates. If you’re looking for unmatched performance, look no further than the TripleTOF 5600+ system.

High-resolution, high-sensitivity data with acquisition speed up to 100 spectra/sec makes the TripleTOF 5600 system a perfect compliment to ultra-fast chromatography. The system also provides 4-5 orders of magnitude of linearity to ensure accurate quantitation in MS and MS/MS modes.

EasyMass™ Accuracy delivers high mass accuracy without continuous recalibration. With external calibration, the mass accuracy holds rock-steady at <1ppm over 30 minutes, and RMS=1.69 over 100 hours.

Reserpine and fragments demonstrate high resolution at low mass, ~30,000 at 100 MS/MS per second. Resolution of insulin (6+) is maintained at >43,000 with data accumulation times of 1 second, 100 milliseconds, and 10 milliseconds.
Applied power

In-depth identification and expression analysis for omics and biomarker studies.

**A new standard for protein identification and targeted quantitation:** The TripleTOF™ 5600+ system achieves the highest acquisition speeds while maintaining maximum resolution and mass accuracy for unmatched protein identification. The resolution and speed also enable MRM-like quantitation without significant method development.

**Comparative analysis for metabolomics studies** can be performed on the TripleTOF 5600+ system with greater precision and confidence than ever before. Profiling of endogenous metabolites can be achieved with unmatched speed and sensitivity in a single injection to determine statistical differences between samples for the rapid determination of putative biomarkers.

**Novel workflows for Lipidomic analysis:** Lipid profiling on the TripleTOF 5600+ system can be used to analyze every lipid species simultaneously. With the new MS/MS ALL workflow it is possible to acquire precursor ion data at every unit mass to obtain high quality MS/MS data on every lipid class within a sample.

**Simple, clear metabolite ID, characterization, and powerful quantitation for bioanalysis.**

**Identify and characterize metabolites at new levels of speed, efficiency and data quality:** The TripleTOF 5600+ system is the ideal platform for rapid assessment of metabolic stability and *in vivo* characterization and definitive metabolite ID. With the ability to perform both TOF MS and MS/MS scanning at rates suitable for fast LC, you can apply completely generic methodology to acquire high-quality qualitative and quantitative data simultaneously.

**Quantify drug metabolites** with performance equivalent to MRM on a triple quad. The TripleTOF 5600+ system is the first accurate-mass, high-resolution MS system with the speed and sensitivity to deliver triple quad-like quantitation.

**Accurate mass for regulated bioanalysis:** The TripleTOF 5600+ has a full suite of tools for to support 21 CFR Part 11 compliance and and uses the Analyst® software platform, recognized as the industry standard for quantitative LC/MS/MS. With Scheduled MRM®, the selectivity of accurate mass is merged with the added utility of sensitive full-scan data in your quantitative workflows.
MS/MS\textsuperscript{ALL} with SWATH\textsuperscript{™} Acquisition

MS/MS\textsuperscript{ALL} with SWATH\textsuperscript{™} Acquisition is changing the way scientists work in quantitative proteomics. Driven by the superior speed and high-resolution performance of the TripleTOF\textsuperscript{™} 5600+ system in both MS and MS/MS mode, this technique provides comprehensive quantitative MS/MS data on every component in a sample in a single injection.

SWATH Acquisition requires no sample-specific method development, yields better dynamic range than methods that derive quantitation from MS (precursor) data, and delivers limits of detection that were previously only attainable using targeted MRM strategies on triple quadrupole systems.

Finally, one of the greatest benefits of using MS/MS\textsuperscript{ALL} with SWATH Acquisition is that for every sample analyzed, the technique creates a complete digital archive of all possible fragment ions in that sample. As your research evolves and new hypotheses are formed, you can re-interrogate a sample without the need to re-acquire data. 
Eksigent NanoLC-Ultra® with cHiPLC®

The most precise quantitation requires the most reproducible nanoflow separations

Quantitative results using MS/MS™ with SWATH™ Acquisition

- 4 orders of dynamic range
- Low detection levels

LCMS reproducibility is a key component of targeted quantitation experiments such as MS/MS™ with SWATH™ Acquisition. Eksigent nano LC systems using the cHiPLC® provide high quality, reproducible separations, as illustrated by these 10 replicate injections of depleted plasma acquired using SWATH Acquisition.
Your success is our success.
We take it personally.

As an AB SCIEX customer you have access to a world-class customer support organization. Wherever you are, we’re there with you as a trusted partner to answer questions, provide solutions, and maximize lab productivity.

The expertise of our service engineers covers the entire LC/MS system. Whether you need help with an ion source, an autosampler, or running an application, they can put your mind at ease. They understand that you can’t afford downtime and need problems fixing fast. In fact, they do what it takes to make sure everything is working to your satisfaction and that your results look like they should.

Our application chemists specialize in making workflows flow. They can streamline your sample preparation and eliminate manual steps. They can help you develop methods for fast implementation and scale up for higher throughput. They can help you find ready-to-use iMethod™ Applications that get you up and running fast. They’re also only a phone call away if you need help quickly.

When it comes to training, different labs have different needs. Our training specialists can design programs specific to your lab that make the experience as effective and efficient as possible. Choose from hands-on system training for LC/MS techniques or application-specific courses given by leading experts. You can also learn at your own pace with our e-learning modules.

Our customer support organization has access to the latest product updates, software revisions, methods and repair procedures to make sure that you stay on top of your game.

When you have questions, we have answers.

Learn more at www.absciex.com/customersupport