The accurate mass workhorse

AB SCIEX TRIPLETOF® 4600 SYSTEM

AB SCIEX

The new AB SCIEX TripleTOF® 4600 System extends the TripleTOF family, making the ground-breaking features of the original TripleTOF® 5600 system – sensitive, high-resolution, accurate mass MS and MS/MS data acquired at unrivaled speeds – available in a value-priced, workhorse platform.

Comprehensive workflows in any research or routine analytical testing laboratory

For applications ranging from drug metabolism, proteomics, metabolomics and lipidomics to general unknown screening in food, environmental or forensic toxicology samples, the TripleTOF 4600 provides the most comprehensive, and most confident, data acquisition for your workflow.

A new workhorse for accurate mass applications

With the fastest data acquisition speeds in an accurate mass platform, the TripleTOF 4600 enables more data collection, higher-throughput, and higher-quality compound identification and quantitation in a single injection.

One touch productivity

Create valuable information using the most intelligent data acquisition strategies, including the qualitative and quantitative Profile and MS/MS^{ALL} workflows, assisted by powerful application-specific software solutions.

A complete solution

The AB SCIEX Accelerated Lab Integration™ packages take one-touch productivity a step further by merging the TripleTOF 4600 with advanced LC solutions, software, reagents, training, and validation services for a comprehensive workflow matched to your application requirements.

Pushing the limits in mass spectrometry

AB SCIEX has taken accurate mass technology and made it accessible to any laboratory that requires maximum uptime, ultimate robustness, and high accuracy in compound identification and quantitation, all in an easy-to-use, value-priced platform.

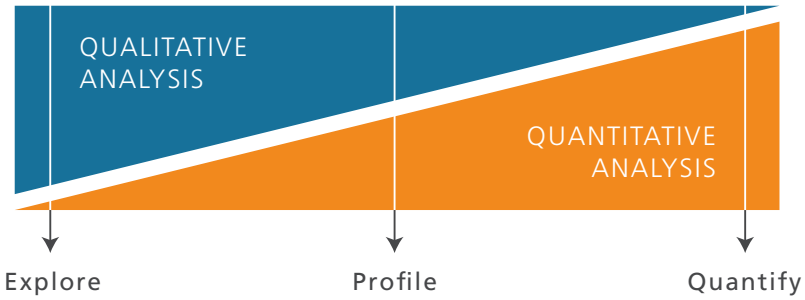
The AB SCIEX TripleTOF® 4600 System combines the world's fastest acquisition rates with intelligent acquisition strategies to give analytical scientists a dependable accurate mass LC/MS/MS workhorse for routine comprehensive analysis of complex samples.

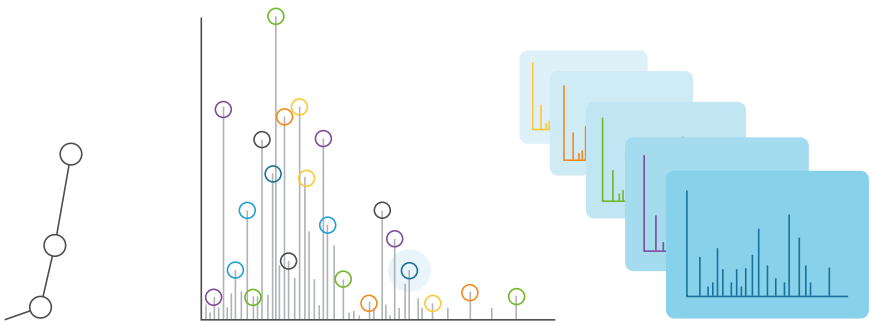
- High-resolution accurate mass MS and MS/MS data at unparalleled speeds
- Quality performance for discovery, identification, and quantitation of low-abundance analytes
- Proven robustness through the reliable Turbo V® source
- SmartSpeed™ 100 Hz data acquisition rates
- EasyMass™ accuracy of less than 2 ppm RMS with external mass calibration, 1ppm achievable with internal calibration
- Typical operating mass resolution of >25,000 FWHM
- High mass resolution in excess of 30,000 FWHM at m/z 956 using a 10 ms accumulation time
- TOF mass range up to 40,000 m/z
- Ideal solution for UHPLC separations with fast data acquisition speeds
- One-touch productivity with advanced software solutions to quickly create useable information from your accurate mass data

Achieve speed, resolution, and sensitivity simultaneously, in a single workhorse platform.

One system, flexible workflows

For the first time, pharma, academic and routine 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?"



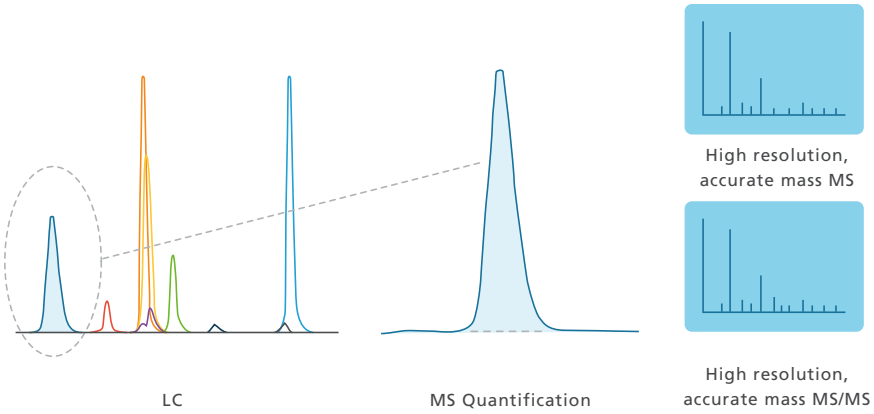


EXPLORE

Explore complex samples in greater depth: Select up to 50 precursors – and generate high resolution and high mass accuracy MS/MS spectra in a second using powerful IDA (information-dependent acquisition) algorithms and high-resolution, accurate-mass MS and MS/MS.

Speed and resolution for definitive identification

- Select up to 50 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

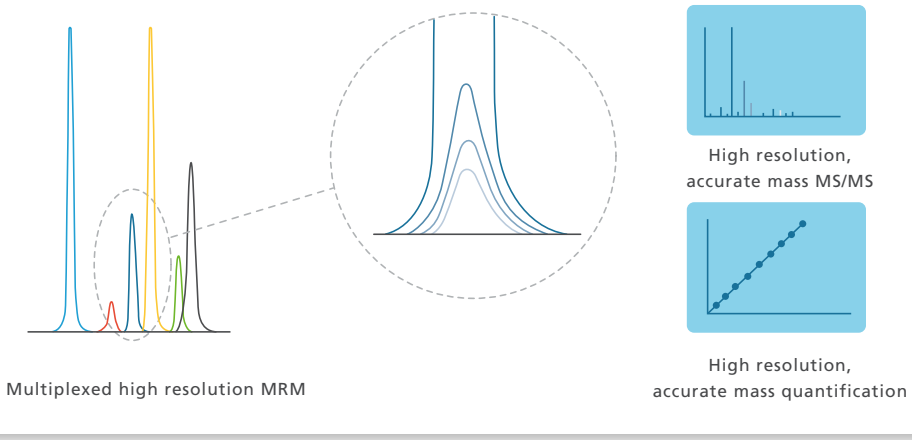


PROFILE

Profile samples for quant and qual in a single run: Quantify virtually every compound in the sample with high-resolution MS quantification and fast chromatography; confirm compound identity with high-resolution, accurate-mass MS/MS; then mine the data for the information you need.

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



QUANTIFY

Quantify analytes with High Resolution MRM for highest specificity and confidence: Obtain high-resolution at high mass and low mass in the same spectrum for high-resolution MRM-like quantification. LOQ's and dynamic range are equivalent to high-performance triple quad instruments. Cycle times as low as 10 msec generate superior peak definition even with fast LC separations. Quantification requires little optimization, and you can choose multiple fragments per precursor from the acquired full scan MS/MS data.

Relative and absolute quantitation with high resolution MRM (MRM^{HR})

- Maximize specificity using MRM-like quantitation with high resolution fragment ions
- Analyze many analytes with triple quadrupole MRM acquisition rates and collect full scan MS/MS spectra for each precursor without 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

Inspired engineering

Beginning with the best-in-class quantitative performance of the AB SCIEX Triple Quad™ 5500 system, AB SCIEX researchers developed the Accelerator TOF™ Analyzer to deliver high resolution at the speed and sensitivity required to maintain the precision and limits-of-quantitation associated with MRM. This innovation is featured in the AB SCIEX TripleTOF® 4600 System – the newest addition to the AB SCIEX quadrupole TOF family of products.

Automated Calibrant Delivery System

DuoSpray™ source

QJet® Ion Guide

Automated Calibration Delivery system allows easy, automated instrument calibration from a reference spray using the DuoSpray™ source.

Software selectable dual ionization system with the DuoSpray™ source – ESI and APCI – provides experimental flexibility with highest performance.

> TurboIonSpray® Probe 5-3000 µL/min

> APCI Probe 50-3000 µL/min

> System also compatible with Turbo V™ source and NanoSpray® III source with heated interface

Patented QJet® ion guide improves ion containment and operates at high pressure, providing better collisional focusing and improved ion transmission.

Next generation eQ™ electronics enable faster scan speeds with improved sensitivity and robustness.

Patented Q0 High Pressure Cell collisionally focuses ions for maximum transmission and sensitivity.

LINAC® collision cell increases speed of analysis and eliminates cross-talk. True collision induced fragmentation provides reliable, information-rich, library searchable spectra.

- 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

Accelerator TOF™ Analyzer

for improved resolution and sensitivity

- 10kV acceleration voltage for optimal resolution
- High transparency grids throughout for minimal ion loss
- Two-stage ion reflector compensates for energy dispersion to maximize resolution

One touch productivity

Take advantage of fast data acquisition, and get reliable information from your accurate mass data, using powerful, workflow-driven software solutions. Whether your application is drug discovery and metabolism, food and environmental contaminant analysis, forensic toxicology sample screening, or proteomics discovery and quantitation, intelligent software solutions help you get the most information from a single analysis.

Drug Metabolism with MetabolitePilot™ Software

Streamline data analysis for metabolite identification with tools for easy structural elucidation and relative quantitation of metabolites.

General Unknown Screening with PeakView™ Software

Process large batches of accurate mass data, interpret structures of unknown compounds, manage large lists of compounds and libraries, and perform automatic extracted ion chromatogram (XIC) calculations in a single software package.

Protein identification and quantitation with ProteinPilot™ Software

Easily identify hundreds of peptides and fragments, distinguish isoforms, suppress false positives, and visualize peptide-protein associations in this streamlined software platform.

Sample component profiling with MarkerView™ Software

Rapidly profile your sample to determine up and down regulation of endogenous compounds or to highlight variance between multiple samples analyzed in a batch.

Lipid characterization with LipidView™ Software

Profile, characterize, and quantify lipid data in this data processing tool, which contains a database of over 25,000 lipid fragment entries to support your analysis.

Quantitative analysis with MultiQuant™ Software

Process data sets consisting of both large numbers of MRM transitions and study samples, with an emphasis on the requirements for processing protein/peptide quantitative workflows. Results can easily be exported to other software packages, or use the software's flexible reporting features to generate custom reports.

Accurate mass performance delivered in a workhorse platform

Keep the 'accurate' in accurate mass data acquisition for hour-after-hour performance

AutoTune and EasyMass provide high confidence in mass accuracy for long sample batches, producing reliable data hour-after-hour, day-after-day.

Matrix is no longer an interference

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.

More data in a single injection

Unmatched speeds enable routine quant/qual analysis, so labs can not only collect accurate mass MS/MS data for the detection and identification of unknowns, but they can also collect high resolution MRM data (MRM^{HR}) for targeted compound quantitation, all in a single run.

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.

Neutral loss triggered IDA provides unique specificity by triggering MS/MS when two TOF MS scans (high and low energy) detect a specified mass difference. The result is higher efficiency IDA experiments with fewer runs.

Get your methods up-and-running quickly

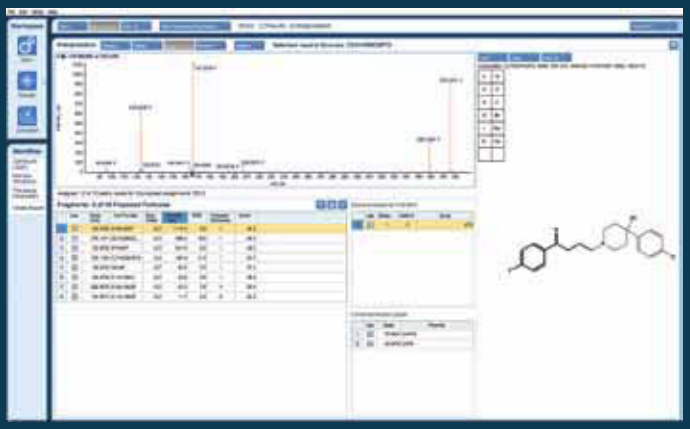
Methods Wizard enables easy creation of acquisition methods with templates for common workflows.

Accelerated Lab Integration™ packages merge hardware, software, reagents, training, and support into a complete workflow solution for easy technology adoption in any laboratory.

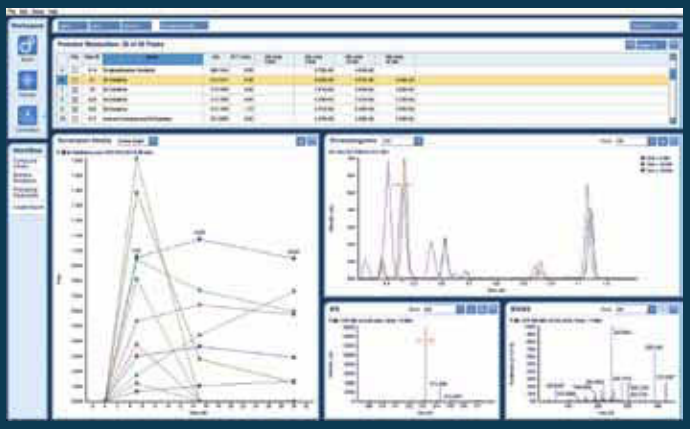
World-class applications specialists are available for intensive training and support to get your lab's customized methods running and analysts trained in no time.

The power of accurate mass for any application

Confident metabolite identification



Use MetabolitePilot™ Software for Integrated MS/MS Interpretation to perform structural editing and automatic fragment assignments, directly within the results workspace.



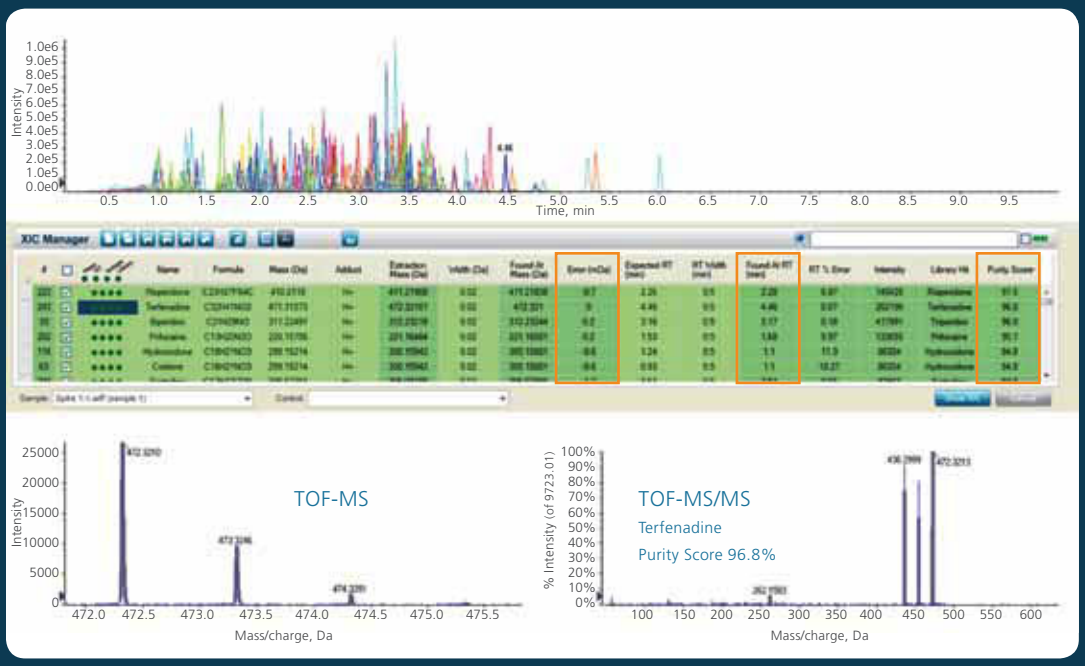
The Correlation Workspace allows qualitative and quantitative data visualization to assess metabolite kinetics or to review metabolites across species.

Comparative unknown screening analysis in food and environmental samples

Easily identify chemical contaminants in a variety of different food and environmental samples, and perform both targeted analysis and unknown screening in a single run. Using the accurate TOF-MS and TOF-MS/MS spectra, detected compounds can be accurately identified against a compound library (targeted analysis shown here).

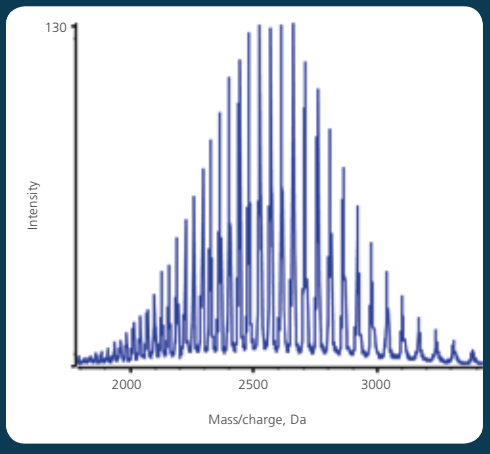
For contaminants detected but not identified in the compound library, the MS/MS spectra can be used to more deeply investigate the structure and chemical composition of the detected unknown (general unknown screening).

Screen forensic toxicology samples for drugs of abuse, analogs, and metabolites

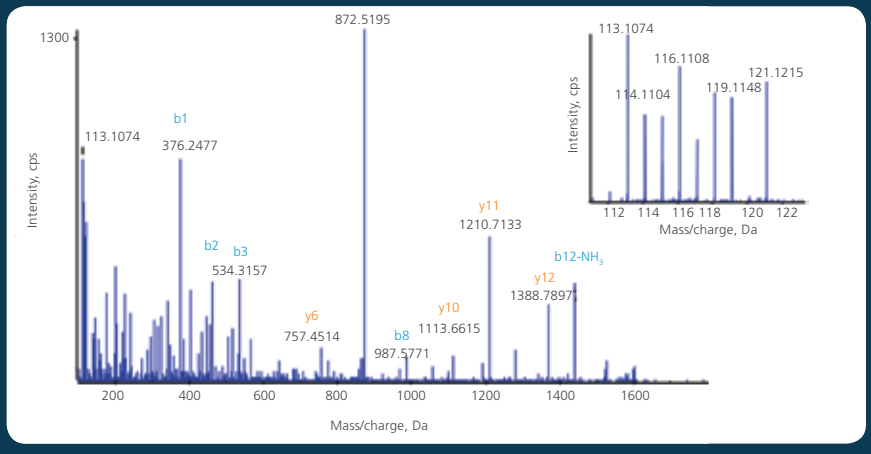


Confidently screen and identify hundreds of drug compounds in a single run using PeakView® Software with the XIC Manager. Identify compounds by searching against a library, and get confident identification by mass error, retention time, and MS/MS purity score.

Elevate biologics analysis and discovery proteomics workflows



Accurately determine the molecular weight of a protein using high quality MS spectra. The resolution and mass range of the TripleTOF® 4600 allows protein mass reconstruction for both small and large proteins, including the IgG protein shown here.



By coupling the high speed, high resolution MS/MS acquisition capabilities of the TripleTOF™ 4600 System with multiplexed workflow solutions such as the iTRAQ® Reagents, discovery proteomics workflows are elevated to a new level.

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.

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