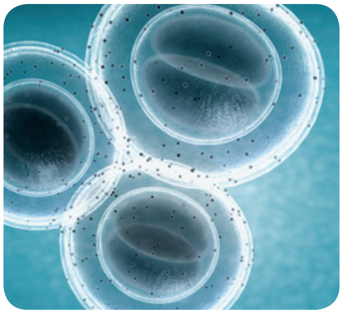


Improving the world we live in

Integrated LC/MS/MS Solutions

Dear customer:

AB SCIEX is committed to providing you with best-in-class analytical solutions that enable you to **push the limits** in your field.

As a **partner who listens**, we work relentlessly every day to help support you in addressing complex analytical challenges.

We are proud of our supportive role in **advancing science and improving our world** by empowering you with technologies for basic research, drug discovery and development, food and environmental testing, and clinical research and forensics.

I trust that the information presented in this brochure will help you select the best solution for your challenges. AB SCIEX aims to help you redefine what is achievable and advance science with reliable, sensitive and intuitive solutions. We offer you what you expect from an industry leader – simply the best.

Regards,
Rainer Blair
President, AB SCIEX

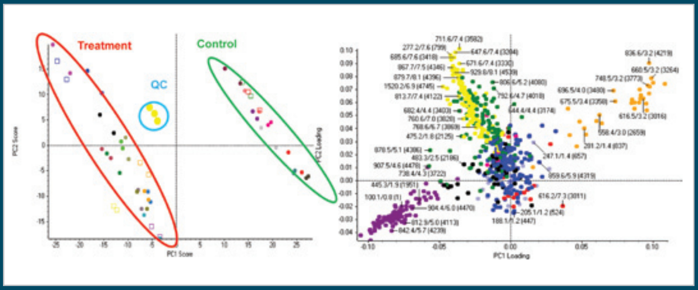
Biomarker and omics research

The goal of biomarker research is to identify genes, proteins, lipids and metabolites that have potential diagnostic or prognostic value in managing human disease. Biomarker discovery is facilitated by omics research, which promises to uncover relevant biomarkers even in the absence of detailed insight into disease mechanisms.

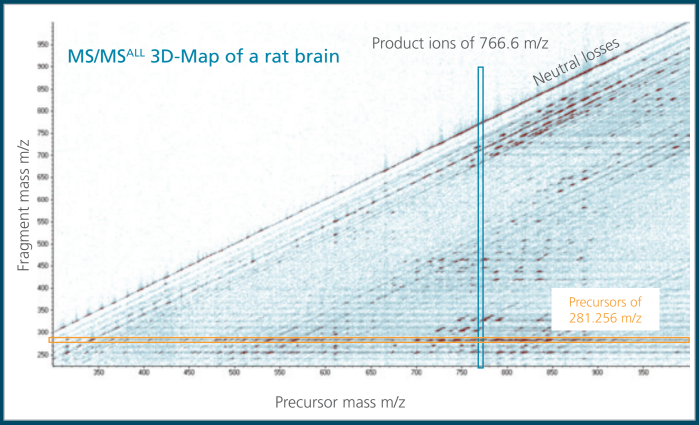
AB SCIEX is a global leader in developing mass spectrometry tools for omics research and biomarker discovery. Our instrumentation, software, reagents, and workflows allow you to dig deeper into complex biological systems, analyze prospective biomarkers and deliver results with potential use in clinical applications.

Find metabolites of interest – MarkerView™ Software

Global metabolite profiling is used to identify interesting metabolites and potential biomarkers in a non-targeted fashion. MarkerView™ Software enables simultaneous feature finding, alignment, and statistical analysis to highlight metabolites of interest.



Highlighting metabolites of interest: The principal component analysis (PCA) scores plot (left) shows samples that group together due to common variables. The PCA loadings plot with principal component variable grouping (PCVG) shows correlation between common and significant variables.

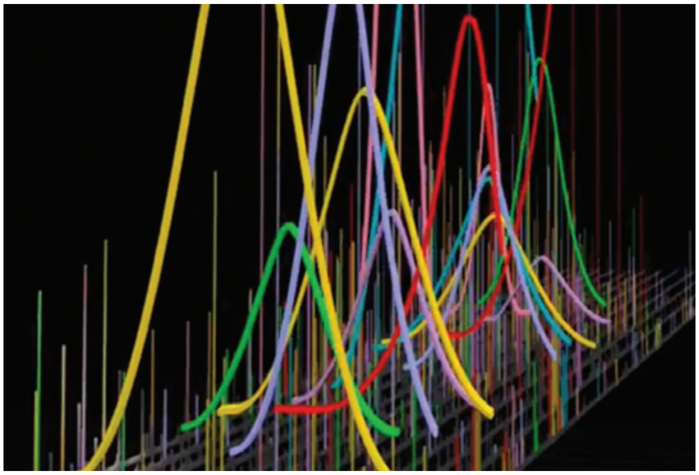


With the MS/MS^{ALL} workflow on a TripleTOF® system, every lipid precursor ion is fragmented sequentially which provides a fragmentation map of all lipid species in the sample. This powerful profiling technique means that the data can be interrogated for specific lipid ions or even lipid-classes post-acquisition.

MS/MS quantitation for all detectable peptides –SWATH™ Acquisition

SWATH™ Acquisition provides the highest level of multiplexing for MS/MS quantitation of thousands of peptides in complex biological samples.

A single generic data acquisition method captures MRM data for all detectable ions, enabling you to acquire first and hypothesize later.



Confident protein ID and advanced analysis of results – ProteinPilot™ Software

Protein identification and expression analysis of proteins from LC/MS/MS, LC/MALDI and gel-based experiments is possible with ProteinPilot™ Software. The software supports all AB SCIEX platforms as well as other platforms using MGF (MASCOT Generic Files) format.

Drug discovery and development

Delivering innovation

AB SCIEX technology is central to the drug discovery and development pipeline. From the rapid structural identification and *in vitro* metabolic stability needs of the early discovery phase, through to the integrated qual/quant and low-level quantitation requirements of the development phase, AB SCIEX offers an innovative set of chromatography, software and mass spectrometry workflow solutions to meet the demands of the most challenging assays.

MRM^3 workflows for enhanced quantitative selectivity

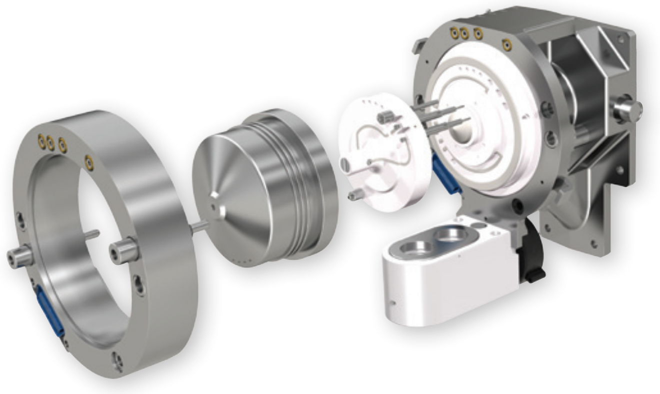
When high background or challenging co-eluting interferences make standard MRM quantitation difficult, the MRM^3 workflow can be used to enhance quantitative selectivity and improve signal to noise ratios.

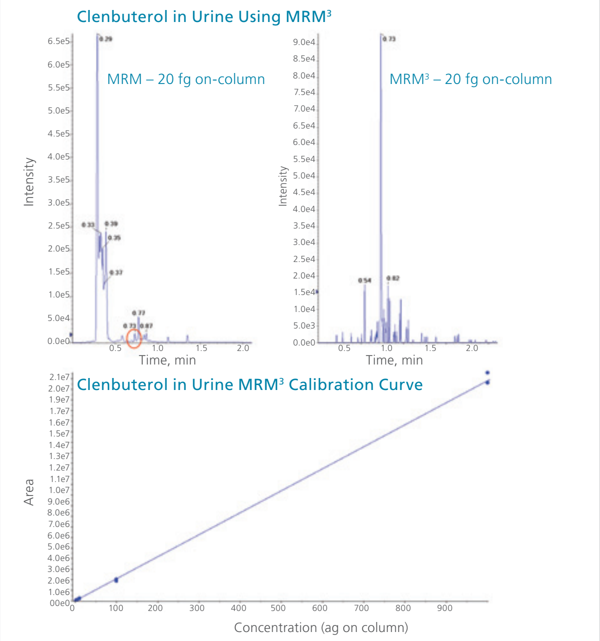
- Boost selectivity and reduce inferences
- Reduce sample cleanup and chromatographic complexity

Differential ion mobility separation of isobaric species and challenging co-eluting contaminants – SelexION™ technology

Improve data quality by combining sensitivity and selectivity in a single platform with SelexION technology.

- Reduce isobaric interferences
- Increase signal to noise ratios
- Accelerate chromatographic separation times

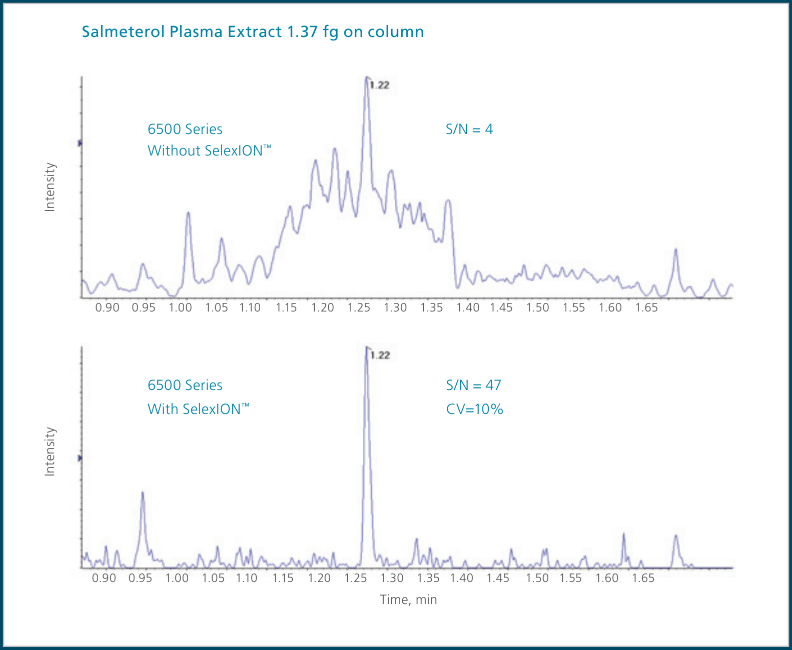




Clenbuterol in Urine Using MRM^3

Clenbuterol in Urine MRM^3 Calibration Curve

MRM^3 workflow reduces background interferences while maintaining linearity across the range.



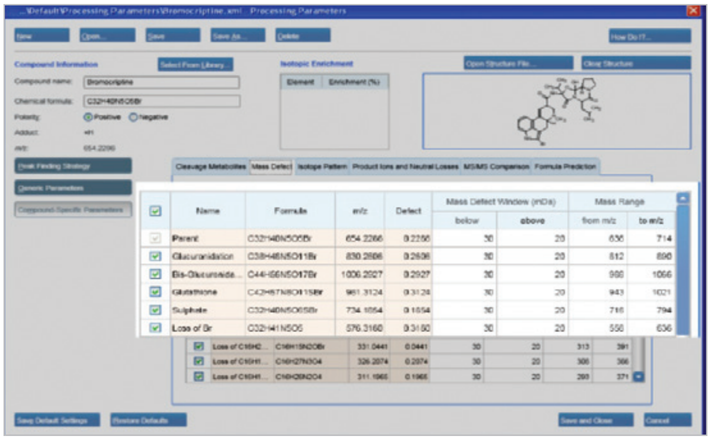
Salmeterol Plasma Extract 1.37 fg on column

SelexION differential ion mobility delivers true gains in data quality and signal to noise ratios.

Effective metabolite identification with real time multiple mass defect filtering

Real time multiple mass defect filtering (RT-MMDF) is a powerful accurate mass technique for the detection of phase I and II metabolites related in elemental composition to the parent compound. It is particularly beneficial for complex in vivo samples.

- Gives IDA priority to ions matching the mass defect of the parent compound
- No need to perform filtering post processing or perform additional injections
- Uses separate mass defect windows for phase I and phase II metabolites
- Compatible with fast cycle times and UHPLC chromatography



Compound name: Bromocriptine
Chemical formula: $C_{32}H_{40}N_5O_5Br$
Polarity: ● Positive ○ Negative
Adduct: +H
m/z: 654.2266

☑	Name	Formula	m/z	Defect	Mass Defect Window (mDa)		Mass Range	
					below	above	from m/z	to m/z
☑	Parent	$C_{32}H_{40}N_5O_5Br$	654.2266	0.2266	30	20	636	714
☑	Glucuronidation	$C_{38}H_{48}N_5O_{11}Br$	830.2586	0.2586	30	20	812	890
☑	Bis-Glucuronide...	$C_{44}H_{56}N_5O_{17}Br$	1006.2927	0.2927	30	20	988	1066
☑	Glutathione	$C_{42}H_{57}N_8O_{11}SBr$	961.3124	0.3124	30	20	943	1021
☑	Sulphate	$C_{32}H_{40}N_5O_8SBr$	734.1854	0.1854	30	20	716	794
☑	Loss of Br	$C_{32}H_{41}N_5O_5$	576.3160	0.3160	30	20	558	636
☑	Loss of C16H2...	$C_{16}H_{15}N_2OBr$	331.0441	0.0441	30	20	313	391
☑	Loss of C16H1...	$C_{16}H_{27}N_3O_4$	326.2074	0.2074	30	20	308	386
☑	Loss of C16H1...	$C_{16}H_{25}N_3O_4$	311.1965	0.1965	30	20	293	371

Information-Dependent Acquisition (IDA) Methods	Peak Intensity	Dynamic Background Subtraction (DBS)	MMDF + DBS
Metabolites detected by processing full MS data	31	31	31
MS/MS spectra of metabolites acquired	17	27	31
Success rate (%)	53	87	100

Diclofenac metabolites in bile using RT-MMDF.

Scientists who are dedicated to improving life push the limits in mass spectrometry

> “Recent gains in sensitivity in analytical instrumentation have opened up remarkable new possibilities for pharmaceutical companies to take advantage of DBS analysis.”
>
> SHANE NEEDHAM, LABORATORY DIRECTOR, ALTURAS ANALYTICS, INC

Clinical research

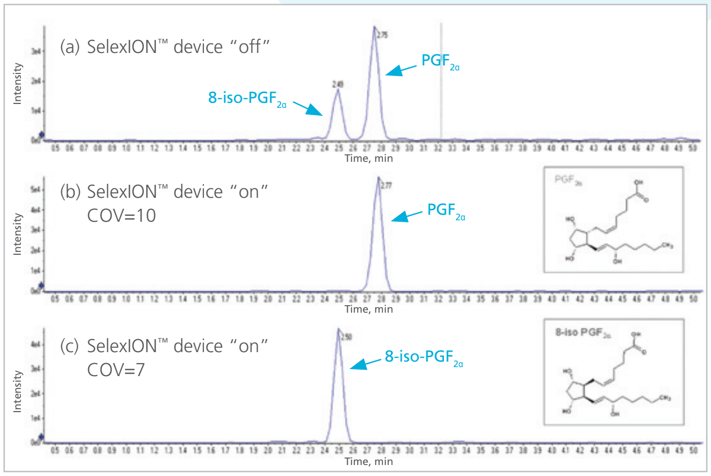
Analysis of multiple immunoassays in a single-run

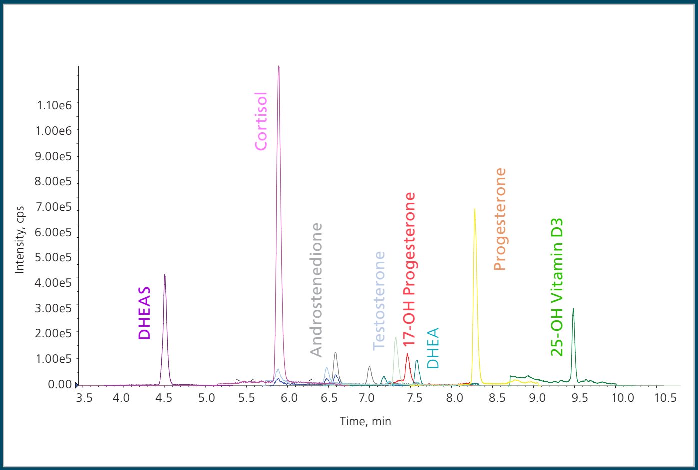
Tandem mass spectrometry is becoming an essential tool for clinical research applications involving detection of low-level or difficult analytes in complex matrices such as urine, blood, saliva and whole cell lysates. Unlike immunoassay methods, LC/MS/MS enables highly selective and specific analysis of multiple compounds in a single run, leading to more confidence in results and opening up new discoveries.

In addition to state-of-the-art hardware and software AB SCIEX offers an extensive portfolio of pre-configured, research methods to help you confidently implement tandem mass spectrometry in your laboratory, even if you are new to the technology. All backed-up with an extensive service and support organization.

Enhanced selectivity with LC/MS/MS analysis of prostaglandins using SelexION™ ion mobility technology

The SelexION differential ion mobility device is able to completely resolve the isomers Prostaglandin F2a and 8-iso-Prostaglandin F2a. This allows dramatic reduction of chromatographic run-times and significant increase of throughput and efficiency while maintaining confidence in the accuracy of results.





The chromatogram above shows a method that measures the levels of a wide variety of compounds in a single analytical run. Combining multiple analytes into a single analysis increases throughput and minimizes sample consumption when samle volume is limited.

Forensic toxicology

Reduce run time and lower cost

Transferring analysis from GC/MS to LC/MS/MS simplifies sample preparation (without the need for time-consuming solid phase extraction (SPE) and derivatization), reduces analytical run time, and lowers operating and labor costs.

AB SCIEX solutions for forensic toxicology provide an easy and rapid method for simultaneous multi-drug identification and quantitation from various sample matrices. The sensitivity of AB SCIEX solutions make it possible to detect and quantitate forensic drugs at extremely low levels allowing complex analysis in challenging matrices such as oral fluids and hair. And by using general unknown screening techniques, unexpected drugs, drug analogs, and drug metabolites can also be detected and identified with utmost confidence.

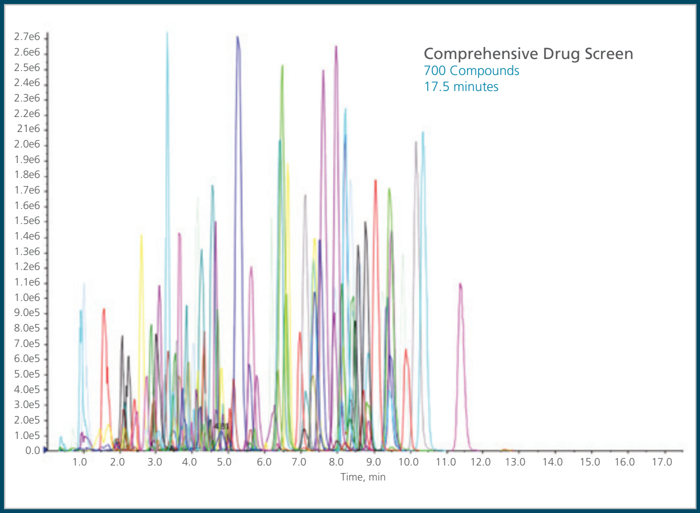
Identify and quantify hundreds of drugs in a single analysis

Unique AB SCIEX QTRAP® system technology enables you to shorten analysis time and gives forensic toxicologists more useful information from every experiment. Combined with Cliquid® Software, iMethod™ Applications, and a 1250 drugs of abuse compound library, you are equipped with a rapid, high-throughput solution that is easy to implement and quick to deliver results.

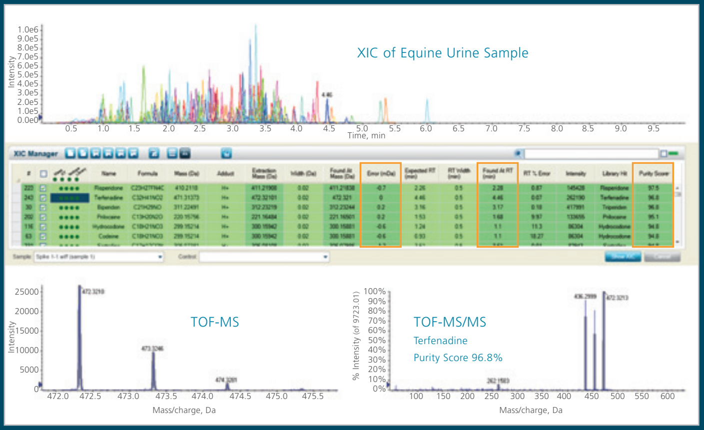
AB SCIEX LibraryView™ Software

A fast way to analyze large volumes of data for forensic screening applications.

- Analyze large screening batches in minutes
- Define criteria for interactive library searching
- Customize your own libraries for faster library searching
- Create dynamic libraries for more robust searches
- Review data interactively
- Export libraries for easy transfer across multiple instruments



Multi-target LC/MS/MS screening for >700 drugs. MRM mode was combined with dependent full-scan MS/MS spectral acquisition. The MS/MS spectra were searched against a library for compound identication and confirmation.



#	☐		Name	Formula	Mass (Da)	Adduct	Extraction Mass (Da)	Width (Da)	Found At Mass (Da)	Error (mDa)	Expected RT (min)	RT Width (min)	Found At RT (min)	RT % Error	Intensity	Library Hit	Purity Score
223	☐	●●●●	Risperidone	C23H27FN4C	410.2118	H+	411.21908	0.02	411.21838	-0.7	2.26	0.5	2.28	0.87	145428	Risperidone	97.5
243	☐	●●●●	Terfenadine	C32H41NO2	471.31373	H+	472.32101	0.02	472.321	0	4.46	0.5	4.46	0.07	262190	Terfenadine	96.8
30	☐	●●●●	Biperiden	C21H29NO	311.22491	H+	312.23219	0.02	312.23244	0.2	3.16	0.5	3.17	0.18	417991	Triperiden	96.8
202	☐	●●●●	Prilocaine	C13H20N2O	220.15756	H+	221.16484	0.02	221.16501	0.2	1.53	0.5	1.68	9.97	133695	Prilocaine	95.1
116	☐	●●●●	Hydrocodone	C18H21NO3	299.15214	H+	300.15942	0.02	300.15881	-0.6	1.24	0.5	1.1	11.3	86304	Hydrocodone	94.8
63	☐	●●●●	Codeine	C18H21NO3	299.15214	H+	300.15942	0.02	300.15881	-0.6	0.93	0.5	1.1	18.27	86304	Hydrocodone	94.8

TripleTOF® analysis in equine urine. 259 drugs were detected and identified using retention time, mass error, isotope pattern and confirmed with MS/MS library matches.

Food and beverage testing

AB SCIEX food and beverage testing solutions are optimized to identify and quantify hundreds of analytes in a single run, providing throughput and performance to help you meet and exceed regulatory demands. AB SCIEX solutions also include pre-configured iMethod™ Applications, consumables and reagents, and advanced software solutions that make food analysis and contaminant identification easy, fast, robust, and accurate.

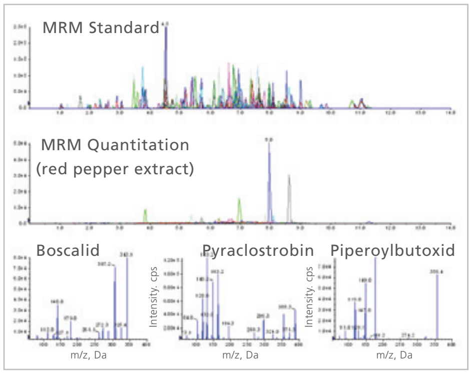
Screen large panels of compounds across different compound classes

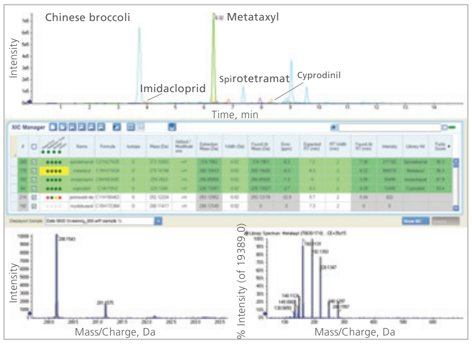
With QTRAP® technology, you can screen, identify, and quantify hundreds of pesticides in a single analysis via library search and automated MRM ratio calculation.

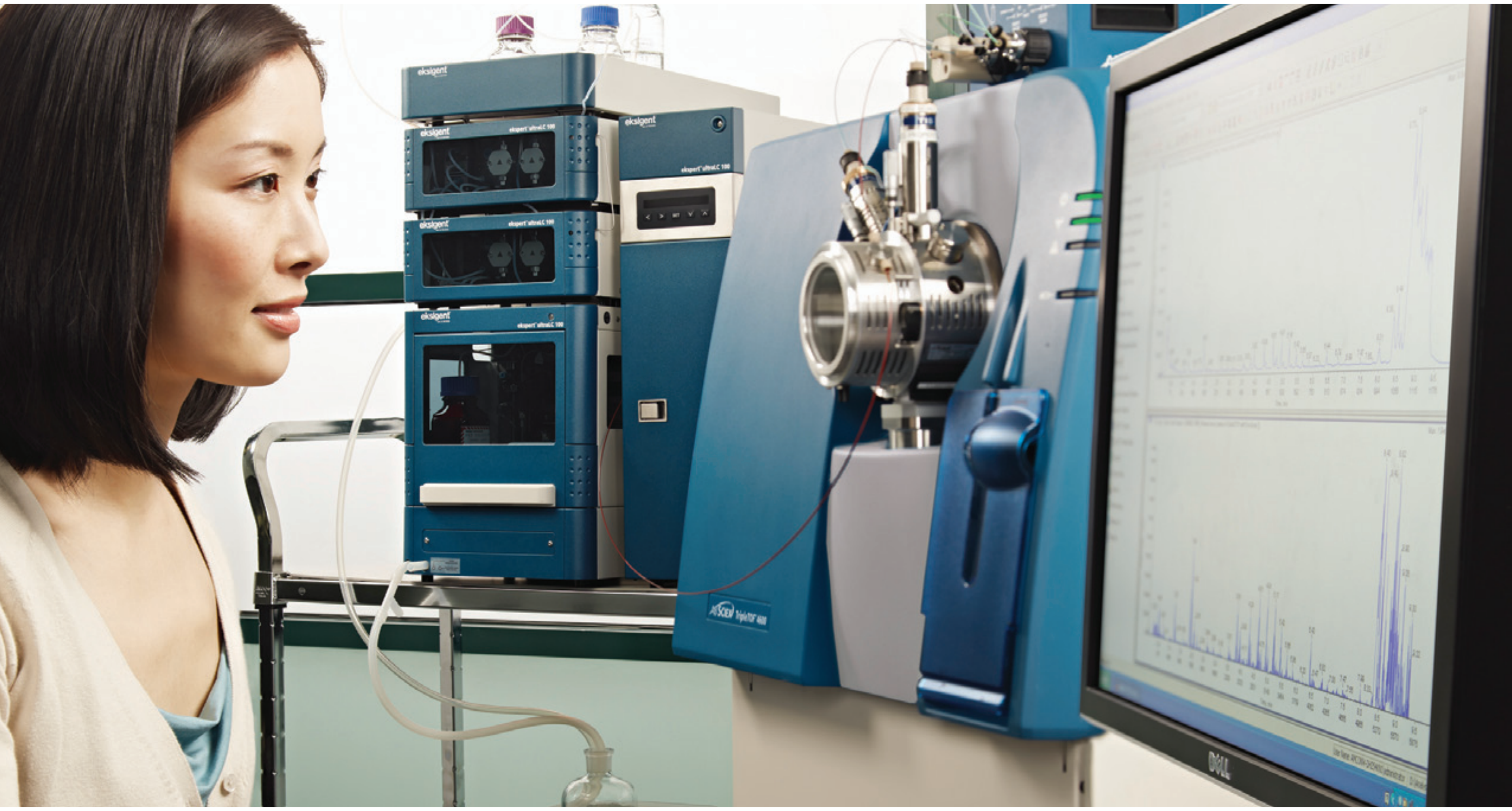
Identify adulterants you didn't expect to find

With high-resolution and accurate mass MS and MS/MS, the TripleTOF® systems enable detection of targeted and non-targeted food contaminants, and AB SCIEX software solutions make it easy to identify and quantify those contaminants with high accuracy.

Additionally, LC/MS/MS libraries containing MRM catalogues and spectral libraries for hundreds of contaminants and residues are readily available for easy method set-up and fast and accurate data analysis.







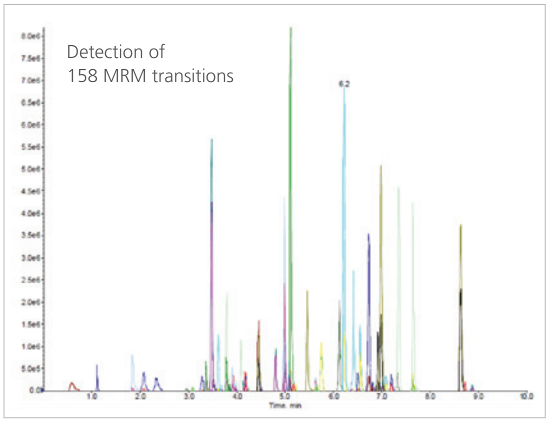
Environmental analysis

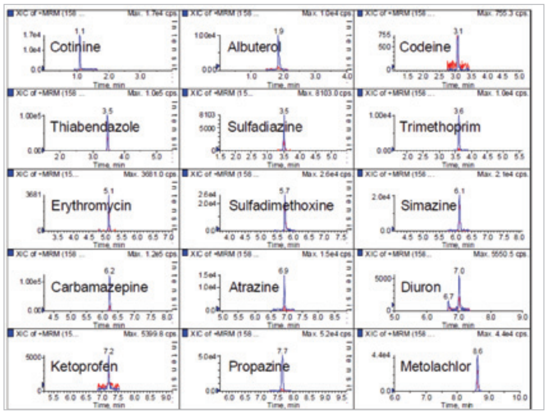
AB SCIEX solutions, including pre-configured iMethod™ Applications, offer exceptional sensitivity, specificity, and throughput, enabling laboratories to characterize and monitor hundreds of compounds in sensitive environmental samples simultaneously, with fast analysis times and minimal sample clean up.

Analysis of contaminants, including PPCP, pesticides, explosives, and drug residues with ultra-high sensitivity in environmental samples

AB SCIEX QTRAP® 5500 Systems offers phenomenal sensitivity for residue detection and identification in water samples. In addition to MRM detection, QTRAP technology offers added sensitivity and selectivity, including robust library searching for accurate compound identification.

iMethod Applications, including methods for analysis of pesticides and herbicides in water are at your fingertips for easy method implementation for analysis of environmental samples.





For direct injection of water samples, limits of detection of < 10 ppt have been achieved for many PPCP compounds, eliminating the need for sample clean-up and increasing throughput.

Simplify your research with application specific software

Analyst® Software offers powerful tools for automating method development, data analysis review, and reporting.

- Automates MS to MS/MS acquisition with Information Dependent Acquisition
- The *Scheduled* MRM™ Algorithm uses overlapping MRM monitoring periods to maximize quantitative performance and accuracy
- Provides easy database searching, traceability, security, and tools for 21 CFR Part 11 compliance

Cliquid® Software for routine screening and quantitation provides a simple four step workflow for LC/MS/MS analysis.

- Offers multiple pre-configured iMethod™ Applications, including libraries and MRM catalogues for food, environmental, forensic and clinical research analysis.
- Bi-directional LIMS compatibility with any LIMS or LIS
- Barcode reading for "chain of custody" workflows

MetabolitePilot™ Software for the TripleTOF® systems streamlines the detection and identification of metabolites for drug discovery.

- Simple, clear data processing that supports quick, effective decision-making
- Exhaustive sets of biotransformations are built into the software, or you can build custom biotransformation sets
- Enables inter sample and intra species metabolite correlation analysis

LightSight® Software for metabolite identification.

- Seamlessly create data acquisition methods based on the structure of the drug, and analyze and mine the resulting data
- Simple, clear data processing that supports quick, effective decision-making
- Exhaustive sets of biotransformations are built into the software, or you can build custom biotransformation sets

DiscoveryQuant™ Software improves the speed of analysis and information gathering of pre-candidate drugs.

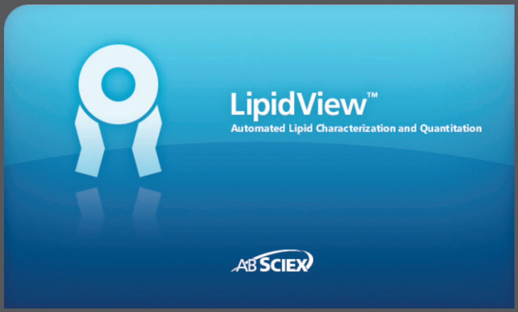
- The optimize module performs a rapid single-injection compound optimization on every compound using a unique MRM-based approach and then populates a database with this information
- The analyze module uses the same database to access MS methods for use in assays.
- The database can be shared among labs and among sites around the world to allow collaboration with colleagues and avoid duplicating effort.

MultiQuant™ Software processes MRM data for quantitative information with a comprehensive user interface for superior data visualization.

- SignalFinder™ algorithm allows more reliable integration, less user intervention and extend dynamic range functionality
- Audit trail functionality makes data review easier
- Streamlined electronic signature functionality improves productivity without sacrificing data queries
- Supports multi-analyte/MRM transition workflows such as peptide quantitation assays

PeakView® Software enables the qualitative review of LC/MS and MS/MS data for the TripleTOF® systems.

- Processing parameters can be applied across large sample sets saving time during data processing and review
- Filter data based on criteria such as quality, mass defect, and isotopic pattern
- Specialized tools such as Formula Finder and Structure Elucidation enable detailed investigation and characterization at the molecular level



LipidView™ Software streamlines the molecular characterization and quantification of lipid species from electrospray MS data.

- Profile lipids by searching parent and fragment ion masses against a lipid fragment database containing over 25,000 entries
- Streamlines a number of key steps such as automated data processing derived from template methods, method editing and selection, lipid species identification, comprehensive isotope contribution removal, multiple internal standards-based quantification, visualization and result reporting

MarkerView™ Software for metabolomics and biomarker profiling across multiple samples.

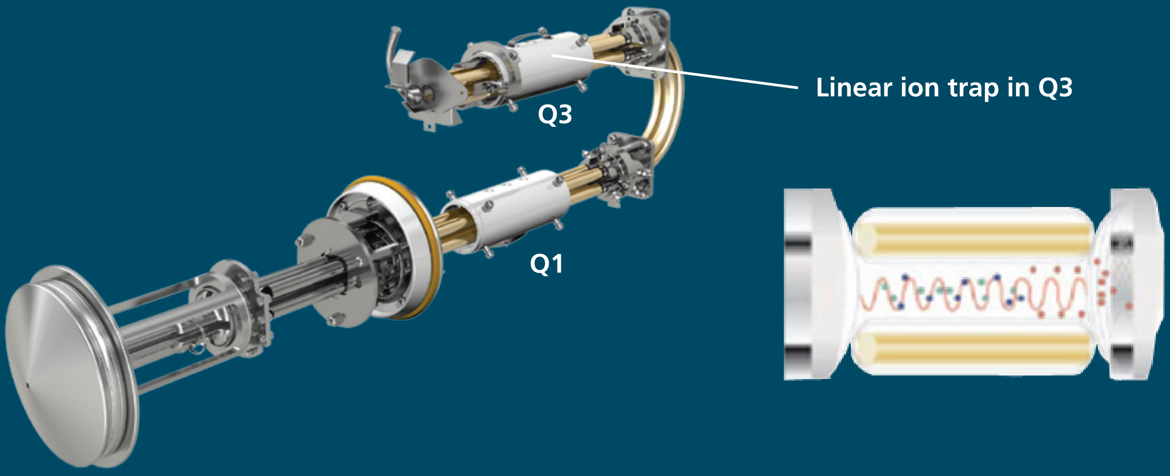
- Align mass and retention time to ensure accurate comparison of identical compounds in different samples
- Process data using classified and/or non-classified workflows such as principal component analysis or T-tests
- Generate custom reports to track your work and record potential biomarkers

ProteinPilot™ Software streamlines protein identification and quantitation.

- Searches for hundreds of biological and other modifications, genetic variants, and unexpected cleavages simultaneously with the Paragon™ algorithm
- Distinguishes protein isoforms, protein subsets, and suppresses false positives
- Intelligently determines all search parameters using the unique user interface – no need for informatics expertise
- Supports quantitative workflows using SCIEX iTRAQ®, ICAT, and SILAC reagents

Pushing the limits of what is possible

AB SCIEX specializes in triple quadrupole, linear ion trap, and TOF based instruments. These are the technologies that provide mass spectrometry capabilities with the sensitivity, resolution, speed, and selectivity to meet the demands of today’s challenging applications.

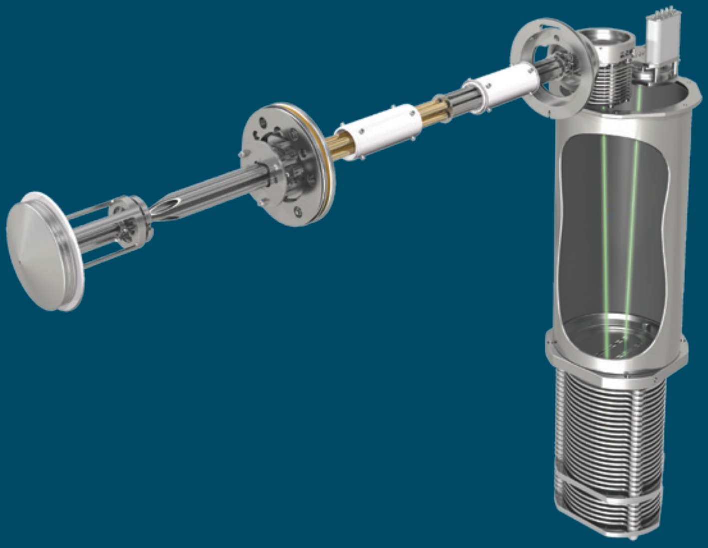


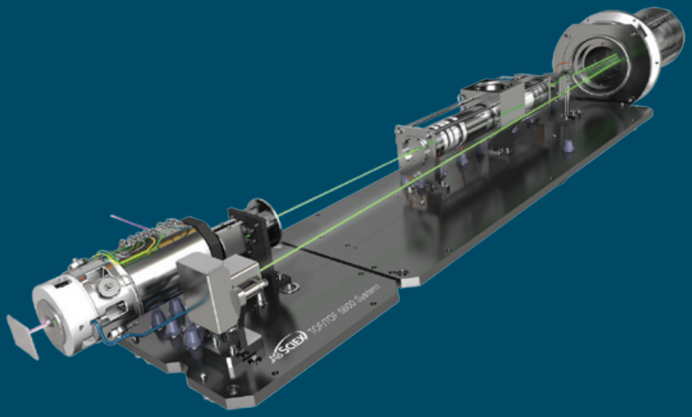
Triple quad system – for quantitation

Tandem mass spectrometry (MS/MS), is a technique in which quadrupole mass analyzers are used in series to obtain quantitative information for a variety of different analytes. In MS/MS mode the first mass analyzer, Q1, selects the ions of interest, the ions are then fragmented in the collision cell, Q2, and the fragments are analyzed in the third quadrupole, Q3. In MS/MS operation, different scan modes can be used to get complementary qualitative information about the sample.

QTRAP® system – for simultaneous quantitation and confirmation

The QTRAP platform is a unique tandem mass spectrometer which is capable of functioning as either a dedidated triple quadrupole mass spectrometer for quantitative workflows or as a highly sensitive linear ion trap mass spectrometer for qualitative workflows. The QTRAP technology can also increase selectivity by reducing interferences for quantitative applications using the MRM^3 workflow in which the MRM transition is based on the MS/MS/MS fragmentation pattern of the compound of interest.





TripleTOF® system – high resolution quantitative and qualitative analysis

The first system to combine comprehensive qualitative exploration, rapid profiling, and high-resolution quantitation on a single accurate mass platform. No other accurate mass MS/MS instrument has the speed and sensitivity to deliver comprehensive qualitative and quantitive information in complex matrices – all in a single injection, on a single platform.

- Explore with speed and resolution for definitive identification
- Profile through quantitative and qualitative information in a single run
- Quantify with relative and absolute quantitation workflows in high resolution

TOF/TOF™ system – speed and sensitivity to expand protein discovery and tissue imaging

Continuing the legacy of innovation in MALDI technology that made it the world leader in life science mass spectrometry, AB SCIEX offers the most advanced MALDI TOF/TOF systems ever. All aspects of the system including hardware, software, workflows and support are perfectly integrated into an optimized platform, allowing you to discover more from every sample.

- Protein identfication
- Tissue imaging
- Carbohydrate analysis
- Polymer analysis

Triple quadrupole technology

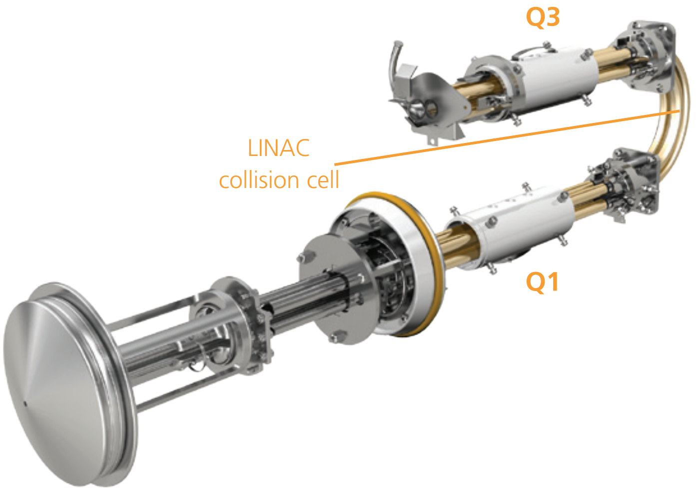
Don't miss a thing

With over 30 years of experience developing LC/MS/MS solutions, AB SCIEX offers an unmatched heritage of technological innovation and dependability. Whether your research is focused on ADME, regulated bioanalysis, food and environmental contaminant screening, targeted quantitative proteomics, forensic toxicology or clinical research, AB SCIEX's integrated triple quadrupole mass spec solutions covers your key performance criteria.

Offering a broad range of LC/MS/MS solutions, the AB SCIEX triple quadrupole portfolio addresses your research needs. You can choose just the right instrument for your lab, from entry level triple quads such as the API 3200™ system for basic quantitation, to the Triple Quad™ 4500 system, a workhorse for sensitivite routine quantitation and up to the Triple Quad™ 6500 system, AB SCIEX's most sensitive triple quadrupole system on the market.

The future path of LC/MS/MS quantitation

AB SCIEX brings together the latest hardware from the world's best selling triple quadrupole family, delivering unmatched quantitative and qualitative analysis.



AB SCIEX triple quadrupole LC/MS/MS portfolio

Triple Quad™ 6500 system
Exceedingly sensitive.
Sharply focused.

- SelexION technology enabled
- 5 to 2000 m/z mass range
- Turbo V IonDrive™ technology
- 20ms polarity switch
- LINAC collision cell
- *Scheduled* MRM algorithm

Triple Quad™ 5500 system
New levels of quantitative
Performance and selectivity

- SelexION™ technology enabled
- 5 to 1250 m/z mass range
- Turbo V source
- 50ms polarity switch
- LINAC collision cell
- *Scheduled* MRM algorithm

Turbo V ionization source – an icon of reliability, reproducibility and confidence

The Turbo V ionization source provides optimal ion production through its enhanced gas flow dynamics and optimized "V" heater configurations while deliverying the "gold standard" in reliability, reproducibility and robustness.

The Turbo V source possess quick-change APCI and TurboIonSpray® probes and accommodates the new low dispersion electrodes for use with microflow UHPLC methods.

Sensitivity, speed and selectivity at every level

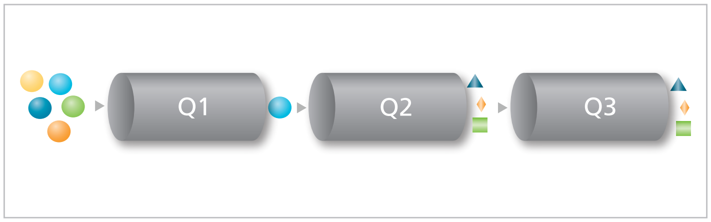
AB SCIEX tandem mass spectrometry (MS/MS) solutions

Tandem mass spectrometry (MS/MS), is a technique in which quadrupole mass analyzers are used in a series to obtain quantitative measurements of concentrations and confirmation of identification by selectively focusing on the precise molecular weight of the analytes of interest.

In MS/MS operation, different scan modes can be used to get complementary information about the sample. Functional in either MS or MS/MS mode, the triple quadrupole MS system offers a blend of quantitative and qualitative experiments to answer your reasearch needs.

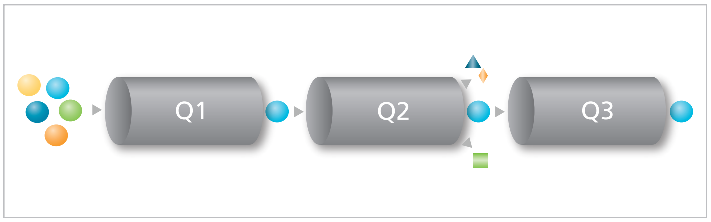
Product ion scan

Provides structural information and identification of fragment ions



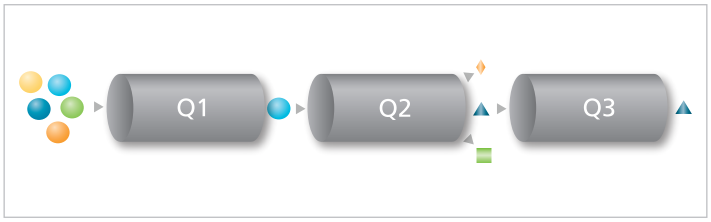
Constant neutral loss

Indicates which ions lose a neutral species equal to Q1-Q3 difference



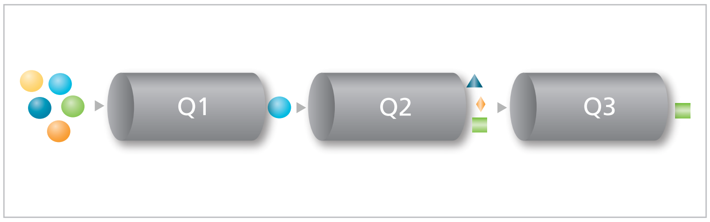
Precursor ion scan

Determines the "origin" of particular product ion(s) created in the collision cell and is frequently used for drug metabolite identification



Multiple reaction monitoring (MRM)

Used primarily for quattitalion studies, this mode allows monitoring of multiple precursor-to-production pairs and is the best way to maximize signal/noise ratio of compounds



Triple Quad™ 4500 system
The new LC/MS/MS workhorse

- 5 to 2000 m/z mass range
- Turbo V source
- 50ms polarity switch
- LINAC collision cell
- *Scheduled* MRM algorithm

API 3200™ system
Performance, productivity and value combined

- 5 to 1800 m/z mass range
- Turbo V™ source
- LINAC® collision cell
- *Scheduled* MRM™ algorithm

QTRAP® technology

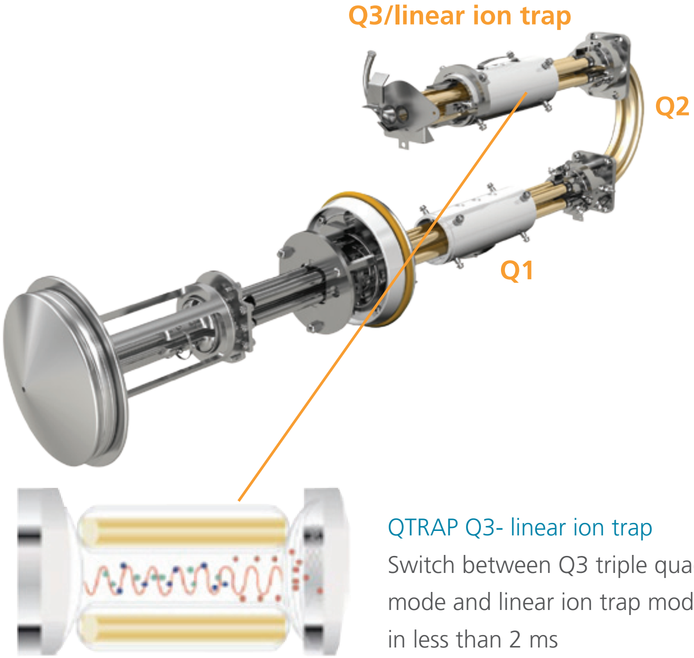
QTRAP technology – quantitate, search and confirm

As an innovator of LC/MS/MS solutions, AB SCIEX prides itself not just in developing new mass spectrometry technology but in developing mass spectrometry solutions that deliver new intelligent workflows that simplify a workstream while improving the quality of the data generated.

QTRAP technology is such an example. This patented triple quadrupole linear ion trap mass spectrometry platform merges the quantitative sensitivity and robustness of our proven triple quadrupole platforms with the qualitative full scan MS/MS sensitivity of a high capacity linear ion trap. The linear ion trap functionality is built into the Q3 and can automatically switch between quadrupole mass analyser mode and linear ion trap mode within 2 miliseconds.

The speed of this switch allows QTRAP enabled triple quadrupoles to not only deliver all of the quantitative functionality expected from a tandem MS/MS but also deliver rich qualitative workflows such as full scan library searching, structural identification, and confirmation.

The future path of LC/MS/MS quantitation



QTRAP Q3- linear ion trap

Switch between Q3 triple quad mode and linear ion trap mode in less than 2 ms

AB SCIEX QTRAP® LC/MS/MS portfolio

QTRAP® 6500 system

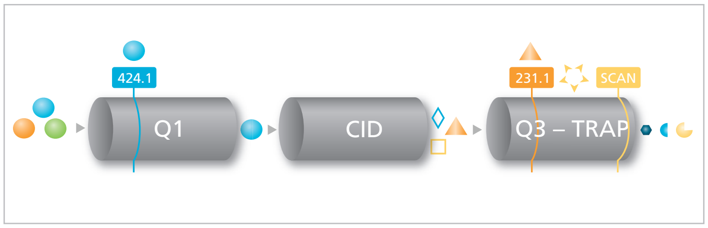
Exceedingly sensitive.
Sharply focused

- SelexION technology enabled
- 5 to 2000 m/z mass range
- IonDrive™ technology
- 20ms polarity switch
- LINAC collision cell
- *Scheduled* MRM algorithm
- Linear ion trap capabilities

QTRAP® 5500 system

New levels of quantitative
Performance and selectivity

- SelexION™ technology enabled
- 5 to 1250 m/z mass range
- Turbo V source
- 50ms polarity switch
- LINAC collision cell
- *Scheduled* MRM algorithm
- Linear ion trap capabilities

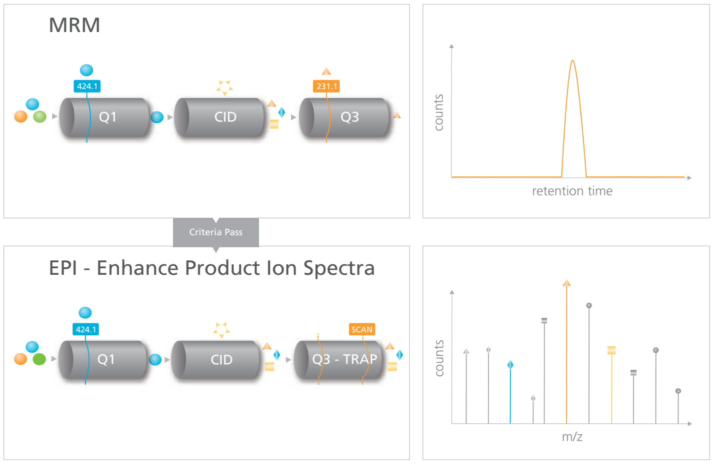


New levels of confidence for screening and quantitation applications

TripleTrap™ scanning

In addition to delivering all the functionality of a standard triple quadrupole mass spectrometer, the QTRAP® platforms enable productive, time-saving workflows that simply cannot be done with other mass spectrometry systems.

Up to 100X gain in full scan sensitivity of the linear ion trap, over the full scan product ion mode of the triple quadrupole, allows QTRAP enabled platforms to provide clear benefits in screening and confirmation workflows making it ideal for food and environment contaminant screening, forensic toxicology research or as an additional tool to increase selectivity of your MRM assay.



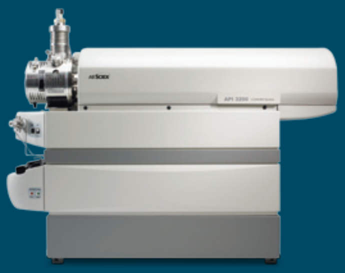
With TripleTrap scanning, MRMs can be used to trigger high quality full scan linear ion trap product ion spectra for use in library searching.

Contaminants at the lowest levels can be confidently identified with the available library of thousands of QTRAP spectra for library matching.

QTRAP® 4500 system

The new LC/MS/MS workhorse

- 5 to 2000 m/z mass range
- Turbo V source
- 50ms polarity switch
- LINAC collision cell
- *Scheduled* MRM algorithm
- Linear ion trap capabilities



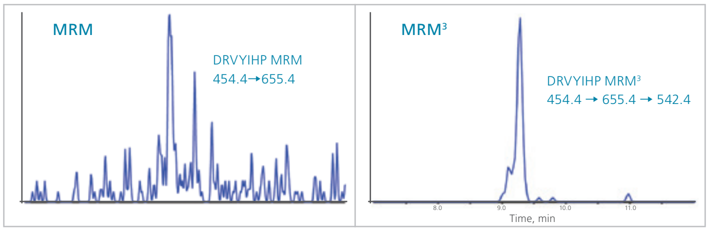
3200 QTRAP® system

Performance, productivity and value combined

- 5 to 1800 m/z mass range
- Turbo V™ source
- LINAC® collision cell
- *Scheduled* MRM™ algorithm
- Linear ion trap capabilities

MRM^3 - enhanced selectivity

Additionally, the unique MRM^3 workflow enabled by the QTRAP technology provides enhanced quantitative selectivity and therefore better LLOQs in complex matrices over MRM workflows when high background or challenging co-eluting interferences make standard MRM quantitation difficult.

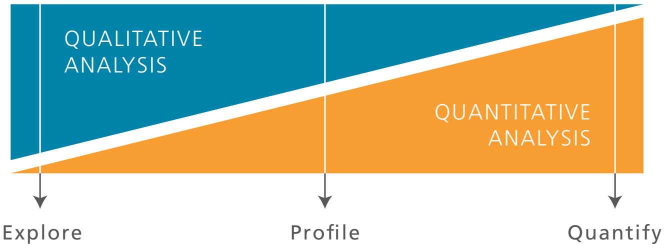


TripleTOF® technology

Speed, sensitivity, resolution, mass accuracy – all at the same time

High resolution qual and quant on one platform

The TripleTOF platform elegantly combines comprehensive qualitative exploration, rapid profiling and high resolution quantitation on single accurate mass platform enabling research that was previously impossible. Fast scanning is engineered into our systems from the ground up. The TripleTOF family of instruments allows data acquisition at speeds up to 100 spectra per second.



Speed and resolution for definitive identification

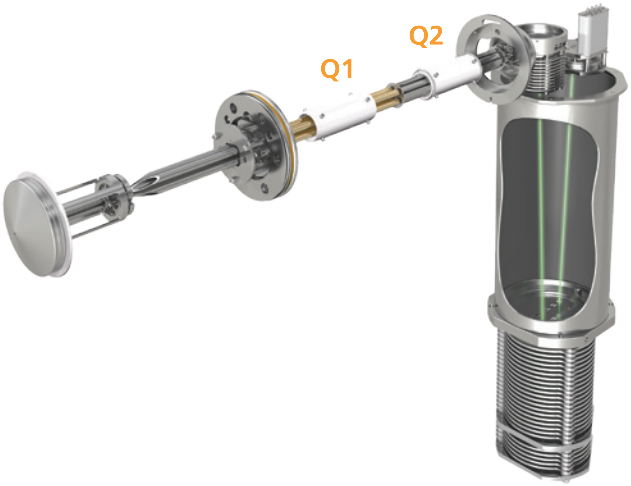
- Up to 100ms/ms spectra per second

Quantitative and qualitative information in a single run

- High resolution MS and MS/MS in UHPLC timescale

Sensitive high resolution quantitation

- Linear dynamic range of up to 4 orders



Accelerator TOF™ Analyzer

AB SCIEX TripleTOF® HRMS portfolio

TripleTOF® 5600⁺ system
Extended limits of HRMS performance

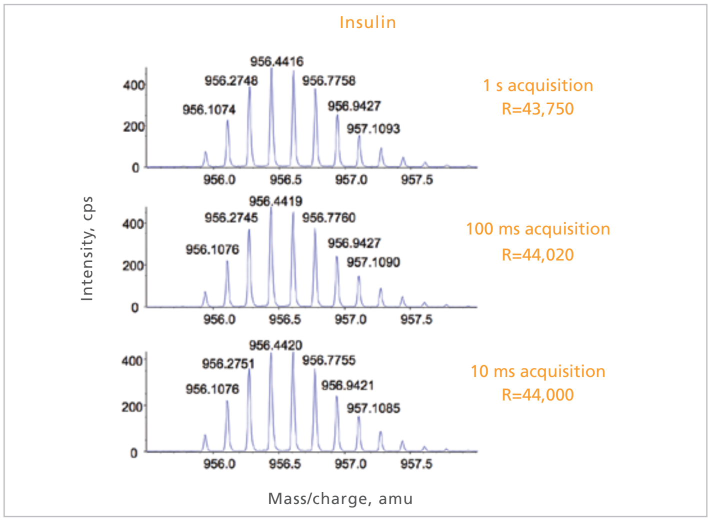
- R= 35,000
- 1.0ppm mass accuracy
- 100 MS/MS spectra /second
- 40,000 m/z mass range
- MS/MS^{ALL} with SWATH acquisition
- 21CFR Part 11 Compliant
- SelexION Technology ready

TripleTOF® 4600 system
The accurate mass workhorse

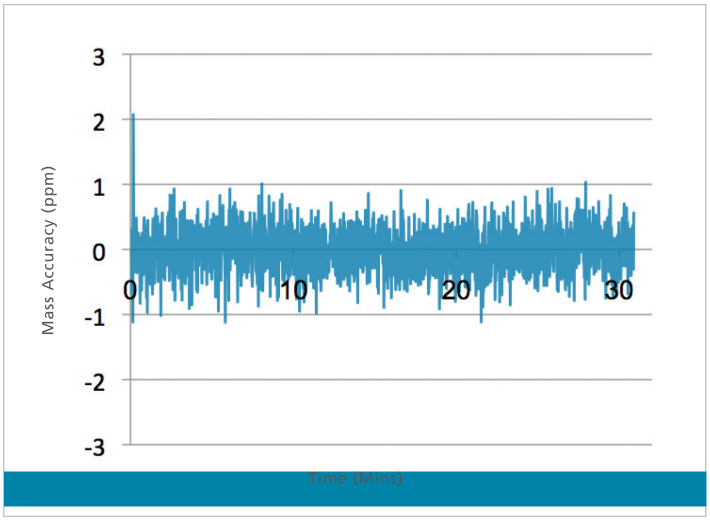
- R= 25,000
- 1.0ppm mass accuracy
- 100 MS/MS spectra /second
- 40,000 m/z mass range
- *Scheduled* MRM algorithm

Resolution you can rely on

High resolution is important to minimize contamination of peaks from overlapping species and to definitively identify and quantify a compound. With the TripleTOF® platform high resolution is maintained even when acquiring data at the highest acquisition speeds, thus affording the greatest analytical power without compromise.



Resolution of insuline (6+) is maintained at >43,000 with data accumulation times of 1 second, 100 milliseconds and 10 milliseconds

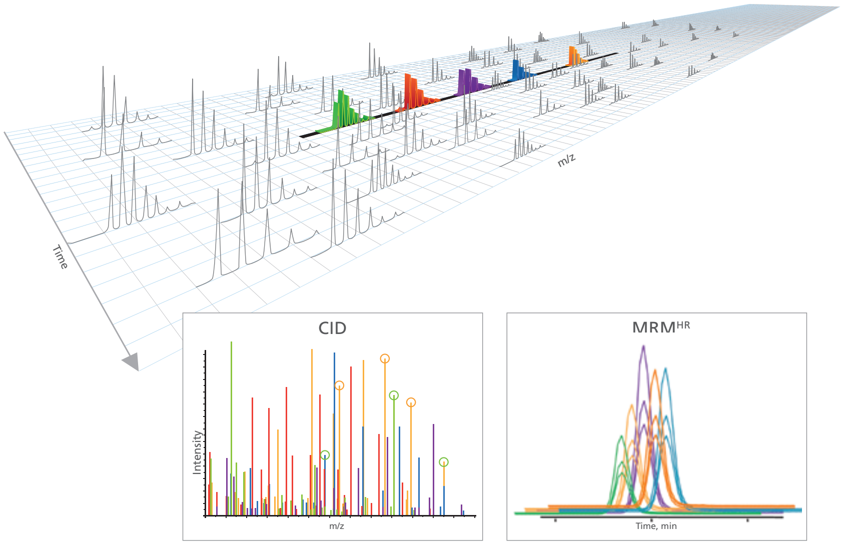


The EasyMass™ accuracy functionality delivers high mass accuracy without the need for continous recalibration. With external calibration, the mass accuracy holds rock-steady at <1ppm over 30 minutes and RMS=1.69 over 100 hours.

Intelligent implementation for improved productivity

MS/MS^{ALL} with SWATH™ Acquisition

A powerful workflow enabled by the speed and sensitivity of the TripleTOF technology, in which high quality MS/MS spectra are generated for all masses in the sample without the need for sample specific methodologies. This technique creates a complete digital archive of all possible fragment ions in the sample allowing the user to re-interrogate the sample for new hypotheses without the need to re-acquire data.



Intelligent data acquisition

This function improves workflow efficiency by acquiring relevant MS and MS/MS data in every run, eliminating the need for re-injection in many cases. Priority for MS/MS acquisition is given to ions with elemental compositions logically associated with the parent, to eliminate the acquisition of irrelevant MS/MS data.

TOF/TOF™ technology

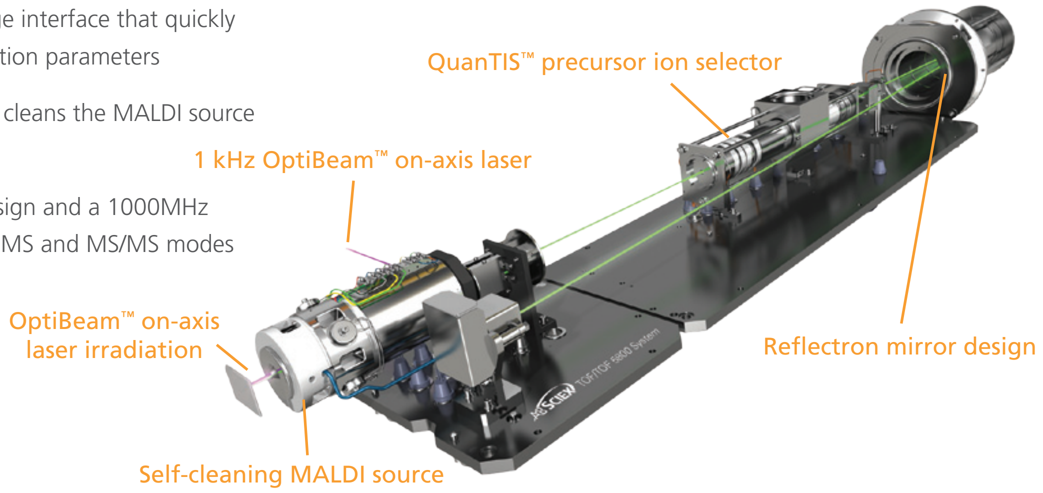
Don’t miss a thing

The AB SCIEX TOF/TOF™ platform provides a fast, confident path to protein identification and relative quantitation. The platform’s unmatched speed and sensitivity make it the ideal platform for gel spot analysis, protein biomarker discovery and MALDI mass spectrometry imaging.

- 10X faster acquisition speed with 1kHz OptiBeam™ on-axis laser delivering ultra fast ionization
- EasyAccess™ Wizard has a single-page interface that quickly guides you through set up of acquisition parameters
- User-programmable baking routuine cleans the MALDI source when its convenient for you.
- Next generation reflectron mirror design and a 1000MHz digitizer provide higher resolution in MS and MS/MS modes

TOF/TOF™ technology from the company that invented it

The AB SCIEX TOF/TOF platform takes performance to a new level to give you answers faster. All aspects of the system, including hardware, software, workflows and support, are perfectly integrated into an optimized platform, so you can discover more from every sample.



AB SCIEX MALDI portfolio

AB SCIEX TOF/TOF™ 5800 System
Extended limits of MALDI performance

- R= >33,000
- <1.0ppm mass accuracy (internal cal)
- On-axis laser irradiation
- 1 kHz solid state laser

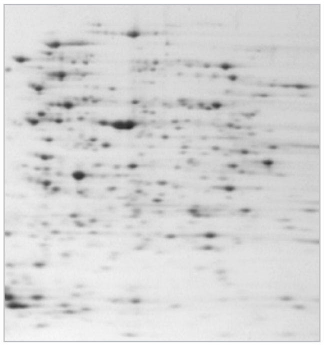
Eksigent ekpert™ nanoLC 400 System

Eksigent EKSpot™ MALDI spotting System

Speed and sensitivity to expand protein discovery

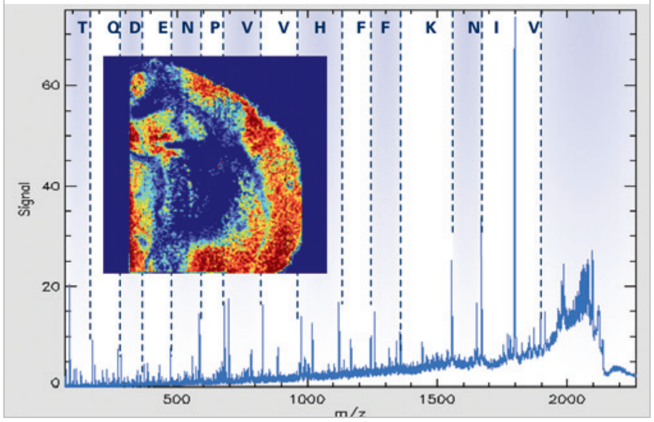
Fast, easy, walk up mass spec for gel spot analysis

The AB SCIEX TOF/TOF™ platform features a simplified workflow for fast, definitive protein identification that is ideal for multi-user environments and gel spot analysis. The EasyAccess Wizard simplifies the selection of parameters for acquisition and the QuanTIS™ precursor ion selector prior to fragmentation produces clean, database-searchable MS/MS spectra for unambiguous identification of peptides and proteins.



MALDI imaging

The AB SCIEX MADLI TOF/TOF platform is a fast, sensitive and flexible platform for MALDI based mass spectrometry imaging of tissue, a widely-used technique for determining the spatial distribution of various types of analytes within biological tissues. Delivering high-sensitivity MS and MS/MS data for small molecules and well as peptides and proteins – in any tissue.

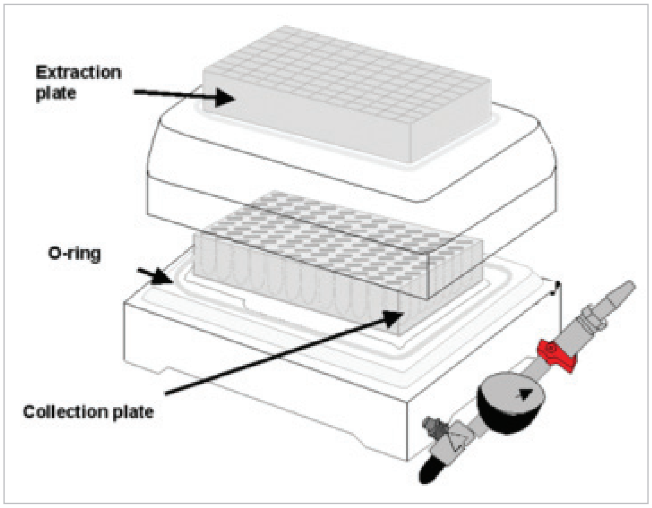


MS/MS of peptide m/z 2141.2 in rat brain

Glycoprotein characterization

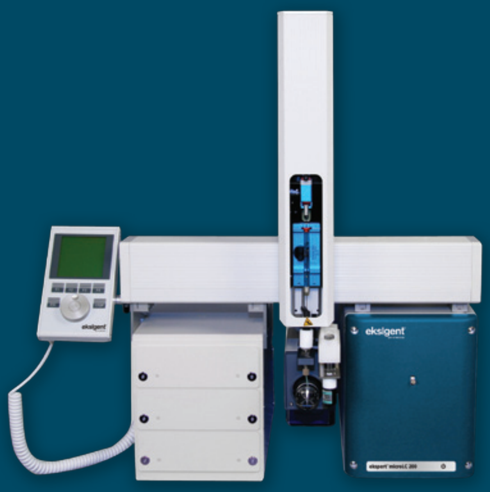
Because glycosylation of a glycoprotein may influence the properties of a protein in the body, the bio-pharmaceutical industry must characterize the glycosylation patterns on therapeutic protein drugs.

The AB SCIEX MALDI TOF/TOF workflow for glyco protein characterization offers a rapid GlycoAnalysis sample preparation system combined with the benefit of an adjustable high and low energy CID providing a wider range of glycan fragments vs electrospray MS/MS. The resulting complimentary cross-ring fragmentation ions allow the user to determine branching patterns and provide linkage information for the monosaccharide residues. SimGlycan Software further facilitates the identification of MS/MS data obtained for glycans and glycopeptides.



Integrated front-end solutions

State of the art analytical, micro and nanoflow UHPLC solutions to enable your life science research



Eksigent ekspert™ microLC 200 System

As the industry pioneer in micro flow UHPLC, Eksigent understands that sensitivity, throughput, and cost of ownership are of the utmost importance for high-throughput LC/MS/MS laboratories. The ekspert microLC 200 system is engineered from the ground up with these priorities in mind and redefines what is possible in high-throughput LC/MS/MS compared to analytical flow:

- Up to a 4X increase in sensitivity
- Accelerate separations up to 5X
- Reduce sample consumption up to 10X
- Use up to 95% less mobile phase

Eksigent ekspert™ ultraLC 100 column oven/100xL system

Designed specifically for use with AB SCIEX mass spectrometers, the Eksigent ekspert ultraLC systems provide speed, sensitivity, resolution, and reliability for your routine LC/MS/MS analysis. The ekspert ultraLC systems employ accurate high pressure solvent mixing to deliver precise and reproducible gradients over a wide flow range:

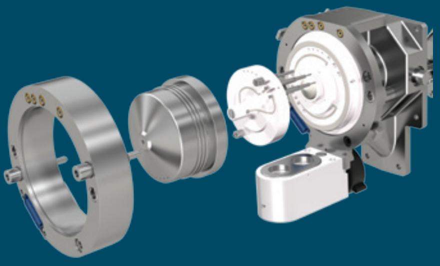
- Flow range: 1 µL / min - 5.0 mL/min
- Maximum pressure: 18,000 psi
- Injection volume: 1 - 20 µL
- Sample cooling and column oven
- Sample capacity: 2 microtitre plates or 84 (2mL) vials

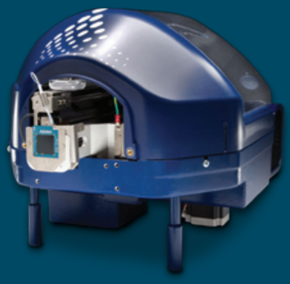
Eksigent ekspert™ nanoLC 400 System with cHiPLC® instrument or system column

The next generation of nanoLC system from Eksigent delivers high resolution separations, combined with excellent reproducibility, resulting in improved identification of low abundance peptides and proteins, with nanoLC-MS.

A range of different nanoLC system configurations are available – from single gradient systems for direct sample injection, to dual gradient systems for multidimensional separations, dual column set-up for increased throughput and chip based Microfluidic components such as the cHiPLC-Nanoflex system making nano LC/MS easier and more reproducible.

New dimensions of separation





SelexION™ differential ion mobility

AB SCIEX SelexION technology adds a new dimension of selectivity to LC/MS/MS analysis for enhanced quantitative and qualitative performance. Leverage the power of ion mobility for any application requiring the separation of isobaric species or challenging co-eluting contaminants. The SelexION hardware can be installed and removed in less than than five minutes.

LDTD ionization source

The Phytronix Laser Diode Thermal Desorption source combines automated sample introduction and ionization with sample-to-sample analysis times as low as 4 seconds. Transform your AB SCIEX MS platform into the ultimate platform for sensitive ultra high throughput analysis without the complications of LC.

Advion LESA Clarity

The Liquid Extraction Surface Analysis (LESA) capabilities of the LESA Clarity for AB SCIEX MS systems combines the benefits of liquid chromatography, mass spec, chip-based infusion, fraction collection and direct surface analysis into one integrated system.

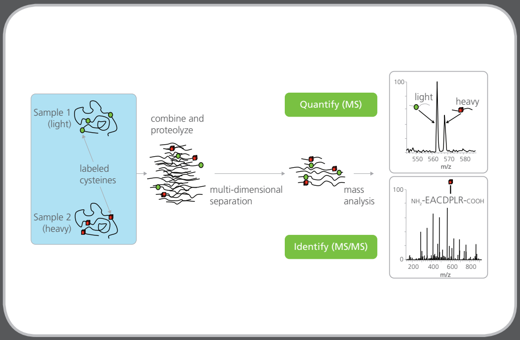
SCIEX iChemistry™ solutions – boost your MS workflows

SCIEX iChemistry solutions for MS qualification

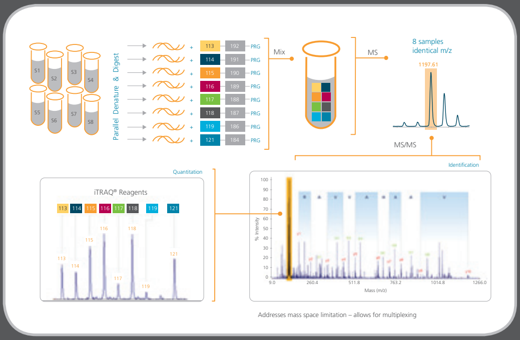
iChemistry MS Performance Calibrants and Standards ensure your AB SCIEX mass spectrometer is tunded for optimal performance and delivers reproducible results

SCIEX iChemistry solutions for biomarker and omics

Clevable ICAT reagents for selective fractionation of cysteine-containing proteins for reduced sample complexity

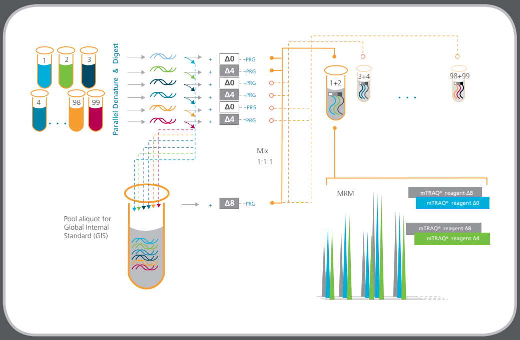


SCIEX iTRAQ® reagents are the industry standard citied in over 840 peer-reviewed papers. A simple peptide-based labelling workflow that allows protein coverage of post translational modifications, affinity pull-downs and membrane proteins.



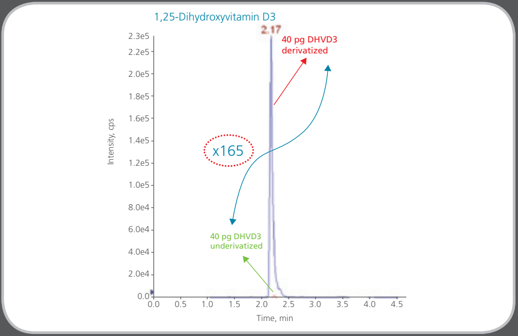
Addresses mass space limitation – allows for multiplexing

SCIEX mTRAQ® reagents for peptide quantitation results you can trust eliminating the need to synthesize internal standards. Available as duplex or triplex to increase sample throughput.



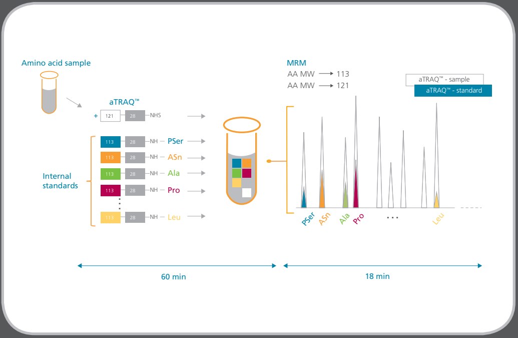
SCIEX iChemistry solutions for food and environment

SCIEX iD*Quant*™ standards kit for simplified preparation of contaminant standards. Containing certified reference materials, the iD*Quant* standards helps eliminate the need to source individual chemical contaminants improving sample turnaround times.



SCIEX iChemistry solutions for clinical research

SCIEX Amplifex™ reagents for enhanced intensity. Derivatizing agents intelligently designed and tested to boost ionization efficiencies and improve fragmentation and chromatographic properties. Available for cis-diene, keto and aldehyde compounds.



SCIEX iChemistry solutions for amino acid analysis

SCIEX aTRAQ™ reagents for faster, more complete amino acid analysis. Quantitate up to 45 amino acids and amines from a wide variety of samples, physiological fluids, protein hydrolysates, food and beverages and culture media.

Short and Simple Workflow

Amenable to 100s of Samples per Day

Starting sample of microsomes or S9 cells

Reduce and alkylate sample for 1 hour at 60°C

Digest sample with Trypsin for 4 hours at 37°C

Add isotope-labeled peptides to the digested solution

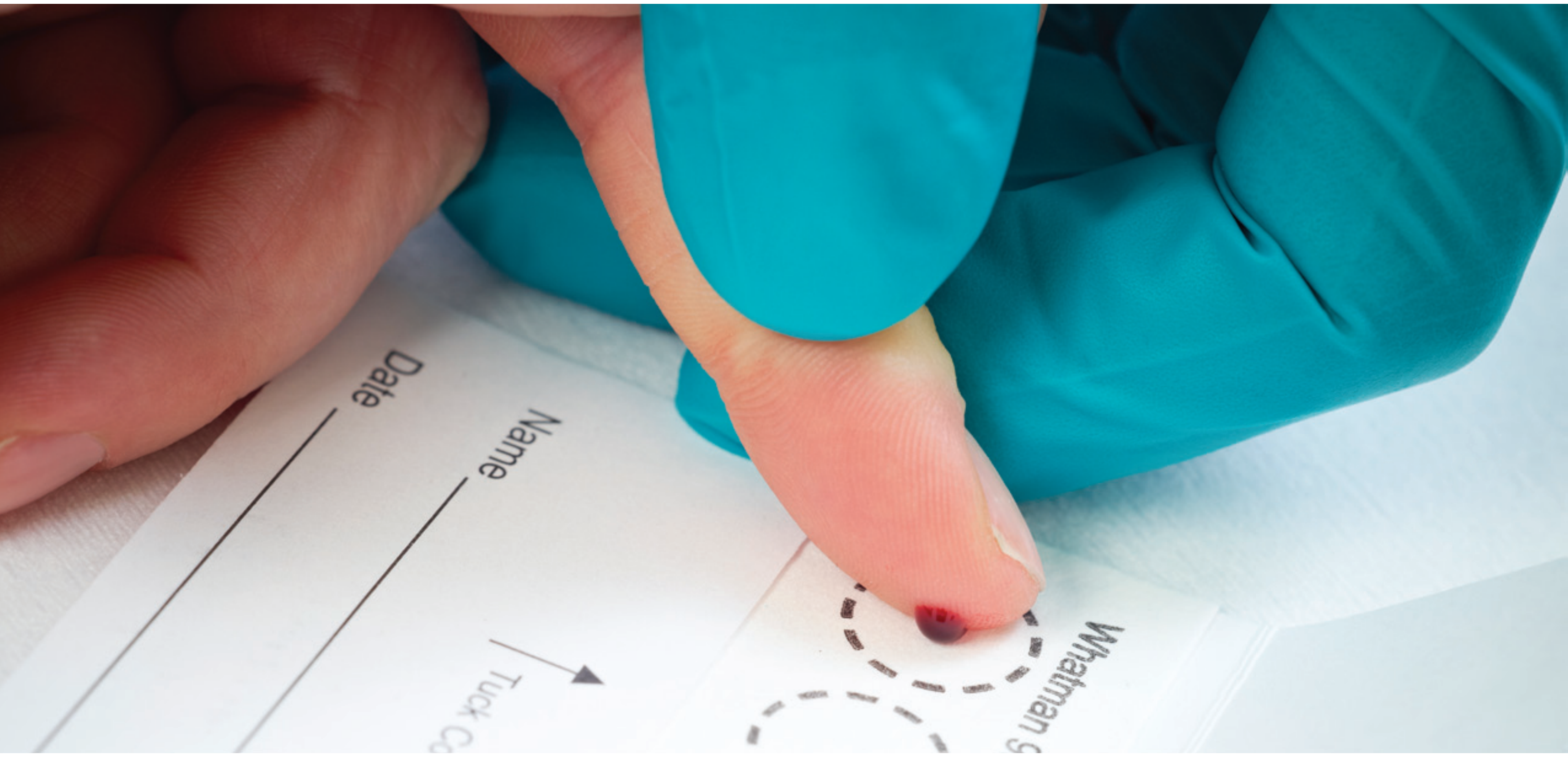
Perform LC-MS/MS analysis

SCIEX iChemistry solutions for cytochrome P450

SCIEX iChemistry CYP450 protein assay enables direct measurement of protein expression changes for induction assays.

AB SCIEX solutions are backed by a global network of certified engineers, technical specialists, training experts, application support chemists and regional logistics centers. Our teams optimize your applications, troubleshoot your workflows, and keep you online and up to date with the latest technology advances. You can have confidence in AB SCIEX.

Application Support



Making workflows flow

Whether you are a novice or expert, we can help you become more successful with the applications that are important to you. Every one of our application specialists has years of experience in their dedicated field – experience and extensive knowledge that can help you reach your research goals more easily.

We can get you started by streamlining your sample preparation and eliminating manual procedures, help you develop methods for faster implementation, scale up a method for higher throughput, or get up and running easily with an iMethod™ Application. We're dedicated to optimizing your applications and making your workflows flow.

Whenever you need assistance we can help

Application optimization – Optimize your workflows to help ensure that you get consistent and reliable results

Application development – Develop applications to meet your requirement through collaboration with our dedicated teams

Application installation – Save time by improving the efficiency of application installation and methods integration, or opt for an iMethod Application™ for quick implementation

Application trouble shooting – Use our expertise knowledge to help with a problem when you are not getting the results you need

Software optimization – Optimize your software to ensure your applications work seamlessly

www.absciex.com/applicationsupport

Training

Let us help you stay one step ahead

Nobody is born an LC/MS expert. We all have to learn step by step. AB SCIEX training specialists are here to take those steps with you and share their expertise and experience with your laboratory. Working closely with you we can customize a training program that gets everyone in your lab up to speed. Whether it's helping on complex workflows, delivering basic instrument operation courses or getting your staff up to speed on data interpretation, we can help keep you ahead of the curve.

Whether you or your team are just getting started in LC/MS or you are a seasoned pro we're here to make your job easier. Choose from:

Classroom based training – LC/MS hands-on system training routine and advanced LC/MS techniques. Application-specific courses given by leading LC/MS experts

e-Learning – Self-paced e-learning modules so you can learn at your own pace

On-site-training – On-site training in your lab focusing on your specific applications. Customized option with content specific to your lab's needs

www.absciex.com/training

Service

We make you our priority

We understand you can't afford downtime so we make sure we fix your problems fast using all the resources available. Our engineers have access to a global network of specialists, regional technical experts, R & D scientists, engineers, manufacturing and a global supply chain so that you have the latest hardware, software and accessory revisions, parts and technical updates. Our expertise also covers the entire LC/MS system. We can troubleshoot your whole workflow, whether you need help with an ion source, an autosampler, valve, or running an application.

Choose from flexible service options that combine value with customized coverage.

AB SCIEX Complete – Our comprehensive coverage option that runs your lab at peak performance

AB SCIEX Assurance – Full coverage maintenance and repair plan that maximize's productivity

AB SCIEX Parts – Provides parts coverage for all required repairs as determined by AB SCIEX service and technical assistance center representatives

AB SCIEX Repair – Provides labor and travel coverage for all required repairs by an AB SCIEX certified field service engineer

AB SCIEX Maintenance – Optimal instrument performance even if you are on a limited budget

AB SCIEX Time and Materials – On-site instrument repair purchased on a time-and-materials basis

Compliance Services – An integrated approach that includes qualification, re-qualification and validation for your complete AB SCIEX system workflow

www.absciex.com/service

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.

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, or locate your local account representative at www.absciex.com/contactus

For Research Use Only. Not for use in diagnostic procedures.

1411113-01 05/2013 RUO-MKT-03-0590-A

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