Agilent

Trusted Answers

Identify. Quantify. Simplify. See the Whole Picture

Agilent 7250 GC/Q-TOF system

Ready to Achieve More?

Discovering what's in your sample, at what levels, helps you make the conclusions and breakthroughs that your organization depends on.

The all-in-one Agilent 7250 GC/Q-TOF system with comprehensive Agilent MassHunter software ensures confidence across GC/MS workflows. It's the premier instrument for your toughest GC/MS identification, quantification, and exploration challenges:

- Performing complex metabolomics studies
- Screening for pesticides in challenging matrices
- Identifying compounds in herbal extracts
- Testing contaminant levels in chemical feedstock

Designed for real-world performance and built for laboratory robustness, the 7250 delivers what your organization needs: consistently excellent results.

Ultimate confidence for routine screening workflows and once-in-a-lifetime discoveries

The 7250 gives you more…

- Sensitive detection
- Accurate quantification
- Power to explore
- Simplified spectra
- Reproducible data

So you can worry less about…

- Future regulation
- Uncertain results
- True unknowns
- Data interpretation time
- Replicate ambiguity

Evolving analytical challenges call for new methods and novel approaches

For over 40 years, Agilent innovations have helped diverse labs meet the demand for ever-more-detailed analysis.

The 7250 is our most advanced GC/Q-TOF. It can analyze nearly any kind of molecule or element, and is designed to provide outstanding performance for labs across the analytical spectrum.

Need More Confident Identification?

"The Agilent instruments are very useful in our laboratory for three reasons: they're reliable, accurate, and easy to use."

– **Mike Thurman, PhD**
Center for Environmental Mass Spectrometry, University of Colorado

Not seeing the whole picture can have serious implications for your research, development, and quality control. The analytical prowess of the 7250 and MassHunter software brings you unmatched compound identification abilities.

– **Know your compounds.** Undistorted library-quality spectra let you confidently identify compounds against commercial libraries.

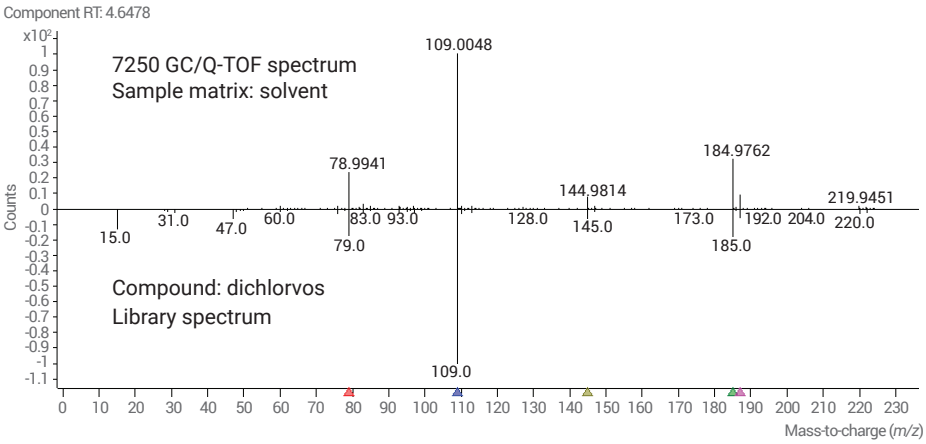
– **Confirm formulas.** Isotopic fidelity gives you greater certainty when assigning molecular formulas.

– **Detect trace analytes.** Ensure a broad in-spectrum dynamic range, even with abundant coelution.

– **Elucidate structures.** MS/MS measurements with high-resolution, accurate mass product ion spectra can provide structural information, increase selectivity, and circumvent matrix interferences.

Spectral fidelity and mass accuracy: dichlorvos analysis

Now you can easily identify compounds by doing a spectral search against commercially available libraries. The 7250 supports the quality of hundreds of thousands of compound library spectra, most of which were generated by our quadrupole GC/MS systems. True-to-library fragmentation patterns, together with full-spectrum acquisition, make the 7250 the ideal platform for GC/MS identification.



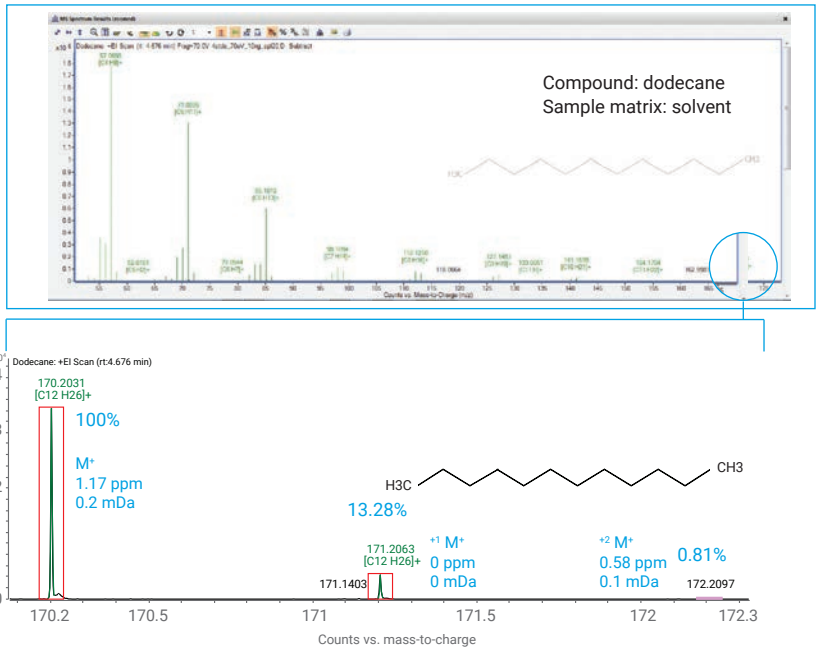
Agilent Value Promise

We guarantee you at least 10 years of instrument use from the date you buy. Otherwise, we will credit you with the residual value of the system toward an upgraded model.

Isotopic fidelity: dodecane analysis

Confident compound identification demands more than good mass accuracy. It also requires you to consider independent compound characteristics, like isotopic pattern matching.

You can easily picture isotopic fidelity through MassHunter qualitative analysis. It allows you to identify compounds complementary to accurate mass measurement. The 7250 exhibits excellent isotopic fidelity, even for trace-level isotopes, as shown in this dodecane spectrum with a minor M^+ peak cluster.

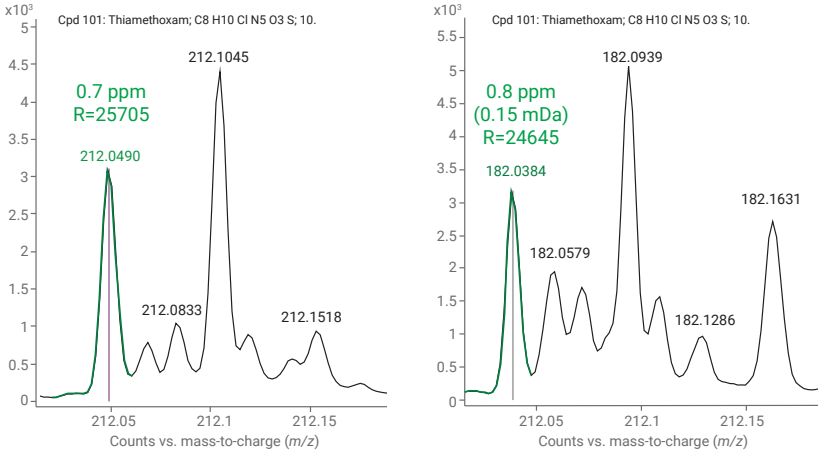


High resolution and mass accuracy: thiamethoxam analysis

High resolution is necessary to separate analytes from interferences. However, this performance characteristic must be usable under challenging conditions, like complex matrices and trace-level analytes.

The example shown here represents such a scenario: analyzing the insecticide thiamethoxam at 5 ppb in avocado, a complex matrix with significant background levels. Even under these conditions, characteristic mass peaks are separated from background with mass accuracy that complies with SANTE/11945/2015 guidelines.

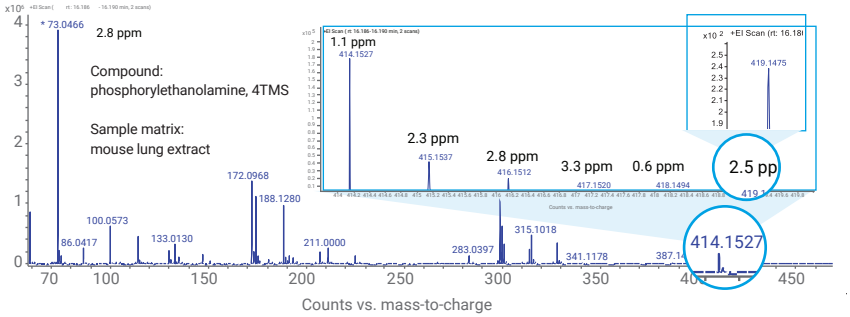
What's more, this level of spectral performance is achieved regardless of acquisition speed or mass range.



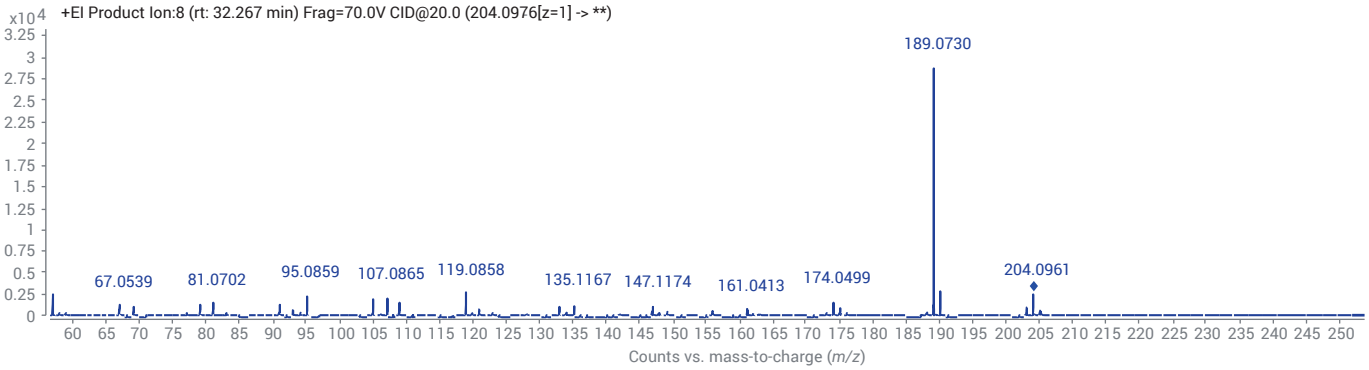
Wide dynamic range: phosphorylethanolamine analysis

A wide in-spectrum dynamic range lets you confidently detect trace-level analytes in the presence of abundant background or other coeluents.

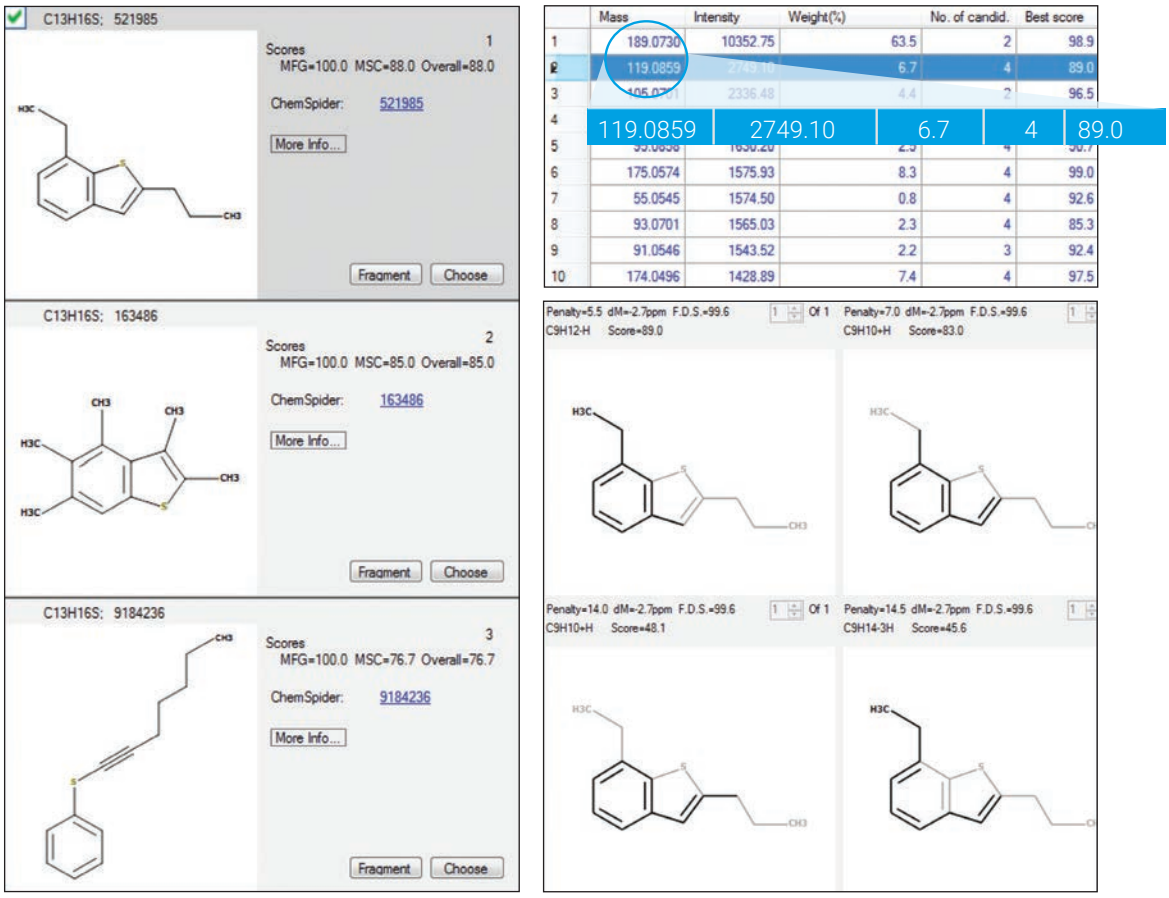
The 7250 typically provides four orders of in-spectrum dynamic range magnitude, even in heavy matrices. This example displays a range of 16,000+:1 for phosphorylethanolamine (4TMS) in a complex biological sample of mouse lung extract.



Elucidate chemical structures and reveal greater detail

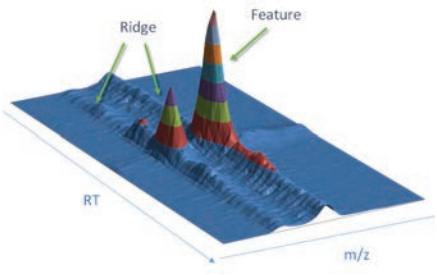


With MS/MS product ion spectra generated from a putative molecular ion, powerful Molecular Structure Correlator software can propose compound structure possibilities and likelihoods based on fragment data.



Compounds with unknown identities or unknown structures can be interrogated to narrow the range of possibilities.

Searching for Better Quantitative Answers?



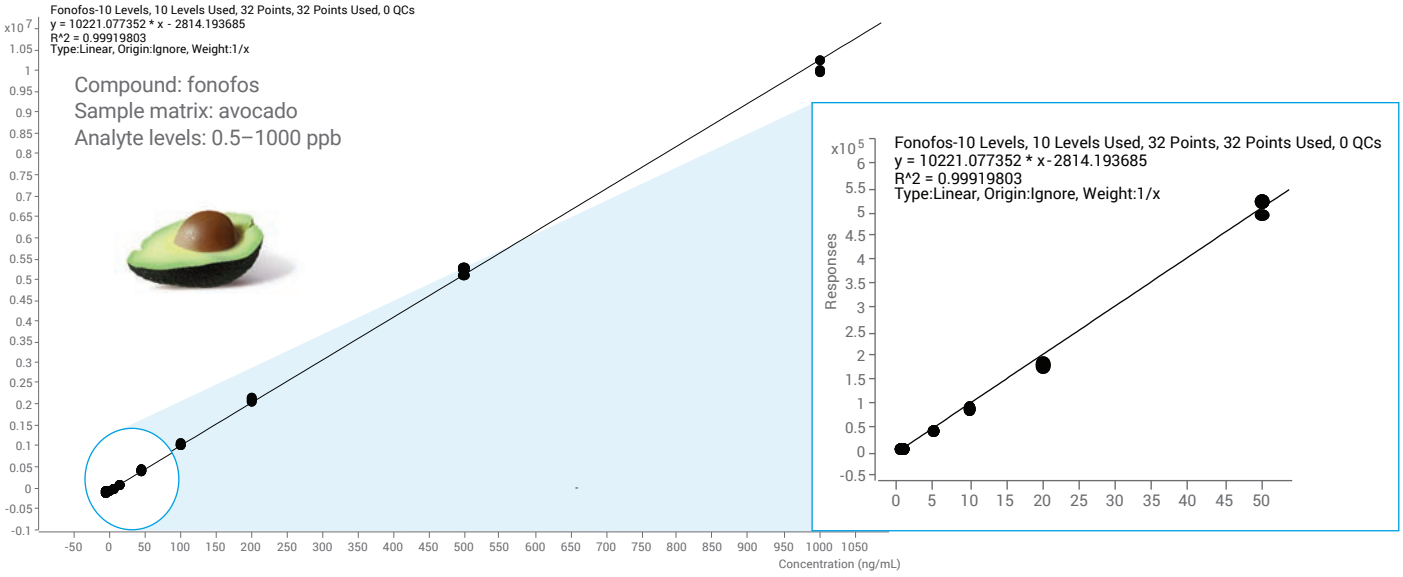
The Agilent MassHunter SureMass algorithm for detecting chemical features is designed specifically for high-resolution MS profile data.

Targeted quantification with untargeted acquisition is a powerful combination. The Agilent 7250 GC/Q-TOF system delivers unmatched quantitative accuracy with its superior chromatography, high mass resolution, and a wide dynamic range.

- **Extend linear dynamic range with high resolution.** Broad linearity in quantitative measurement is enabled by state-of-the-art electronics for mass separation and detection.
- **Precisely analyze real-world samples.** Achieve consistent response factors, even for trace analytes in abundant matrices.
- **Quantify at high speeds.** Fast acquisition speeds with high-resolution spectra facilitate accurate deconvolution of narrow, coeluting GC peaks.
- **Detect and extract component features.** MassHunter SureMass, a unique signal processing algorithm, optimizes mass accuracy and signal intensity.

Accurate quantification: fonofos analysis

A wide linear dynamic range brings quantitative accuracy across varying concentrations. Response factors are maintained even at low concentrations in complex samples, as shown in this separation of fonofos at 0.5 to 1,000 ng/mL in avocado matrix.



Want to Simplify Your Analysis?

Enable workflows that were previously impractical or impossible with the 7250, the world's only high-resolution GC/Q-TOF. It lets you create simplified spectra without relying on specialty techniques, and while retaining the universal applicability of electron ionization.

The electron ionization source in the 7250 is based on the proven high-efficiency source (HES) in the Agilent 5977B GC/MSD and 7010B GC/TQ systems. It has been optimized for low-energy operation, yet still performs at conventional 70 eV ionization. In addition, HES design modifications amplify the analytical sensitivity of low-energy electron ionization for a paradigm shift in GC/MS soft ionization.

Combined with available interchangeable chemical ionization sources, the soft ionization options for the 7250 simplify your most challenging analyses.

- **Identify with confidence.** Preserve or enhance molecular ions for sensitive MS/MS experiments (application dependent).
- **Stretch your limits.** Ionize across analyte classes while avoiding analytical sensitivity losses common with other soft ionization techniques.
- **Improve efficiency.** Harness the proven performance of ion source technology from the global GC/MS leader.

Low-energy electron ionization delivers accessible analytical sensitivity for universal ionization and confident detection.

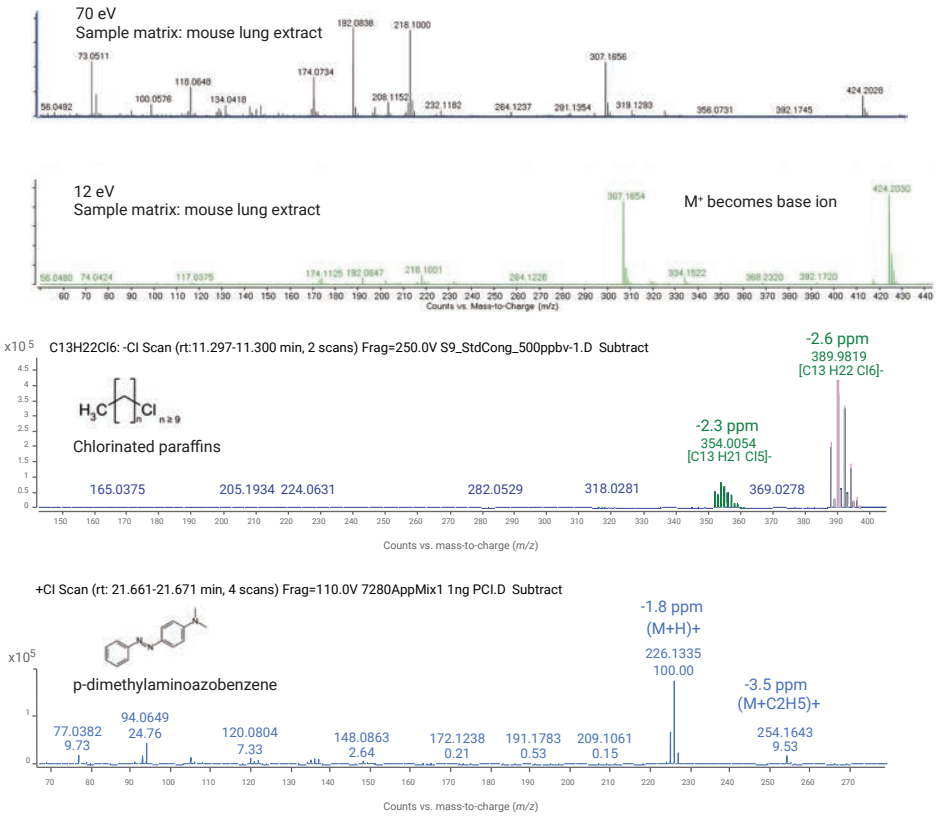
Available interchangeable chemical ionization sources give you easy access to conventional GC/MS soft ionization.

Soft ionization in challenging matrices: kynurenine analysis

Identifying metabolites (and other compound classes with similar structures) in complex matrices can be challenging. In this metabolomics experiment, kynurenine was detected in a mouse lung extract.

Lowering the source ionization energy creates a spectral tilt toward the molecular ion. Here, both the relative and absolute amounts of the molecular ion increased at 17 eV, ideal for MS/MS experiments.

At even lower ionization energies, the proposed molecular ion becomes the base ion in the component spectra, lending further assurance to the identification.



Protect Customers and Your Reputation

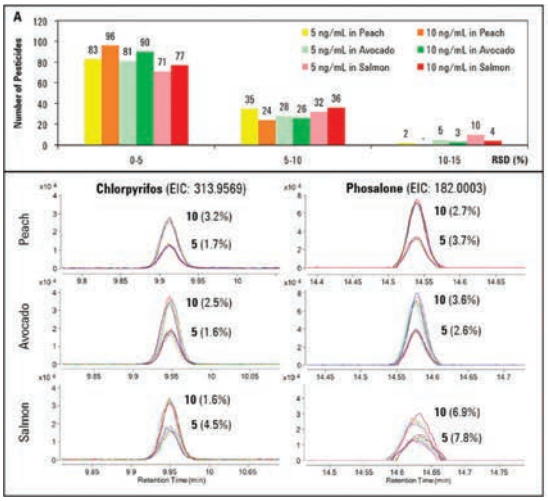
Food producers and consumers face threats from food adulteration and fraudulent labeling. In addition, global trade, stringent regulations, and increased public awareness are driving the need for more frequent and detailed food testing.

The 7250 helps you meet these challenges with a single platform that optimizes target, suspect, and unknown compound screening.

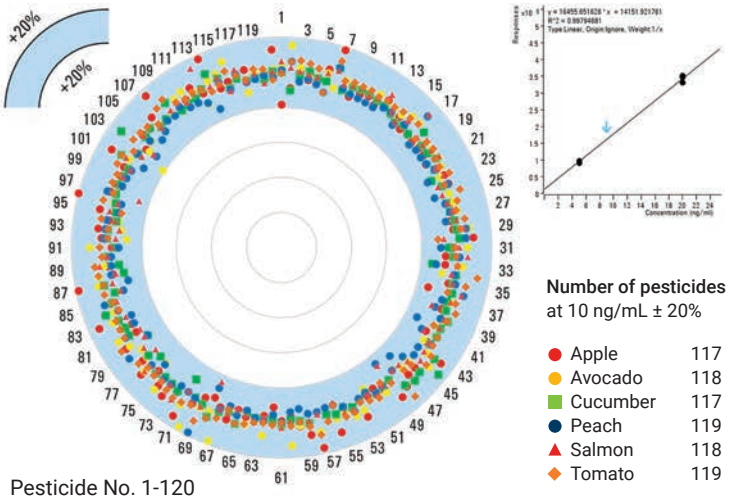
- Our customizable, high-resolution spectral library of pesticides and environmental pollutants lets you qualitatively screen for over 1,000 compounds of interest.
- Our comprehensive screening workflow identifies suspect analytes using high-resolution library matching performed in parallel with target quantitation.
- SureMass signal processing lets you quantify targets across a broad linear dynamic range and identify unknowns using commercial libraries.

Matrix matters

Untargeted acquisition and high-resolution spectral libraries let you comprehensively screen for pesticides in food matrices.



120 pesticides spiked into three different food matrices, including avocado and salmon. The repeatability (RSD %) values for spiking levels of 5 ng/mL and 10 ng/mL confirm excellent analytical performance. Two examples of detected characteristic ion replicates are also shown.



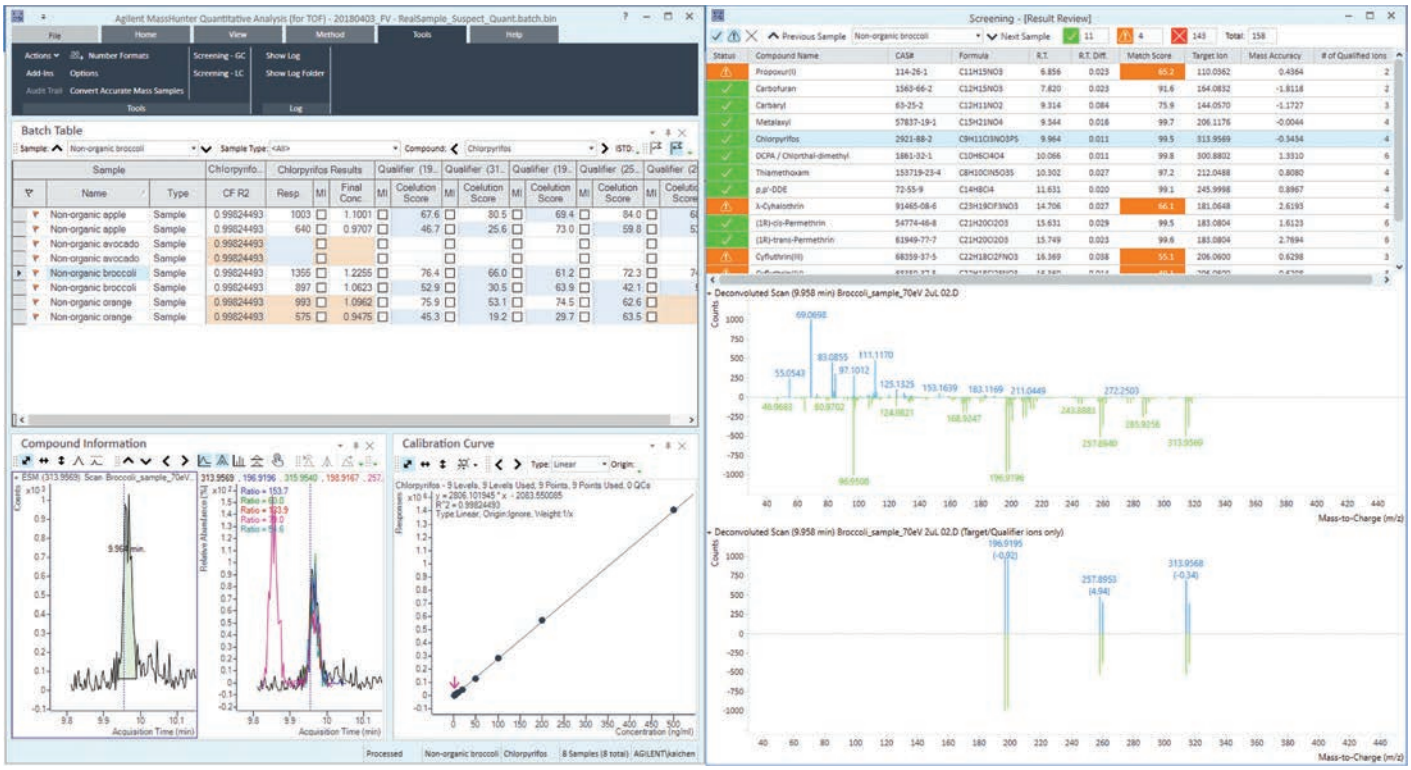
Quantitative accuracy at 10 ng/mL. A rapid comparison against maximum residue limits (MRLs) is shown for six food matrices of varying complexity. Even for complex matrices like avocado and salmon, quantitative accuracy complies with EU SANTE/11813/2017 guidelines for over 97% of the pesticide/food pairs tested.

"The GC/MS Q-TOF system enabled us to confirm the positive, but also to avoid false positive results."

– **Peter Furst, PhD**
Department of Central Analytical Services, Chemical and Veterinary Analytical Institute, Munsterland-Emscher-Lippe

High throughput with low effort

Easily evaluate large sample batches for hundreds of target and suspect compounds with a single analysis method. MassHunter provides simultaneous quantitative measurement for calibrated compounds. It also lets you screen against high-resolution spectral libraries for suspect compounds with no calibration reference.



MassHunter includes Quant-My-Way customization options that display only the desired details for your workflow.

Now you can perform simultaneous target and suspect compound screening using one data analysis tool. The 7250, combined with our GC/Q-TOF Personal Compound Database and Library (PCDL) of pesticides and environmental pollutants, lets you qualitatively screen for over 1,000 compounds of interest. All without the need for chemical standards. A simplified workflow lets you customize any PCDL to expand your screening scope.

Take the Fight to the Next Level

Every day, new questions arise about the impact of humanity on the environment—and about the environment's impact on us. The revolutionary technological enhancements in the 7250 are designed to provide meaningful answers with ease and efficiency.

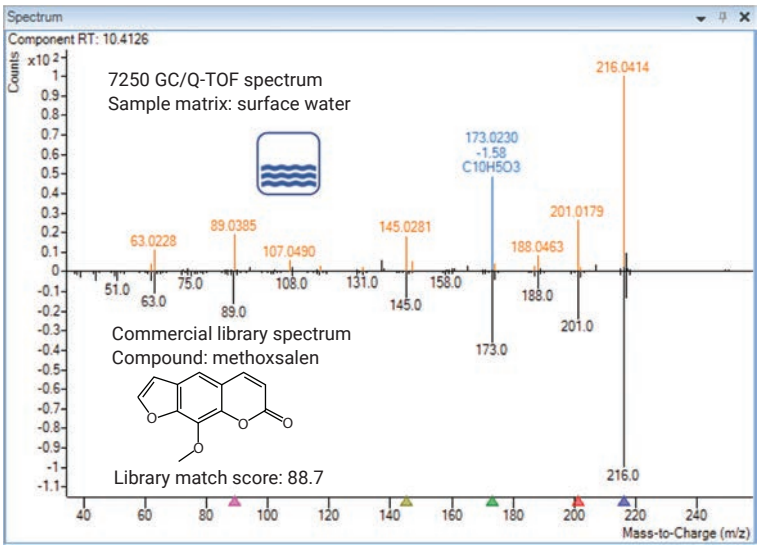
- Retrospective processing lets you measure once and analyze repeatedly with full-spectrum data that you can interrogate for future emerging targets.
- Full-spectrum high resolution generates spectra across a broad mass range (up to 3,000 m/z) for congener detection and speciation.
- Low-energy electron ionization and chemical ionization transcend 70 eV EI while maintaining signal intensity with highly efficient interchangeable source designs. The designs are optimized to support ionization at various electron energies, as well as positive and negative analyte polarities.

Be sure in your identification of unknowns

MassHunter Unknowns Analysis software, using SureMass signal processing and exact-mass searching, gives you insight and accuracy beyond conventional deconvolution techniques. Even minor components are accurately extracted and identified in the presence of a dominating background signal.

Exact-mass accuracy for proposed fragment formulas lets you identify compounds with confidence, even when using MS libraries with nominal mass spectra from quadrupole MS systems.

The data shown here represents the trace detection of a pharmaceutical compound in surface water with a NIST library match combined with an exact-mass comparison.



Exact Mass

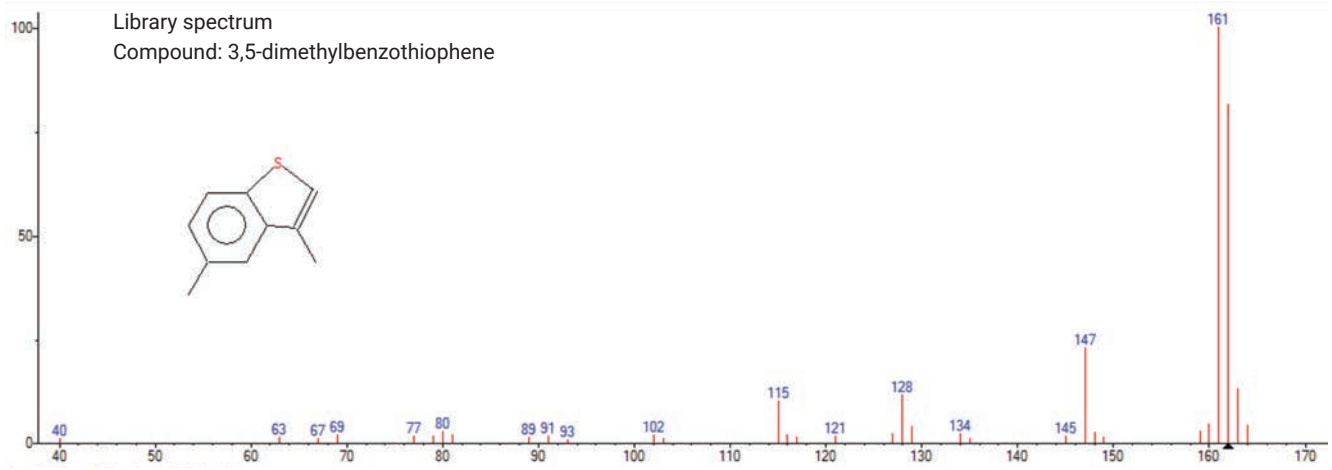
Source Ion (m/z)	Exact Mass (m/z)	Mass Delta (ppm)	Fragment Formula
63.0228	63.0229	-1.35	C5H3
89.0385	89.0386	-0.40	C7H5
107.0490	107.0491	-0.93	C7H7O
117.0339	117.0335	3.26	C8H5O
145.0281	145.0284	-1.77	C9H5O2
173.0230	173.0233	-1.58	C10H5O3
174.0265			
187.0386	187.0390	-2.22	C11H7O3
188.0463	188.0468	-2.90	C11H8O3
201.0179	201.0182	-1.61	C11H5O4
202.0212			
216.0414	216.0417	-1.48	C12H8O4

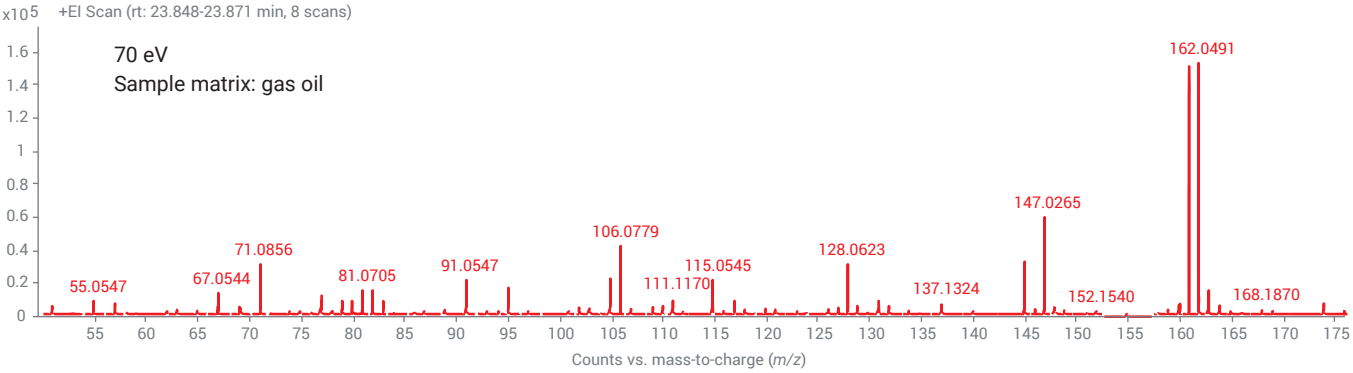
The data shown here depicts the trace detection of dibromophenyl ether with a match score of greater than 95 in complex combustion byproducts.

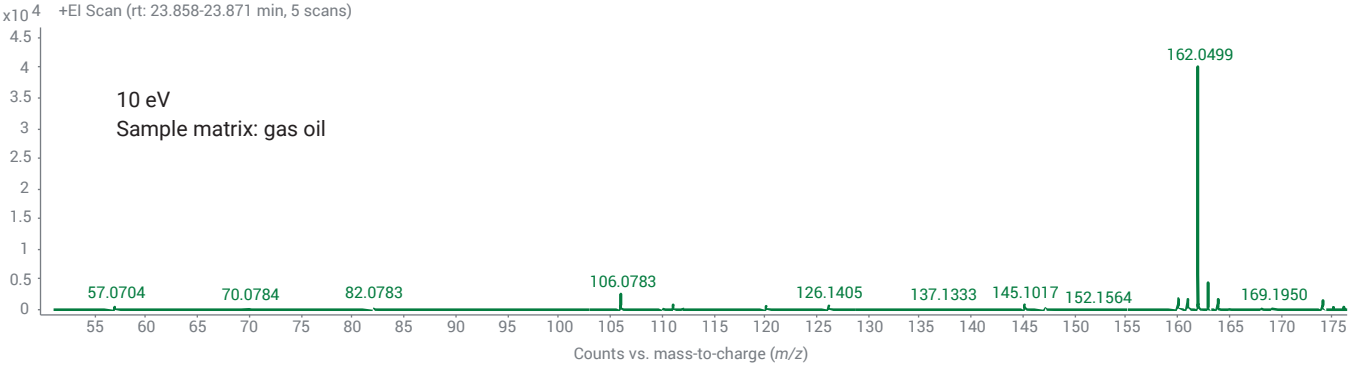
Powerful Analytical Capabilities

Characterizing what's in a complex sample is no simple task. It takes knowledge, insight, and the powerful analytical capabilities found in the Agilent 7250 GC/Q-TOF system. Capabilities like high-resolution accurate mass measurements, low-energy electron and chemical ionization options, fast spectral acquisition for comprehensive GC x GC compatibility, and highly sensitive MS/MS measurements.

- Fast acquisition rates let you characterize narrow chromatographic peaks or ultranarrow 2D GC peaks with data rates of up to 50 Hz and speed-independent resolving power.
- Spectral simplification allows you to deduce molecular ions for similar chemical species with soft GC/MS ionization options. You can confirm these ions by sensitive MS/MS measurements.
- High-resolution accurate mass product ion spectra, combined with powerful Molecular Structure Correlator software, yield insights on chemical structures.







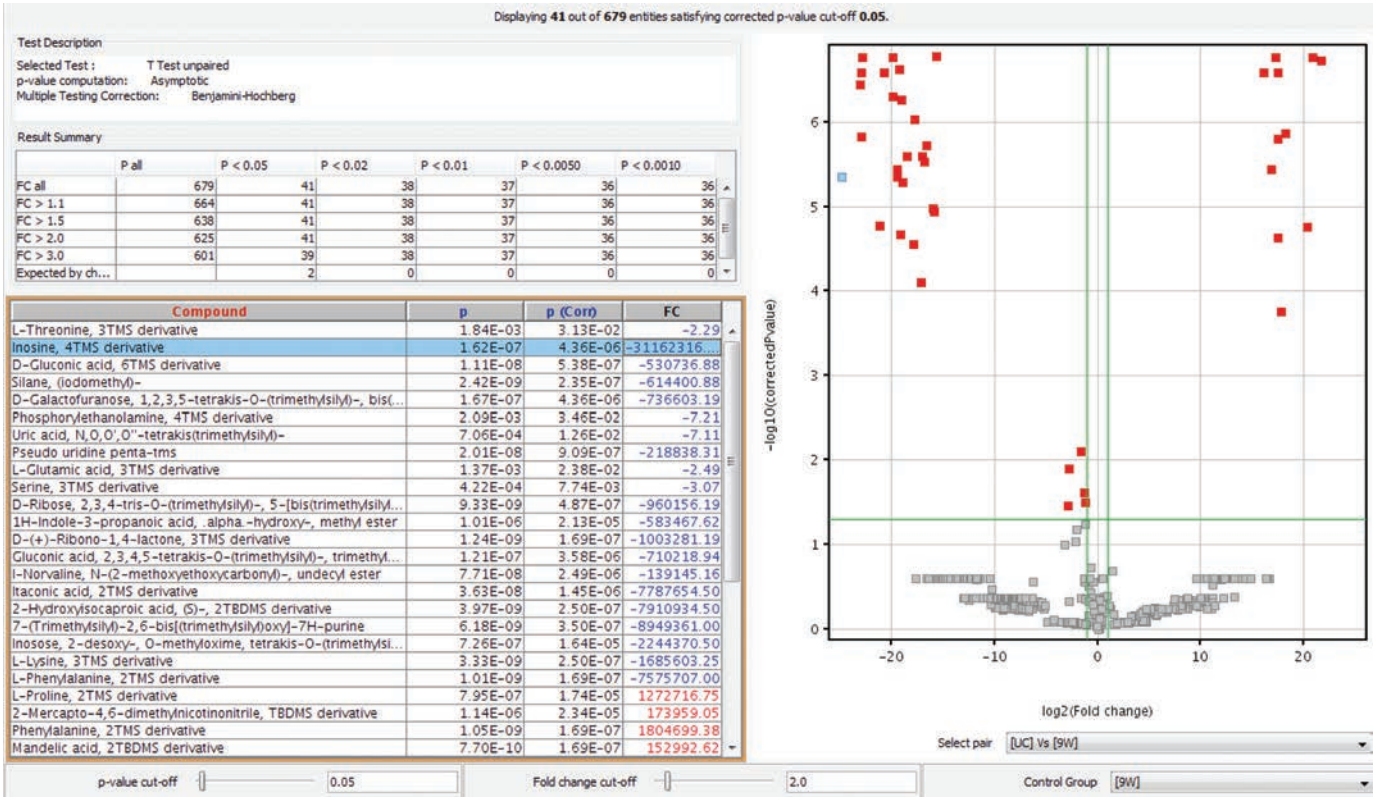
Spectral ambiguity is reduced with revolutionary low-energy electron ionization on the 7250. Based on the high-efficiency source found on the Agilent 5977 HES GC/MSD and 7010 GC/TQ platforms, the low-energy-capable electron ionization source greatly maintains compound analytical sensitivity while enabling a spectral tilt toward molecular ion. This example shows 3,5-dimethylbenzothiophene detected in gas oil, with identification facilitated by use of low-energy electron ionization.

Focus on What's Important

Each day brings advances in human health and protection. The research that drives these advances requires painstaking experimental design and execution. Move your research forward with the Agilent 7250 GC/Q-TOF system, with full-spectrum, high-resolution data and powerful software.

Mass Profiler Professional software transforms complex data into clear results

Differential analysis between sample groups brings focus to what is statistically important when performing comparative studies. Here, we identified metabolite differences between tuberculosis-infected and uninfected mouse lung tissue at nine weeks. Progression is depicted through fold change analysis on a volcano plot for easy visualization.



Complex data is changed into simplified results through powerful Mass Profiler Professional software. Differential analysis between sample groups brings focus to what is statistically important when performing comparative studies. Here, the data shows metabolite differences between mouse lung tissue of uninfected vs. tuberculosis-infected specimens at nine weeks. Progression is depicted through fold change analysis on a volcano plot for easy visualization.

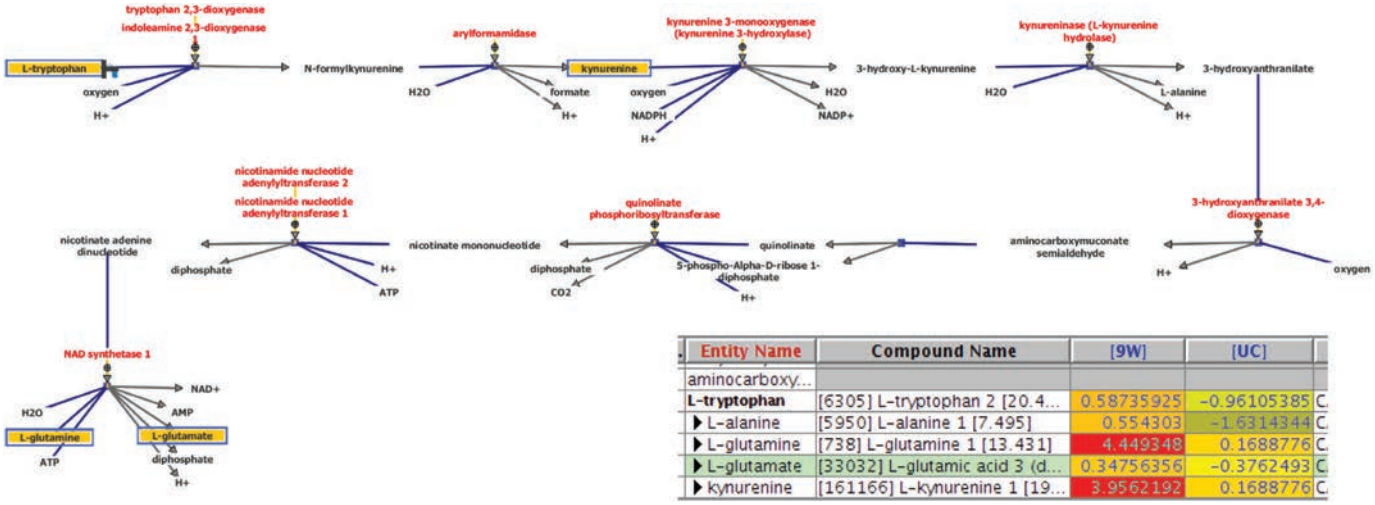
"The high-resolution Q-TOF MS, combined with the Mass Profiler software, has enabled us to study the different matrix components that coelute with the pesticides of interest."

– **Carmen Ferrer, PhD**
Analytical Department, University of Almeria

Metabolomics workflows: advance your study of systems biology

Complex metabolomic studies benefit from the full-spectrum analytical sensitivity and mass accuracy of the 7250, as well as its MS/MS ability to structurally elucidate unknown metabolites. The system's extended dynamic range allows accurate, simultaneous quantification of metabolites present in a cell.

Pathway Architect, available with Mass Profiler Professional, brings a biological context to mass spectral data. With Pathway Architect, you can take results from single or multiple "omics" experiments and map them onto canonical biological pathways. You can concurrently analyze, picture, and interpret pathway information. This pathway-centric workflow speeds the route from discovery and insight to validation. It also enables you to efficiently plan and execute your next series of experiments.



Entity Name	Compound Name	[9W]	[UC]	
aminocarboxy...				
L-tryptophan	[6305] L-tryptophan 2 [20.4...	0.58735925	-0.96105385	C
▶ L-alanine	[5950] L-alanine 1 [7.495]	0.554303	-1.6314344	C
▶ L-glutamine	[738] L-glutamine 1 [13.431]	4.449348	0.1688776	C
▶ L-glutamate	[33032] L-glutamic acid 3 (d...	0.34756356	-0.3762493	C
▶ kynurenine	[161166] L-kynurenine 1 [19...	3.9562192	0.1688776	C

Find the Answers You Seek

The advanced data mining and processing tools in our MassHunter suite help you to quickly and accurately extract available information from the analytes in your samples. You'll experience unprecedented productivity with time-saving features.

- MassHunter's Find-by-Fragment capability enables targeted qualitative screening with at-a-glance results.
- Simple quantitative method creation is based on detecting qualified targets.
- Powerful multivariate analysis reduces data sets to differentiate relevant analytes.

It's just one more way that Agilent supports your complete analytical workflow, from sample preparation to reporting.

Profile

MassHunter Acquisition software

- Familiar, flexible operation
- SWARM autotune for optimal performance with every sample

MassHunter Unknowns Analysis software

- High-quality compound detection and extraction based on SureMass signal processing

Mass Profiler Professional software

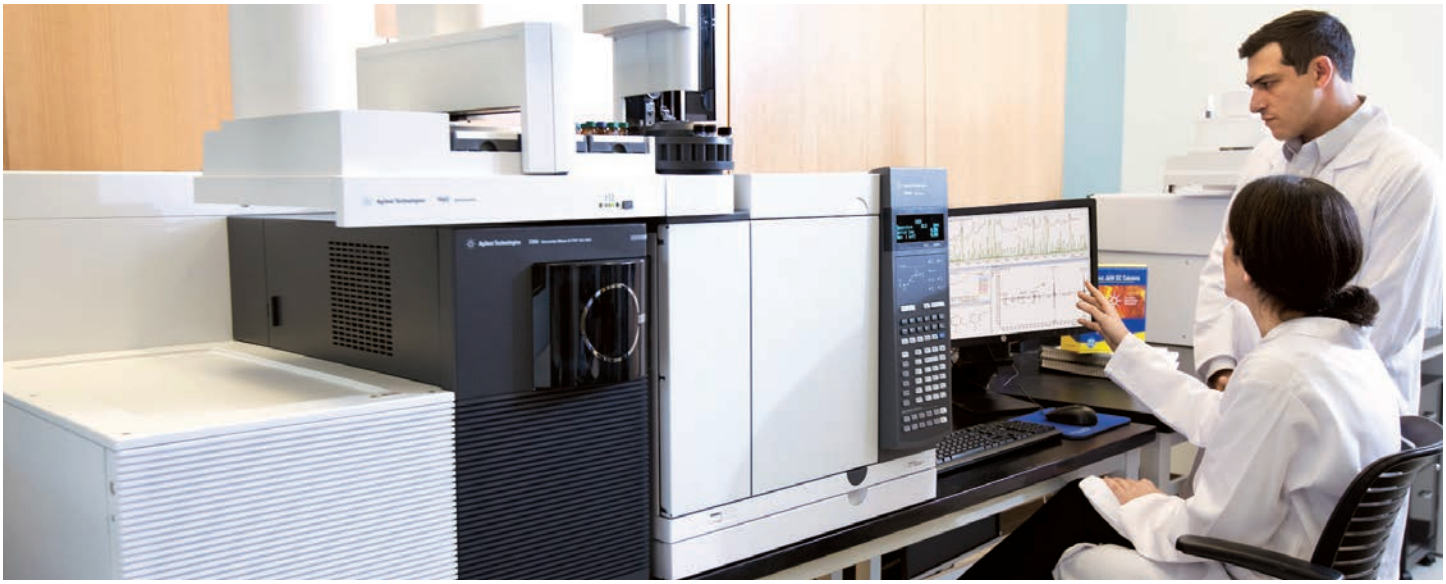
- Multivariate statistical analysis for chemometrics
- Visualization tools to quickly and clearly report results

ID Browser software

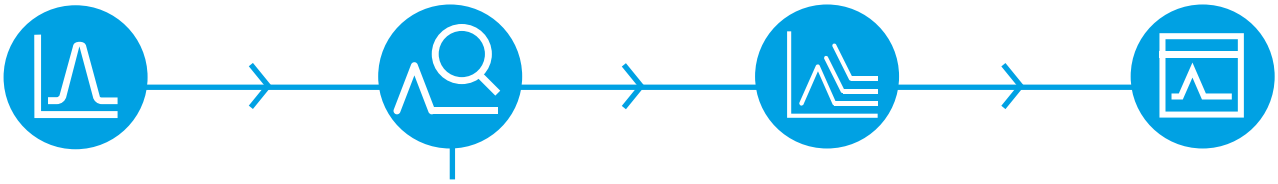
- Integrated compound identification for entities of interest

Pathway Architect software

- Visually contextualize biological pathways from major sources using statistically relevant data



Screen



MassHunter Acquisition software

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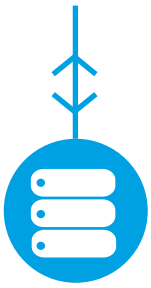
MassHunter Qualitative Analysis software

- Targeted qualitative screening using Find-by-Fragment and customizable spectral libraries for easy method development



Personal Compound Database and Library (PCDL) manager

- Curated HRAM library of 1,000+ pesticides and environmental pollutants
- Easy annotations and compound additions

MassHunter Quantitative Analysis software

- One-click compound import from MassHunter Qualitative Analysis
- Accurate quantification and SureMass signal processing
- Simultaneous target and suspect screening with an intuitive, unified workflow

MassHunter Reporting software

- Reporting solution customizable to your lab's needs

Discover

MassHunter Acquisition software

- Familiar, flexible operation
- SWARM autotune for optimal performance with every sample
- Low-energy electron and chemical ionization for molecular ion enhancement
- MS/MS spectra for structural insight

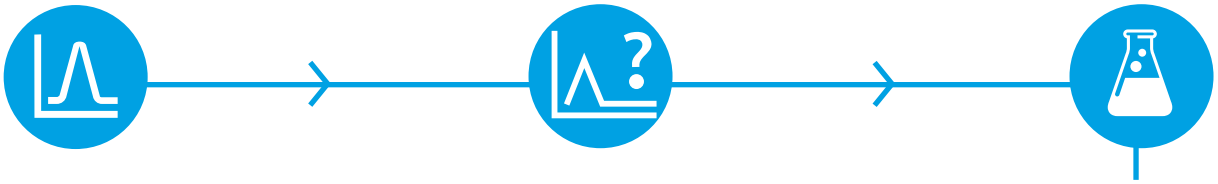
MassHunter Qualitative Analysis software

- High-quality compound detection and extraction

MassHunter Molecular Structure Correlator software

- Unknowns identification and structure elucidation
- Abundant online resources expand depth of search

Predict



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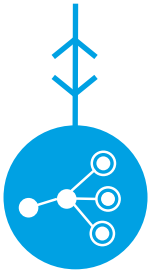

MassHunter Classifier

- Training and validation of class prediction models for streamlined future classification

From routine testing to cutting-edge research, Agilent supports data analysis workflows with a suite of powerful software tools that deliver the answers your analytical success depends upon.

Agilent CrossLab
From Insight to Outcome

CrossLab is an Agilent capability that integrates services, consumables, and lab-wide resource management to help laboratories improve efficiency, optimize operations, increase instrument uptime, develop user skill, and more. Our industry-leading services keep your instruments running at peak performance, and include technology refreshes, application consulting, repairs, preventive maintenance, compliance verification, and education.

Agilent CrossLab supports Agilent and select non-Agilent instruments and provides consultative support for workflow enablement, lab analytics, compliance, inventory management, and asset management, including relocation services.

Learn more about Agilent CrossLab, and see examples of insight that leads to great outcomes, at **www.agilent.com/crosslab**

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U.S. and Canada
1-800-227-9770
agilent_inquiries@agilent.com

Europe
info_agilent@agilent.com

Asia Pacific
inquiry_lsca@agilent.com

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