Agilent 7250 GC/Q-TOF

SEE THE WHOLE PICTURE



Agilent Technologies

SEE THE WHOLE PICTURE

The new Agilent 7250 GC/Q-TOF is the premier instrument for all of your GC/MS identification, quantification, and exploration challenges. Discovering confidently what's in your sample at what levels helps you to see the bigger picture to make the conclusions, breakthroughs, and promises your organization depends on. Agilent delivers this confidence across GC/MS workflows with the 7250 GC/Q-TOF and comprehensive MassHunter software.

More is less

From routine screening workflows, to labs focused on once-in-a-lifetime discoveries, your GC/MS applications demand only the best. Whether being used in complex metabolomics studies, pesticide screening in challenging matrices, compound identification in herbal extracts, or testing of contaminant levels in chemical feedstock, today's instruments need to stand up to the increasingly complex challenges that scientists are facing. Designed for real-world GC/MS performance and built for laboratory robustness, the 7250 GC/Q-TOF delivers what your organization needs: consistently excellent results, consistently.

This revolutionary all-in-one GC/Q-TOF delivers the power to achieve more.

The Agilent 7250 GC/Q-TOF gives you MORE:	So you manage LESS:
Sensitive detection	Concern about future regulation
Accurate quantification	Uncertainty about results
Power to explore	True unknowns
Simplified spectra	Time on data interpretation
Reproducible data	Ambiguity with replicates

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

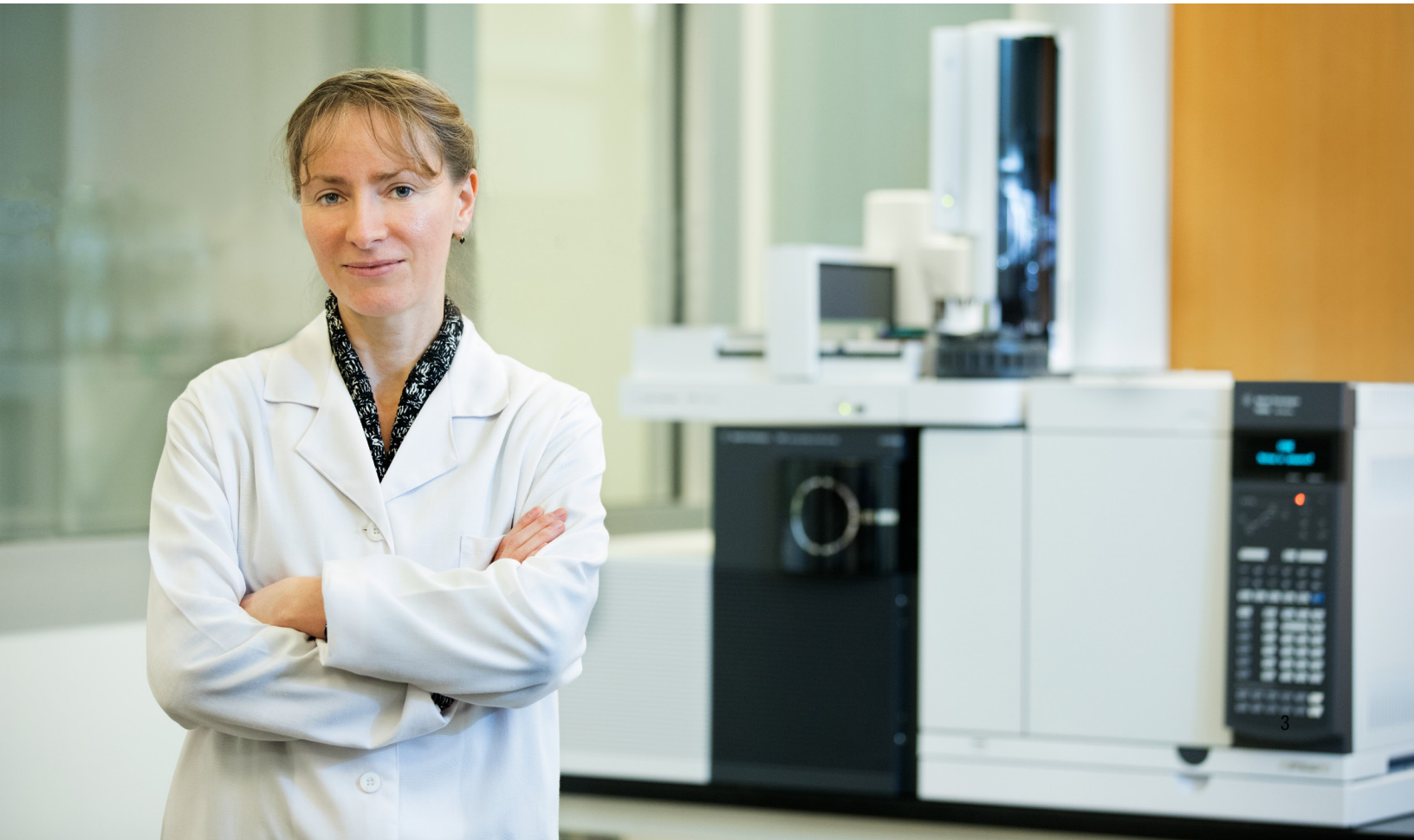
– **MIKE THURMAN, PHD,** CENTER FOR ENVIRONMENTAL MASS SPECTROMETRY, UNIVERSITY OF COLORADO

Trust the experts

For over 40 years, Agilent has served diverse labs to meet their increasingly demanding needs in mass spectrometry. Evolving analytical challenges call for new methods and novel approaches, and Agilent has answered once again. The Agilent 7250 GC/Q-TOF is designed to provide the ultimate in performance for labs across the analytical spectrum – solving the toughest GC/MS challenges.

This instrument is the newest and most advanced GC/Q-TOF in Agilent's comprehensive range of mass spectrometers that can analyze virtually any kind of molecule or element. Agilent MS solutions benefit from more than 40 years of continual innovation. The result is analytical systems that set the standard for reliability, flexibility, and exceptional performance.

Identify. Quantify. Simplify. See the whole picture with the Agilent 7250 GC/Q-TOF.



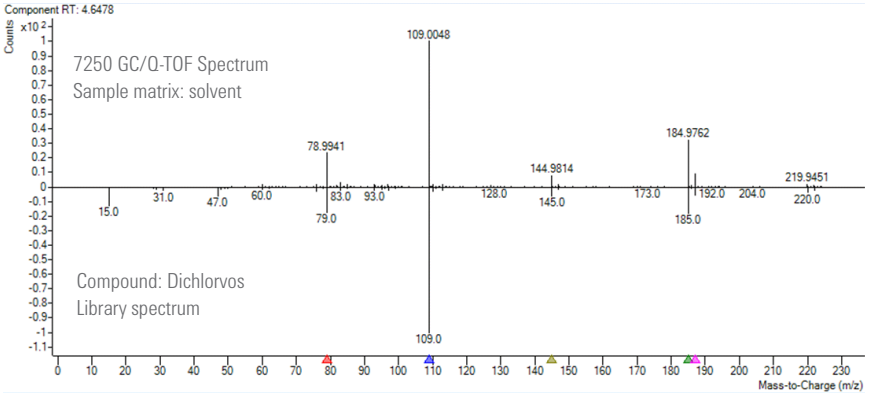
CONFIDENT IDENTIFICATION

Not being able to see the whole picture of what's in your sample can have serious implications for your research, development, and QC activities. True confidence is derived from experience and ability. Agilent's experience in GC/MS is unparalleled, and the analytical prowess of the 7250 GC/Q-TOF and MassHunter software gives the platform unmatched abilities in compound identification.

- **Library-quality spectra** – undistorted spectral fidelity provides trustworthy compound identification against commercial libraries.
- **Isotopic fidelity** – preservation of isotope patterns allows greater certainty in molecular formulae assignment.
- **Broad in-spectrum dynamic range** – confident detection of trace analytes, even in the presence of abundant co-elution.
- **Structural elucidation** – MS/MS measurements with high-resolution, accurate mass product ion spectra can provide structural information, further increase selectivity, and circumvent matrix interferences.

Spectral library match

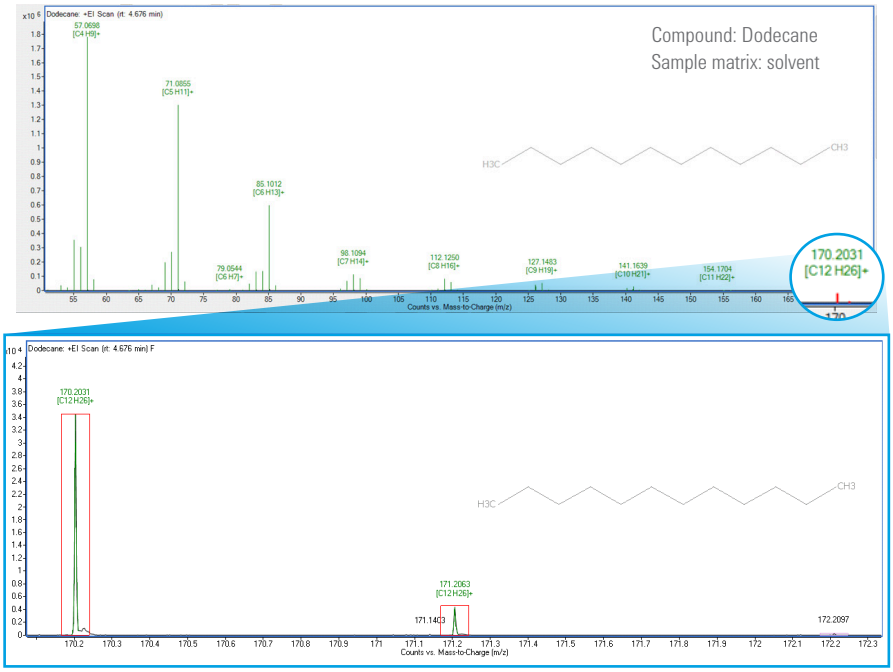
Perform compound identification by spectral search against commercially available libraries with ease. True-to-library fragmentation patterns and full spectrum acquisition makes the 7250 GC/Q-TOF the premier platform for identification by GC/MS. The 7250 GC/Q-TOF was designed to support the spectral quality of hundreds of thousands of compound library spectra, most of which have been generated by HP/Agilent quadrupole GC/MS systems. The example shown of Dichlorvos shows excellent spectral fidelity and mass accuracy.



Isotopic fidelity

Increased confidence in compound identification requires more than good mass accuracy. Consideration of independent compound characteristics, like isotopic pattern matching, is essential.

Isotopic fidelity is easily visualized through MassHunter Qualitative Analysis for confidence in compound identification that is complementary to accurate mass measurement. The 7250 GC/Q-TOF exhibits excellent isotopic fidelity, even for trace-level isotopes, as shown in this compound spectrum for Dodecane with a minor M^+ peak cluster.

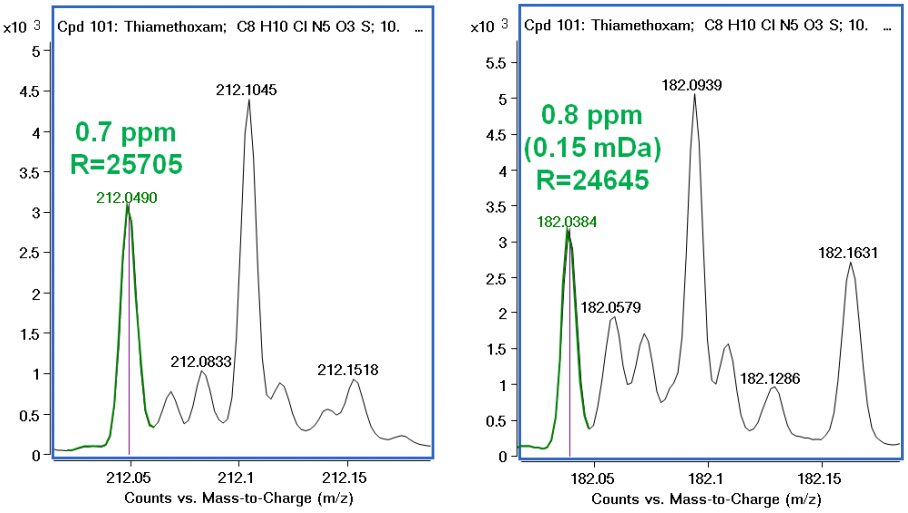


High-resolution and mass accuracy

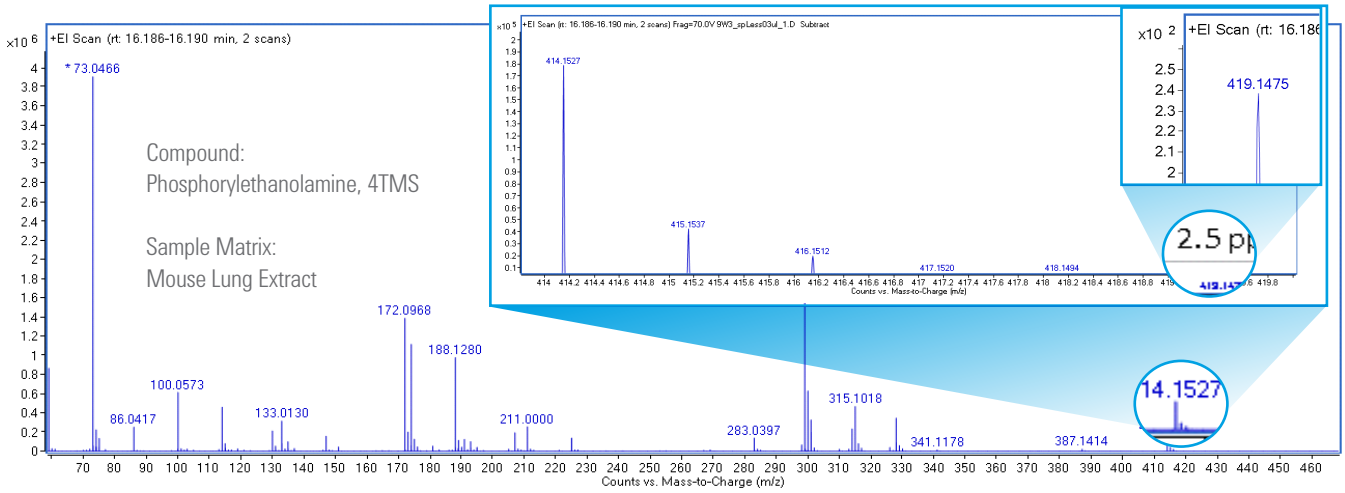
High-resolution is necessary to separate analytes from interferences. But, to provide the most analytical utility, this performance characteristic must be usable under challenging conditions, like complex matrices and trace level analytes.

The example shown here represents such a challenging 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 on compound identification.

What's more, this level of spectral performance is achieved regardless of acquisition speed or mass range. The 7250 GC/Q-TOF delivers maximum HRAM usable utility for the most challenging GC/MS applications.



Wide in-spectrum dynamic range

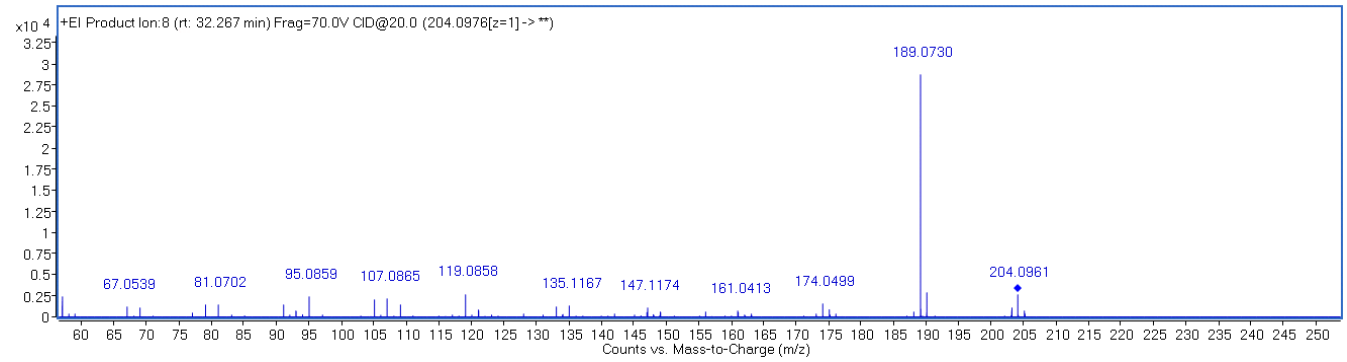


A wide in-spectrum dynamic range enables confident detection of trace level analytes in the presence of abundant background or other coeluents.

The 7250 GC/Q-TOF typically provides four orders of magnitude of in-spectrum dynamic range, even in heavy matrices. The example shown displays a range of 16,000+:1 for the identified compound Phosphorylethanolamine (4TMS) in a complex biological sample of mouse lung extract.

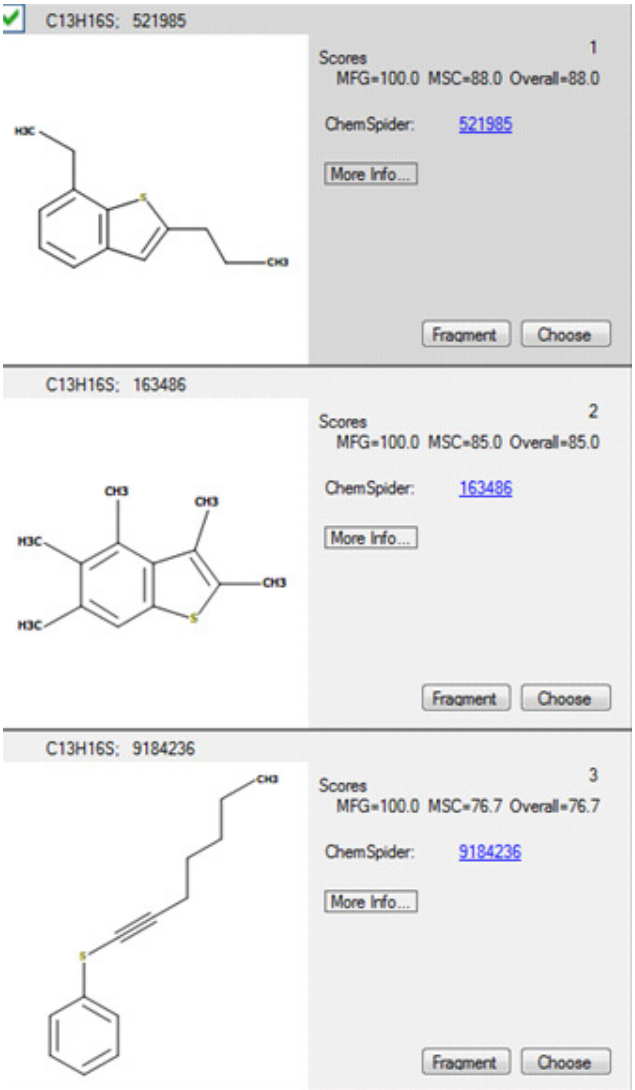


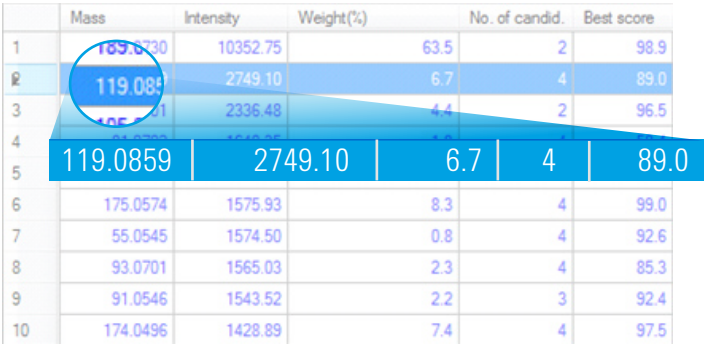
MSC workflow



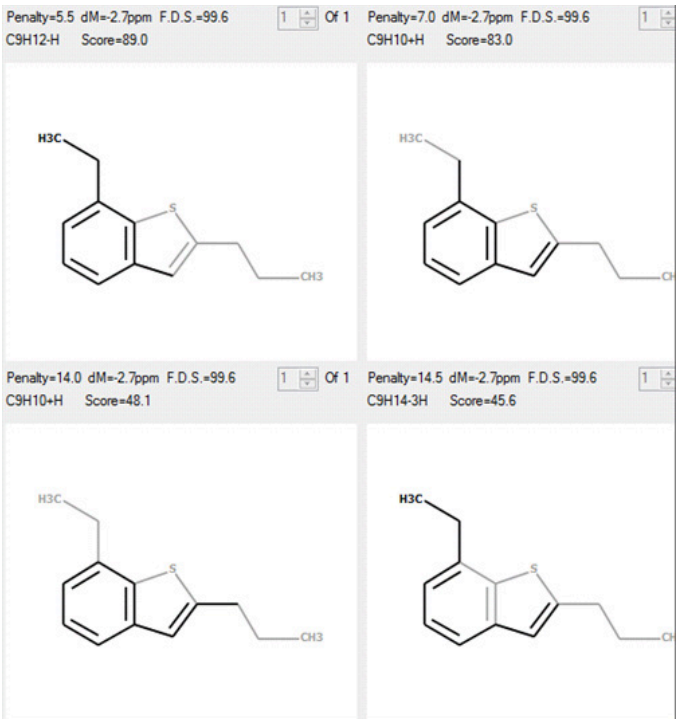
With MS/MS product ion spectra generated from a putative molecular ion, powerful Molecular Structure Correlator software can propose compound structure possibilities and likelihoods based on fragment data.

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





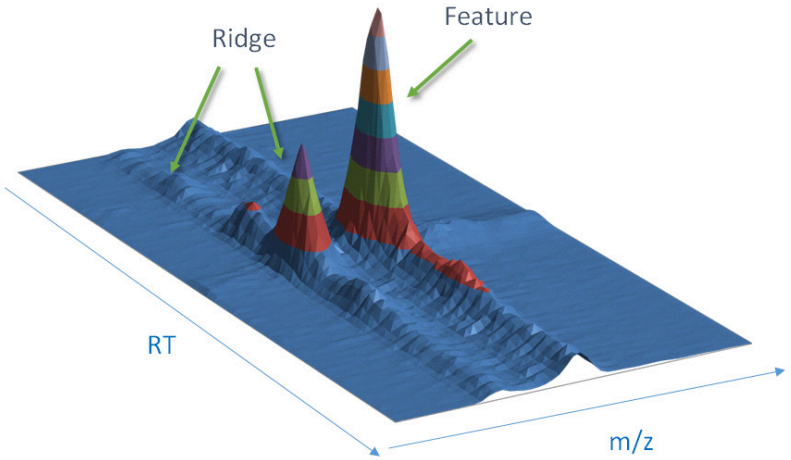
	Mass	Intensity	Weight(%)	No. of candid.	Best score
1	189.0730	10352.75	63.5	2	98.9
2	119.0859	2749.10	6.7	4	89.0
3	204.0961	2336.48	4.4	2	96.5
4	67.0539	1649.35	4.1	4	77.3
5	81.0702	1648.25	4.1	4	77.3
6	175.0574	1575.93	8.3	4	99.0
7	55.0545	1574.50	0.8	4	92.6
8	93.0701	1565.03	2.3	4	85.3
9	91.0546	1543.52	2.2	3	92.4
10	174.0496	1428.89	7.4	4	97.5



ACCURATE QUANTIFICATION

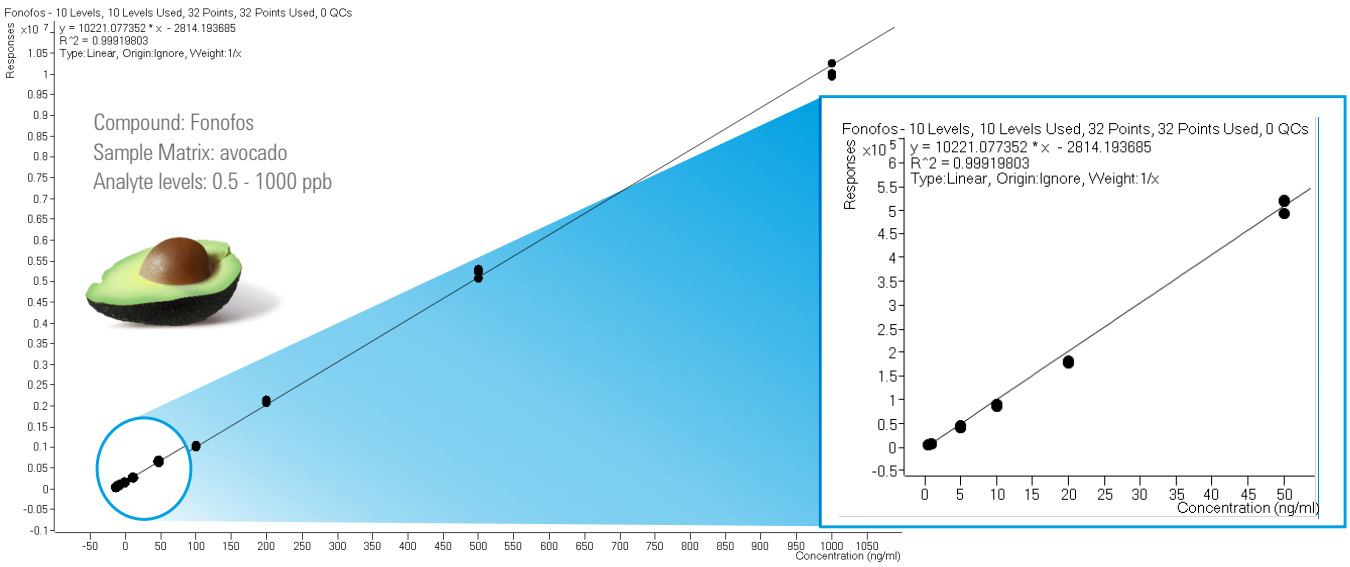
Targeted quantification with untargeted acquisition is a powerful combination. Combined with superior chromatography, high mass resolution, and a wide dynamic range, the Agilent 7250 GC/Q-TOF delivers accuracy, quantitatively.

- **Extended linear dynamic range with high resolution** – broad linearity in quantitative measurement enabled by state-of-the-art electronics for mass separation and detection.
- **Precision and trueness** – consistent response factors, even for trace analytes in the presence of abundant matrix, deliver analytical performance for real-world samples.
- **Chromatographic compatibility** – fast acquisition speeds with high-resolution spectra facilitate deconvolution of narrow, co-eluting GC peaks for accurate quantification at high speeds.
- **SureMass** – optimized mass accuracy and signal intensity with Agilent's proprietary signal processing algorithm for compound detection.



SureMass Signal Processing

Quantification



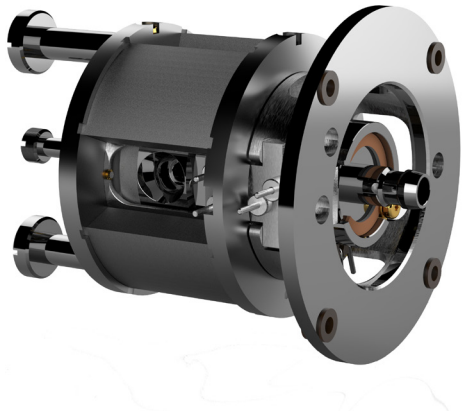
A wide linear dynamic range brings quantitative accuracy across a range of compound concentrations. Response factors are maintained even at low concentrations in a complex sample, as shown in this data depicting Fonofos at 0.5 – 1000 ng/mL in an avocado matrix.



ANALYTICAL SIMPLIFICATION

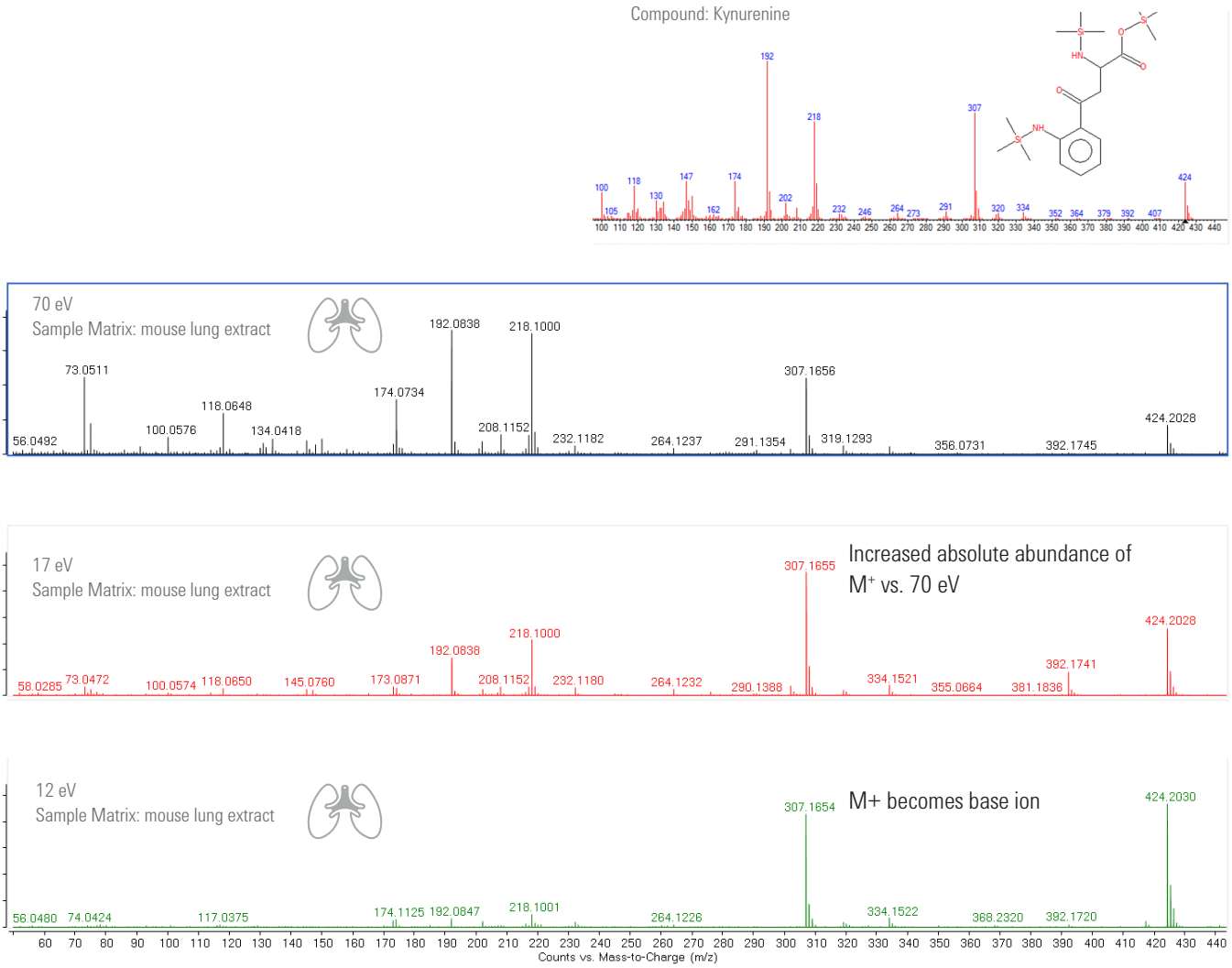
The world's only high-resolution GC/Q-TOF, now with Low Energy EI, enables new workflows that were previously impractical or impossible. Based on the revolutionary High Efficiency Source (HES) proven in the Agilent 5977B HES GC/MSD and 7010B GC/TQ, the EI Source in the 7250 GC/Q-TOF has been optimized for Low Energy operation, yet still exceeds at conventional 70 eV ionization. Modifications to the patented HES design allow Low Energy EI with useful sensitivity levels for a paradigm shift in GC/MS soft ionization. The creation of simplified spectra without relying on chemical ionization or other specialty techniques and while retaining the universal applicability of EI promise to equip GC/MS laboratories with new, powerful identification and elucidation capabilities.

- **Preserved molecular ion** – preserve or enhance analyte molecular ions for improved identification confidence and sensitive MS/MS experiments (application dependent).
- **Universal applicability** – provide ionization across analyte classes greatly avoiding compound limitations and analytical sensitivity losses experienced with PCI and other soft ionization techniques.
- **Proven performance** – efficient ionization with proven proprietary ion source technology from the global GC/MS leader.



Based on revolutionary Agilent HES technology
Low Energy EI with accessible sensitivity levels for universal ionization and confident detection

Low Energy EI



In a metabolomics experiment, the compound Kynurenine was detected in a mouse lung extract. However, identification of metabolites (and other compound classes with similar structures) in complex matrices can be challenging. By lowering the source ionization energy, there is a spectral tilt towards the molecular ion. In this case, both the relative and absolute amount of the molecular ion increase at 17 eV, making the system ideal for MS/MS experiments. At even lower ionization energies, the proposed molecular ion becomes the base ion in the component spectra, yielding further confidence to the identification.

FOOD SAFETY

Never compromise

Global trade, stringent regulations, and increased public awareness of food safety issues are all driving the need for more frequent and detailed food testing. Food producers and consumers are facing threats from food adulteration and fraudulent labeling. You're committed to consistent quality and uncompromising consumer safety – protecting both consumers and your reputation – and Agilent is here to help.

To meet these challenges, you need a single platform that optimizes screening for targets, suspects, and unknowns all at once. The 7250 GC/Q-TOF was developed to meet this need with fit-for-purpose measurement capabilities and powerful, comprehensive software tools.

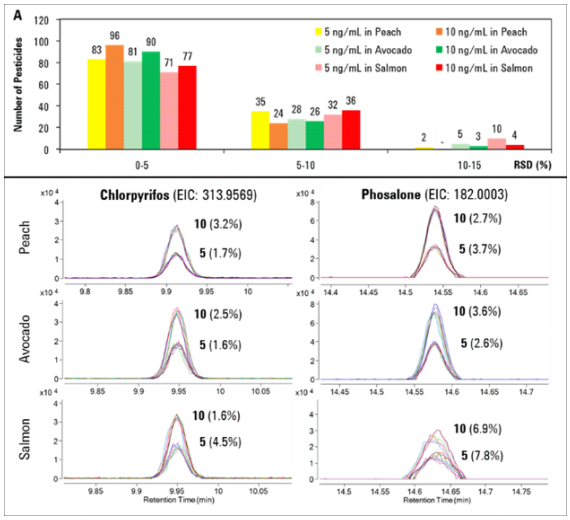
- Over 850 pesticide analytes are available in a customizable, high-resolution spectral library.
- Suspect analytes are confidently identified using co-elution matching and ion ratio scoring of selective ions with Agilent's Find-by-Fragments workflow.
- Quantification of targets across a broad linear dynamic range and identification of unknowns using commercial libraries are both enhanced with SureMass signal processing.

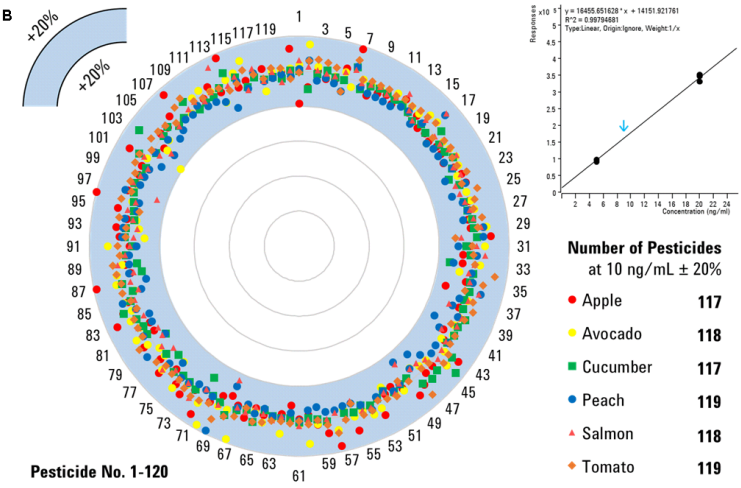


FOOD TESTING

Matrix matters

Food and feed matrices can be simple or complex. Agilent provides the expertise, supplies, and tools needed to generate results confidently and reproducibly with ease across the range of matrices that matter in your lab.





Comprehensive screening for pesticides in food matrices is greatly empowered with untargeted acquisition and high resolution spectral libraries. A) The GC/Q-TOF data presented here shows 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 show excellent analytical performance, with two examples of detected characteristic ion replicates shown. B) Quantitative accuracy at 10 ng/mL for rapid comparison against Maximum Residue Limits (MRLs) is shown for six food matrices ranging in complexity. Even for complex matrices like avocado and salmon, quantitative accuracy complies with SANTE/11945/2015 guidelines (± 20% vs. standard) for over 97% of the pesticide:food pair for each commodity 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 INSITITUTE MUNSTERLAND-EMSCHER-LIPPE

ENVIRONMENTAL

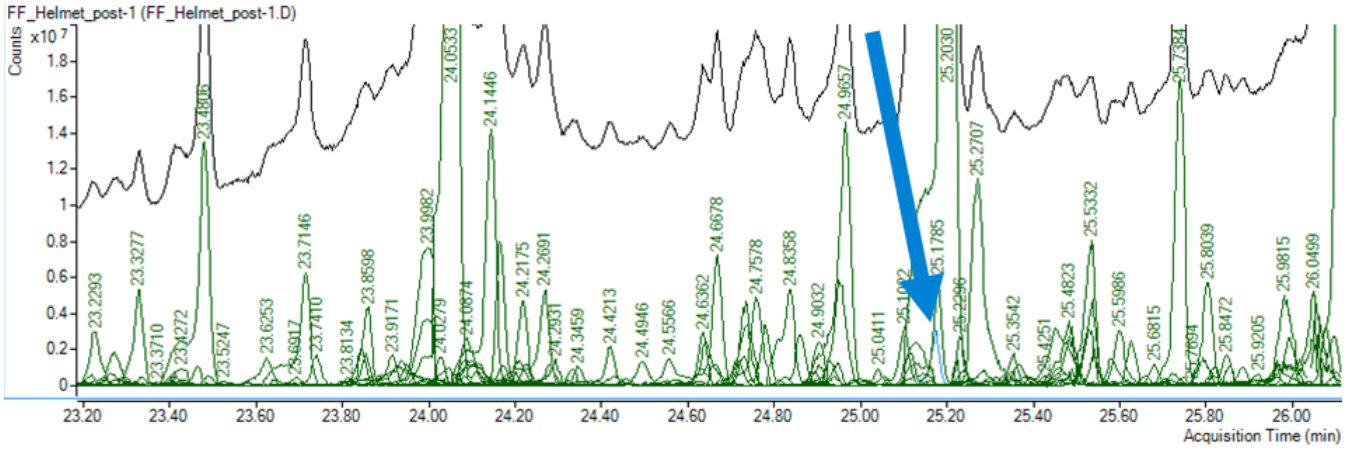
Taking the fight to the next level

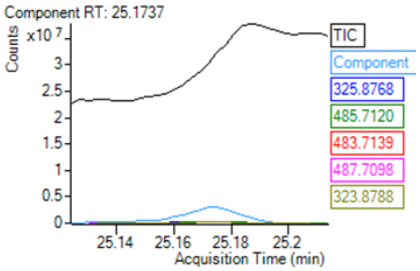
Every day, new questions arise about the impact of humanity on the environment, and about the environment's impact on us. These complex questions require tools of increasing capability to deliver meaningful answers. The revolutionary technological enhancements in the 7250 GC/Q-TOF are designed to provide these answers with ease and efficiency.

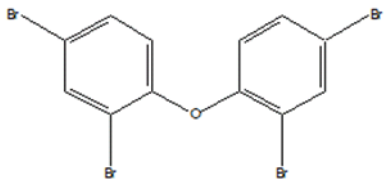
- **Retrospective processing** – measure once and analyze reiteratively with full spectrum data that can be interrogated for emerging targets in the future.
- **Full spectrum high resolution** – generate high-resolution spectra across a broad mass range (up to 3000 m/z) for congener detection and speciation.
- **Low Energy EI** – transcend 70 eV EI while maintaining signal intensity with a highly efficient source optimized to support ionization at varied electron energies.

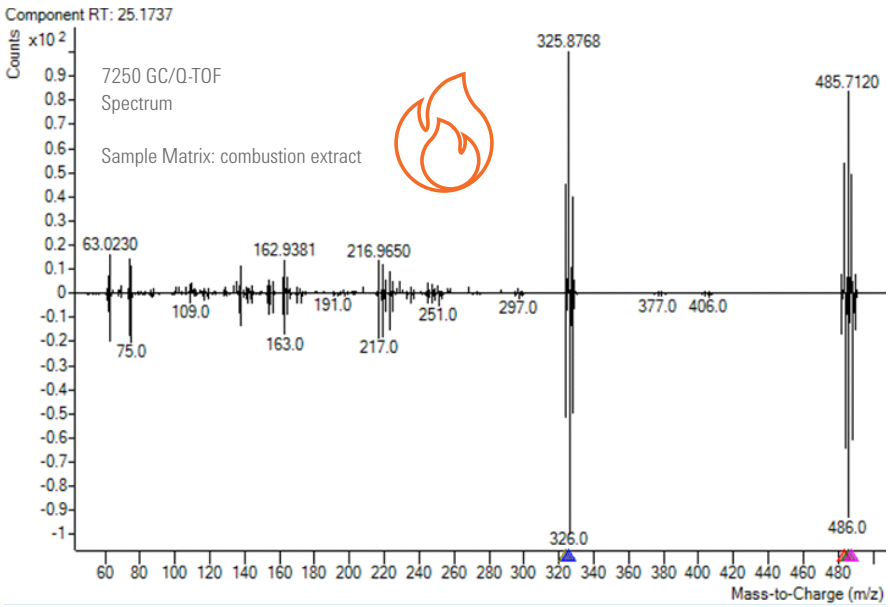


MassHunter Unknowns Analysis









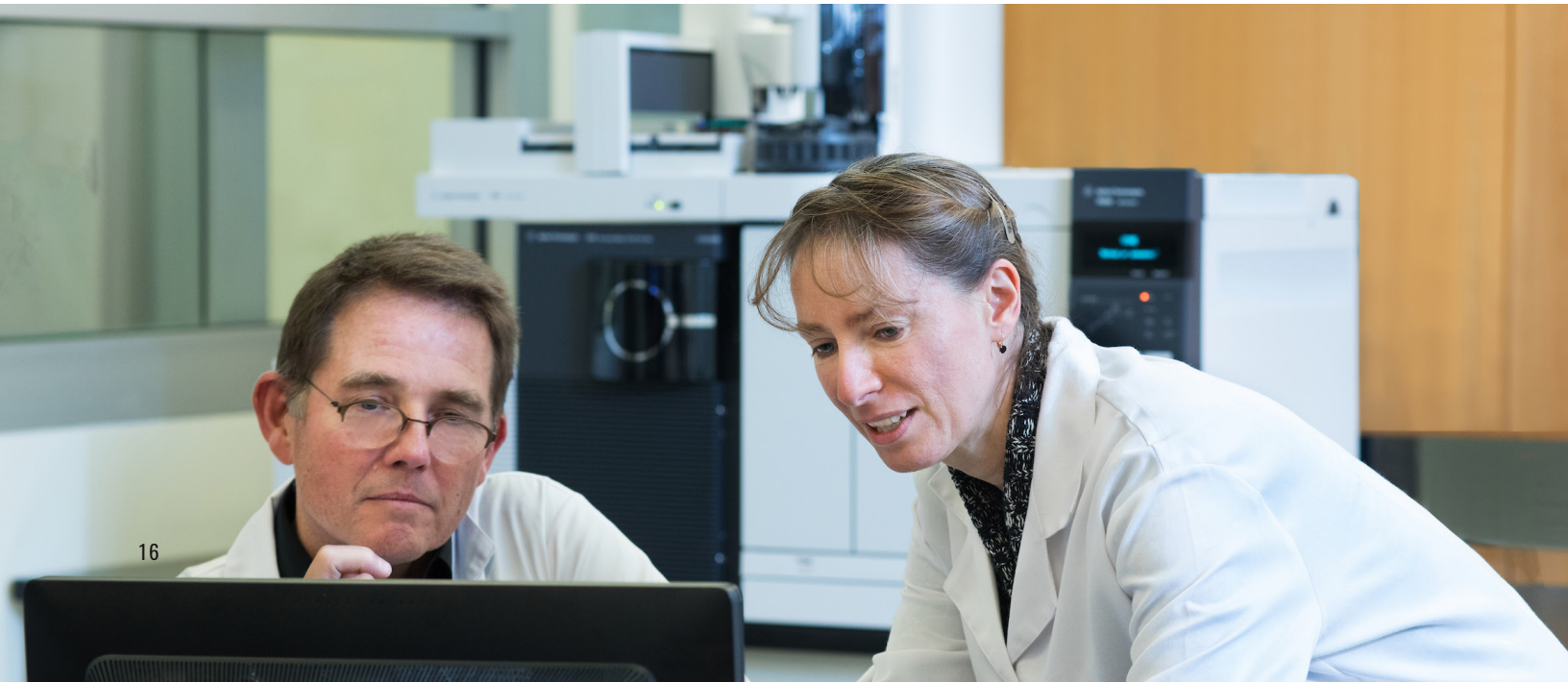
MassHunter Unknowns Analysis software, using SureMass signal processing, provides insight and accuracy beyond conventional deconvolution techniques. Even minor components are accurately extracted and identified in the presence of dominating background signal. The data shown here depicts the trace detection of dibromophenyl ether with a match score of greater than 95 in complex combustion byproducts.

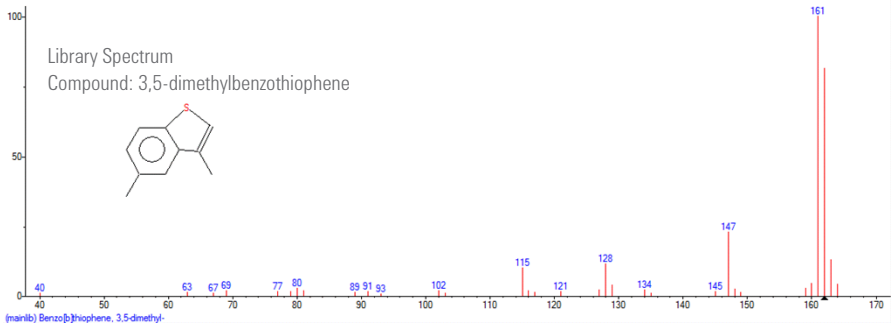
ENERGY AND CHEMICAL

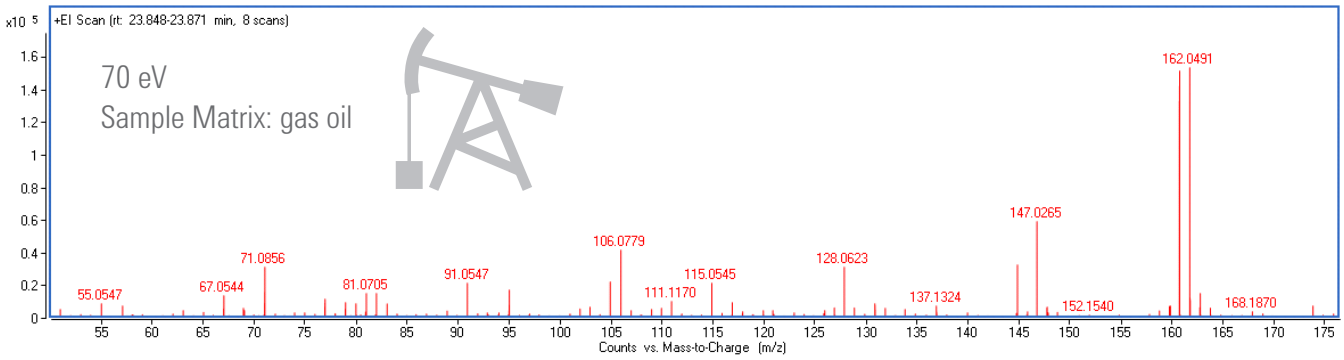
See the whole picture

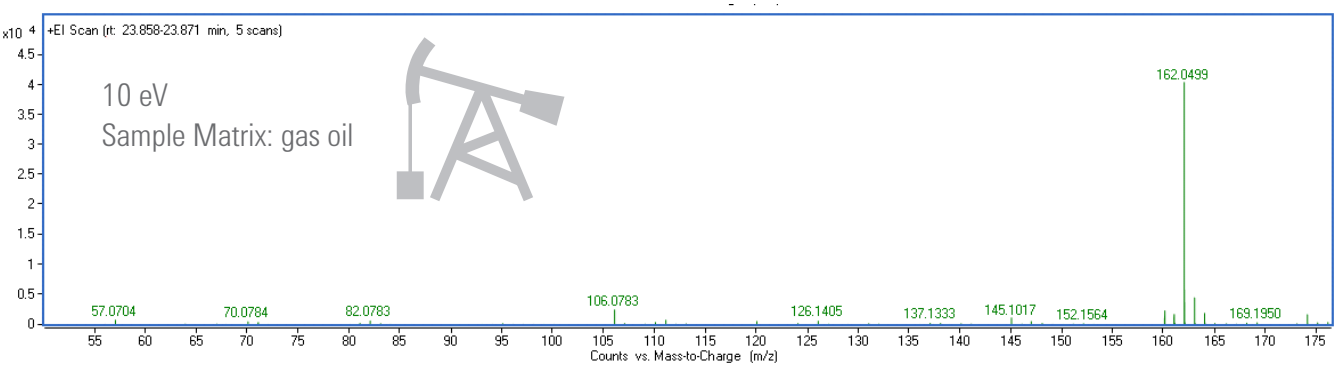
Characterizing what's in a complex sample is no simple task. It takes knowledge, insight, and powerful analytical capabilities. With high-resolution accurate mass measurements, Low Energy EI capability, fast spectral acquisition for comprehensive GCxGC compatibility, and highly sensitive MS/MS measurements, the Agilent 7250 GC/Q-TOF is the platform of choice for complex sample characterization.

- **Fast acquisition rates** – characterize narrow chromatographic peaks or ultranarrow 2-D GC peaks with data rates up to 50 Hz and speed-independent, high resolving power.
- **Spectral simplification** – deduce molecular ions for similar chemical species with Low Energy EI and confirm by sensitive MS/MS measurements.
- **Elucidate structures** – high-resolution accurate mass product ion spectra combined with powerful Molecular Structure Correlator software yield insight on chemical structures of studied analytes.









Spectral ambiguity is reduced with revolutionary Low Energy EI on the 7250 GC/Q-TOF. Based on the High Efficiency Source found on 5977 HES GC/MSD and 7010 GC/TQ platforms, the Low Energy capable EI source greatly maintains compound sensitivity while enabling a spectral tilt towards molecular ion. This example shows 3,5-dimethylbenzothiophene detected in gas oil, with identification facilitated by use of Low Energy EI.

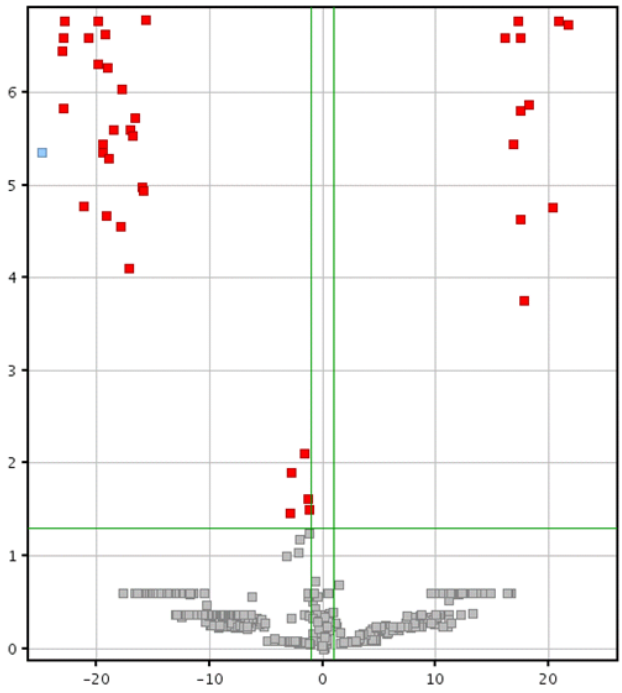
LIFE SCIENCE RESEARCH

Exhaustive analysis

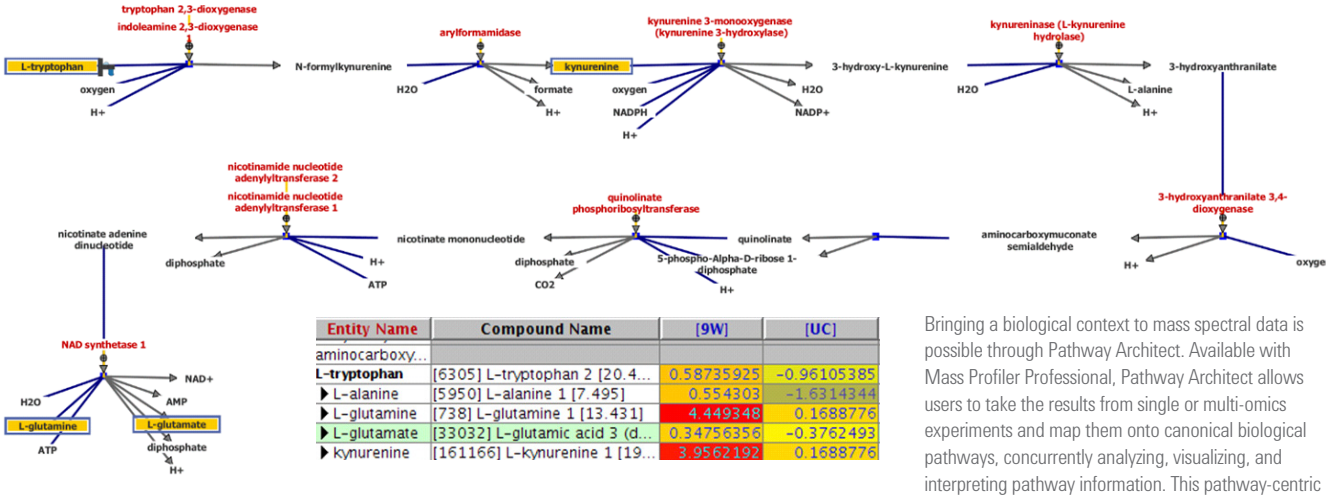
Each day brings new advances in human health and protection. The fundamental research that drives these advancements requires painstaking experimental design and execution. The Agilent 7250 GC/Q-TOF drives research forward with full spectrum, high-resolution data, and powerful software to bring focus to what's important.

	P all	P < 0.05	P < 0.02	P < 0.01	P < 0.0050	P < 0.0010
FC all	679	41	38	37	36	36
FC > 1.1	664	41	38	37	36	36
FC > 1.5	638	41	38	37	36	36
FC > 2.0	625	41	38	37	36	36
FC > 3.0	601	39	38	37	36	36
Expected by ch...		2	0	0	0	0

Compound	p	p (Corr)	FC
L-Threonine, 3TMS derivative	1.84E-03	3.13E-02	-2.29
Inosine, 4TMS derivative	1.62E-07	4.36E-06	-31162316...
D-Gluconic acid, 6TMS derivative	1.11E-08	5.38E-07	-530736.88
Silane, (iodomethyl)-	2.42E-09	2.35E-07	-614400.88
D-Galactofuranose, 1,2,3,5-tetrakis-O-(trimethylsilyl)-, bis(...	1.67E-07	4.36E-06	-736603.19
Phosphorylethanolamine, 4TMS derivative	2.09E-03	3.46E-02	-7.21
Uric acid, N,O,O',O''-tetrakis(trimethylsilyl)-	7.06E-04	1.26E-02	-7.11
Pseudo uridine penta-tms	2.01E-08	9.09E-07	-218838.31
L-Glutamic acid, 3TMS derivative	1.37E-03	2.38E-02	-2.49
Serine, 3TMS derivative	4.22E-04	7.74E-03	-3.07
D-Ribose, 2,3,4-tris-O-(trimethylsilyl)-, 5-[bis(trimethylsilyl...	9.33E-09	4.87E-07	-960156.19
1H-Indole-3-propanoic acid, .alpha.-hydroxy-, methyl ester	1.01E-06	2.13E-05	-583467.62
D-(+)-Ribono-1,4-lactone, 3TMS derivative	1.24E-09	1.69E-07	-1003281.19
Gluconic acid, 2,3,4,5-tetrakis-O-(trimethylsilyl)-, trimethyl...	1.21E-07	3.58E-06	-710218.94
l-Norvaline, N-(2-methoxyethoxycarbonyl)-, undecyl ester	7.71E-08	2.49E-06	-139145.16
Itaconic acid, 2TMS derivative	3.63E-08	1.45E-06	-7787654.50
2-Hydroxyisocaproic acid, (S)-, 2TBDMS derivative	3.97E-09	2.50E-07	-7910934.50
7-(Trimethylsilyl)-2,6-bis[(trimethylsilyl)oxy]-7H-purine	6.18E-09	3.50E-07	-8949361.00
Inosose, 2-desoxy-, O-methyloxime, tetrakis-O-(trimethylsi...	7.26E-07	1.64E-05	-2244370.50
L-Lysine, 3TMS derivative	3.33E-09	2.50E-07	-1685603.25
L-Phenylalanine, 2TMS derivative	1.01E-09	1.69E-07	-7575707.00
L-Proline, 2TMS derivative	7.95E-07	1.74E-05	1272716.75
2-Mercapto-4,6-dimethylnicotinonitrile, TBDMS derivative	1.14E-06	2.34E-05	173959.05
Phenylalanine, 2TMS derivative	1.05E-09	1.69E-07	1804699.38
Mandelic acid, 2TBDMS derivative	7.70E-10	1.69E-07	152992.62



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. The data shown presents identified metabolite differences between mouse lung tissue of uninfected vs. tuberculosis infected specimens at 9 weeks. Progression is depicted through Fold Change Analysis on a Volcano plot for easy visualization.



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

Bringing a biological context to mass spectral data is possible through Pathway Architect. Available with Mass Profiler Professional, Pathway Architect allows users to take the results from single or multi-omics experiments and map them onto canonical biological pathways, concurrently analyzing, visualizing, and interpreting pathway information. This pathway-centric workflow speeds the route from discovery and insight to validation. It also enables researchers to efficiently plan and execute their next series of experiments.

Using metabolomics workflows can be a powerful way to study systems biology. Complex metabolomic studies will take advantage of full spectrum analytical sensitivity and mass accuracy of the GC/Q-TOF, as well as its MS/MS capability to assist structural elucidation of unknown metabolites. The extended dynamic range of the Agilent 7250 GC/Q-TOF will allow for accurate and simultaneous quantification of a broad range of metabolites present in a cell.



MASSHUNTER

Giving you answers

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, such as:

- Find-by-Fragments workflow for targeted qualitative screening with at-a-glance results.
- Simple quantitative method creation based on detection of qualified targets.
- Powerful multivariate analysis to reduce datasets to differentially relevant analytes.

Agilent supports your complete analytical workflow, from sample to report. Take your analytical results to compelling new levels with industry-leading performance from the groundbreaking Agilent 7250 GC/Q-TOF.



Profiling

MassHunter Acquisition

- Familiar, flexible operation
- Swarm Autotune for optimal performance with every sample

MassHunter Profinder
MassHunter Unknowns Analysis

- High-quality compound detection & extraction based on Molecular Feature Extractor (MFE) & SureMass signal processing

MassHunter Profiler Professional

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

ID Browser

- Integrated Compound identification for entities of interest

Pathway Architect

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

Screening

MassHunter Acquisition

- Familiar, flexible operation
- Swarm Autotune for optimal performance with every sample

MassHunter Qualitative Analysis

- Targeted qualitative screening with Find-By-Fragments and customizable spectral libraries

MassHunter Quantitative Analysis

- One-click compound import from MassHunter Qualitative Analysis
- Accurate quantification and SureMass signal processing

MassHunter Reporting

- Customizable solution for reporting to your lab's needs

Personal Compound Database & Library (PCDL Manager)

- Human curated, 850 pesticide compound HRAM library for GC/Q-TOF
- Easy annotations and compound additions

Identify and elucidate

MassHunter Acquisition

- Familiar, flexible operation
- Swarm Autotune for optimal performance with every sample
- Low Energy EI for molecularion enhancement
- MS/MS Spectra for structural insight

MassHunter Profinder MassHunter Unknowns Analysis

- High-quality compound detection & extraction based on Molecular Feature Extractor (MFE) & SureMass signal processing

Molecular Structure Correlator

- Aid in unknowns identification & structure elucidation
- Access abundant online resources to expand depth of search

"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

Class prediction

MassHunter Acquisition

- Familiar, flexible operation
- Swarm Autotune for optimal performance with every sample

MassHunter Profinder MassHunter Unknowns Analysis

- High-quality compound detection & extraction based on Molecular Feature Extractor (MFE) & SureMass signal processing

Mass Profiler Professional

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

Sample Class Predicator

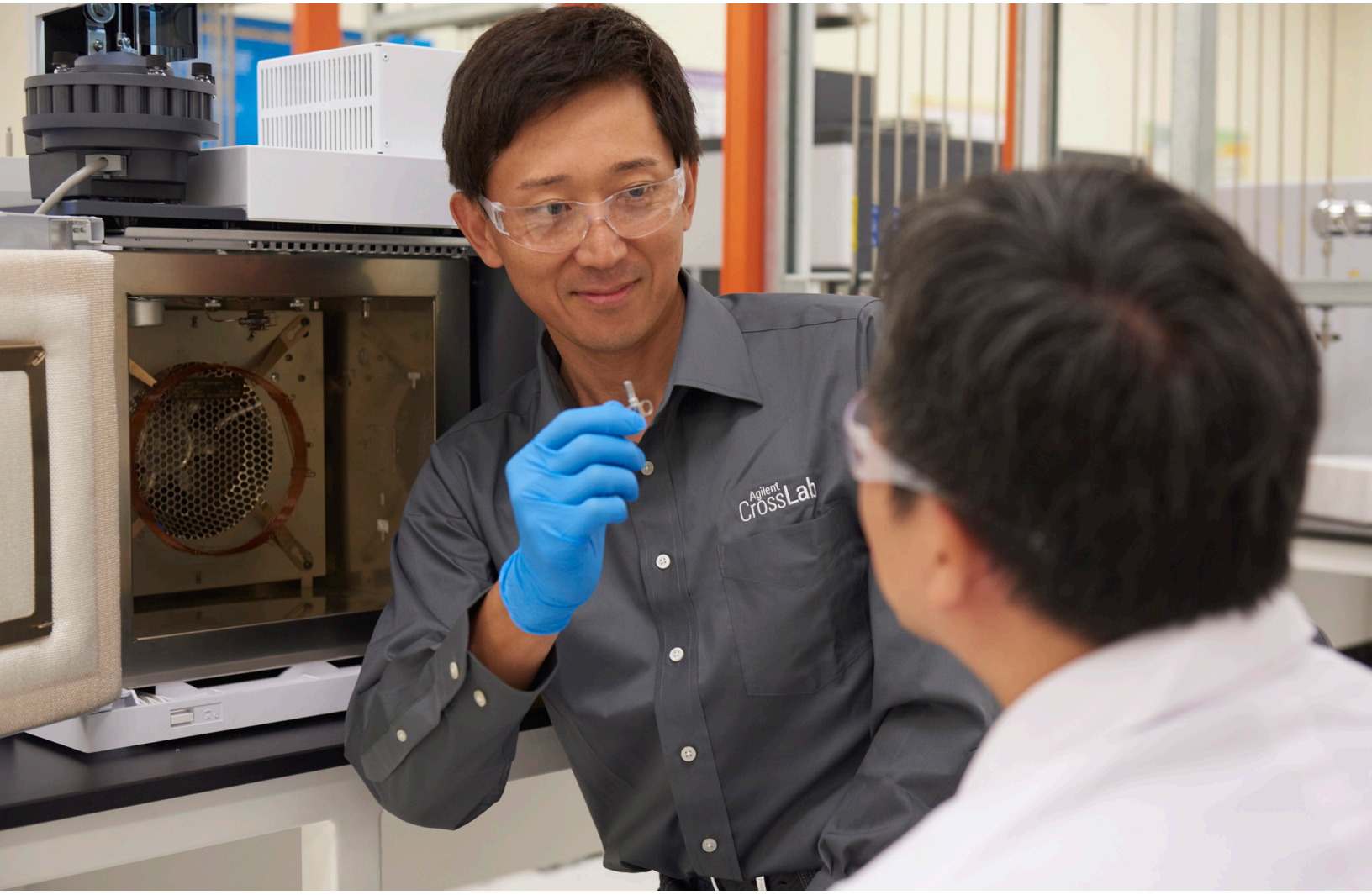
- Training and validation of class prediction models for streamlined future classification

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