



Agilent 7200 Q-TOF for GC/MS

**ACHIEVE MAXIMUM QUALITATIVE
AND QUANTITATIVE POWER FOR
CHALLENGING APPLICATIONS**

The Measure of Confidence



Agilent Technologies

Maximize detection selectivity and confidently analyze both targets and unknowns

Complex matrices and trace-level analyses demand your best qualitative and quantitative data. Now, a new technology helps you find the answers you seek.

Agilent 7200 Q-TOF for GC/MS: Achieve high resolution, accurate mass, full-spectrum sensitivity, and MS/MS selectivity for your toughest analysis

Agilent's 7200 Q-TOF for GC/MS is the world's first Q-TOF designed specifically for gas chromatography. It redraws the boundaries of GC/MS technology by combining the separation power of Agilent's 7890 Series GC with application-tested MS components from our 7000 Triple Quadrupole GC/MS and 6500 LC/Q-TOF systems. The results: robust GC/MS operation, outstanding selectivity, full spectrum acquisition with high sensitivity, fast data rates, and accurate mass information to simplify molecular characterization and structural confirmation.



The world's first Q-TOF for GC/MS combines the proven separation power of Agilent's 7890 GC with the high detection selectivity and accurate mass information of a TOF analyzer.

Your first choice for exceptional qualitative *and* quantitative analysis

The Agilent 7200 Q-TOF for GC/MS combines the sought-after features of our flagship GC/MS systems with the following advanced capabilities:

High resolution and mass accuracy

Low-ppm mass accuracy – combined with 15x to 50x greater resolution than a single quadrupole MS – gives you the power to analyze target, non-target, and unknown compounds with much greater reliability.

Low detection limits and excellent linearity

A full-spectrum with sensitivity greater than that of quadrupole MS lets you capture accurate mass spectra at low pg on-column for most compounds. Dual gain mode expands this range to 10^5 .

Unparalleled MS/MS selectivity

The detection selectivity of high-resolution MS/MS dramatically surpasses other MS/MS analyzers. Moreover, accurate mass product ion spectra help confirm targets and non-targets as well as elucidate unknown compounds.

Simplify your analysis of accurate mass MS and MS/MS files

Agilent MassHunter software provides valuable tools for identification, quantitation, and confirmation.

- Find compounds in complex samples by applying deconvolution optimized for EI or CI data.
- The combination of library search results and calculated formulas for molecular and fragment ions simplifies compound identification.
- Perform multivariate statistical analysis on several data files using Mass Profiler Professional – a mass spectrometry-centric program.

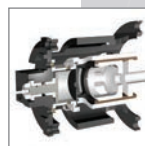
Accurate mass information lets you qualitatively and quantitatively recognize compounds with maximum confidence.

Time-tested design with leading-edge enhancements



Full 7890 GC capabilities

Includes multimode inlet, high-performance backflush, and fast, low-thermal mass column technology.



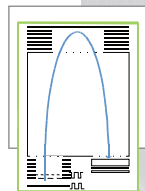
High-sensitivity extractor ion source

Programmable up to 350 °C for robust compatibility with complex matrices.



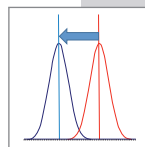
Hot quartz monolithic hyperbolic quadrupole

Can be heated to 200 °C – without resolution or sensitivity loss – to eliminate contamination from high-temperature GC peaks.



Stable, high-performance TOF technology

Agilent's orthogonal TOF technologies deliver consistent performance for thousands of LC/TOF and LC/Q-TOF systems.



Internal reference mass (IRM) correction

When necessary, an IRM compound can be introduced into the source for maximum mass accuracy.



Removable ion source

Computer control of both the transfer line and vacuum interlock position ensure trouble-free ion source replacement in about 30 minutes.

To learn more about the capabilities of the Agilent 7200 Q-TOF for GC/MS, visit www.agilent.com/chem/GCMS_QTOF

Agilent's 7200 Q-TOF for GC/MS system combines proven technologies with new – and unique – features

Dual-stage ion mirror provides second-order time focusing for high mass resolution.

4 GHz ADC electronics enable a high sampling rate (32 Gbit/sec), ensuring high resolution, mass accuracy, and sensitivity for low-abundance samples.

Proprietary INVAR flight tube, sealed in a vacuum-insulated shell, maintains 24/7 mass accuracy by eliminating temperature-related thermal mass drift. Its longer length also improves mass resolution.

Dual gain amplifiers expand the dynamic range up to 10^5 .

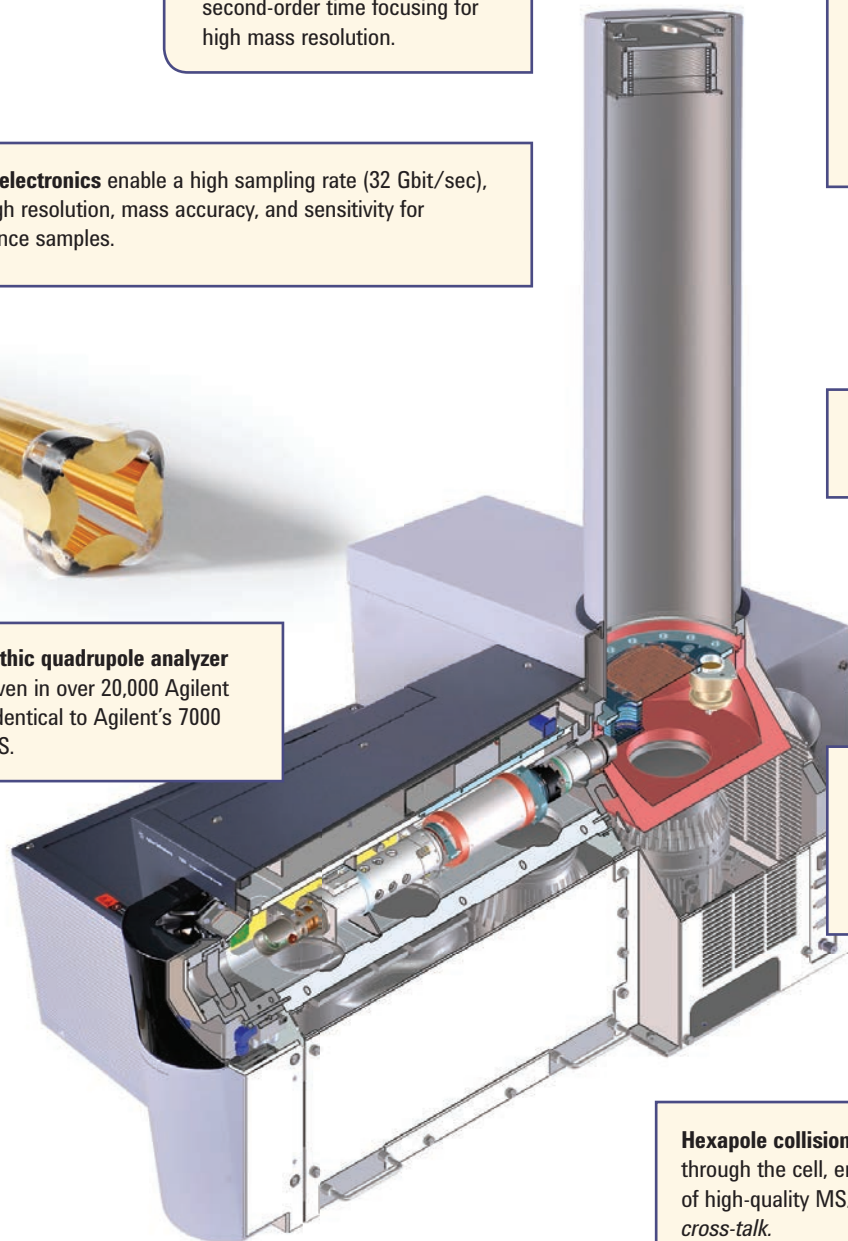


Hot, quartz, monolithic quadrupole analyzer is performance-proven in over 20,000 Agilent MS systems, and identical to Agilent's 7000 Quadrupole MS/MS.

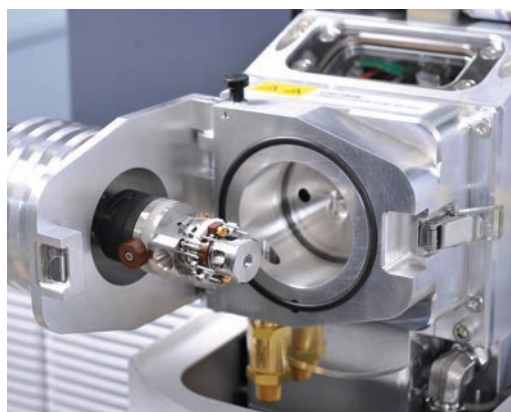
Hybrid channel plate photomultiplier ion detector delivers single ion detection sensitivity, excellent time resolution, and a large linear range.

Hexapole collision cell accelerates ions through the cell, enabling faster generation of high-quality MS/MS spectra *without cross-talk*.

Three turbomolecular pumps, including two single-stage pumps and one split-flow pump for the source and quadrupole analyzer, create an optimal vacuum for every region of the analyzer assembly.

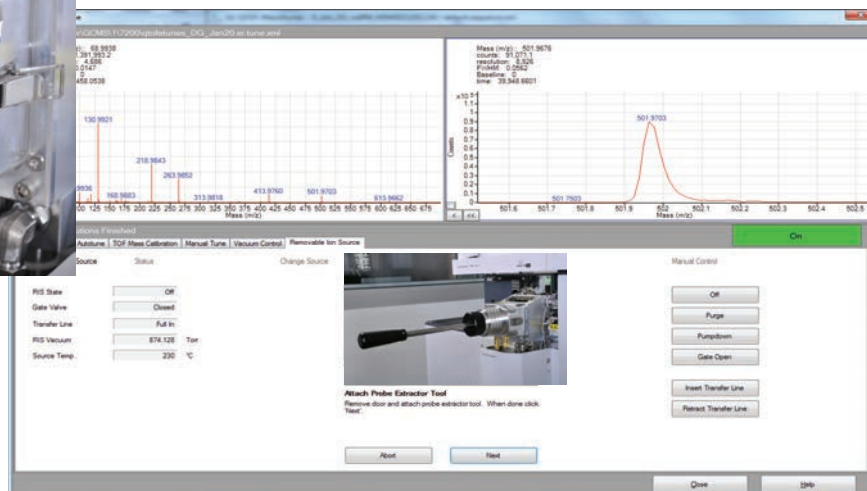


Excellent linearity and mass accuracy enable analysis of targets, non-targets, and unknowns



NEW removable ion source (RIS) lets you change the complete ion source – including repeller, ion volume, extraction lens, and dual filaments – in about 30 minutes without venting.

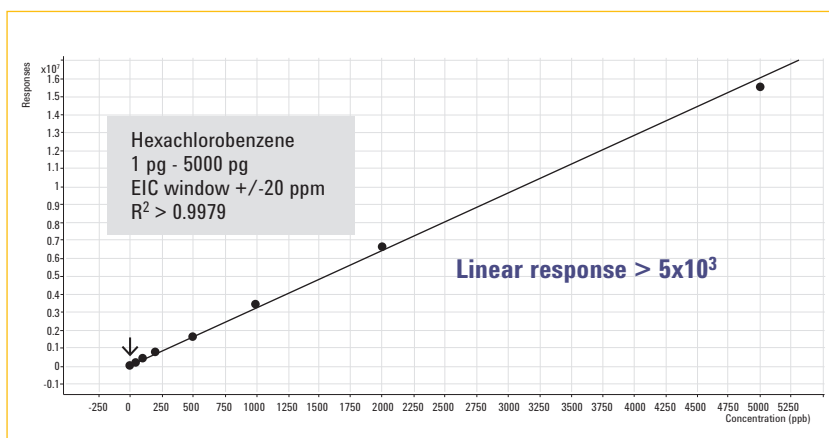
User-friendly videos and software guide you through all the necessary steps for source removal and installation – making the process safe and error free.



pg on-column	mass error, ppm	
	2-formyl thiophene	2-acetyl thiazole
1	-3.57	-0.79
2	-4.46	-0.79
5	-2.68	-0.79
10	-2.68	0.79
20	-2.68	0.00
50	-0.89	1.57
100	0.00	1.57
200	-1.79	1.57
500	2.68	1.57
1000	1.79	-1.57
Average	-1.43	0.31

New Internal Reference Mass (IRM) is a proprietary system that locks the mass axis for each scan to a calibrant compound. IRM ensures low-ppm mass accuracy under the most complex chromatographic conditions.

Analog-to-digital (ADC) Detector: The 4 GHz sampling rate of ADC electronics enables exceptional linearity in high-resolution mode. For an even wider linear range, dual-gain amplifiers simultaneously process detector signals through both low-gain and high-gain channels, extending the dynamic range up to 10^5 .



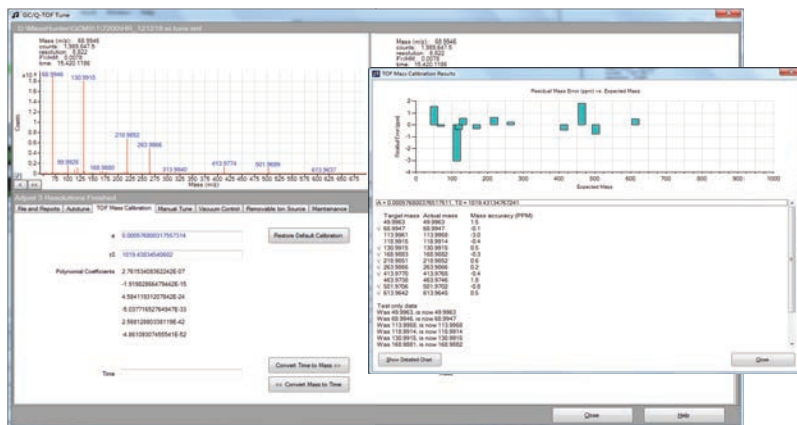
To learn more about the capabilities of the Agilent 7200 Q-TOF for GC/MS, visit www.agilent.com/chem/GCMS_QTOF

Results *prove* how GC/Q-TOF technology makes exceptional qualitative and quantitative analysis *real* – and *easy*

With its low-ppm mass accuracy and high resolving power, Agilent's 7200 Q-TOF for GC/MS can help you reduce uncertainty, minimize false positives, confirm database search results, and generate molecular formulas for unknowns.

Fast, trouble-free setup

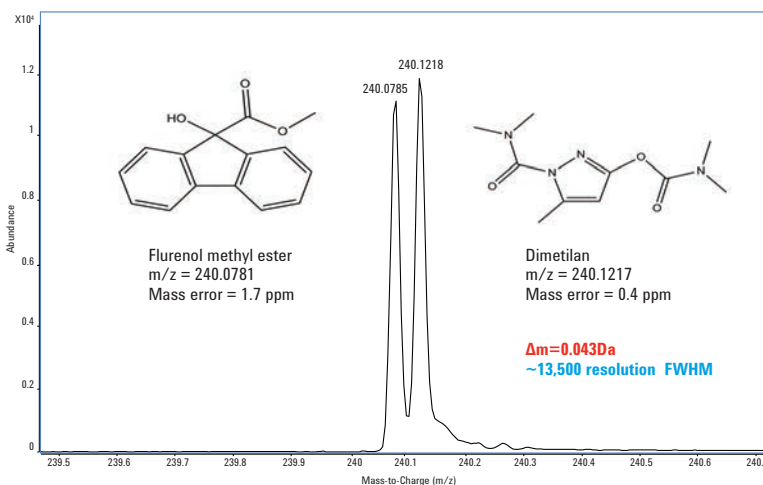
Our automated acquisition software guides you through each step of the tuning and mass calibration process for precise high resolution and accurate mass operation.



Superior resolving power is essential for confident analyte identification

Resolution of 13,500 (FWHM) easily resolves two compounds with nominal masses of 240 Da, whose exact masses differ by only 0.0436 Da.

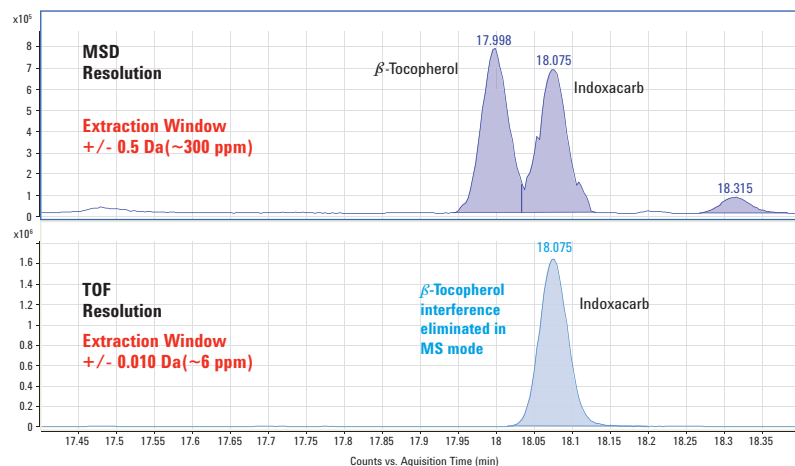
Superior resolving power is indispensable in confidently identifying analytes in complex matrices.



Accurate mass allows for efficient elimination of matrix interferences

Using an extraction window of 0.010 Da, the fragment ion of the target analyte, Indoxacarb (150.01195 Da), can easily be separated from the matrix interference ion of β -Tocopherol (150.06839 Da). This facilitates reliable quantitative analysis.

When more selectivity is needed, MS/MS with accurate mass can help separate target analytes and matrix interferences further.

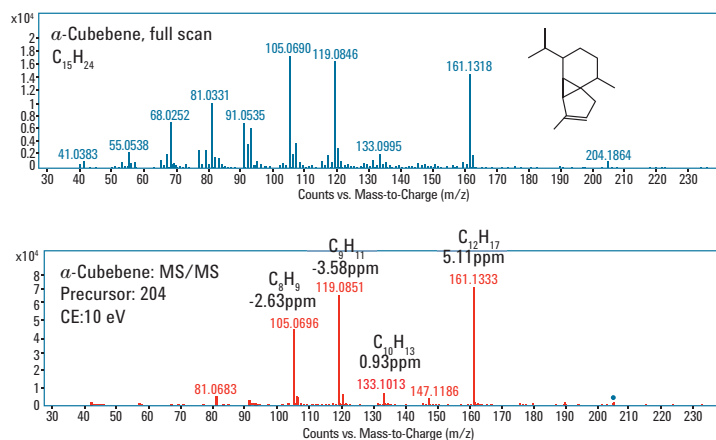


Unambiguous structural clarification and target confirmation

The identity of target and unknown compounds can be confirmed using a variety of techniques.

- Conducting an EI spectra library search
- Determining the PCI molecular ion
- Performing MS/MS dissociation of multiple precursor ions to document fragmentation pathways – *an Agilent exclusive*
- Calculating molecular formulas for all ions from accurate mass data

For very complex separations, such as the α -Cubebene example at right, MS/MS selectivity also generates a simplified spectrum to facilitate structure elucidation.



List of hits after deconvolution and library searching

Component RT	Is Primary Hit	Compound Name	Match Factor	CAS#	Formula
12.6787	<input checked="" type="checkbox"/>	5H-Ter...			
12.9386	<input checked="" type="checkbox"/>	Sulfur			
13.0013	<input checked="" type="checkbox"/>	Sulfur			
13.2311	<input checked="" type="checkbox"/>	alpha-Lindane			
13.4155	<input checked="" type="checkbox"/>	Hexan...			
13.7426	<input checked="" type="checkbox"/>	Arsole, 2,2-dimethyl-1,3-dioxolane			
13.8088	<input checked="" type="checkbox"/>	Dimethoate	56.2	60-51-5	CSH12NO3PS2
14.1361	<input checked="" type="checkbox"/>	2-Propenoic acid, 2-methyl-, octyl...	68.4	2157-01-9	C12H22O2
14.3734	<input checked="" type="checkbox"/>	alpha-Lindane	65.0	319-84-6	C8H16O6
14.6363	<input checked="" type="checkbox"/>	alpha-Lindane	52.0	319-84-6	C8H16O6
15.0550	<input checked="" type="checkbox"/>	2,3-Dimethyl-5-(2,6,10-dimethylun...	66.3	166773-96-4	C20H36O
15.1762	<input checked="" type="checkbox"/>	3-Methylcotechol, decanoate	67.6	1000352-78-9	C11H12O4
15.3821	<input checked="" type="checkbox"/>	2-Propenoic acid, 2-methyl-, octyl...	64.8	2157-01-9	C12H22O2
15.6336	<input checked="" type="checkbox"/>	Diazinone	59.9	333-41-5	C12H21N2O3PS
15.9195	<input checked="" type="checkbox"/>	3,5-diket-6-ethyl-4-hydroxyacetoph...	63.9	14035-33-7	C16H24O2
16.3135	<input checked="" type="checkbox"/>	3-Nonyne	64.2	20184-89-8	C8H16
16.7578	<input checked="" type="checkbox"/>	Cyclopentanemethanol, 3-methyl...	53.4	74793-20-7	C7H12O
17.3253	<input checked="" type="checkbox"/>	1,5-Hexadien-4-one, 3,3,6-trimet...	57.9	546-49-6	C10H16O
17.9993	<input checked="" type="checkbox"/>	Methanone, (3-amino-5-chloro-2...	61.4	313400-50-9	C15H10ON2O2
18.5982	<input checked="" type="checkbox"/>	Romef	65.7	289-84-3	C8H8O3O3PS
18.8971	<input checked="" type="checkbox"/>	2,2-Dimethylpropyl 2,2-dimethyl...	53.6	82360-14-3	C10H20O5S2
19.4124	<input checked="" type="checkbox"/>	Butane, 2-methoxy-2-methyl-	73.1	994-05-8	C8H14O
20.6552	<input checked="" type="checkbox"/>	N,N-Di-Traoctylhydroxylamine	55.0	17720-63-7	C8H18NO4
24.4732	<input checked="" type="checkbox"/>	3-Amino-2,4-dimethylpentane	67.8	4083-87-2	C7H17N
24.8776	<input checked="" type="checkbox"/>	p,p'-DDE	62.2	72-95-9	C14H8Cl4
25.1149	<input checked="" type="checkbox"/>	Propanoic acid, 2-methyl-, anhydr...	75.2	97-72-3	C8H14O3
25.2403	<input checked="" type="checkbox"/>	2,2-Dimethylpropyl 2,2-dimethyl...	54.1	78607-80-4	C10H20O5S2
25.7613	<input checked="" type="checkbox"/>	2,2-Dimethylpropyl 2,2-dimethyl...	52.6	78607-80-4	C10H20O5S2
26.1256	<input checked="" type="checkbox"/>	Furan, 2-methoxy-	58.1	25414-22-6	C5H6O2
26.2806	<input checked="" type="checkbox"/>	4-Fluorobenzylamine, N,N-diunde...	52.5	1000110-48-8	C28H52FN
26.4086	<input checked="" type="checkbox"/>	1,2-Bis(2-chlorophenyl)-1,2-bis(3...	72.4	1000137-94-8	C26H18Cl4
26.4422	<input checked="" type="checkbox"/>	trans-Nonachlor	59.0	38765-80-5	C10H8Cl8
26.8768	<input checked="" type="checkbox"/>	Heptane, 3,3,5-trimethyl-	65.4	7154-00-5	C10H22
27.0193	<input checked="" type="checkbox"/>	Subprofas	69.0	35400-43-2	C12H19O2P6S3
27.2829	<input checked="" type="checkbox"/>	Carbophenothion	54.3	786-19-6	C11H16O3O2P3S3
27.8981	<input checked="" type="checkbox"/>	Oxalic acid, dimooxentyl ester	67.4	1000309-72-7	C12H22O4

TIC and component chromatogram for hits

Deconvoluted spectrum of alpha-Lindane

TIC and extracted ions of alpha-Lindane

Molecular Structure

C1=CC=C(C=C1)C2=CC=CC=C2C3=CC=CC=C3C4=CC=CC=C4

High-speed spectral acquisition is another fundamental advantage of TOF MS. Rates as fast as 50 Hz allow you to efficiently resolve a substantial number of components by chromatographic deconvolution with MassHunter's Unknowns Analysis tool.

To learn more about the capabilities of the Agilent 7200 Q-TOF for GC/MS, visit www.agilent.com/chem/GCMS_QTOF

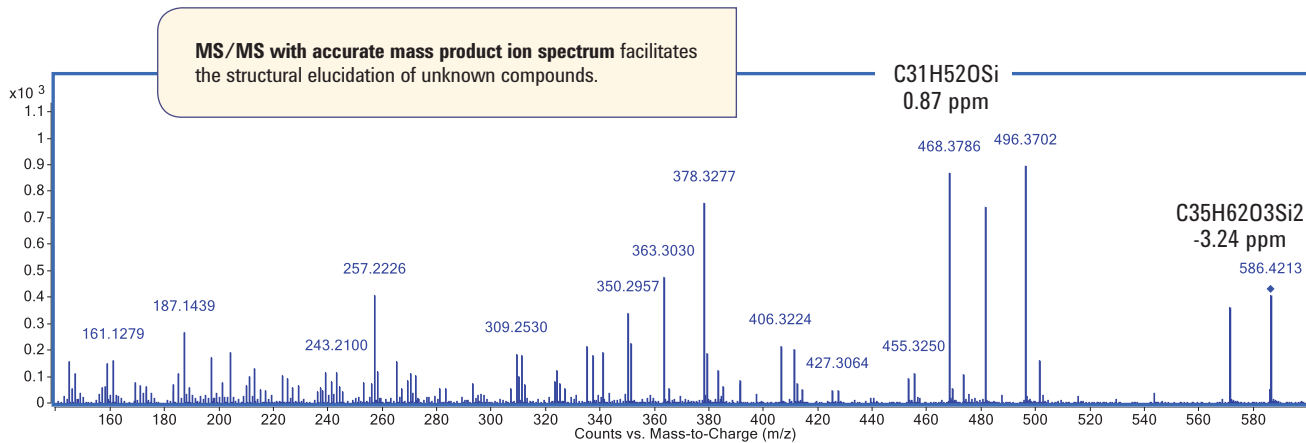
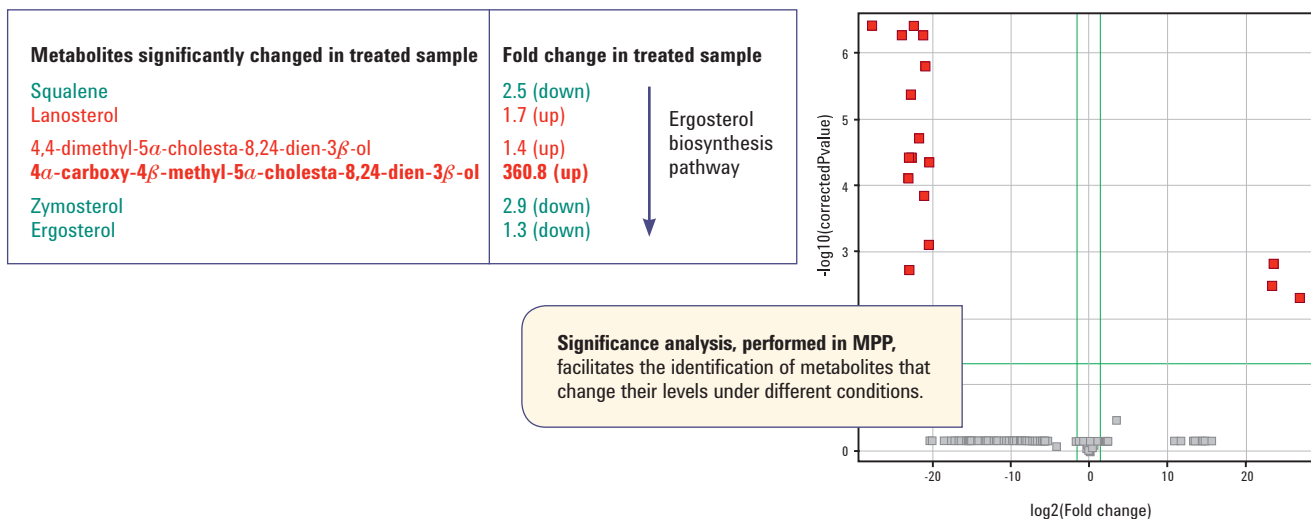
Analyze and visualize changes in cellular function

Metabolomics is a powerful tool in understanding metabolic changes under distinct conditions. Complex metabolomic studies will take advantage of high full spectrum sensitivity and mass accuracy of GC/Q-TOF, as well as its MS/MS capability to assist in structural elucidation of unknown metabolites. The extended dynamic range of the 7200 GC/Q-TOF will allow for accurate and simultaneous quantification of a broad range of metabolites present in a cell.

In one simple experiment, Agilent's 7200 Q-TOF for GC/MS provided the accurate mass information, excellent sensitivity

in full scan mode, and dynamic range essential for identifying and quantifying all pathway intermediates of interest, thus unambiguously revealing the step in the biochemical pathway affected in a treated sample.

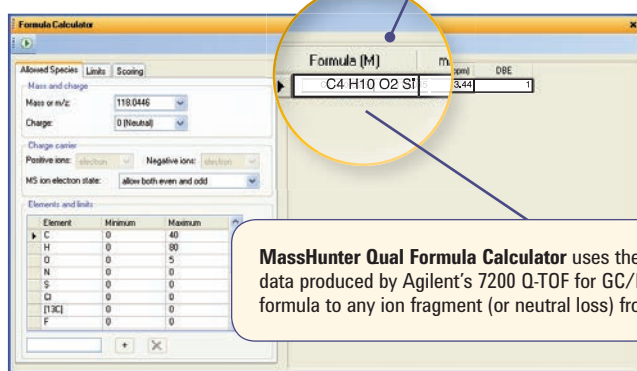
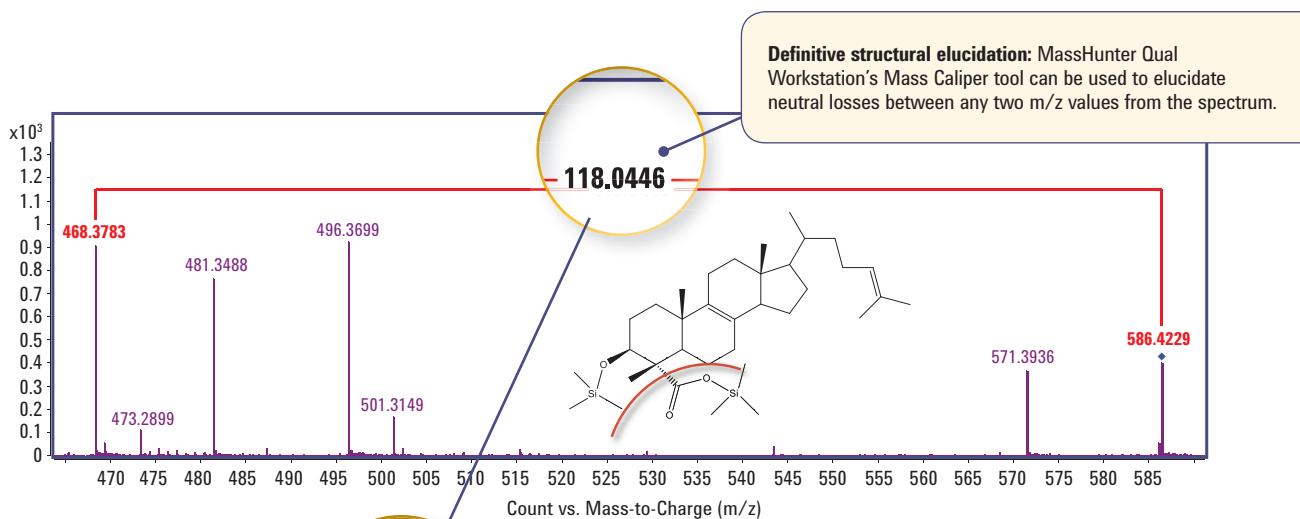
Mass Profiler Professional (MPP) was used for statistical data evaluation. The analysis included data filtering, baseline correction, and significance testing. The software's visualization tools were also indispensable for data interpretation.



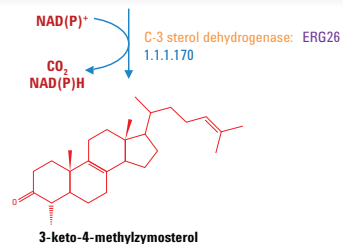
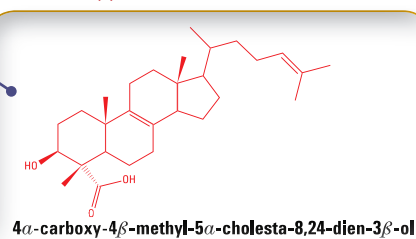
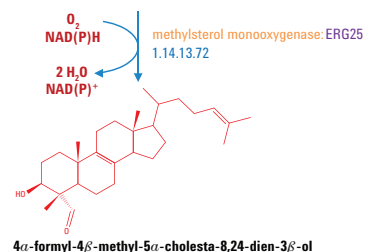
Confirm the proposed structure of a metabolite based on accurate mass product ion spectrum

Metabolomic studies often recognize a significant number of non-targets and unknown metabolites as potentially playing a critical role in biological interpretation of the data. Therefore, the structure of these important metabolites has to be confirmed or elucidated.

The pairing of Agilent's 7200 Q-TOF for GC/MS with MassHunter Workstation software is ideal for this type of study.



MassHunter Qual Formula Calculator uses the accurate mass data produced by Agilent's 7200 Q-TOF for GC/MS to assign a formula to any ion fragment (or neutral loss) from the spectrum.



Acknowledgements:

This application is based upon work supported by Manhong Wu¹, Robert St. Onge², Sundari Suresh², Ronald Davis² and Gary Peltz¹

¹Department of Anesthesia, School of Medicine, Stanford University

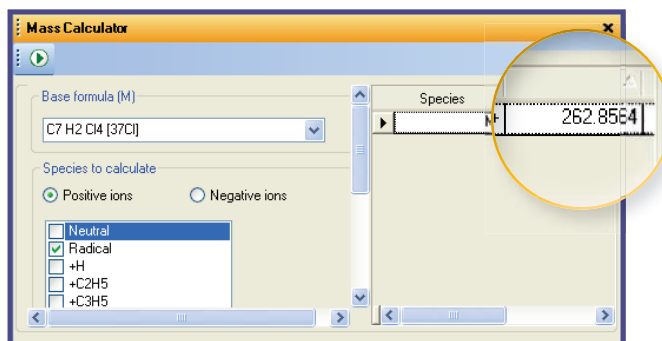
²Biochemistry-Genome Center, Stanford University

To learn more about the capabilities of the Agilent 7200 Q-TOF for GC/MS, visit www.agilent.com/chem/GCMS_QTOF

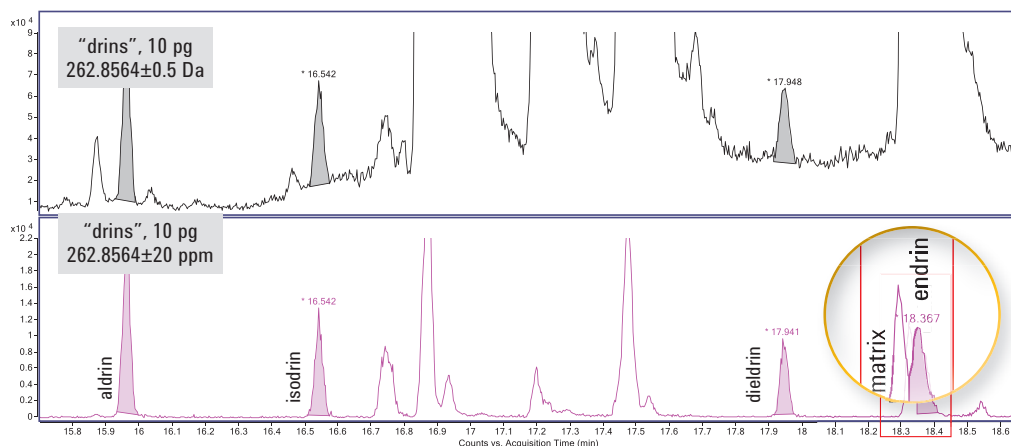
Perform confident screening and identification of contaminants in challenging matrices

Comprehensive food safety screening involves both the quantitative analysis of frequently occurring contaminants and the qualitative analysis of non-target compounds and unknowns.

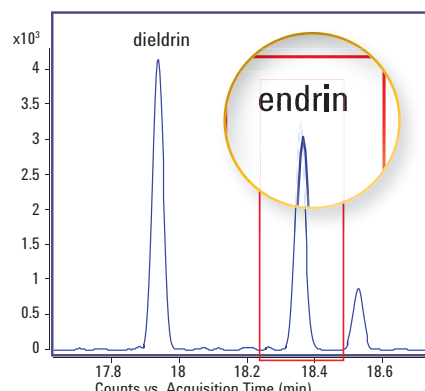
Success often depends upon high sensitivity in full scan mode as well as accurate mass information for target confirmation or unknowns analysis.



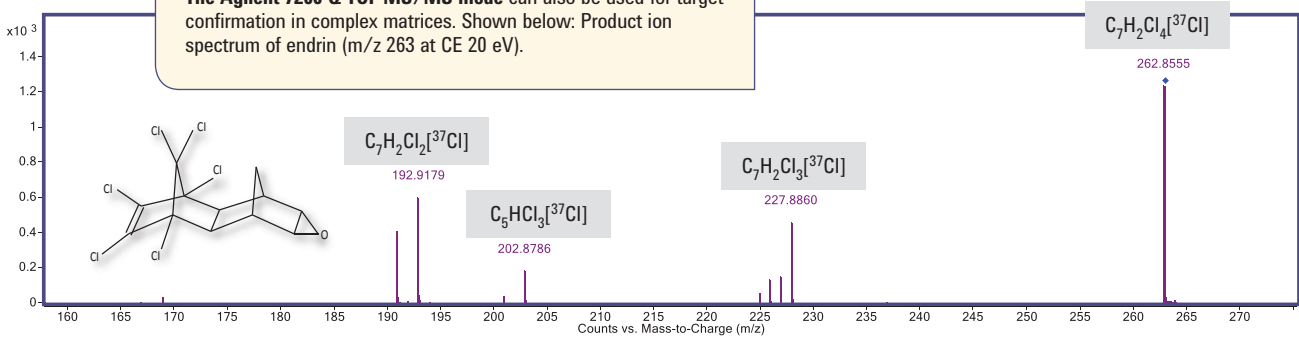
MassHunter Qual Mass Calculator is used to obtain the theoretical masses of the target compounds in both EI and CI modes. Theoretical mass can be used for further qualitative evaluation and quantitative analysis.



Ultimate selectivity in MS/MS mode: Agilent 7200 Q-TOF for GC/MS easily resolves targets from coeluting matrix interferences when high resolution/accurate mass alone is not enough.



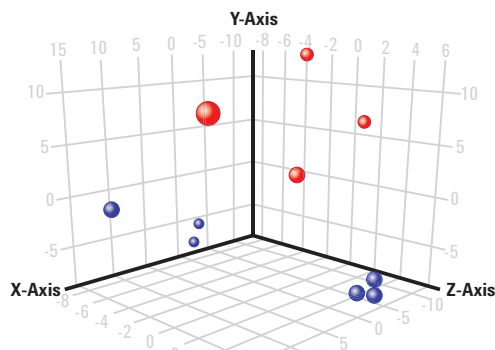
The Agilent 7200 Q-TOF MS/MS mode can also be used for target confirmation in complex matrices. Shown below: Product ion spectrum of endrin (m/z 263 at CE 20 eV).



Evaluation of extra virgin olive oil

To construct a GC/Q-TOF data-based model that could predict whether an olive oil would pass the extra virgin sensory test, Mass Profiler Professional (MPP) software was used. The model utilized five specific compounds to predict the sensory test's outcome.

In addition to the EI spectral data, positive CI accurate mass spectra were necessary to confirm a molecular ion for the compounds used in the model.

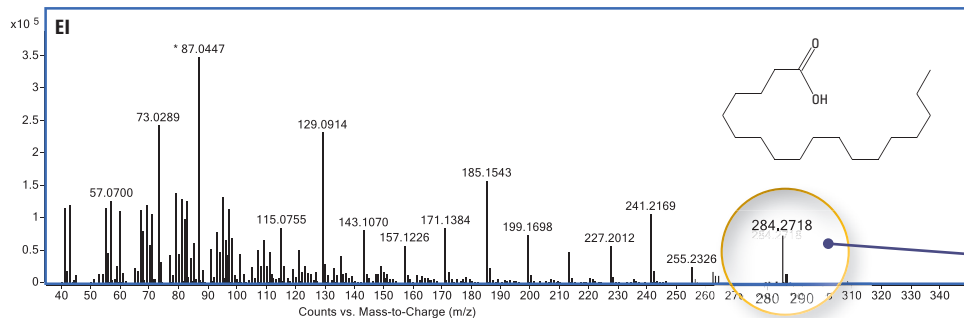
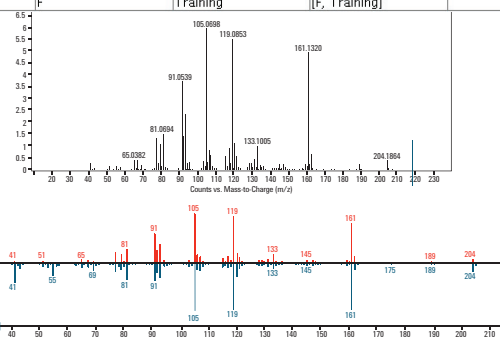


Principal Component Analysis (PCA) in MPP, shows how the data clusters. The blue samples passed the sensory test, while the red samples failed.

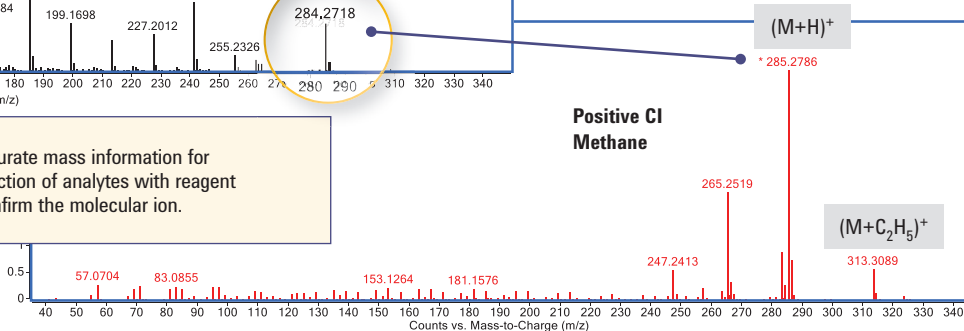
The MPP Prediction Model correctly predicted the pass/fail status of all samples. The samples not used for building the prediction model are listed with the training variable set as "None."

Identifier	Grade	Training	Predicted(Class Pre...	Confidence
PAC1-El-1: Ig2	F	None	[F, Training]	1.000
ESC2-El-1: Ig2	P	Training	[P, Training]	1.000
ESC1-El-1: Ig2	P	Training	[P, Training]	1.000
SAC1-El-1: Ig2	F	None	[F, Training]	1.000
RFC2-El-1: Ig2	P	None	[P, Training]	1.000
RSA2-El-1: Ig2	P	None	[P, Training]	1.000
CSC1-El-1: Ig2	F	Training	[F, Training]	1.000
RSA1-El-1: Ig2	P	Training	[P, Training]	1.000
EFC1-El-1: Ig2	P	None	[P, Training]	1.000
F5W2-El-1: Ig2	F	Training	[F, Training]	1.000

The Agilent 7200 Q-TOF for GC/MS generates spectra that can be searched against the commercially available nominal mass EI spectral libraries.



Positive CI spectral data provided additional accurate mass information for molecular ions. Adduct ions formed by the interaction of analytes with reagent gas can easily be detected, further helping to confirm the molecular ion.



Reference:

Analysis of Medium Volatility Sulfur Compounds in Coffee Using Agilent GC/Q-TOF: Pub. No. 5990-9076EN

Olive Oil Characterization using Agilent GC/Q-TOF MS and Mass Profiler Professional Software: Pub No. 5991-0106EN

To learn more about the capabilities of the Agilent 7200 Q-TOF for GC/MS, visit www.agilent.com/chem/GCMS_QTOF

Carry out reliable screening for target compounds, and identify unknowns

One of the greatest environmental analysis challenges lies in identifying and quantitating large numbers of compounds, many of which are present at trace levels in complex matrices. For this type of application, the following features are essential:

- Highly sensitive accurate mass full spectral acquisition
- A wide dynamic range
- Easily automated qualitative analysis
- Batch processing for target compounds

The "Find by Formula" tool in MassHunter Qual lets you *simultaneously* search for all compounds corresponding to any formula from the given list.

Compound Method	Name	RT	MI	Final Conc.	Mass Accuracy	Mass Match Score	Mass Abundance Score	Mass Accuracy Score	Mass Spacing Score	Ref. Library Match Score	Qualifier 1 Results	Qualifier 2 Results	
	fluorene	8.979	207.4383	1.6953	-1.6953	98.7	98.5	99.4	97.7	94.3	77.3	17.8	
	naphthalene	5.048	217.3482	1.6091	1.6091	47.5	0.0	99.7	0.0	0.0	3.7015	4.6217	
	acenaphthylene	7.268	205.4632	0.6839	0.6839	75.7	16.2	99.2	100.0	57.2	21.4	2.8157	17.0
	acenaphthylene	7.642	159.7733	-0.0549	-0.0549	89.9	65.5	99.7	99.7	90.4	76.5	1.0431	54.1
	phenanthrene	12.520	206.2585	0.7297	0.7297	74.6	11.3	99.8	100.0	79.4	22.3	0.3113	15.2
	anthracene	12.753	205.9017	1.2650	1.2650	73.9	9.5	99.5	100.0	82.4	21.5	0.6437	15.0

Acenaphthylene
0.2 pg - 1000 pg
 $R^2 > 0.999$

Outlier detection tools in MassHunter Quant Workstation facilitate the survey of large data sets.

Reference:

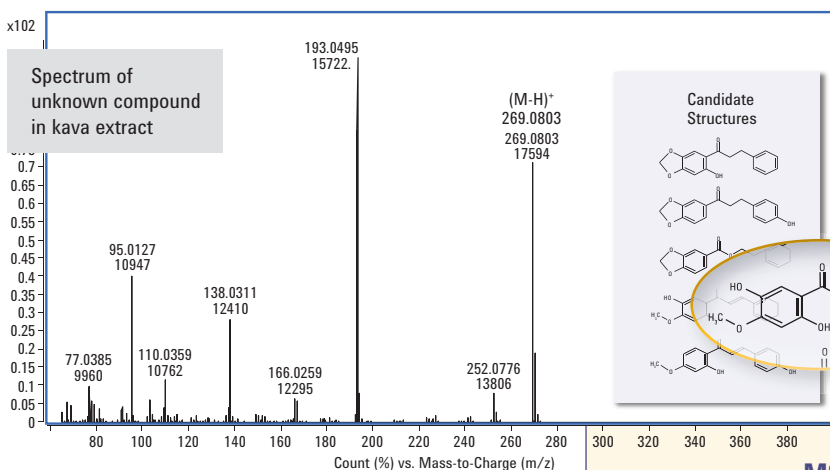
Analysis of Biomarkers in Crude Oil Using Agilent 7200 Q-TOF for GC/MS:
Pub. No. 5990-9477EN

Combine accurate mass and product ion spectra to elucidate the structure of unknown compounds

Herbal extracts contain a large number of compounds that need to be identified; however, commercial EI spectral libraries do not always contain mass spectral data for compounds of interest. In these instances, the accurate mass product ion

spectra generated by the Agilent 7200 Q-TOF for GC/MS can be invaluable for establishing relationships between fragment ions, thus assisting structure correlation.

Identification of unknowns in kava extract



Of the 5 candidate structures, only one fits the losses identified by MS/MS experiments on multiple precursor ions.

Reliable peak identification and compositional data capabilities make the Agilent 7200 Q-TOF for GC/MS ideal for these additional applications

Food Testing and Flavors

- Natural products

Energy/Chemicals

- Quality control
- Detecting trace analytes in petroleum products

Forensic/Toxicology

- Doping control
- Post-mortem screening, discovery and confirmation

MS/MS experimental measurements

	<i>m/z</i> (experimental)	Formula	Error (ppm)	Score
(M-H) ⁺	269.0803	C ₁₆ H ₁₃ O ₄	-1.99	80.7
(M-C ₆ H ₅) ⁺	193.0494	C ₁₀ H ₉ O ₄	-0.18	96.7
(M-CH=CH-C ₆ H ₅) ⁺	167.0334	C ₈ H ₇ O ₄	-2.9	N/A
(M-CH ₂ =CH-C ₆ H ₅) ⁺	166.0259	C ₈ H ₆ O ₄	-0.96	N/A
-CO	138.0311	C ₇ H ₆ O ₃	-0.33	98.1
-CO	110.0359	C ₆ H ₆ O ₂	-3.01	N/A
-CH ₃	95.0127	C ₅ H ₃ O ₂	-0.59	99.5

Accurate mass information of the product ion spectrum helps eliminate any ambiguity between different neutral losses that have the same nominal mass.

To learn more about the capabilities of the Agilent 7200 Q-TOF for GC/MS, visit www.agilent.com/chem/GCMS_QTOF

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