

Gas Chromatograph Mass Spectrometer







GCMS-TQ8040 with Smart Technologies

Smart Performance, Smart Productivity, Smart Operation

Finally, a triple quadrupole GCMS *Smart* enough for everyday use in your laboratory.

The Shimadzu GCMS-TQ8040 is the first triple quadrupole with Smart Performance

for low detection limits and Scan/MRM, Smart Productivity for high efficiency sample throughput,

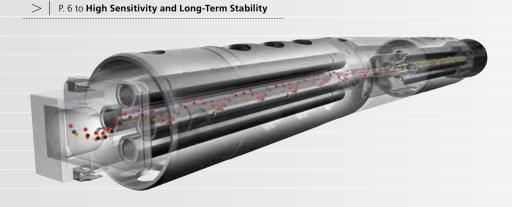
and Smart Operation for quick and easy method development.

These three smart technologies contribute to Smart MRM, and provide the most accurate,

cost-effective, and easy-to-use triple quadrupole GCMS you have ever imagined.

Smart Performance

The ion source, incorporating a highly efficient collision cell, enables high-sensitivity and long-term stable analyses. In addition, with high-speed scan control technology called Advanced Scanning Speed Protocol (ASSP), multiple analysis modes can be measured simultaneously, enabling a great deal of information to be obtained in a single analysis.



>

Smart Productivity

Simultaneous multi-component analysis is now possible for hundreds of target compounds, dramatically improving productivity. Smart MRM produces GC-MS/MS methods with up to 32,768 transitions in a single run.

> P. 8 to Smart Productivity





Performance Productivity Operation

Smart Operation

GC-MS/MS analysis requires multiple settings that can be confusing to the average operator. With *Smart MRM*, the GCMS-TQ8040 software sets the analytical conditions automatically, making method development painless, fast, and easy.

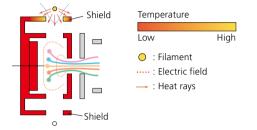


Smart Performance

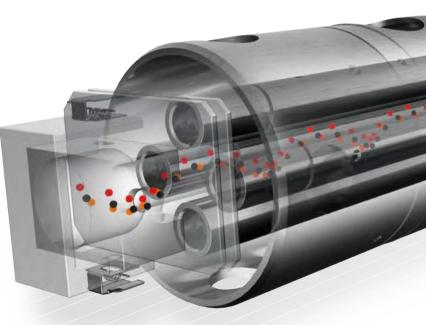
High Sensitivity and Long-Term Stability

Ion Source Featuring High Sensitivity and Long-Term Stability

The filament and the ion source box have been separated, which reduces the impact of the filament potential on the interior of the ion source. In addition, a shield is provided to block radiant heat generated by the filament, achieving a uniform temperature inside

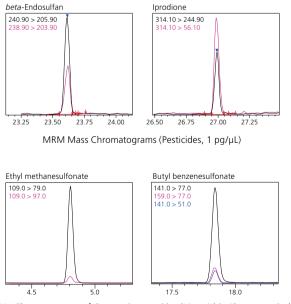


the ion source box. Thus, active spots inside the ion source are not prone to occur, enabling high-sensitivity analysis with long-term stability. (Patent: US7939810)



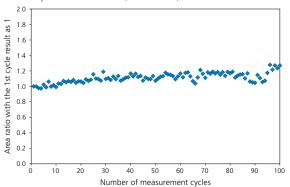
High-Performance Quadrupole Mass Filter

A high-accuracy mass filter equipped with a pre-rod, as well as patented electric field control technology, result in high-accuracy mass separation performance. The pre-rods also minimize contamination of the quadrupole, eliminating the need for quadrupole maintenance.



MRM Chromatograms of Genotoxic Impurities (10 pg/L) in Pharmaceuticals

Response of a Pesticide (Fenitrothion) in a Sesame Extract



OFF-AXIS Ion Optics

Lower detection limits are achieved by OFF-AXIS Ion Optics (Patent Pending). Meta-stable and neutral ions are removed without sacrificing sensitivity. Helium buffer gas is not required in the CID cell.

High-Efficiency Collision Cell UFsweeper

Shimadzu's proprietary UFsweeper technology achieves high-speed MRM analysis at speeds up to 800 transitions per second. It sweeps residual ions from the collision cell to provide high-efficiency CID and fast ion transport. Rapid ion removal minimizes cross-talk and enables trace analysis (patent pending).



15.0

15.1

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15.3

Analysis of Residual Pesticides (Isoprothiolane 1 pg/µL)

Sensitivity and Repeatability in Single GC/MS Mode

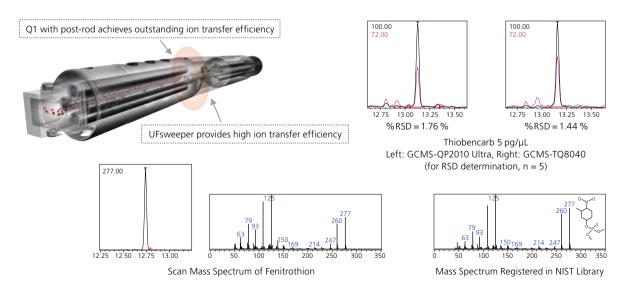
The high-efficiency ion source provides the foundation of an ion generation and transmission system, which creates and then delivers ions to the detector, resulting in a GC/MS with the maximum possible sensitivity and repeatability. These features are not realized just for MRM measurements by GC-MS/MS, but also for scan and SIM measurements in single quadrupole modes, even with the most reactive compounds.

15.3

SIM

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15.1 15.2

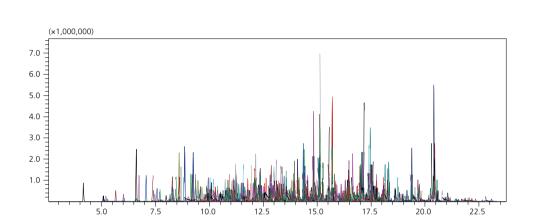


Innovative Technologies that Improve Accuracy and Throughput

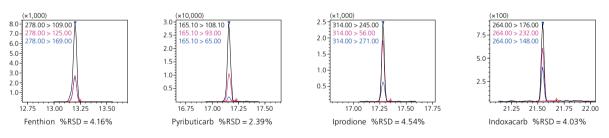
UFMS in the Multiple Reaction Mode can acquire over 800 transitions per second and over 32,000 transitions in a single analysis. The *Smart MRM* technology automatically adjusts the analytical dwell time for each transition, only acquiring data during peak elution, to fully optimize sensitivity. For example, analysis of more than 400 pesticides that used to require two or three methods can now be accomplished in a single acquisition method created by *Smart MRM*, significantly increasing laboratory throughput. The UFMS technology guarantees a minimum of ten data points across each peak for optimum sensitivity and repeatability. Highly accurate, low-level detection of multiple components in complex matrices is finally possible by UFMS and **Smart MRM**.

P. 11 to Smart MRM

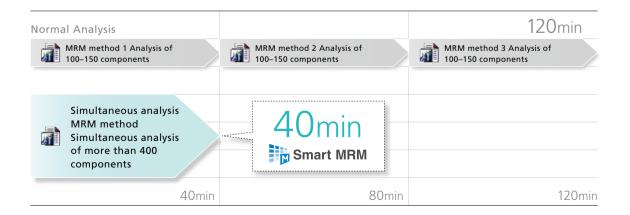
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Simultaneous Analysis of 439 Pesticides Using UFMS and Smart MRM



Mass Chromatogram and %RSD (5 $pg/\mu L)$



27 Reduce Analysis Costs and Minimize Downtime

If simultaneous, multi-component analysis can be performed in 1/2 to 1/3 the time of existing systems, then two to three times the number of samples can be analyzed in the same period of time, and return on investment is improved. In addition, the frequency of maintenance, such as replacing glass liners and columns, is reduced, thereby minimizing downtime.

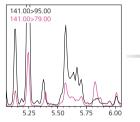


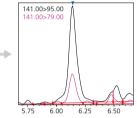
127 Twin Line MS System Eliminates the Need to Vent the MS

The GCMS-TQ8040 is capable of accepting installation of two narrow-bore capillary columns into the MS simultaneously. This allows you to switch applications without venting the MS.

Simply decide which column is best for your analysis and choose the associated injection port.







Column 2 (SH-Rtx-200 MS)

Column 1 (SH-Rxi-5Sil MS)

Methamidophos in Ginger (10 pg/µL), Analyzed on Two Dissimilar Columns Using **Smart MRM**

CID gas control is a method parameter, allowing acquisition of GC-MS and GC-MS/MS data in the same batch. By coupling this with the Twin Line MS System, analysis of phenols by SIM and analysis of pesticides by MRM are possible in a single batch without venting the MS.

i i i	Method File	Data File	
1	Phenols_SIM.qgm	DATA_01.qgd	
2	Phenols_SIM.qgm	DATA_02.qgd	
3	Phenols_SIM.qgm	DATA_03.qgd	GC-MS (CID gas–Off)
4	Pesticide_MRM.qgm	DATA_04.qgd	MRM
5	Pesticide_MRM.qgm	DATA_05.qgd	GC-MS/MS (CID gas–On)

Run SQ and TQ Methods in a Single Sequence

*) The Twin Line MS System requires an optional installation kit and is limited to certain column dimensions.

Simplified GC-MS/MS method development

In order to create an MRM analysis method, complex parameter settings are required,

such as for the optimum transitions and collision energies.

Smart MRM makes method development quick and easy.

Whether starting from scratch to optimize transitions and collision energies for new compounds,

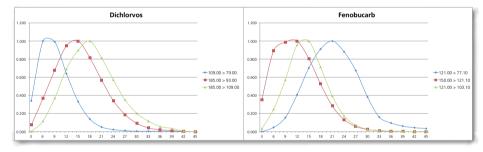
or starting from an MRM database of known target analytes to build a custom MRM method,

Smart MRM takes the stress and difficulty out of method development.

MRM Optimization Tool

Optimize MRM Transitions Automatically

Determining and optimizing MRM transitions for new compounds can require significant development time. The "MRM Optimization Tool" automates the process by collecting product ion scan data and finding the optimum collision energy for each transition. Once established, the transitions are registered to one of the Shimadzu "Smart Database" files, and the MRM or Scan/MRM methods are created using **Smart MRM**.



Smart Database

Compounds and Optimized Transitions

The Shimadzu "Smart Database" is a database of related compounds (e.g. pesticides, drugs, metabolites, etc.) with optimized transitions and collision energies, CAS registry numbers, and Retention Indices (RI). The user can select from hundreds of pre-registered compounds in one of the "Smart Database" files, or add their own optimized transitions. The user selects the compounds to be analyzed, and **Smart MRM** builds the MRM or Scan/MRM acquisition method from the "Smart Database" with the push of a button. In addition to MRM information, the database file can contain Scan and SIM ion information, mass spectra and calibration curve information from the internal standard method. This allows users to easily create their own database.

Serial#	Туре	Acq. Mode	ISTD Group	Level1 Conc (IS)	Method No.	Compound Name (E)	Ret. Index 1	Cas#		lon1		
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1	Target	MRM			1	Aldicarb deg.	881	0 - 00 - 0	Т	115.1>68.0	8	100.00
2	Target	MRM	0		1	DCIP	1058	108 - 60 - 1	Т	121.1>45.0	4	100.00
3	Target	MRM	1		1	Aldoxycarb deg.	1135	0-00-0	Т	80.0>65.0	6	100.00
4	Target	MRM	1		1	Chlofentezine deg.	1182	0 - 00 - 0	т	137.0>102.0	14	100.00
5	Target	MRM	<u>[</u>]		1	Hymexazol	1196	10004 - 44 - 1	Т	99.0>71.0	8	100.00
6	Target	MRM	Ĩ.		1	Methamidophos	1236	10265 - 92 - 6	Т	141.0>95.0	8	100.00
7	Target	MRM			1	Dichlorvos	1253	62 - 73 - 7	т	109.0>79.0	8	100.00
8	Target	MRM			1	Nereistoxin	1283	0 - 00 - 0	т	149.1>71.1	8	100.00
9	Target	MRM			1	Allidochlor	1296	93 - 71 - 0	Т	132.1>56.0	8	100.00
10	Target	MRM			1	Dichlobenil	1358	1194 - 65 - 6	Т	170.9>136.0	14	100.00
11	Target	MRM			1	EPTC	1364	759 - 94 - 4	т	189.1>128.1	4	100.00
12	Target	MRM		· · · · ·	1	Biphenyl	1394	92 - 52 - 4	Т	154.1>128.1	22	100.00
13	Target	MRM			1	Propamocarb	1398	24579 - 73 - 5	Т	188.2>72.0	4	100.00

Smart MRM

Smart MRM

Automatic Method Creation

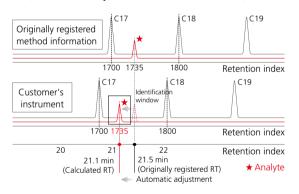
The Smart MRM technology automatically creates methods with measurement times optimized for each component based on the Smart database. The Automatic Adjustment of Retention Time (AART) function incorporated in the system estimates retention times with high accuracy. When creating methods for simultaneous multicomponent analysis, the complicated process of configuring measurement parameters made it difficult to prepare appropriate methods. By using the Smart MRM function, however, it is possible to automatically create methods in which data are acquired with high sensitivity only during the elution time of the target components. In addition to MRM methods, SIM methods can be created.

MS lable Pa

Create	Method Fa	•	Instrument	Type	TO fores . Lang									- MRM,SIM Parameter	
	Pame	witter		-										Loop Time (MRM, SIM)	0.30 sec
	Ret	Index for AART	Ret Index											Required Processing Time : R.T ±	0.30 min
		tane data file	0.0084	Action Calaridina	CatabacePedicit .										and the second sec
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-	-										MRM	Transition	-	and the second	
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2	Tavget	MRM		. T.	DCIP	1068	10/0	1063		108-50-1	T.	121.1>45.0	4	Scan Range Start with End Mit	45 - 600.
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		84054			Dictricochyl	1355	1361	1350		1194 - 88 - 8		170.3>158.0	14 3		OK Cancel

Parameter Setting

 Automatic Adjustment of Compound Retention Time (AART) (Automatic Adjustment of Retention Time)



The AART function adjusts the retention times of target components based on linear retention indices (LRI) and the retention times of n-alkanes. The AART function easily adjusts acquisition and processing method parameters simultaneously.

hos ethyl

IGK 264-2

tazaci

Pendimethali Ethychlozate

Penconazole Heptachlor-ex oxy-Chlordane Chlozolinate

(Z)-Pyrifenoi Thiabendazo

n-1.2

Automatic Estimation

of Retention Times

ethametry

Automatic Creation of Analysis Methods

	Compound Name	Acq. Mode	Event Time(sec)	Ch1 m/z	Ch1 CE	Ch2 m/z	Ch2 CE	Ch3 m/z	Ch3 CE
44-14	MGK 264-2	MRM	0.018	164.10>98.00	12.00	111.10>82.00	8.00	164.10>67.00	8.00
44-15	(E)-Chlorfenvinphos	MRM	0.018	323.00>267.00	16.00	267.00>159.00	18.00	267.00>203.00	12.00
44-16	Dimethametryn	MRM	0.018	212.10>122.10	12.00	212.10>94.00	22.00	212.10>71.00	18.00
44-17	Metazachlor	MRM	0.018	209.10>132.10	18.00	133.10>117.10	24.00	211.10>132.10	20.00
45-1	Diphenamid	MRM	0.014	167.10>152.10	20.00	239.10>167.10	8.00	239.10>72.00	16.00
45-2	Fosthiazate-2	MRM	0.014	195.00>103.00	10.00	195.00>60.00	22.00	195.00>139.00	6.00
45-3	Pirimiphos ethyl	MRM	0.014	304.10>168.10	12.00	318.10>166.10	12.00	318.10>182.10	12.00
45-4	Isopropalin	MRM	0.014	280.10>238.10	8.00	280.10>133.10	18.00	280.10>165.10	16.00
45-5	Isodrin	MRM	0.014	192.90>157.00	20.00	192.90>123.00	26.00	262.90>192.90	28.00
45-6	Cyprodinil	MRM	0.014	224.10>208.10	16.00	224.10>197.10	22.00	224.10>131.10	14.00
45-7	Isofenphos-methyl	MRM	0.010	199.00>121.00	14.00	241.10>121.10	22.00	0.00>0.00	0.00
45-8	MGK 264-2	MRM	0.014	164.10>98.00	12.00	111.10>82.00	8.00	164.10>67.00	8.00
45-9	(E)-Chlorfenvinphos	MRM	0.014	323.00>267.00	16.00	267.00>159.00	18.00	267.00>203.00	12.00
45-10	Dimethametryn	MRM	0.014	212.10>122.10	12.00	212.10>94.00	22.00	212.10>71.00	18.00

. Time	200 : Pinnviphos etnyi (3.3 ms)
1.1008	201 . isopropalin (3.3 ms)
Ψ.	202 : Isodrin (3.3 ms)
23.286	203 Cyprodinil (3.3 ms)
23.415	204 Isofenphos-methyl (3.5 ms)
23.436	205 : MGK 264-2 (3.3 ms)
23.458	206 (E)-Chiorfenvinphos (3.3 ms)
23.500	207 : Dimethametryn (2.7 ms)
23.565	208 Metazachlor (2.7 ms)
23.629	209 Pendimethalin (2.7 ms
23.715	210 Ethychiozate (2.7 ms
23.737	211 Anirazine (2.5 ms
23,780	212 Penconazole (2.7 ms
23,801	213 Heptachlor-exo-epoxide (2.7 ms
and the second se	214 : oxy-Chlordane (2.7 ms
23.844	215 Chiozolinate (2.7 ms
23.887	216 (Z)-Pyrifenox (2.7 ms
23.930	217 Thiabendazole (2.7 ms
23.952	218 Ateinnn-1,2 (2.7 ms
23.952	219 Phosfolan (2 5 ms
23.973	220 Tolyituanid (2.7 ms
23.995	221 Heptachior-endo-epoxide (2 7 r
24.016	222 Bromferwinfos-methyl (2.7 r

Dwell Time Optimization

Z LabSolutions Insight Heightening the Efficiency of Multi-Analyte Data Analysis

With LabSolutions Insight software, quantitative results for a complete series of data files can be displayed side-by-side for comparison and QC review. All of the chromatograms for a selected target compound can be displayed simultaneously, making it easy to review the detected peaks and confirm the quantitative results. Color-coded QA/QC flags quickly identify any outliers that require further examination.

Color-coded Quantitative Flags

In LabSolutions Insight, quantitative results can be compared to established criteria, and any outliers are color-coded for easy identification and further review. Five color-coded criteria levels can be defined, making it easy to determine which data points are outliers, and which specific QC criteria were not met. Any changes made to calibration curves or manual peak integration are immediately reflected in the color-coded flags.



Status Review Function

This function can be used to specify the status of all compounds and samples for their management. By specifying a status, the progress of data analysis work can be accurately recorded and reported.

#	Flags	Data Filename	Status	Sample Type 🔺	#	Name	Status	
V	Ŧ	Y	Ŧ			Ŧ	¥	Rerun
77		Conc-3_001	Pending	Standard	1	MPA-gluc	Pending	
8		Conc-3_002	Accept	Standard	2	d3-MPA		
9		Conc-3_003	Review	Standard	V 3	MPA	Pending	● ↔ ●
V 10	=	Unknown-1	Rerun	Unknown	V 4	d3-MPA		Pending Acc

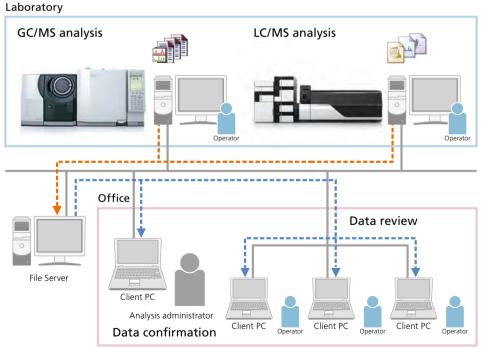
Enhanced Accuracy Controls

Accuracy control results, such as retention time differences, calibration curve linearity and peak shapes (tailing), can be assessed visually. In addition, the QC chart function in LabSolutions Insight allows visual confirmation of variations in target compounds across multiple data sets. This is useful when evaluating variations in internal standard substances between samples, for example.

174	Compound	e.2	AT		Absence	Tailing factor	Tor. Tor.
	Tarrierus	181.03-91.00			15.00	1.500	
	Teristeni	170 005 100 00			15.00	1.500	Hocker - rep opt
	EPTC	184 10-128 10			15.00	1.700	
	Bistand	154 10-128 10	7.845	0.8*00	15.00	1.500	Acerephthene-di0 15TD Area
5	Chlormephos	212.90+121.00			15.00	1,500	135000
	(Incompany)	11500-1106		0.0700	Contraction of the	2.900	
12-	J-Menyloha	110.10+141.10	4.258	0.8 000		1,500	1.30001-
	Moureto	126-10> 95.00	3.656	0.8730		1.500	
	Umechoase	158.00>158.02	9.902	9.9700		1.500	125040
10	Hoper	152 100 130 10	12.137	0.5700		1.500	
11	Tochazone	260.925-202.93	10.161	0.11730		1.500	1.2004
17	Propaction	126-10>52.00	12.329	0.0700		1.500	
17	Dichenylami	389.10>66.00	13.629	00.4.9	G	1.500	1 110et 1
14	Bhoprophes	200.00>158.00	\$3.452	0,0110.0		1.500	8 **Pat
		213.10+171.10				2.500	
	Träusie	306-10-264-10				1.500	1.1000-2
	Duitrates	222.00>202.00				1.500	
	1.1910					1	100001

System Configurations Using Multiple Client Computers

Data acquired from multiple systems can be reviewed or confirmed using client computers connected via a LAN or other network. If multiple systems are used, data obtained from each system can be reviewed from any client computer. Even in the case of multiple analysts using the same system, the ability to separate analytical work from measurement work improves work efficiency.



File management on a file server is recommended for systems with more than five users.

GC-MS/MS Databases Allow Users to Start Analysis Immediately

Offering both quantitative and screening applications, these databases contain pre-optimized MRM transitions and collision energies required for GC-MS/MS analysis, allowing users to start an analysis immediately just by using the AART function to automatically modify the retention times.

Smart Database Series Supporting Accurate Quantitative Determinations in MRM Analysis

The series contains optimized analysis conditions, so users can start an analysis immediately without investigating the conditions. This database is for accurate quantitative determinations using standard samples.

Smart Pesticides Database

It covers the pesticides (530 compounds) subject to GC-MS analysis and used inside and outside Japan. The database also contains information on compounds that can be used as internal standards. Therefore, it also supports analysis with the internal standard method.



Smart Metabolites Database

The database contains 525 compounds including metabolites contained in blood, urine, cells and other biological samples. It also contains information on the stable isotopes of 22 major metabolites, which can be used as internal standards.



Smart Environmental Database

The database contains information on 527 compounds including polychlorinated biphenyl, brominated flame retardants, dioxins, polycyclic aromatic hydrocarbons, and organochlorine pesticides, as well as their stable isotope labeled compounds.



Smart Forensic Database

The database is registered with 201 forensic toxicological substances often involved in poisonings, such as drugs of abuse, psychotropic drugs, pharmaceuticals, and pesticides.



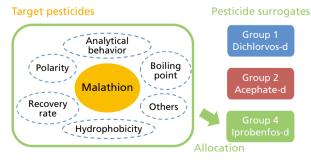
Quick-DB Series Enables Quick Screening Without Using Standards

Preregistered with calibration curve information from the internal standard methods, this database allows users to calculate quantitative values without analyzing standard samples. It can be used for screening when quick confirmation of quantitative results is required.

• Quick-DB GC/MS Residual Pesticides Database

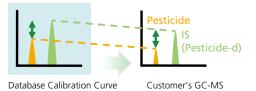
The database contains information on calibration curves created using pesticide surrogates as the internal standards, thus enabling the simultaneous screening of 491 residual pesticides without using standard samples. The registered calibration curves have been created by grouping target pesticides based on similar behavioral and physical properties, and allocating pesticide surrogates with similar physical properties to each group as internal standard substances. This allows highly accurate quantitative values to be calculated.

Allocation of Pesticide Surrogates Based on Physical Properties of Target Pesticides



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Sensitivity Variation Adjustments Using Pesticide Surrogates



Pesticide surrogates can also be used to adjust differences in target pesticide responses observed in calibration curves and a customer's instrument due to variations in GC-MS(/MS) sensitivity.

Smart Operation

Quick-DB Forensic Toxicology Database

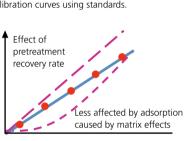
This database contains information on sample preparation, data acquisition, and analysis of 68 compounds often involved in poisonings. Due to the simple QuEChERS method used for the sample preparation, even first-time users can pretreat samples easily. The performance control function, which automatically assesses the system status, quickly determines problematic areas. As a result, users can analyze toxicological substances while consistently maintaining the highest status level.

Using a Calibration Curve for a Pretreated Sample to Correct for Recovery Rates

By using the calibration curve information from a pretreated sample, accurate quantitative values can be obtained. The calibration curve information is used to correct differences in recovery rates for each target compound or correct for effects caused by adsorption, which occurs when creating calibration curves using standards.



Calibration curve for whole blood sample spiked with standard and pretreated





If specific control parameter criteria are not satisfied, the optimal steps for restoring the system status are displayed in a message box.



Quick-DB Forensic Launcher Screen

Quick-DB Forensic

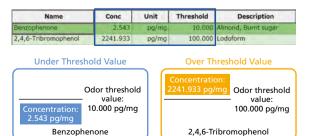
Off-Flavor Analyzer

This analysis system contains information on the major odor-causing substances identified from previous problems and associated sensory information, thus enabling the reliable identification of odor-causing substances. It allows users to calculate quantitative values easily without using standard samples, and to identify odor-causing substances through comparison with registered odor thresholds. The system also supports the use of a sniffer, enabling the efficient confirmation of odors using the predicted retention time display function. In addition, support is provided for a total system, including pretreatment units such as HS, SPME, and thermal desorption units using MonoTrap.

Comparison of Concentration to Odor Threshold Values



Odor-causing substances can be identified through comparisons of odor thresholds with the concentrations of off-flavor components identified in a chromatogram.



Compared lame (E)
Ref. (mix 1)
Comment (E)
Instead

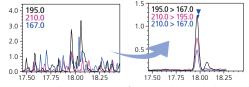
Bestgarenze
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Remote (A pure operation)
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Remote (A pure operation)
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Remote (A pure operation)
100

2.4.6. Francesine
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Remote (A pure operation)
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Primary odor GC/MS analytical Sensory components conditions information



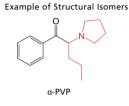
Since some odor components have a low odor threshold, low concentration levels need to be detected to identify the causative substances. High-sensitivity MRM/SIM analysis by GC-MS(/MS) can reliably detect even trace components near the odor threshold (a few pg/g).

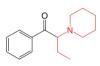


Mass Chromatograms of 2,4,6-Trichloroanisole (estimated concentration of 18.166 pg/g) in Food with an Odd Odor (Left: Scan analysis, Right: MRM analysis)

Qualitative Analysis Using GC-MS/MS

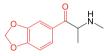
GC-MS/MS allows users to freely select ions cleaved by electron ionization (EI), and then cleave precursor ions via collision induced dissociation (CID), thus enabling the detailed analysis of partial structures. A product ion scan can be used to easily discriminate structural isomers and regioisomers, which are hard to identify with an EI mass spectrum obtained via GC/MS. This mode is optimal for predicting partial structures.



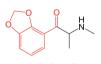


α-PBP Piperidine analog

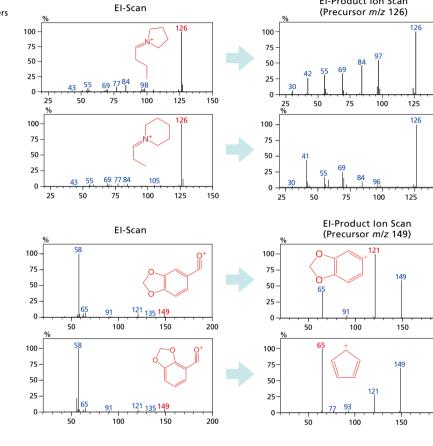
Example of Regioisomers



Methylone (bk-MDMA)



2,3-Methylenedioxymethcathinone



High-Speed Scanning Control (Advanced Scanning Speed Protocol, ASSP)



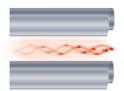
EI-Product Ion Scan

150

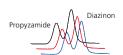
150

200

200



Newly Patented Technology (ASSP)



Black: 1,111 u/sec Red: 5,000 u/sec Blue: 10,000 u/sec

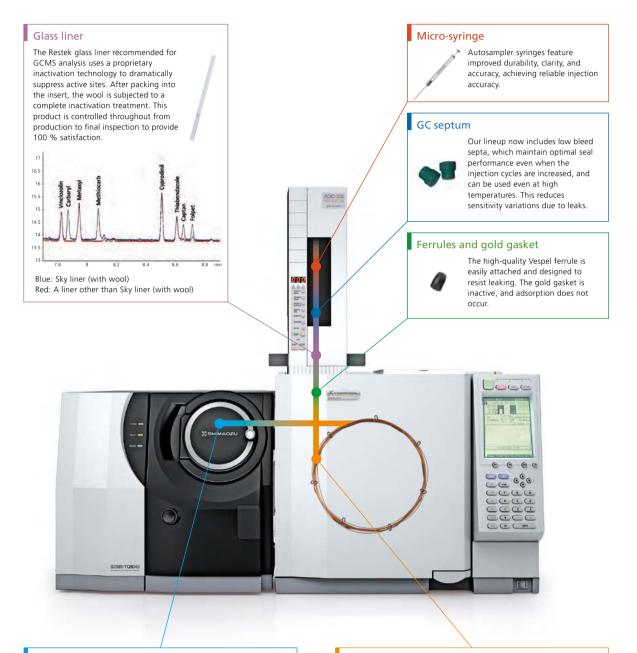
Equipped with a function to automatically optimize the rod bias voltage during high-speed data acquisition, the system can collect data stably through scans as well as product ion scans at 20,000 u/sec (patent: US6610979).

With the GCMS-TQ8040, ten or more product ion scans can be configured for a single measurement, and three or more user-specified analysis modes (Scan, MRM, product ion scan) can be combined.

	Compound Name	Start Time (min)	End Time (min)	Acq. Mode	Event Time(sec)	Scan Speed	Start m/z	End m/z	Precursor m/2	CE
1-1		2.30	43.00	Q3 Scan	0.050	10000	43.00	500.00		
1-2		2.30	43.00	MRM	0.050					
1-3	Amine m/z44	2.30	43.00	Product Ion Scan	0.005	20000	20.00	45.00	44.00	15.00
1-4	Amine m/z58	2.30	43.00	Product Ion Scan	0.005	20000	20.00	59.00	58.00	15.00
1-5	Amine m/z72	2.30	43.00	Product Ion Scan	0.008	20000	20.00	73.00	72.00	15.00
1-6	Amine m/z86	2.30	43.00	Product Ion Scan	809.0	20000	20.00	87.00	86.00	15.00
1-7	Amine m/z98	2.30	43.00	Product Ion Scan	0.010	20000	20.00	99.00	98.00	15.00
1-8	Amine m/2100	2.30	43.00	Product Ion Scan	0.010	20000	20.00	101.00	100.00	15.00
1-9	Amine m/z112	2.30	43.00	Product Ion Scan	0.010	20000	20.00	113.00	112.00	15.00
1-10	Amine m/z114	2.30	43.00	Product Ion Scan	0.010	20000	20.00	115.00	114.00	15.00
1-11	Amine m/z126	2.30	43.00	Product Ion Scan	0.010	20000	20.00	127.00	126.00	15.00
1-12	Amine m/z128	2.30	43.00	Product Ion Scan	0.010	20000	20.00	129.00	128.00	15.00
1-13	Amine m/z140	2.38	43.00	Product Ion Scan	0.010	20000	20.00	141.00	140.00	15.00
1-14	Amine m/z142	2.30	43.00	Product Ion Scan	0.015	20600	20.00	143.00	142.00	15.00

Inert Flow Path Achieves High-Sensitivity GC/MS Flow Path

Minimizing adsorption and other losses in the flow path from sample injection to the detector is important for stable, high-sensitivity measurements using GC/MS. The flow lines in the GCMS-QP series and the TQ series consist of high-quality, highly reliable consumable parts, so even trace concentrations of components can be detected with high sensitivity and favorable repeatability.



lon source



Designed with a shield that blocks radiant heat generated by the filament, and an ion source treated with an oxide coating, active spots inside the ion source are not prone to occur, which enables high-sensitivity analysis with long-term stability.

Capillary columns



For the SH-Rxi series, a high-quality fused silica like no other is used as the raw material. Our proprietary surface inactivation technology and optimal process to mask silanol groups result in a low-bleed column with very impressive inactivation performance, even with respect to polar compounds comparable to acidic and basic substances.

Optional Units Enable a Variety of System Configurations

Various System Configurations

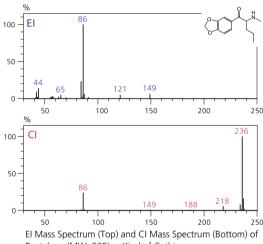
For GC-MS/MS analysis, different system configurations may be required depending on the application and sample-introduction needs. The GCMS-TQ8040 offers a wide variety of system configurations and sample-introduction devices to enable an expanded range of applications.



% Chemical Ionization and Negative Chemical Ionization

In addition to electron ionization (EI), chemical ionization (CI) and negative ion chemical ionization (NCI) are available for the GCMS-TQ8040. The CI method softly ionizes sample molecules and is effective for confirming molecular weights, while the NCI method enables selective, high-sensitivity detection of compounds with functional groups that have a large electron affinity such as halogens.

The Quick-CI function allows users to switch between the EI and CI modes with the same ion source, so EI and CI data can be obtained from the same sample. If confirmation of molecular ions is difficult with the EI mode, molecular information can be collected from the CI mode data.



Pentylone (MW: 235), a Kind of Cathinone

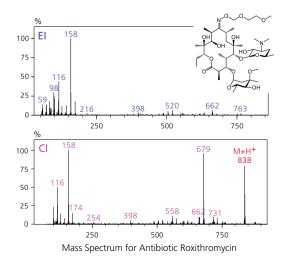


Ø DI-2010 Direct Sample Inlet Device

Direct sample injection (DI) is a method in which a sample is injected directly into the ion source without passing through the gas chromatograph (GC). This is an effective method for measuring the mass spectra of synthetic compounds, and can be used easily for the usual GC-MS

configuration. By using this in combination with Quick-CI, EI and CI mass spectra can easily be collected.

Components that are thermally degradable or difficult to vaporize are not suited to GC analysis. Their mass spectra can be obtained easily using the DI probe.



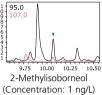
Ø AOC-6000 Multifunctional Autosampler

The AOC-6000 supports three sample injection methods: liquid sample injection, headspace (HS) injection, and solid phase micro extraction (SPME) injection, so samples in a variety of forms can be analyzed. It allows the sample injection method to be switched automatically, enabling different sample injection methods to be combined in a continuous operation.

With the automatic syringe exchange and stirring function, standard samples can be prepared automatically with a variety of dilution levels, and everything from the creation of calibration curves to the quantitative determination of unknown samples can be fully automated.







HS-20 Headspace Sampler

The HS-20 headspace sampler provides strong backup for the analysis of volatile components at every stage from research to quality control departments. The high-sensitivity electronic cooling trap enables quantitative and qualitative determination of trace components that cannot be detected with a conventional headspace sampler.

The HS-20 transfer line is built into the GC unit, which makes it easy to combine the HS-20 with the AOC-20 liquid sample injector, as well as to switch between these units.

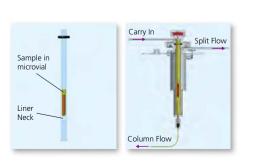
Ø OPTIC-4 Multimode Sample Inlet

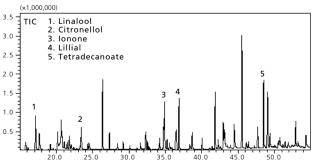
The OPTIC-4 multimode sample inlet is a GC injection port that enables a variety of sample injection modes for GC-MS, including large-quantity injection, inlet derivatization, thermal desorption, and DMI (difficult matrix introduction).

Combining this with an autosampler enables automatic replacement of inserts, improving productivity in multisample analyses.



DMI (Difficult Matrix Introduction) Mode Simplifies Pretreatment





An undiluted shampoo solution was placed directly in a microvial and measured in DMI mode, enabling the selective analysis of volatile components.



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