Access to **your** success

SHIMADZU

GCMS-QP2010 Plus

Shimadzu
Gas Chromatograph
Mass Spectrometer

The performance you
have been waiting for is here.
GCMS-QP2010 Plus

GCMS-QP2010 Plus

Shimadzu Gas Chromatograph Mass Spectrometer

Setting a new standard for performance and sensitivity

Precise and reliable measurement of trace level compounds

Highly accurate identification of target analytes

Strong demand for faster analysis times, more efficient work flow and assurance of data quality

These were the requests of researchers, lab managers and high thru-put production managers from the Environmental, Drug testing and Food Safety industries.

Shimadzu Corporation stepped up to develop a GCMS that satisfies these demands. Introducing the "GCMS-QP2010 Plus"!

Based on the GCMS-QP2010, we proudly present this innovative new model.

The world's highest level of performance
• Superb trace level detection for a wide range of applications

Software that focuses on functionality and ease of use
• Advanced workstation software with the versatility to meet demanding needs

Solutions to many applications
• Preprogrammed Method Packages to facilitate a short start-up time

1. Highest sensitivity resulting from new innovative design

2. High-Speed Scan/SIM data acquisition technology

3. Automatic Scan/SIM acquisition parameter set-up

4. Necessary tools for high-speed analyses

5. Expanded mass range 1.5 – 1090

6. Automatic adjustment of retention times

7. Library search using retention index

8. Report customization functionality

Contents

Superb Trace Analysis Technology for High Sensitivity and Stability

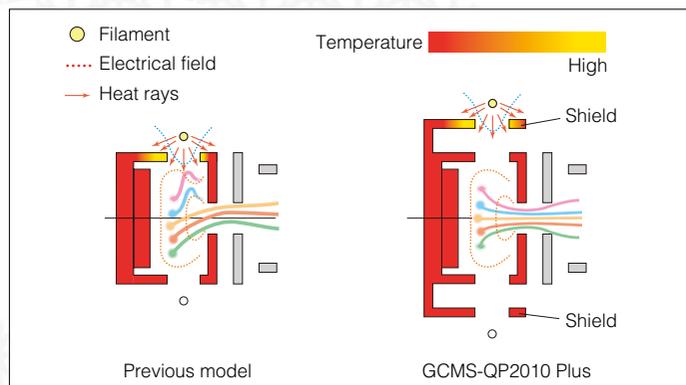Front-opening chamber for easy maintenance

Three technologies that achieve high sensitivity and stability

1. Enhanced ion source
2. High capacity differential vacuum system
3. Detector equipped with overdrive lens

The detection and quantitation limits of an instrument are lowered by enhancing sensitivity and stability. The Similarity Index of library searches improve along with the quality of acquired spectra, especially at trace levels.
The GCMS-QP2010 Plus achieves this thru innovative ion optics design technology.

High-efficiency ion source provides uniform temperature control for increased sensitivity

- ○ Filament
- ····· Electrical field
- → Heat rays

Temperature — High

Shield

Shield

Previous model   GCMS-QP2010 Plus

The effect of filament potential on the ion source is reduced by placing more distance between the filament and ion source box, and installing a shield plate. The result is that generated ions are transported more efficiently to the MS.
Filament shielding ensures efficient ion transport to the detector while protecting thermally labile compounds.
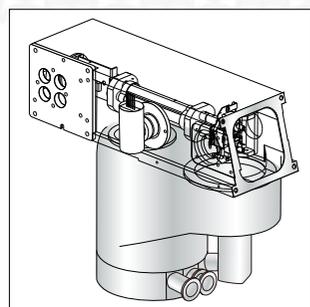

The differential dual inlet turbomolecular system provides a higher level of vacuum in the ion source and mass analyzer regions. This is achieved by a unique dual-ported manifold.

The result of increased vacuum is a suppression of the space-charge effect. Allowing for more efficient ion transmission thru the mass filter thus greater sensitivity, especially in Negative Chemical Ionization mode.


OFN 1pg EI data [*m/z*: 272 Scan]

OFN 100 fg NCI data [*m/z*: 272 Scan]
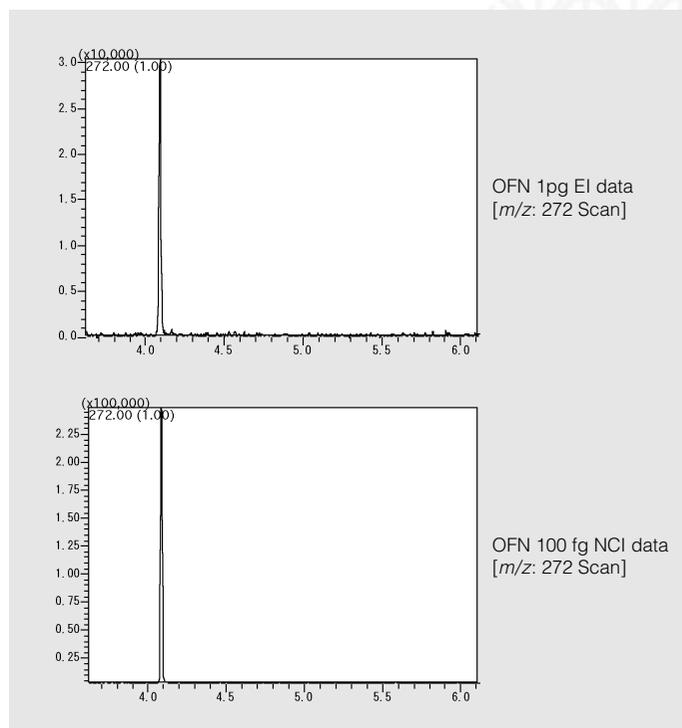
Ultra Trace-Level Quantitation and Mass Spectrum Simultaneous Analysis Technology
Scan/SIM Simultaneous Analysis

A traditional scan measurement will provide a great deal of qualitative information from the mass spectrum including information about compounds other than target analytes. A traditional SIM measurement provides much greater sensitivity than scan but, only for compounds specified in the acquisition method. FASST (Fast Automated Scan/SIM Type) data acquisition is a new technique that will allow the analyst to take advantage of the strengths of both data acquisition modes.
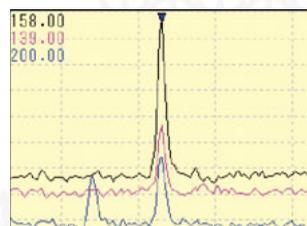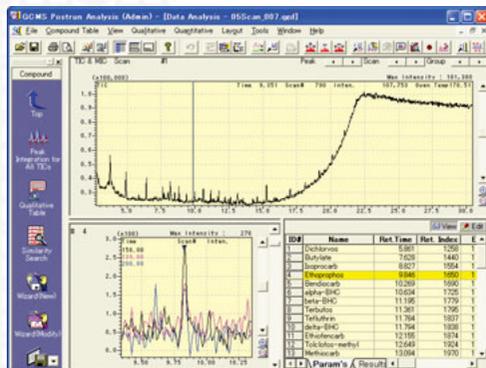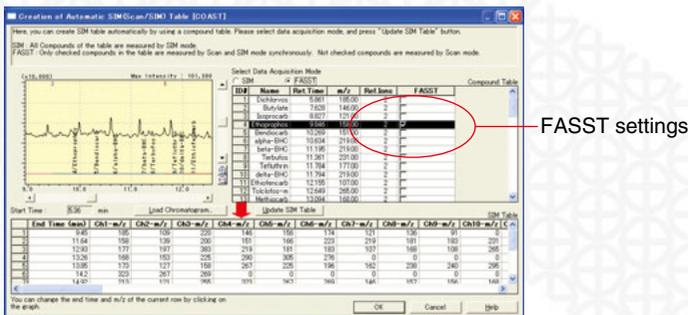

Scan data
SIM data

Scan data
SIM data

Mass spectrum information
Unknown compound information

High sensitivity
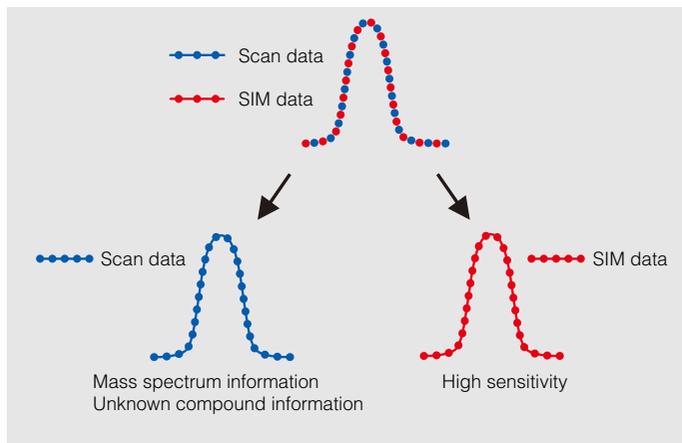
Advancement in Technology:
Simultaneous Scan/SIM Data Acquisition
FASST (Fast Automated Scan/SIM Type)

Scan data

S/N ratio increase

FASST data
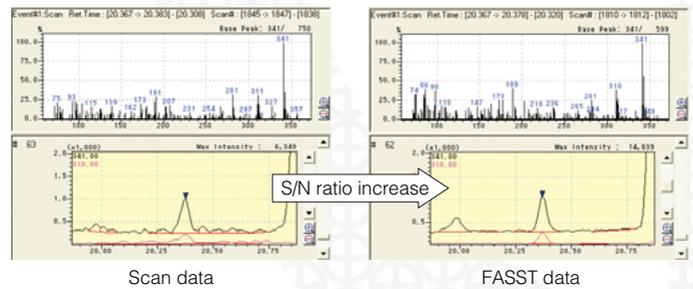
With the FASST technique, a scan chromatogram and SIM chromatogram can both be obtained by switching at high speed between Scan and SIM modes for data acquisition. Even with simultaneous data acquisition in both modes, there is no degradation of sensitivity from the high speed data acquisition technology employed in the GCMS-QP2010 series. The FASST measurement parameters are easily set using the GCMSsolution automatic setting function.


FASST settings

Ease of Use:
COAST (Creation of Automatic Scan/SIM Table)

COAST is a wizard that allows the user to quickly set up a Scan/SIM data acquisition method. The user will run the wizard while viewing a chromatogram to quickly and easily create a Scan/SIM table. FASST measurements can be specified for the entire analysis or just in regions where sensitivity enhancement is desired. It is also possible to alternate acquisition modes between Scan, SIM and FASST.


High sensitivity SIM chromatograms can be obtained using the COAST Scan/SIM simultaneous measurement settings.
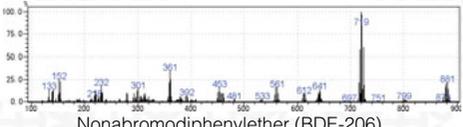
Enhance Productivity:
Tools that allow you to easily increase productivity, perform more sensitive analyses and analyze a greater variety of compounds at lower detection limits.
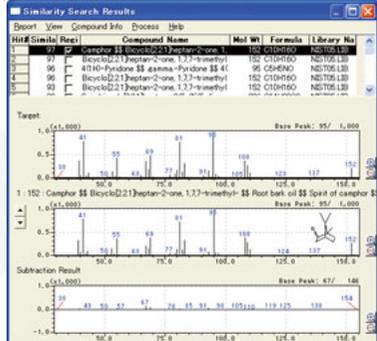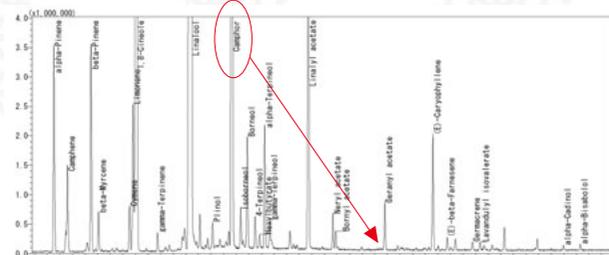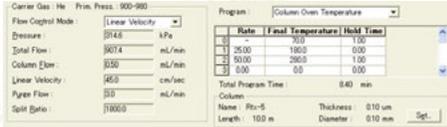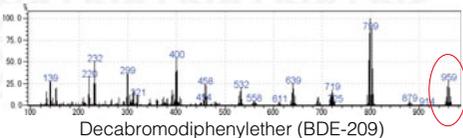

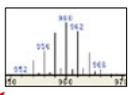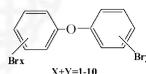Superior similarity search indices will be obtained from spectra acquired at 10,000 amu/second
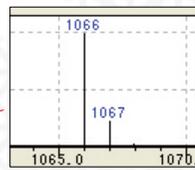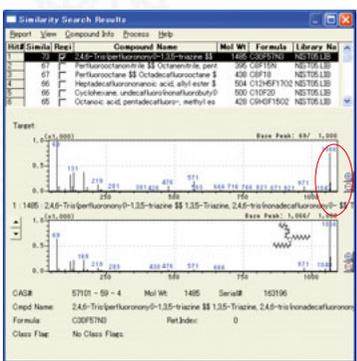
Tris(perfluorononyl)-S-triazine mass spectrum library check

Nonabromodiphenylether (BDE-206)

Decabromodiphenylether (BDE-209)

High-Speed GCMS:

Electronic Carrier Gas Flow Controller

AFC
(Advanced Flow Controller)

Several important parameters play roles in shortening the analysis time while maintaining column separation performance. The "constant linear velocity control" mode maintains the highest separation characteristics. Carrier gas control of up to 970kPa and 1200 ml/minute total flow allows for higher flow rates and greater split ratios when using micro-bore capillary columns. Use Constant Linear Velocity when separations are critical.

High speed data acquisition technology

High speed digital control technology was adopted early in the GCMS-QP2010 series, enabling high speed scan data collection at up to 10,000 amu/sec. Stable mass spectral data can be acquired with very narrow chromatographic peaks. Neither distortion nor reduced intensity is observed in the mass spectrum.

High-performance quadrupoles and pre-rods allow mass range to be extended up to *m/z* 1090.

High Performance Quadrupole Mass Filter

Highly accurate quadrupoles and pre-rods combine to create our patented electronic field control for ideal mass filter performance. Pre-rods act to prevent contamination and enhance long term stability, while the quads deliver superior ion transmission and resolution.

Wide Mass Range up to *m/z* 1090

The result of our quadrupole technology is the ability to analyze for compounds that have masses of up to 1090 *m/z*. Compounds in that mass range are becoming more important. The GCMS-QP2010 Plus is ready to meet that challenge.

Brominated Flame Retardant Analysis

Analysis results of the brominated flame retardants Nonabromodiphenylether and Decabromodiphenylether show that accurate spectra are routinely obtained for these high-mass compounds.

Productivity

Workstation Software Combines Ease of Use and Versatile Functionality

A GC/MS workstation must incorporate many functions, from data acquisition to qualitative or quantitative data analysis to versatile reporting. GCMSsolution incorporates these features and many more into the latest version.

GCMS-QP2010 Series Software   GCMSsolution
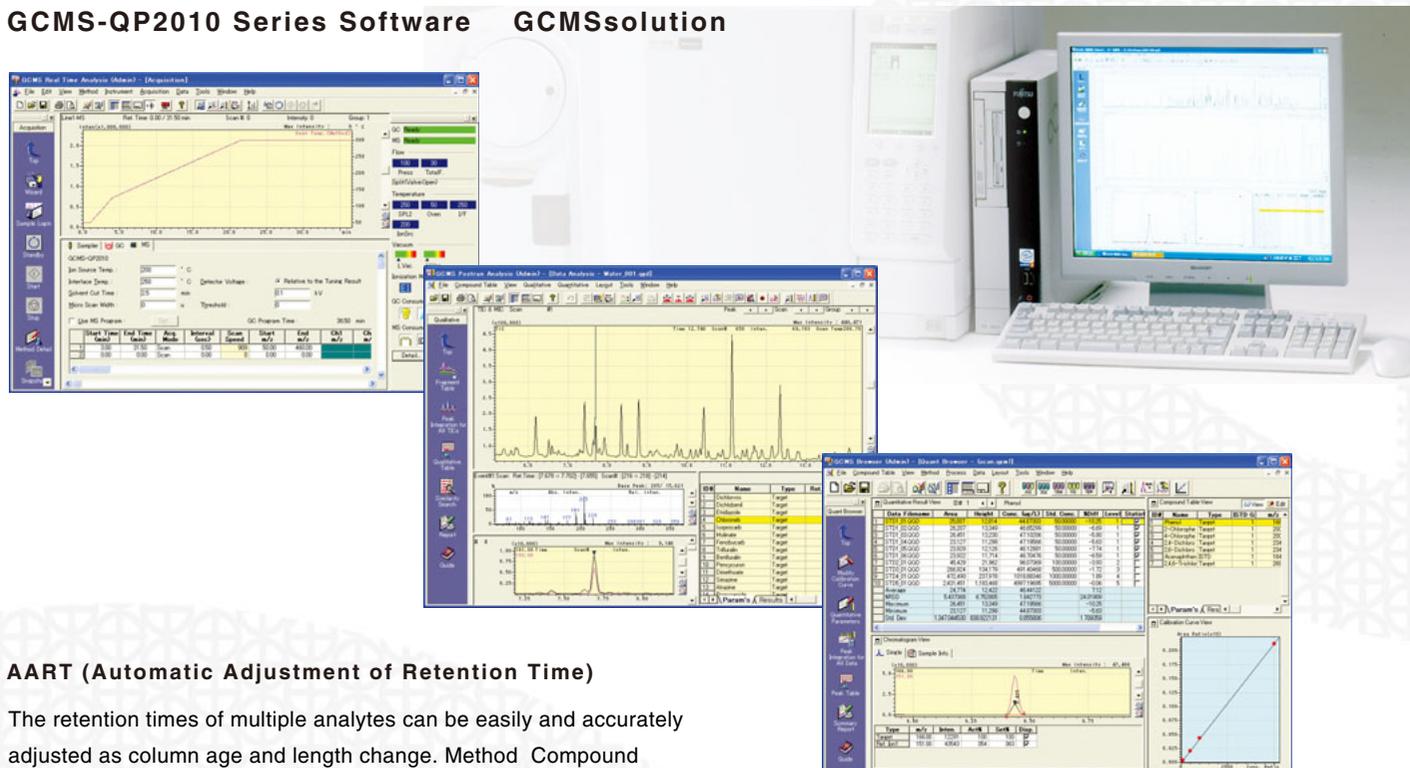
AART (Automatic Adjustment of Retention Time)

The retention times of multiple analytes can be easily and accurately adjusted as column age and length change. Method Compound Tables containing a large number of analytes can be easily updated or Methods may be transferred to other instruments easily by using this wizard.

Similarity Search with Linear Retention Indices

Often times compounds of similar class or molecular weight will produce identical spectra. Their library searches will be refined to identify the actual isomer with the help of this retention time indexing feature.

COAST (Creation of Automatic SIM (Scan/SIM) Table)

This function is used to automatically create a SIM table, which defines the conditions for SIM analysis. It can also be used to automatically set up a Scan/SIM table when conducting FASST analysis.

Intuitive user interface

Intuitive operation is assured with adoption of the GCMSsolution's approach, featuring such useful elements as the "Assistant Bar" and "Data Explorer".

Abundant wizard functions

Wizard functions free the user from such bothersome tasks as specifying target compound identification information and retention time adjustments. They also facilitate the setting of SIM and other analytical conditions as well as batch analysis parameters.

Highly flexible report customization

Allows free positioning and sizing of all report elements, including chromatograms, spectra, spectrum search results, and qualitative and quantitative results. The report settings can be saved as a report format, allowing the same format to be used repeatedly for report output.

GLP/GMP support

The software is fully equipped with security, audit trail, hardware/software verification and QA/QC functions for GLP/GMP compliance.

Automatic Adjustment of Compound Retention Time
GCMSsolution Workstation
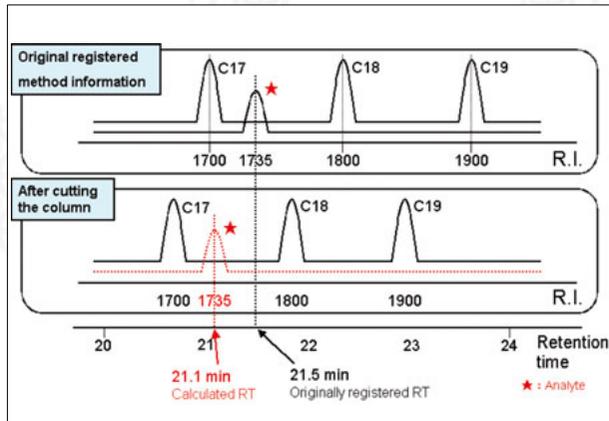
Adjustment Example

ID	Compound Name	Corrected Time	Actual Time	Error
1	Hexachlorocyclopentadiene	6.599	6.592	0.007
2	Dimethyl phthalate	7.508	7.513	-0.005
3	Acenaphthylene	7.669	7.663	0.006
4	Acenaphthene-d10	7.935	7.929	0.006
5	2-Chlorobiphenyl	8.053	8.050	0.003
6	Diethyl Phthalate	8.848	8.853	-0.005
7	Fluorene	8.966	8.960	0.006
8	2,3-Dichlorobiphenyl	10.196	10.192	0.004
9	Hexachlorobenzene	10.400	10.394	0.006
10	Simazine	10.490	10.496	-0.006
11	Atrazine	10.595	10.604	-0.009
12	Pentachlorophenol	10.853	10.852	0.001
13	Lindane	10.955	10.955	0.000
14	Phenanthrene-D10	11.150	11.146	0.004
15	Phenanthrene	11.208	11.203	0.005
16	Anthracene	11.321	11.316	0.005
17	2,4,5-Trichlorobiphenyl	11.877	11.875	0.002
18	Alachlor	12.536	12.539	-0.003
19	Heptachlor	12.627	12.619	0.008
20	di-n-Butyl phthalate	13.049	13.056	-0.007
21	2,2',4,4'-Tetrachlorobiphenyl	13.222	13.220	0.002
22	Aldrin	13.483	13.472	0.011

Note) The retention times registered in the method are the times used for identification and verification of compounds based on the retention index data from the method and the results of the n-alkane standard analysis.
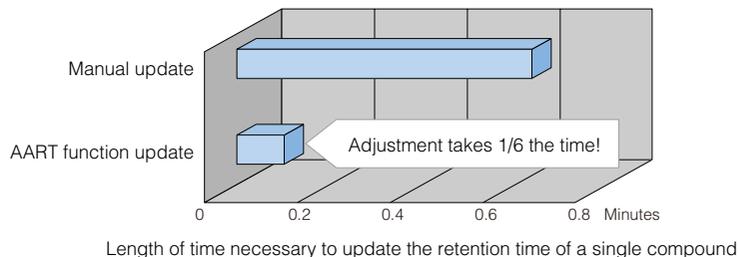
AART (Automatic Adjustment of Retention Time)

Retention times may change as a result of capillary columns being trimmed during maintenance or exchanged with a new one from a different lot. The AART feature is used in this case to update the retention times of your compounds in the peak table. This is accomplished by generating a linear retention index based on an alkane standard mix*. Your peak table may then be updated as required without changing the instrument acquisition parameters.

*The alkane standard mix is available from RESTEK Corporation (P/N 560295).

Retention Index

A retention index is information unique to a compound for a given analytical column. A unique index value is assigned to a compound based on its retention time relative to those of an alkane series.

Length of time necessary to update the retention time of a single compound

Work load comparison** between manual and automatic retention time adjustment* after replacing column
  *Using a method with compound names, measurement ions and time information already entered for 200 compounds.
**Excluding updating of SIM acquisition parameters. These values may also be updated by AART.

AART (Automatic Adjustment of Retention Time) Features

● Retention times of up to 1000 compounds can be updated with analysis of a single n-alkane solution.
● Correction is performed at multiple points from low to high boiling points, enabling accurate correction over a wide range of retention times. The carbon numbers of the alkane series is chosen based on the analytes. Indexing compounds other than alkanes may be used.
● Retention time updating based on analysis of n-alkanes is easily accomplished using the AART wizard function.
● Time correction of SIM acquisition parameters may be updated using AART.
● AART can easily be applied to an existing method by just adding the retention index information to the method.

Sharing a method between instruments is easy.

AART enables easy method transfer between instruments. Retention times may be updated with the analysis of an indexing standard. Then the system is ready for use.
Various method packages are available with the compound list and calculations pre-entered.

Note) Excellent correction accuracy is maintained by using the same type of column and the same analytical conditions.

Similarity Search Using Retention Index
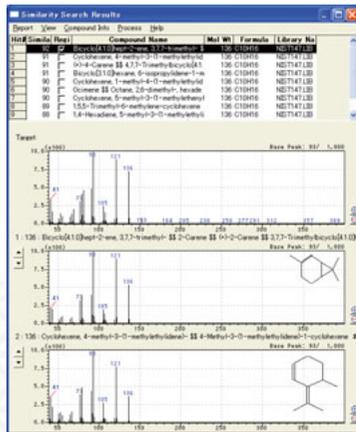## Functional Analysis of Scan/SIM Data

Similarity Search using Retention Index

In the retention-indexed similarity search, the existing mass spectrum similarity search is used in conjunction with a retention index to perform a more specific library search, enabling more certain component identification, particularly for isomers with similar mass spectra.
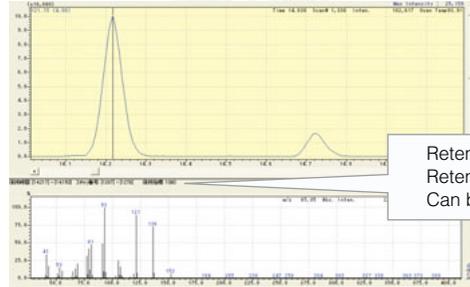
Library with Retention Indices is Easily Created

Library searched results may be further refined with the help of retention index data. Enabling the clear identification of compounds with similar spectra but different retention times. GCMSsolution allows for the easy creation of an indexed mass spectral library.

Retention index display
Retention index: 1090
Can be registered to library

Similarity search using
retention index

Retention index tolerance
range setting

Hits on more than
10 high similarity
compounds
(similarity greater than 88)

Ordinary Similarity Search
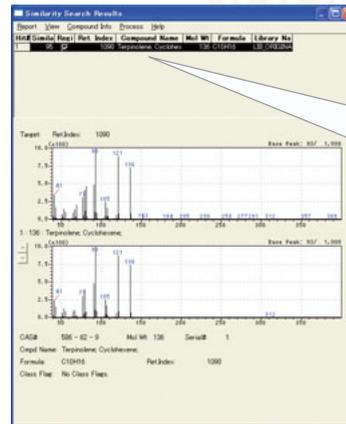
Ret. Index	Compound Name
1090	Terpinolene; Cyclohex

**More certain search
is provided.**

Functional Analysis of Scan/SIM Data

FASST data may be viewed and analyzed in the same window. GCMSsolution take full advantage of Scan/SIM data. ① shows SIM traces, ② is the spectrum of the same trace, ③ view non-target peaks and ④ search their spectra.
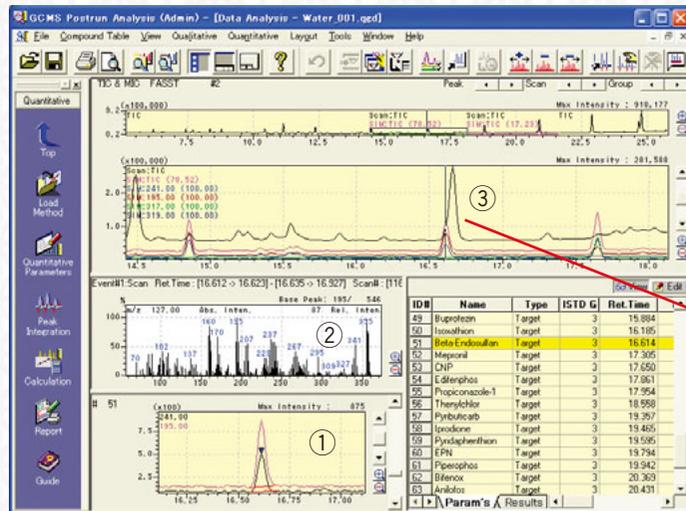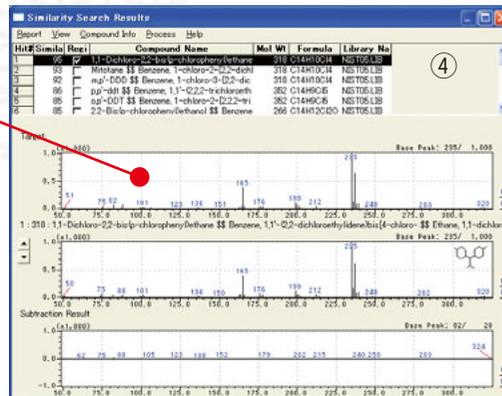
While viewing the scan data TIC, the background can be subtracted from the ③ unknown compounds. The compounds can be confirmed using a background-subtracted mass spectrum.

Identification of unknown compounds is easily accomplished using the Scan data mass spectrum.

Report Customization
Variety of Optional Software

Highly Flexible Report Creation

Items to be output in a report format can be pasted into the layout and freely edited. After preparing the various items such as chromatograms, spectra, spectrum search results and quantitation results, the user can compose a report format as desired. Report formats optimized for environmental, drugs, and pesticide residues in food analyses are provided as templates. Those templates can be further customized or a report can easily be formatted starting with a blank page. In addition, the preview function can be used to check the created format using WYSIWYG.

Examples of report formats for different applications

Summary Report

Multiple components simultaneous analysis report format

EPA Initial Calibration Format
Requires EPA optional software.

Optional Software

● **AOC-5000 Control Software**
Allows management of AOC-5000 parameters in GCMSsolution, and works with GCMSsolution to perform batch analysis.

● **EPA Optional Software**
Supports analysis according to the regulations of the US EPA. Specialized reports and quality assurance functions are available.

● **Compound Composer Database Software 2nd edition for Simultaneous Analysis**
The retention times, mass spectra and calibration curves for 942 hazardous chemicals are registered in the database. In combination with the prediction of retention times using n-alkanes (retention index), the database supports highly reliable compound identification. In addition, approximate quantitative results for hazardous chemicals can be confirmed without using calibration standards.

Mass Spectral Libraries

● **NIST Library**
The main library contains spectra for 191436 general compounds, and 28307 of these spectra are registered in a sub-library. More than 99.9% of these spectra are accompanied by structural information. In this library, retention indices are given for about 90% of the compounds.

● **Wiley Library**
This library contains spectra for about 310000 general compounds.

● **Pesticide Library 3rd edition**
This is a library containing mass spectra for 578 compounds measured using the electron ionization (EI) method and 383 compounds measured using the negative chemical ionization (NCI) method. Highly reliable identification is possible using the mass spectra of the EI and NCI modes together. The library also includes a method for analyzing pesticide residues in food and tap water.

● **FFNSC (Flavor and Fragrance Natural and Synthetic Compounds) Library**
This is a library for 1156 fragrance-related compounds. The library contains mass spectra as well as retention indices, allowing retention-indexed searches.

● **Drug Library**
This library contains spectra for 7840 compounds, including drugs, poisons, pesticides and environmental pollutants.

● **GC/MS Metabolite Mass Spectral Database**
This database contains mass spectral library and method files that specify analytical coditions and data analysis parameters for amino acids, fatty acids, and organic acids.
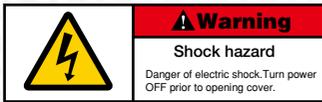
Founded in 1875, Shimadzu Corporation, a leader in the
development of advanced technologies, has a distinguished
history of innovation built on the foundation of contributing to
society through science and technology. We maintain a
global network of sales, service, technical support and
applications centers on six continents, and have established
long-term relationships with a host of highly trained
distributors located in over 100 countries. For information
about Shimadzu, and to contact your local office, please visit
our Web site at **www.shimadzu.com**

⊕ SHIMADZU