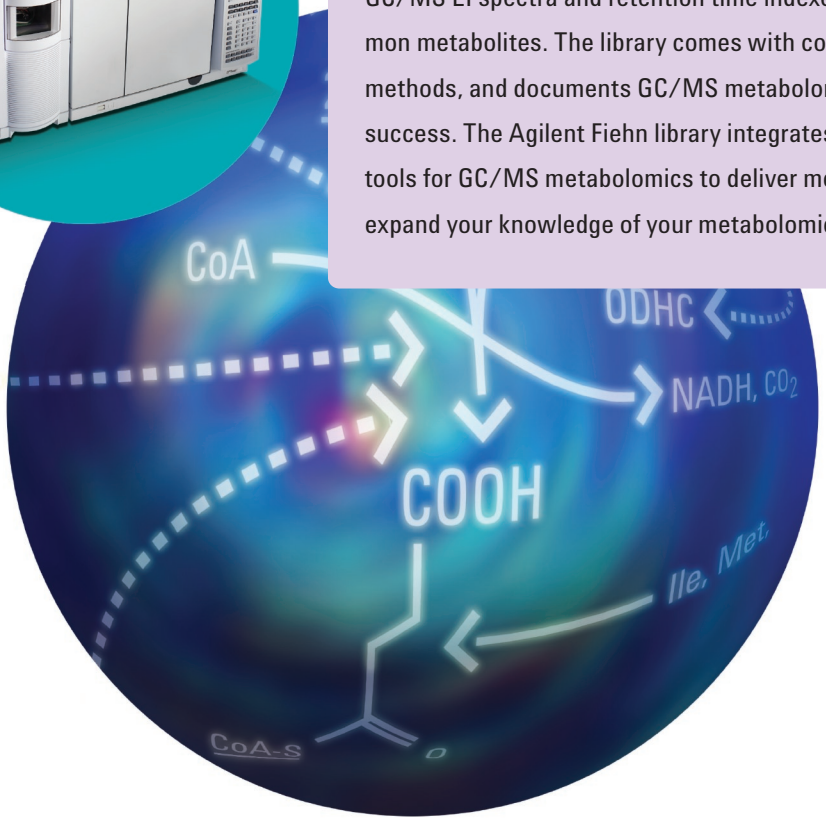
Agilent Fiehn GC/MS Metabolomics RTL Library

A complete GC/MS solution for metabolite identification

Product Note

Gas chromatography/mass spectrometry (GC/MS) offers high separating power and high sensitivity for metabolomic research. High-quality, searchable EI spectra can lead to positive identification of metabolites flagged during profiling experiments. To further facilitate identification of known metabolites through untargeted metabolomics, Agilent Technologies offers the Fiehn GC/MS Metabolomics RTL (retention time locked) Library. Developed with Dr. Oliver Fiehn, this growing metabolomics-specific library contains searchable GC/MS EI spectra and retention time indexes from approximately 700 common metabolites. The library comes with complete, preprogrammed GC/MS methods, and documents GC/MS metabolomic analysis to maximize research success. The Agilent Fiehn library integrates with Agilent's other software tools for GC/MS metabolomics to deliver metabolite identities faster and expand your knowledge of your metabolomic samples.



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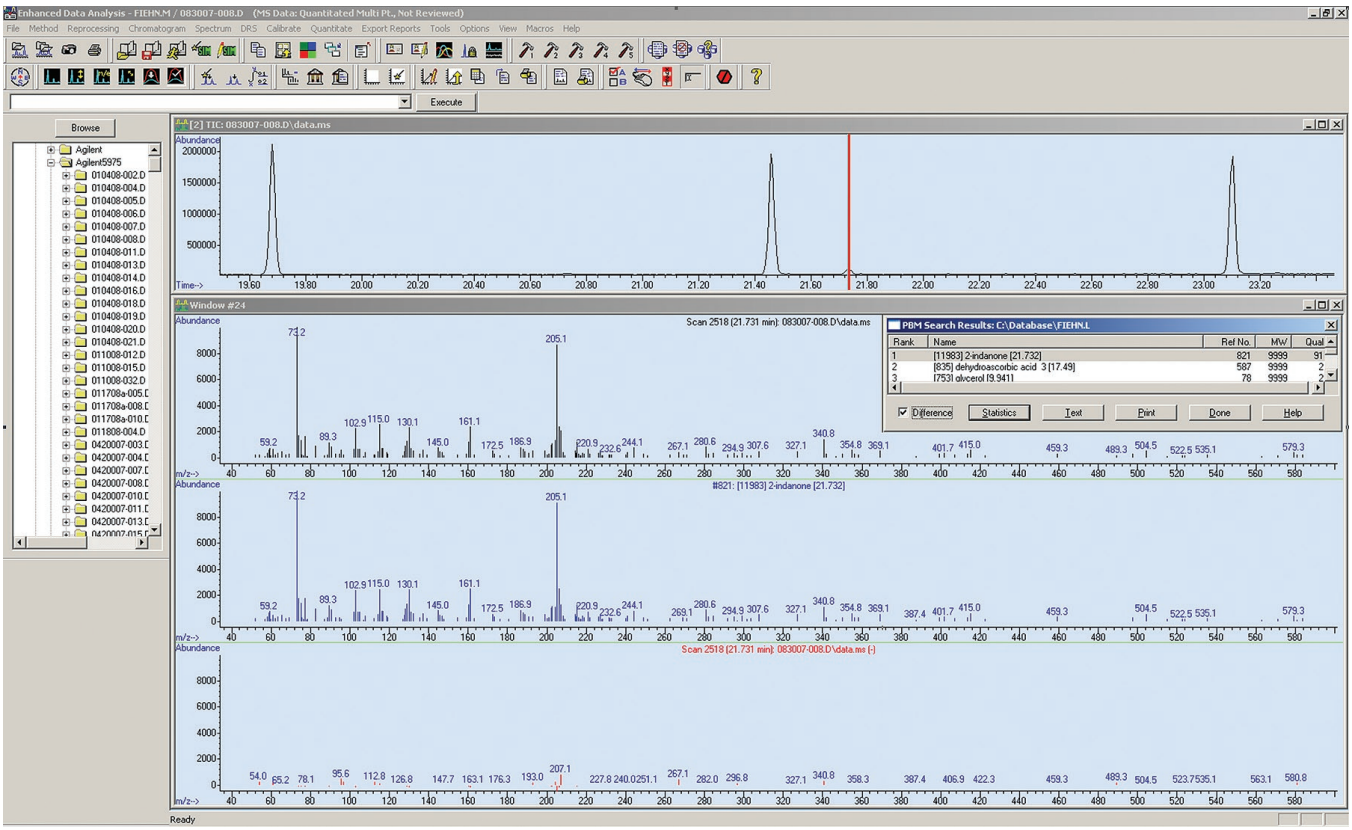
More library compounds for more positive identifications

The Agilent Fiehn GC/MS Metabolomics RTL Library is the most comprehensive library of metabolite GC/MS spectra that is commercially available. This expanding library currently contains 1050 entries for approximately 700 common metabolites, including entries corresponding to partially derivatized metabolites for metabolites that do not always derivatize completely. Each entry includes a searchable EI spectrum and retention index. It also includes the name and CAS number of the native molecule for easier compound recognition and subsequent literature or software searching.



The Agilent Fiehn library can be searched using the ChemStation software's native probability-based matching (PBM) algorithm. Here, PBM searching of a minor peak produces a high-confidence library match.

Retention time indexing increases identification confidence

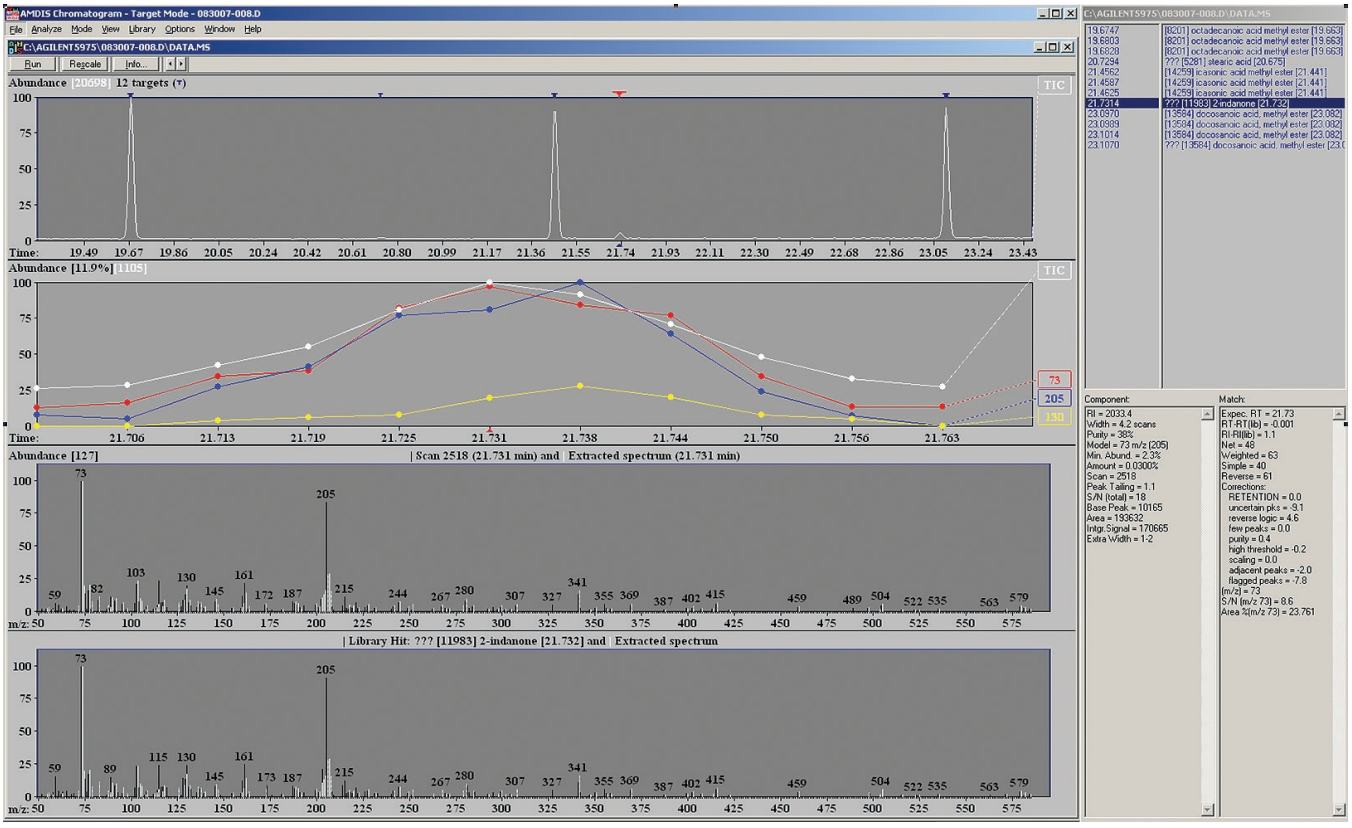
The Agilent Fiehn library takes advantage of retention indexing and retention time locking to increase your confidence in the search results. Retention indexing and the use of retention ladder compounds – internal standards with well-spaced retention times – allow you to make significant changes to the method and still use chromatographic retention as an independent criterion for metabolite identification. Retention time locking reduces run-to-run retention time variation and reduces the frequency with which you need to analyze the retention ladder compounds.

Fast, flexible, high-throughput searching

The Agilent Fiehn GC/MS Metabolite RTL Library is supplied with the well-known AMDIS automated GC/MS identification program from the U.S. National Institute of Standards and Technology. GC/MS data analysis methods that automatically invoke AMDIS to deconvolute merged chromatographic components and identify metabolites are provided.

AMDIS results can be imported into Agilent's GeneSpring MS software to take advantage of its powerful statistical analysis and data visualization capabilities.

The Agilent Fiehn library can also be searched using the native probability-based matching (PBM) capabilities of the Agilent MSD Productivity ChemStation software. ChemStation methods for quantitative data analysis and qualitative screening are also provided.



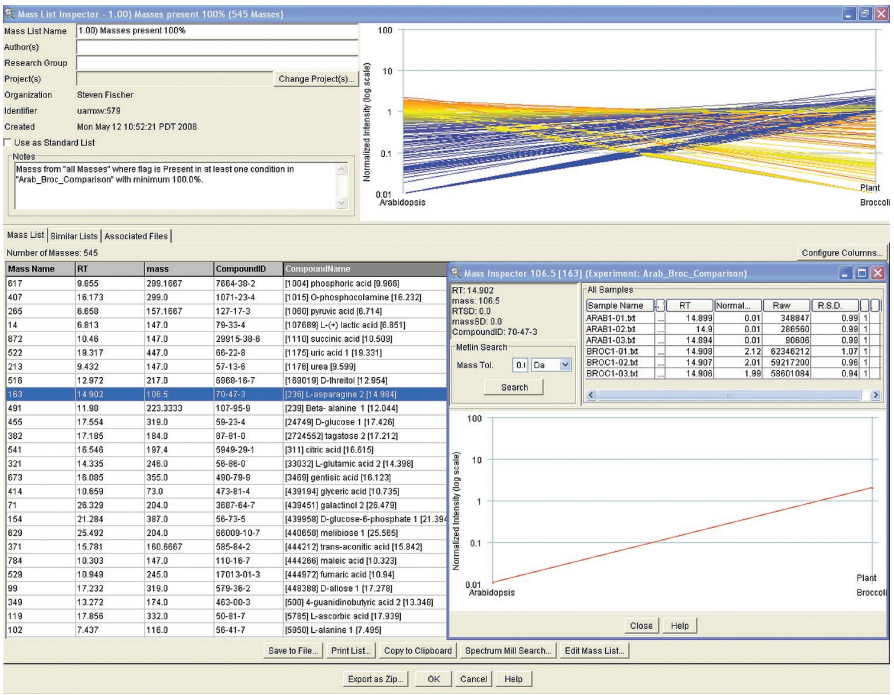
AMDIS automated GC/MS identification program is supplied with the Agilent Fiehn library. It can be used to deconvolute co-eluting chromatographic components and to search the library.

Complete workflow for more successful research

In addition to finding and identifying metabolites through library searching, the Agilent Fiehn library includes extra features that help you through the entire workflow for untargeted metabolomic studies. The library includes proven, preconfigured data acquisition methods suitable for a 6890 or 7890 GC and 5973 or 5975 MSD. It also includes a user's guide that covers virtually every aspect of the analysis including derivitization, standards, retention indexing, and retention time locking.

Ordering information

G1676AA – Agilent Fiehn GC/MS Metabolomics RTL Library



The AMDIS results can be imported into Agilent's GeneSpring MS software. GeneSpring MS software provides powerful statistical analysis and data visualization capabilities that can help you learn more from highly complex experiments.

About Agilent Technologies

Agilent Technologies is a leading supplier of life science research systems that enable scientists to understand complex biological processes, determine disease mechanisms, and speed drug discovery. Engineered for sensitivity, reproducibility, and workflow productivity, Agilent's life science solutions include instrumentation, microfluidics, software, microarrays, consumables, and services for genomics, proteomics, and metabolomics applications.

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1-800-227-9770
agilent_inquiries@agilent.com

Europe
info_agilent@agilent.com

Asia-Pacific
adinquiry_aplsca@agilent.com

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