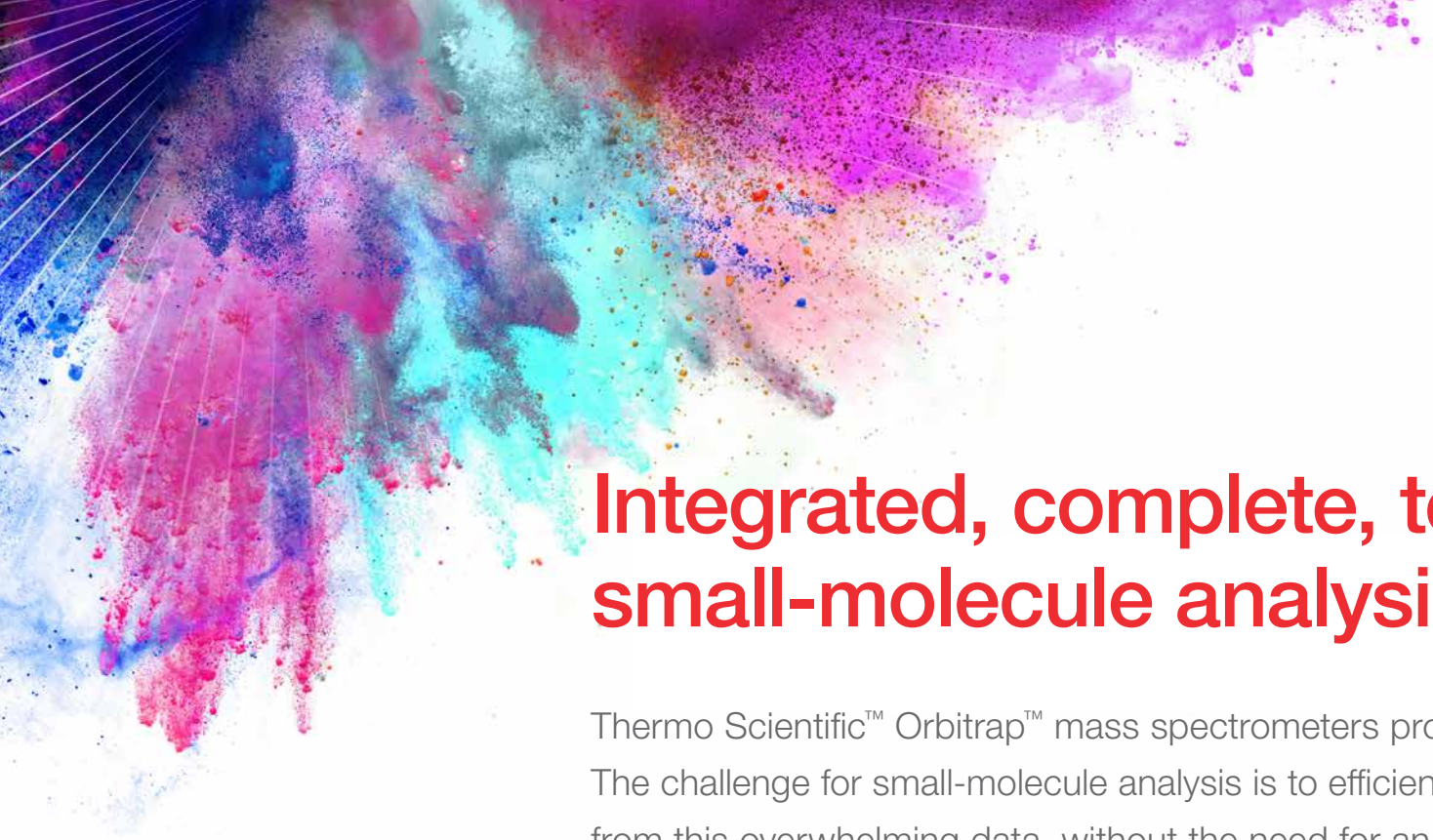

ThermoFisher
SCIENTIFIC
Compound Discoverer software
Venture into the unknowns



Integrated, complete, toolset solves small-molecule analysis challenges

Thermo Scientific™ Orbitrap™ mass spectrometers produce information-rich data. The challenge for small-molecule analysis is to efficiently extract meaningful information from this overwhelming data, without the need for an expert user.

Thermo Scientific™ Compound Discoverer™ software solves this challenge. With a comprehensive, integrated set of libraries, databases, statistical analysis, and visualization tools linked in customizable workflows, the software streamlines unknown identification, determination of real differences between samples, and elucidation of the biological pathways involved in the processed studies.

When connected to the Thermo Scientific™ Ardia™ Platform, you gain direct access to raw data and result file uploads. This eliminates data management barriers in the laboratory and allows users to collaborate remotely from anywhere with automated file centralization.

Reveal the highest confidence data using Compound Discoverer software on liquid chromatography (LC), gas chromatography (GC) mass spectrometry (MS) data

Thermo Scientific™ Orbitrap Exploris™ mass spectrometers

Thermo Scientific™ Orbitrap Exploris™ GC 240 mass spectrometer

Thermo Scientific™ Orbitrap™ Ascend Tribrid mass spectrometer

Sample to structure—pathways to insight

Know more unknowns

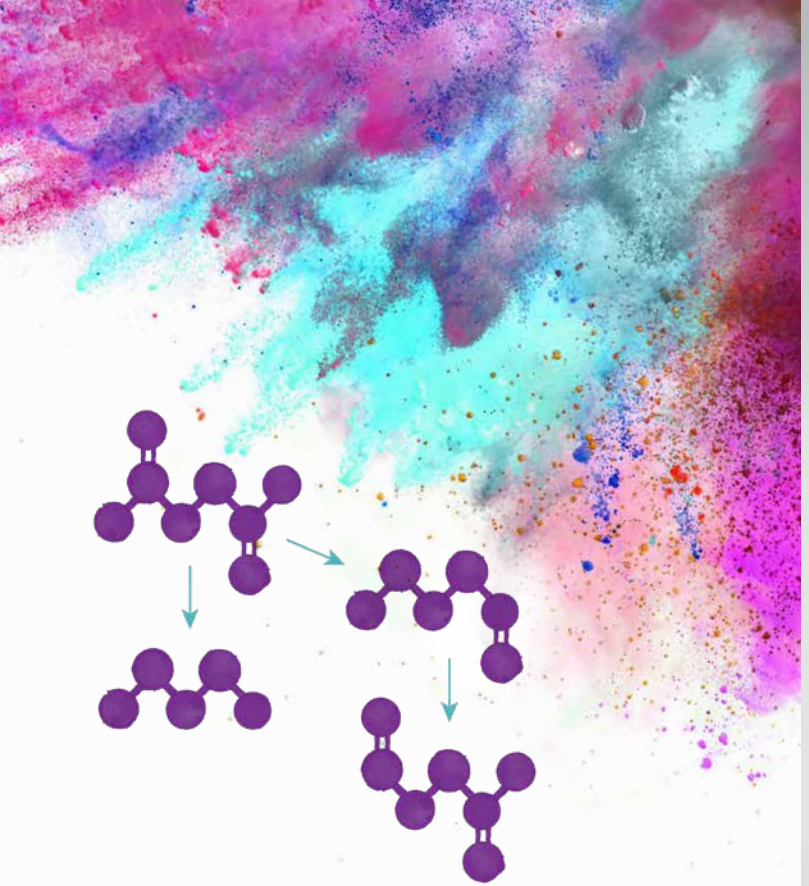
- Increase certainty using multi-factorial Peak Quality scoring to reveal, identify, and quantify with confidence
- Determine elemental composition using the isotopic fine structure of full scan HRAM data
- Separate co-eluting components by auto-deconvolution in GC workflows and identify components with dedicated high-resolution GCMS libraries
- Gain confidence in ID with automatic batch searching of MS/MS and MS^n data against Thermo Scientific™ mzCloud™ library

Go from spectra to structure

- Automatically search spectral libraries with integrated identity and similarity search modes to identify compounds
- Annotate spectra with predicted fragmentation, automatically
- Query chemical databases for putative candidates and rank these candidates according to spectral properties to accelerate compound identification process

Find real differences

- Perform differential statistical analysis using univariate paired and non-paired t-tests, ANOVA, multiple-hypotheses testing adjusted p value, fold-change
- Mine your data deeper with multivariate statistical analysis of HCA, PCA, PLS-DA, and plots
- Visualize statistical results using volcano plots, box-and-whisker plots, heatmaps, user-defined 2D- and 3D-plots, and more
- View trend charts to visualize peak areas, average peak area per group, or fractional label incorporation over time



Understand biological pathways

- Map detected compounds, statistical data and fractional label incorporation to pathways
- View pathways using Metabolika and BioCyc databases
- Analyze stable-isotope labelling data in an untargeted, hypothesis-free process and gain unlimited insights about biological changes

Supports a breadth of applications

Impurities and degradants

Identification of impurities and degradation products in drugs and foods is a critical aspect of product safety testing. Compound Discoverer software tools and customizable approaches enable confident detection of related components in complex samples.

Environmental and food safety

Food and environmental fate studies, and the analysis of contaminants in soil and water, often require identification of unknown compounds. Compound Discoverer software is ideally applicable to the analysis of metabolic fate and unknown compound identification of food and environmental degradants and contaminants.

Metabolite identification

The detection of related components in biological samples and the subsequent determination of their structures are key aspects of drug discovery research. Compound Discoverer software allows you to find, identify and flexibly report metabolites of interest.

Forensic toxicology

Targeted screening applications only find what is targeted. Compound Discoverer software enables forensic toxicologists to find unknown metabolites of drugs of abuse and structurally related designer drugs. This information can then be transferred back to screening methods to help you.

Metabolomics and lipidomics

By integrating the tools necessary to determine components of interest in small- and large-scale, complex metabolomics datasets, Compound Discoverer software offers an ideal solution for processing large-scale studies, correcting signal drift, and quickly finding and identifying compounds of univariate and multivariate statistical significance between sample groups. The software also provides a unique approach to stable-isotope labeling (SIL) studies, with a completely untargeted, hypothesis-free analysis to maximize potential for discovery. The visualization of fractional label incorporation over times or sample groups, along with overlaying results with metabolic pathways, eliminate the tedious manual steps. Additionally, the integration of the Thermo Scientific™ LipidSearch™ software as a node within Compound Discoverer software enhances lipid identification confidence and streamlines analysis.

Extractables and leachables

Extractables and leachables (E&L) analysis is crucial in the development of pharmaceuticals, food packages, and medical devices to ensure product safety and quality. The complexity of this analysis mandates extensive investigations for known and unknown and the use of multiple analytical techniques for volatile and semi-volatile (GCMS) and non-volatile (LCMS). Compound Discoverer software is positioned to match the required needs with its powerful unknown analysis tools in both GCMS and LCMS data files, and its integrated search of mzCloud library which contains over 500 E&L compounds with >40,000 spectra.

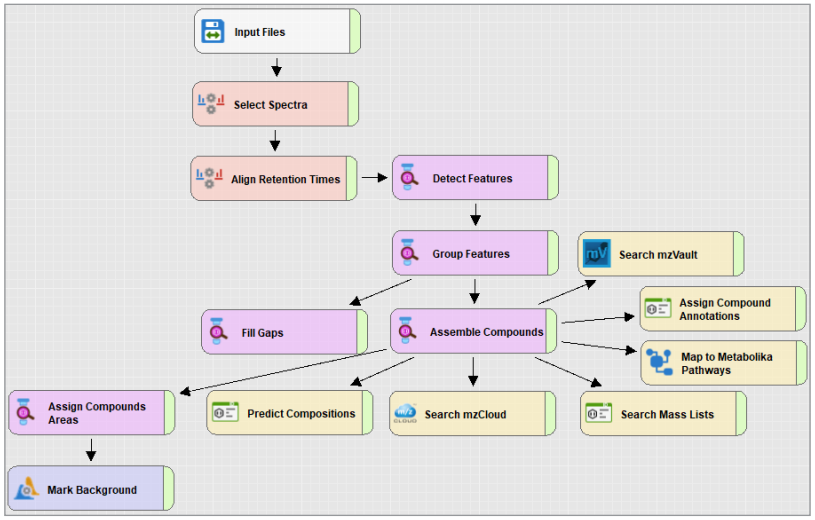
Speed, simplicity, and flexibility match your requirements

Easily customizable workflows

Empower your data processing with customizable workflows. Drag and drop workflow nodes, from an extensive list of processing tools, into workflow trees that specify your desired data flows. Save your workflow as a template or pick from many pre-made templates to simplify setup. Get up and running quickly with the Study and Analysis Wizard. Add your data, define your study and sample groups, pick a workflow template and start processing. You can also save time by partially re-running a workflow if needed.

Interactively linked results

The software makes it easy to visualize results in a meaningful way. Customizable data visualization allows you to review only the data you choose. Configurable layouts let you quickly change between views. Multiple monitor support ensures that you can view more data at once. Expand your processing horizon with the scripting node which allows the integration of your code, made in R or Python™, to process results and add functionalities.



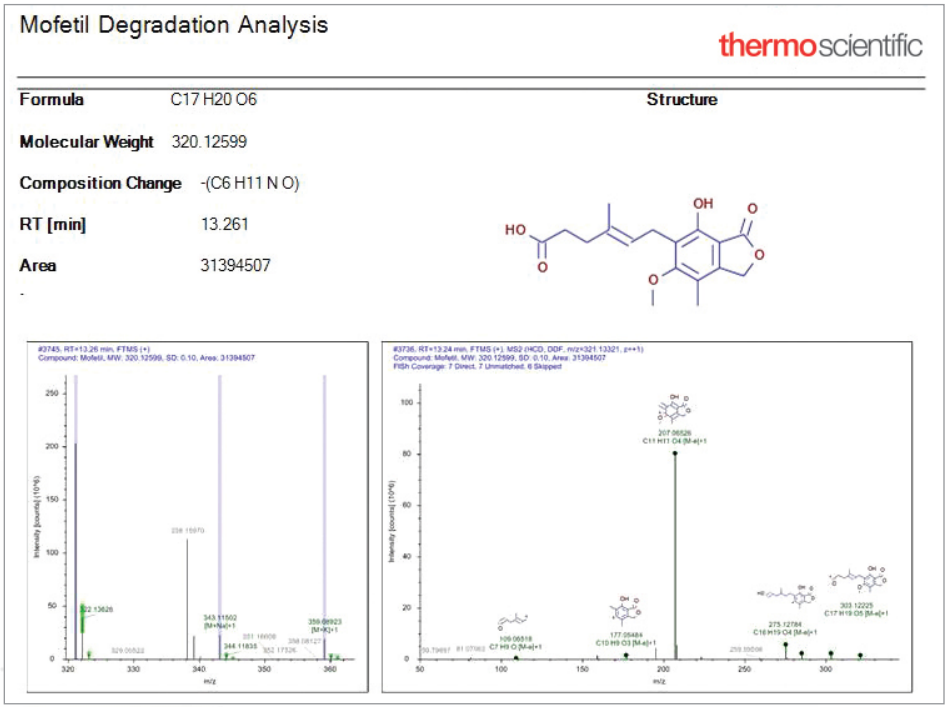
Compound Discoverer workflows reduce the processing clicks needed to transform mass spectral data into results.

"Compound Discoverer software, as an integrated, well-optimized and user-friendly platform, saved an additional and valuable time by preventing us from getting lost among thousands of raw spectra, individual databases and exported data."

— Engin Bayram, MS Application Scientist, Reotek Cihazlar Ltd.

Share results with customizable reporting

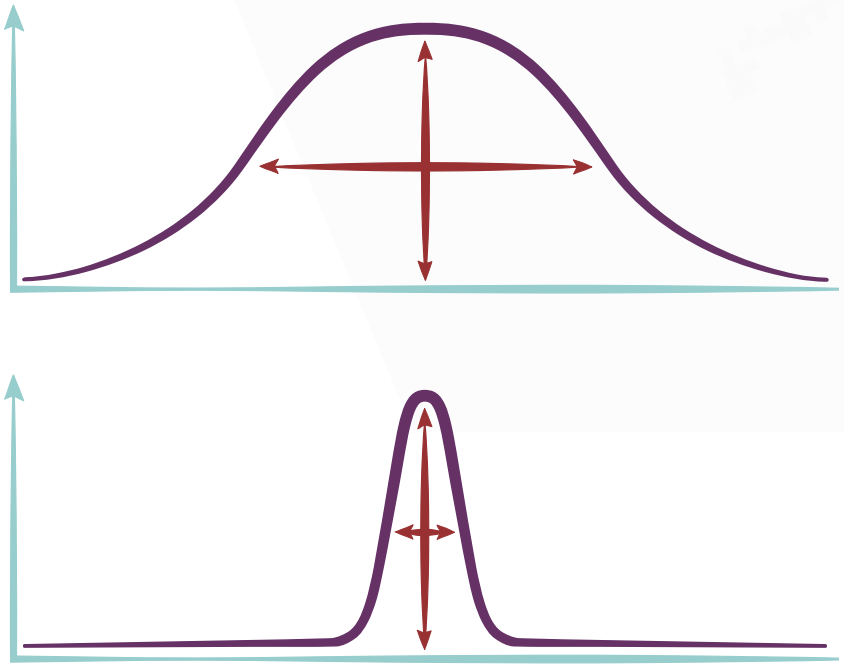
Powerful data-processing tools quickly create valuable results, but these results and supporting information must also be shared. Compound Discoverer software provides customizable reporting so results can be easily transferred to others that need them. Multiple output formats also allow you to transfer data to informatics software.



Customized reporting helps you make real use of results.

Reveal higher quality chromatographic peaks

Peak Quality Factors provide a powerful scoring mechanism to identify good chromatographic peaks, by measuring certain properties, such as jaggedness or symmetry, which describe the overall peak performance. The aggregated Peak Quality Factor score can then be used to filter out poor peaks, resulting in better data. In addition, the automatic detection and grouping of MS^1 fragment ions reduce data complexity.



Compound Discoverer software measures and reports peak quality.

Know more unknowns

Unknown identification is one of the toughest challenges in many small-molecule analyses. It requires both comprehensive high-quality spectral acquisition, such as those achieved when using Thermo Scientific™ AcquireX™ software workflow, as well as a collection of matching algorithms. By seamlessly integrating multiple tools for gathering identification information, Compound Discoverer software provides a faster route towards solving this challenge and enables you to identify more of your unknowns.

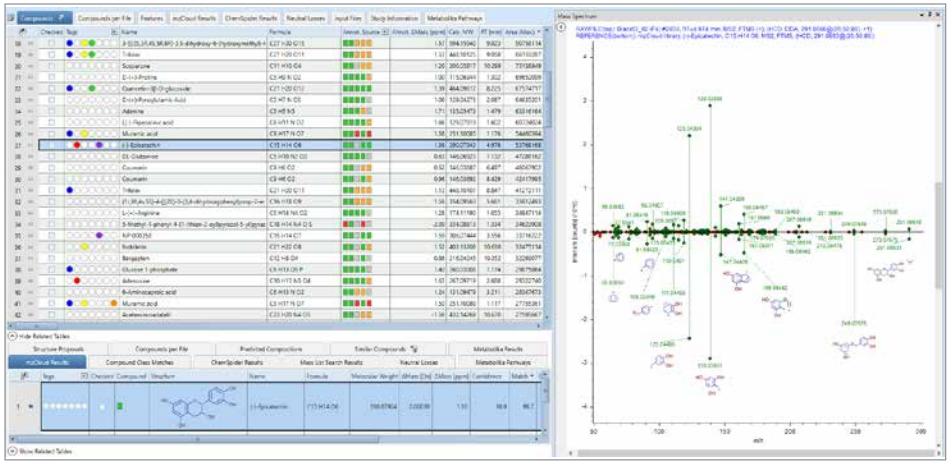
Automatically identify components

Identify more unknowns automatically and faster—with connection to the online mzCloud 2.0 spectral libraries or local Thermo Scientific™ mzVault™ spectral libraries:

- Search mzCloud libraries, in identity mode with MS/MS or MS^n data to annotate compounds or similarity mode to provide structurally similar candidates or substructures, to gain even more information to use for unknown identification
- Effortlessly export spectra and compounds with spectra to mzVault libraries directly from Compound Discoverer software to expand your scope of identified compounds

Determine elemental composition—including fine isotopes, using HRAM MS, MS/MS, and MS^n data

Access further annotations—use compound information to search online user-defined or local user-made multiple chemical databases for annotation

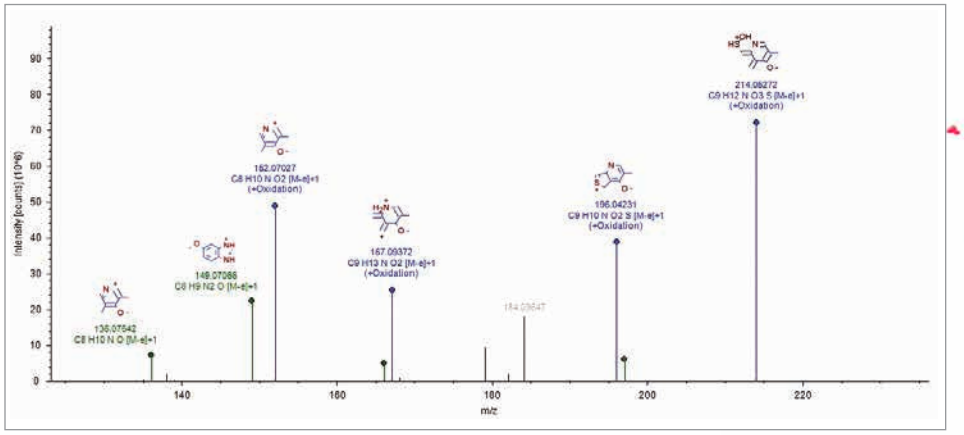


Automatically identify unknown compounds using the mzCloud spectral library, within the environment of Compound Discoverer software.

Elucidate structures

Simplify determination of compound structure by predicting and displaying fragments onto spectra using the built-in HighChem Fragmentation Library of reference fragmentation mechanisms.

This feature allows annotation of either expected compounds, such as metabolites, impurities, or breakdown products, and of putative structures supplied by chemical databases or the user.



Structurally annotated peaks provide more certainty in results and allow visualization of modified portions of expected compounds.

Rank order putative results

Database searches alone only produce putative candidates for identification. With Thermo Scientific™ mzLogic™ algorithm, you can use the extensive fragmentation spectral information in mzCloud library to rank order putative database results.

Combining mzCloud library similarity searching with structure similarity matching provides improved candidate ranking.

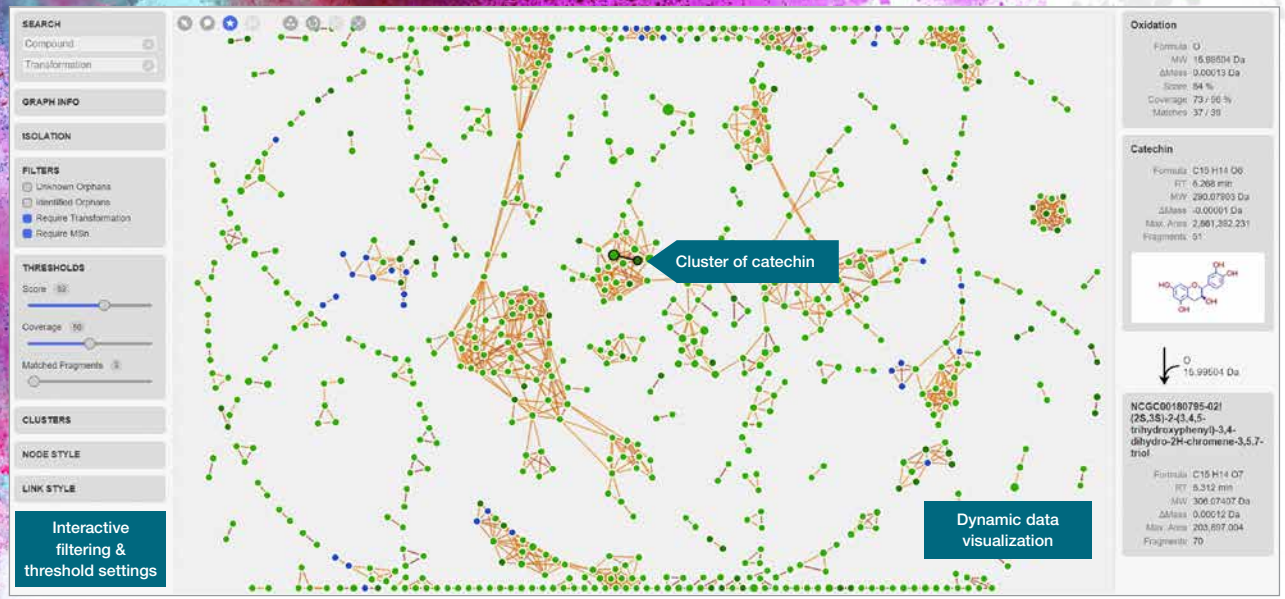
mzCloud 2.0 library, new format and features, same multi-dimensional comprehensive mass spectral library

mzCloud 2.0 library is the world's most extensively curated mass spectral fragmentation library, with over 16.5 million spectra in the repository. Beyond generating matches for identification, integrated batch searching of mzCloud library can also produce similarity matches. Searching makes use of stepped collision energy scans to automatically model results using the library's multiple energy levels of reference fragmentation data.

mzCloud 2.0 library

- Extensively-curated online library with highest quality data
- Includes small molecule compounds relevant to all applications
- Highly-curated, highest-quality data
- Multiple energy levels, multiple activation types, and MS^n spectral trees
- Supports both research and targeted screening workflows
- Faster batch searching of data
- More meta-data available (including compound class, CAS numbers, HMCD IDs)

m/z™ CLOUD



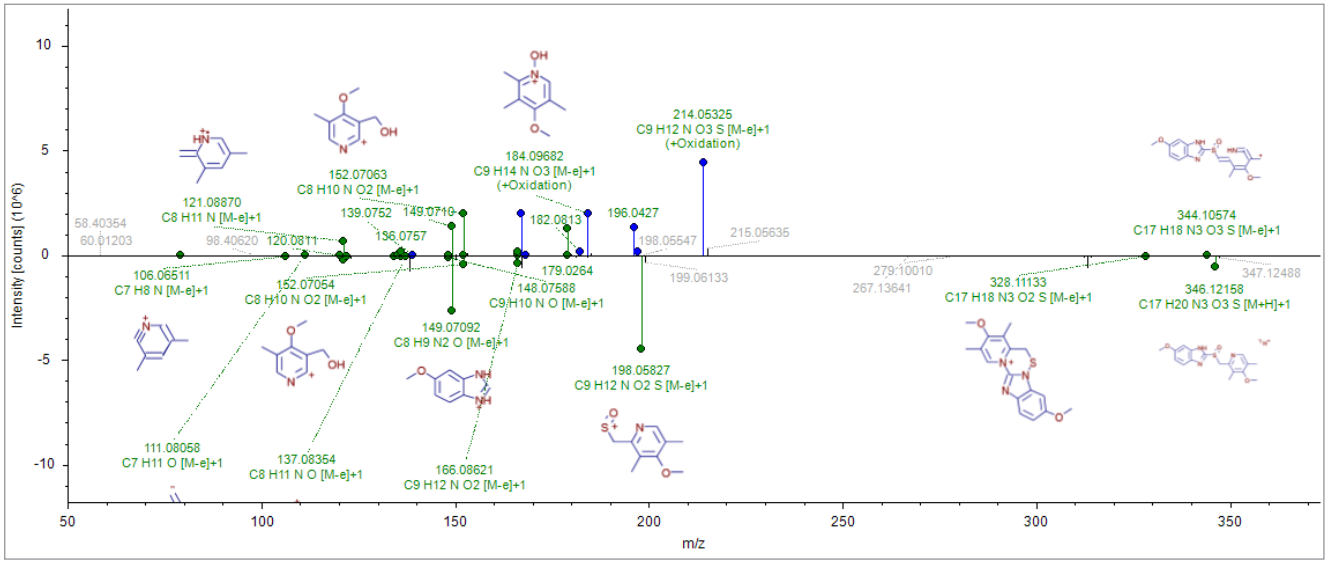
The software builds intrinsic compound-based molecular networks. The networks are interactive with dynamic data visualization through node and edges coloring and annotation in the associated panes. Parameters are adjustable from within the network page and important findings can be tagged back in the Compounds table.

Know more with molecular networks

While the journey to discovery often focuses on connections between samples, the intrinsic relationship between compounds within a study offers a great added value. Compound Discoverer software enables the exploration of such links through molecular networks, where you can interactively explore relationships between compounds in your analysis based on transformations and spectral similarity. These interactive networks can reveal insights, for example, in Phase I and Phase II transformations, in emerging contaminants, and even in unknown identification via the transitive relation of an identified linked compound or via homologous series/clusters.

Identify drug metabolites more confidently

Metabolite identification is a critical part of drug discovery research. Scientists in this field are often challenged to characterize the metabolic fate and rate of the parent molecule once it is introduced into the subject's biological system. Compound Discoverer software provides the tools to predict metabolic transformations in a combinatorial system, query these predictions in the study samples, and help elucidate the structure of the found metabolites utilizing matching to mzCloud and mzVault spectral libraries and the advanced spectral annotation algorithms powered by Thermo Scientific™ Mass Frontier™ spectral interpretation software.

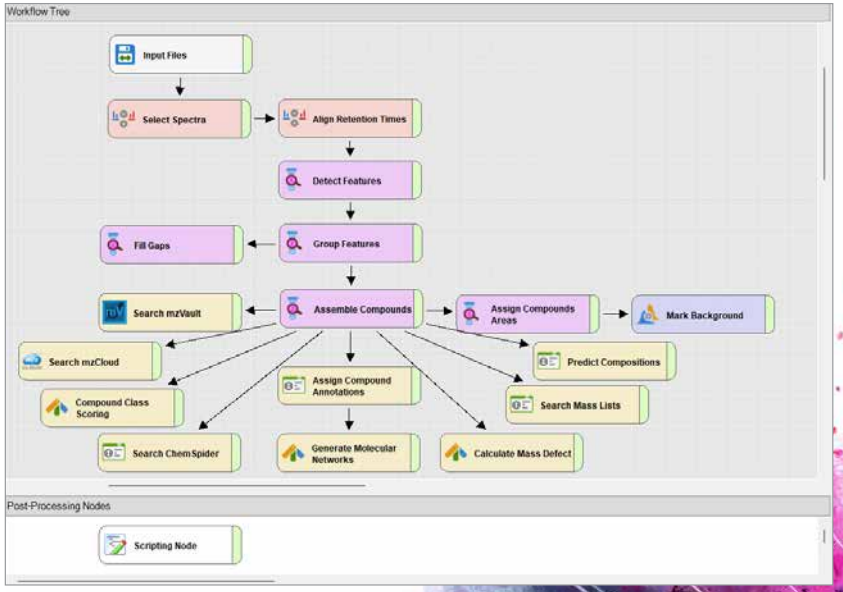


The software helps in impurity profiling and metabolite identification by comparing the suspect MS^n spectra (up) to those of the parents (down), using FiSH scoring and fragment annotation, and taking into consideration preserved fragments (green sticks) and transformation-associated modified fragments (blue sticks).

Untargeted per- and polyfluoroalkyl substances (PFAS) analysis workflow

PFAS, an expansive class of enduring toxic chemicals surpassing 15,000 members, is globally monitored by regulatory agencies. In addition, thousands of potential transformation products are actively being discovered in the environment. Regulatory methods typically use conventional quantitative analysis based on available reference standards. However, this approach fails to see the whole picture, as non-targeted workflows are critical to help define the true extent of PFAS contamination. Untargeted analysis utilizes tools which deploy PFAS' intrinsic properties such as negative mass defect (MD), homologous series formation, and progressive retention times tied to chain length. These tools are vital to ensure the consideration of all PFAS in evaluating health and environmental outcomes. Compound Discoverer software unifies and extends these tools in a pre-defined turnkey workflow by adding spectral library matching against mzCloud library, in-silico compound databases containing over 48,000 structures, screening for over 700 PFAS signature fragments via the integrated Fluoromatch suite database, and molecular networking using a CF2 transformation to connect homologous series. Additionally, suspect compounds can be ranked by mzLogic algorithm, through their spectral similarity to known compounds, adding a layer of confidence in PFAS subclass assignment.

A



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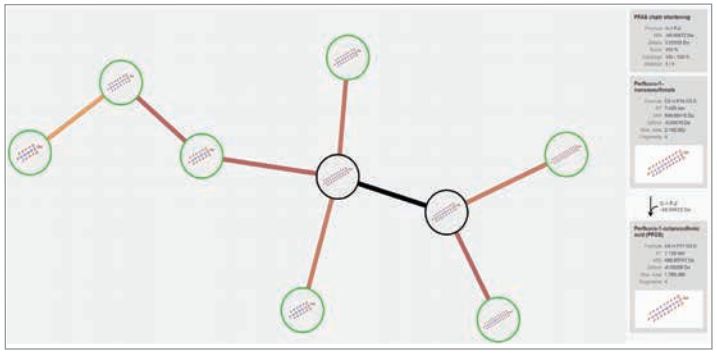

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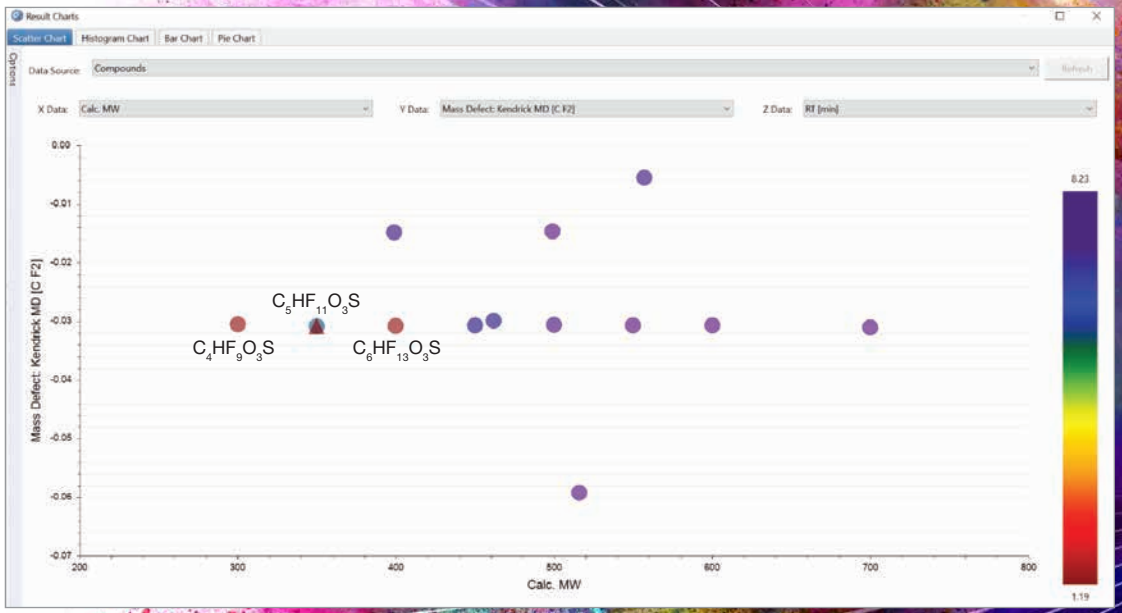


(A) Compound Discoverer workflows reduce the processing clicks needed to transform mass spectral data into results. (B) Molecular network cluster of PFAS related compounds (C) Mass Defect plot, showing a PFAS related homologous series of compounds.

Turn data into knowledge

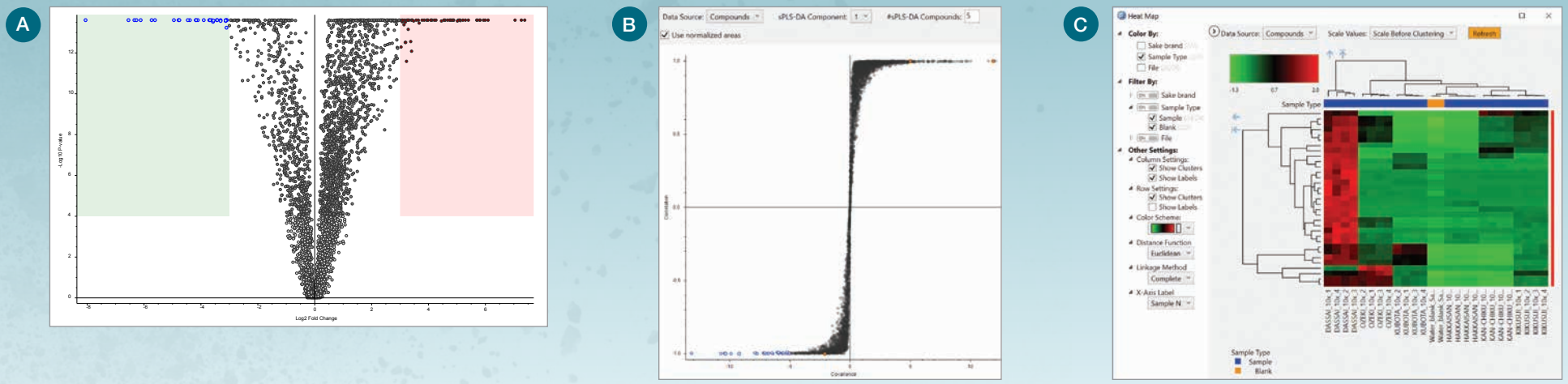
Support your study with a suite of tools that turn raw data into knowledge. This powerful software has the ability to reduce data complexity, provide flexible data visualization, advanced statisics, including multiple-hypothesis testing corrections, and biological pathway mapping through BioCyc and Metabolikia databases. These tools build on the certainty provided by Compound Discoverer's unique identification and structural elucidation capabilities because confidence in pathway analysis is dependent on the confidence in underlying identifications.

Find and visualize real differences

Whether you are performing metabolomics research or looking for emerging environmental contaminants, this powerful software toolset enables you to quickly find real statistical differences—the differences that matter—between sample groups. Quickly view trends in components across a study or identify the key components of interest between multiple sample groups using interactively linked displays. Move quickly from high-level PCA visualizations to individual components with one click.

Capabilities

- Differential statistical analysis: univariate (t-test, ANOVA, fold-change) with multiple-hypothesis testing correction, and multivariate (PCA, HCA, and PLS-DA)
- Visualization of fractional label incorporation for multiple samples (isotopologue plot) and for trends over time (trendline chart)
- Monitoring of study performance at compound level with area, CV%, and median values at sample group and quality control levels
- Pathway mapping and visualization using Metabolika and BioCyc databases
- Interactive heatmaps with hierarchical clustering analysis
- Automatic background removal with powerful and flexible filtering, single compound, or multiple compound selection, and assigning compounds into customized tagged groups



(A) 33 compounds were selected (blue) in the volcano plot based on p-value (ANOVA, Tukey test) and fold change. The same set of compounds is automatically highlighted in the S-plot (B) of the PLS-DA and the heat map (C). When clicking on a point in a plot, the software will navigate to the corresponding compound in the table and display XIC and spectrum.

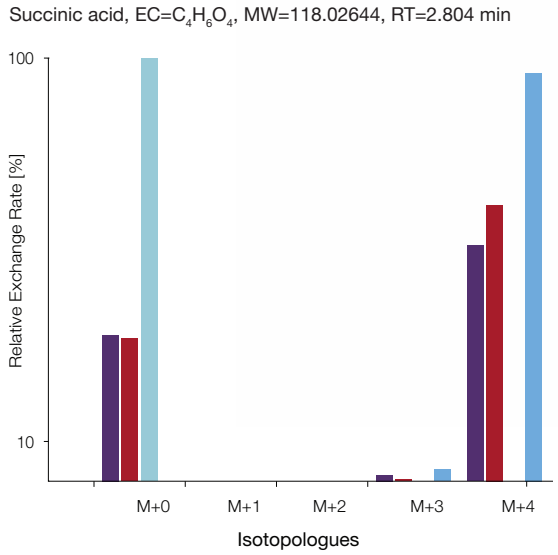
Streamline stable isotope labeling analysis

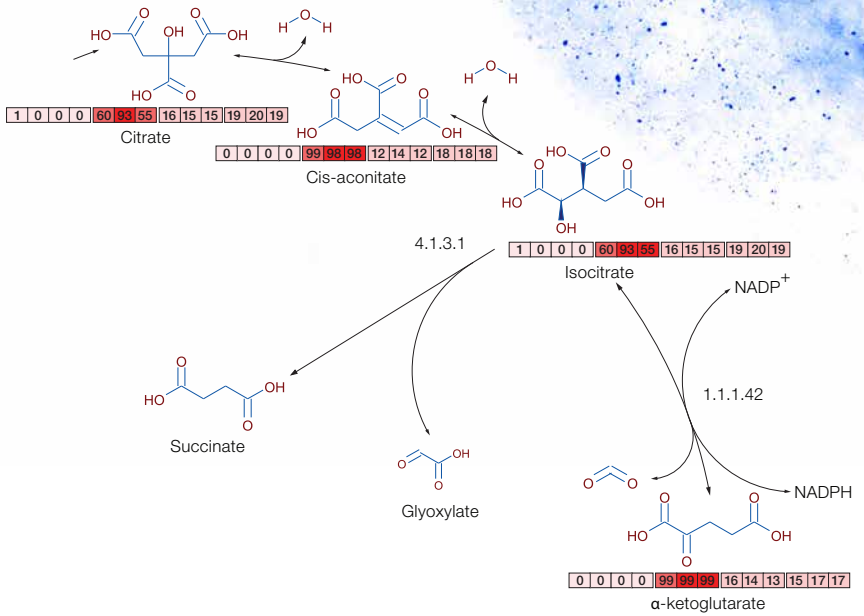
Stable-isotope labeling experiments are fundamental to understanding metabolic pathways and providing mechanistic insights into biological processes. Compound Discoverer software makes full use of high-resolution Orbitrap mass spectrometer data to offer advanced, streamlined untargeted workflows for stable-isotope labeling. Using an unlabeled reference sample, it automatically detects all compounds, determines their elemental composition, and identifies their labeled counterparts in labeled samples. Any isotopically labeled element can be used for automatic isotopologues detection.

The software reports the fractional label incorporation (exchange rate) after natural abundance correction for each compound. The exchange rate and other statistical data can be overlaid onto pathways using Metabolika, which is fully integrated.

Exchange Rate [%]

0	1	2	3	4
0	0	0	3	97
0	0	0	3	97
0	0	0	4	96
30	0	0	1	69
32	0	0	0	68
34	0	0	2	65
38	0	0	2	60
39	0	0	2	59
41	0	0	0	59
100	0	0	0	0
100	0	0	0	0
100	0	0	0	0
100	0	0	0	0
100	0	0	0	0
100	0	0	0	0





Compound Discover software supports untargeted stable-isotope labeling workflows with visualizations of fractional label incorporation. Left-to-right: Details for fractional label incorporation (exchange rate) for isotopologues of succinic acid (C4H6O4) across 15 samples; isotopologue plot showing exchange rates for isotopologues of succinic acid measured for 4 samples; Metabolika pathways showing a detail of the TCA cycle with data overlay of the overall exchange rates measured across 4 sample groups with multiple replicates.

The complete package for small-molecule unknown data processing

Providing a complete software platform for small-molecule research in a customizable single platform enabling sample to structure information. Address your small molecule identification needs and workflows including untargeted metabolomics, drug metabolism, impurity, E&L, environmental, food & beverage, and forensic research.

Offering in-depth support: visit the help portal

Connect with support and explore the operation manuals, release notes, quick start guides and more-all from one location.
https://docs.thermofisher.com

mzCloud advanced mass spectral database

www.mzcloud.org

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