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Orbitrap GC-MS HRAM Metabolomics Library

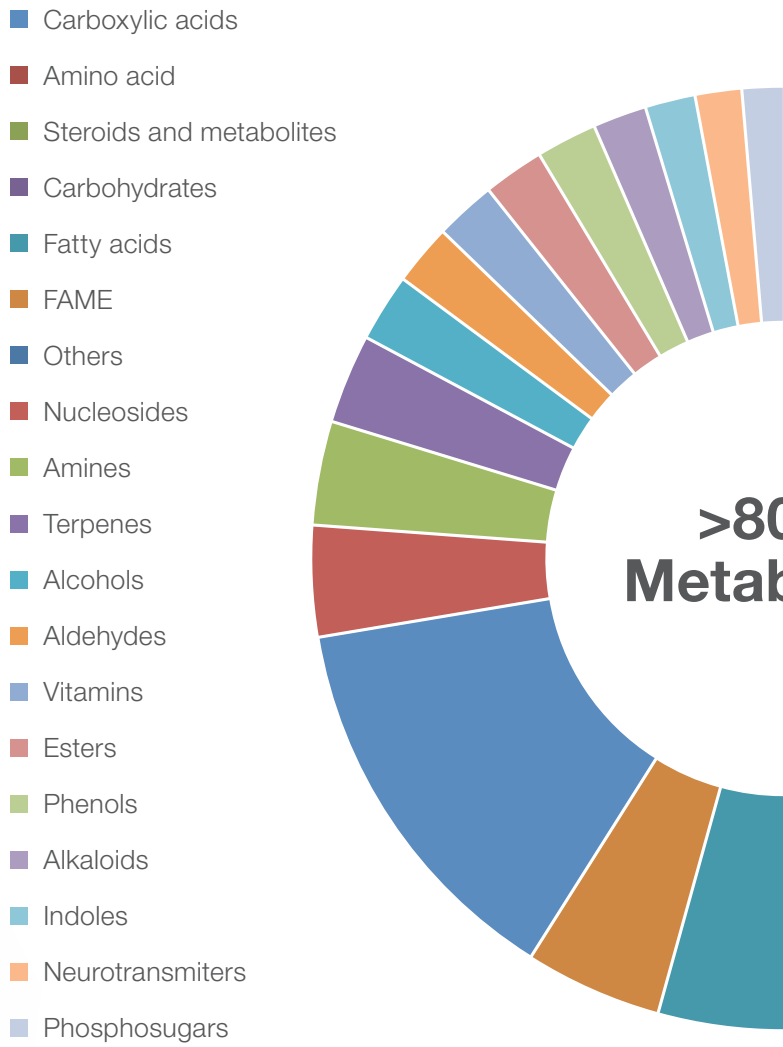
Explore deeper into the metabolome

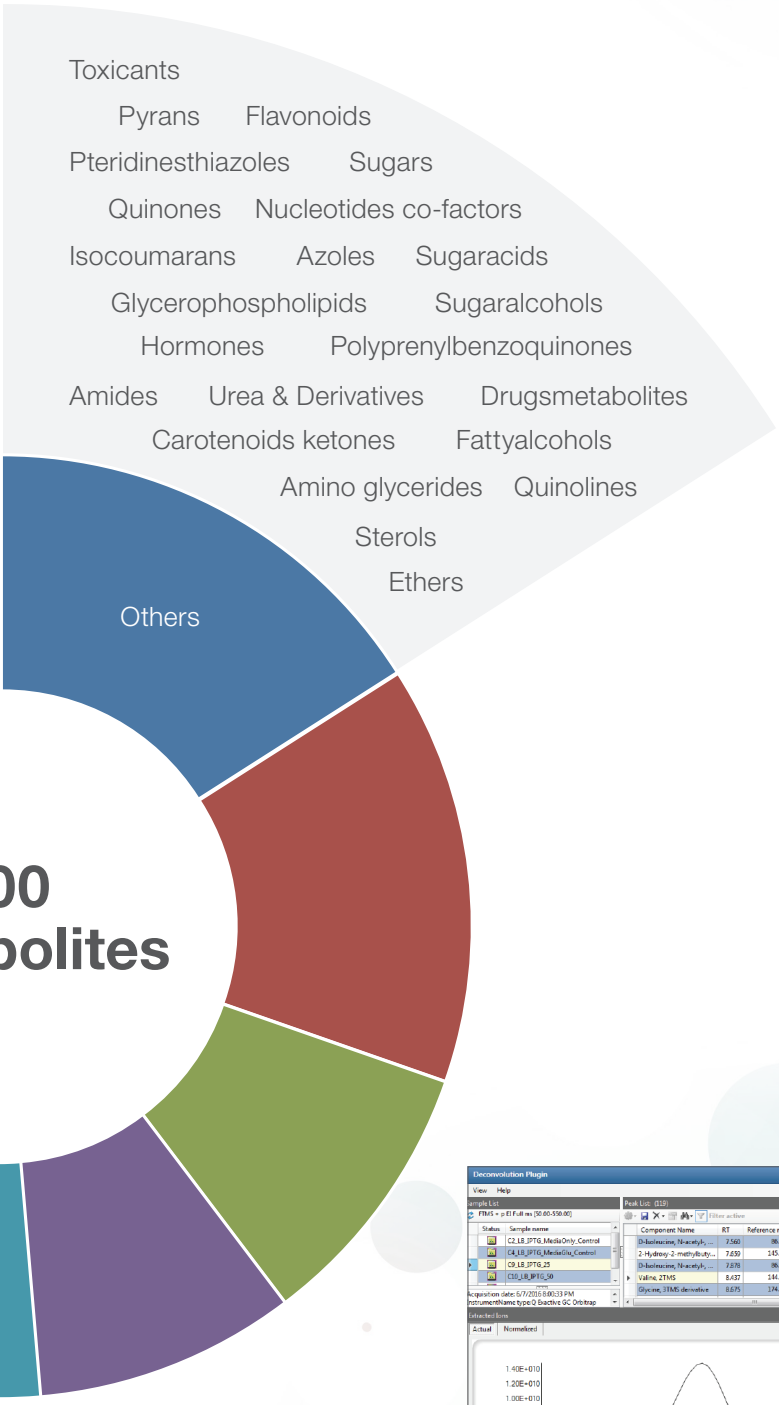
ThermoFisher SCIENTIFIC

Identify more metabolites

Biology is complex. To decipher these complexities, metabolomics analysis demands sophisticated analytical technologies and advanced software solutions. The Thermo Scientific™ Orbitrap™ GC-MS HRAM Metabolomics Library is the first commercially available high resolution accurate mass (HRAM) metabolomics library for electron ionization (EI) GC-MS. It contains more than >900 retention indexed unique entries from more than 800 metabolites, providing a broad coverage of primary and secondary metabolites (including volatiles) in plants, animals and microbes. When used in combination with powerful Orbitrap GC-MS technology and unique Thermo Scientific software data processing tools, the difficult challenge of metabolite identification in untargeted experiments is easier than ever before.

- High resolution, high mass accuracy spectra acquired at 60,000 RP (*m/z* 200)
- Spectra refined and curated with elemental composition of each EI fragment verified
- Kovats retention index entries
- PubChem ID for unique metabolites
- Can be used in combination with existing unit mass libraries



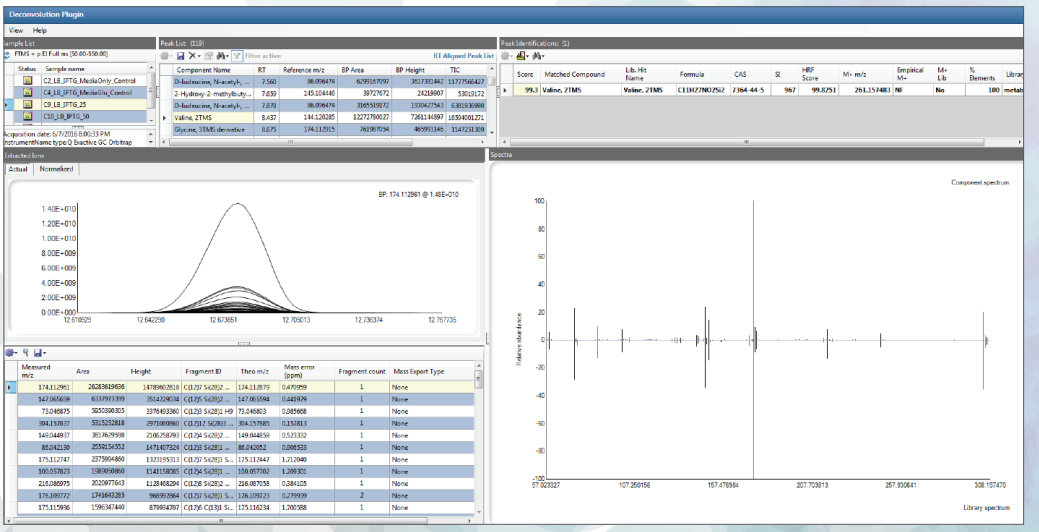


Automated metabolite identification

Automatic compound identification in a non-targeted way was once science fiction. Today, with the Orbitrap™ GC-MS and unique proprietary data mining tools, it's a reality.

The sensitivity, selectivity and dynamic range of the Orbitrap GC-MS provides an unprecedented level of compound coverage in GC-MS, and intelligently mines data sets using automated software workflows that ultimately identify metabolites within the sample.

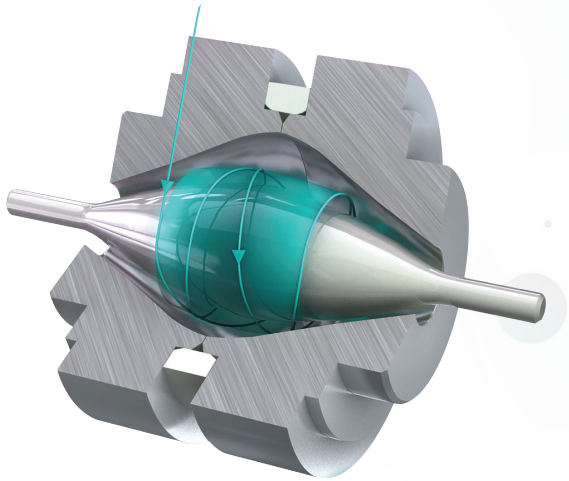
Data interpretation is available in minutes, instead of weeks, and an entirely new host of new possibilities is unleashed within your laboratory.



The core of successful metabolomics—powered by Orbitrap mass spectrometry

The success of metabolomics research lies with proven Thermo Scientific™ Orbitrap™ technology. Workflows that include Orbitrap mass spectrometers have already been widely adopted for life science applications such as proteomics. Based on published reports, the same technology is also suited for metabolomics.

The Orbitrap mass spectrometers represent the leading mass spectrometry (MS) technology for analyzing samples that are complex both in the sheer number of analytes present and in the type of sample matrix, such as blood, food, urine, etc. Additionally, with a breadth of chromatographic separations and integrated data analysis tools, the Orbitrap mass spectrometer enables researchers to successfully analyze physicochemically diverse samples in metabolites—making us the leader in metabolomics, delivering solutions to keep you at the forefront of science.



Thermo Fisher Scientific would like to acknowledge and thank the following people for their contributions:

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Find out more at **thermofisher.com/OrbitrapGCMS**

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