Designed to unravel complex chemical structures
Thermo Scientific Orbitrap IQ-X Tribrid mass spectrometer
The future of small-molecule analysis is here

Designed for small-molecule analysis, the Thermo Scientific™ Orbitrap IQ-X™ Tribrid™ mass spectrometer redefines small molecule identification and characterization of unknown compounds. The trusted Tribrid architecture provides the richest MS^n data by leveraging the best quadrupole, linear ion trap and Thermo Scientific™ Orbitrap™ mass analyzers combined with intelligent data acquisition. Ease-of-use hardware improvements for automatic, hands-free calibration along with a fit-for-purpose software interface allow you to overcome the traditional bottlenecks in small molecule structure elucidation workflows.

The Orbitrap IQ-X Tribrid instrument seamlessly integrates with our industry-leading solutions—including Thermo Scientific™ Vanquish™ Duo UHPLC Systems, Thermo Scientific™ FAIMS Pro Duo interface, and Thermo Scientific™ Compound Discoverer™ software—for a complete workflow for small molecule structural characterization.
• Increase certainty
Real-Time Library Search increases confidence in unknown metabolite annotation and structure assignment of lipid isomers through search-driven, real-time spectral matching against local mzCloud™ or Thermo Scientific™ mzVault™ spectral libraries. Using decision-based triggering of MSⁿ or alternate fragmentation scans, you can tailor the analysis based on what information is needed and what is already known about the analytes in question.

• Acquire rich, meaningful data
Expanded Thermo Scientific™ AcquireX™ intelligent data acquisition workflows increase sample profiling efficiency and depth of analysis by automating inclusion/exclusion list creation for MSⁿ. The MSⁿ mass range has also been extended down to m/z 40 to capture low-mass fragments and differentiate challenging isomers.

• Expand experimental possibilities
The Orbitrap IQ-X Tribrid mass spectrometer provides experimental versatility for structural determination with collision-induced dissociation (CID), high-energy collision dissociation (HCD), and optional Thermo Scientific™ Ultraviolet Photodissociation (UVPD). Collision energies (CE) can be optimized in real time by making use of assisted CE determination. Optionally available are the Thermo Scientific™ 1 Million (1M) Resolution option to resolve isobaric components and fine isotopes, and the FAIMS Pro Duo interface for orthogonal selectivity based upon differential ion mobility.

• Spend more time on reviewing results, less on instrument setup
The Auto-Ready ion source standardizes calibration for consistent instrument performance with automated, remote calibration. Pre-built methods and optimized templates enable you to analyze complex samples effortlessly. Method templates define data acquisition for a variety of small molecules using combinations of high-resolution accurate-mass (HRAM) and ion trap mass analyzers with MSⁿ fragmentation using CID, HCD, or optional UVPD. The instrument increases sample throughput with fast polarity switching to acquire positive and negative mode data in a single run.
Next-generation Tribrid mass spectrometer for small molecules

Designed with new capabilities, the Orbitrap IQ-X Tribrid mass spectrometer is the cutting edge of small molecule analysis. Proven and trusted Tribrid architecture combines quadrupole, ion trap, and HRAM Orbitrap mass analyzer technologies for acquisition of the richest MS^n data for every sample. All fragmentation techniques—CID, HCD, and optional UVPD—are available at any stage of MS^n, with subsequent mass analysis in either the ion trap or ultra-high-resolution Orbitrap mass analyzer.

Enhanced capabilities

Real-Time Library Search uses Real-Time MS² spectral matching against local mzCloud or mzVault spectral libraries for decision-based triggering. This leads to higher confidence metabolite annotation, and improved characterization of unknowns.

Segmented quadrupole delivers higher transmission at narrower isolation widths, down to 0.4 m/z, improving selectivity for co-eluting compounds.

New AcquireX acquisition workflows increase coverage and throughput with the flexibility to submit several experiments from a single sequence, and with new algorithms for improved background exclusion and component detection.

Auto-Ready ion source provides scheduled, or on demand, remote system checks and calibrations, without disruption to your LC-MS system.

Expanded experimental options

UVPD produces fragment ions indicative of double bond locations and other unique structurally diagnostic information for analysis of various compound classes, including lipids and glucuronides.

1M provides higher resolution and fine isotope information to help determine elemental composition of the analytes.

FAIMS Pro Duo interface is a differential ion mobility device that increases selectivity and reduces interferences, for improved detection with expanded lower limits of quantitation (LOQ).
Advanced Active Ion Beam Guide
Prevents neutrals and high velocity clusters from entering mass resolving quadrupole

EASY-IC source
Introduces a calibrant ion to help maintain high mass accuracy

Electrodynamic Ion Funnel
Focuses ions; has broad tuning curves

Round Bore Ion Transfer Tube
Controls ion flux into the mass spectrometer for reduced unintended fragmentation

Segmented Quadrupole
Improves transmission at higher resolution; symmetric transmission across the isolation window

Auto-Ready ion source
Automatically calibrates the instrument without needing to disconnect the LC

Extended Mass Range
Analyzes MS^n fragments down to m/z 40 to help differentiate isomers

Real-Time Library Search
Allows the instrument to perform decision-driven scans based on real-time spectral library search results

1M resolution option
Increases resolution up to 1,000,000 FWHM at m/z 200 for enhanced isotopic pattern assessment

Orbitrap Mass Analyzer
Offers resolution up to 500,000 FWHM at m/z 200 and scan rates up to 40 Hz at 7500 FWHM at m/z 200

UVPD option
Provides photon-driven fragmentation to generate unique fragments

Linear Ion Trap Mass Analyzer
MS^n and sensitive mass analysis of fragments resulting from CID, HCD, and UVPD

Ion Routing Multipole
Enables parallel analysis and HCD at any MS^n stage

OPTIONS
UVPD | 1M | FAIMS Pro Duo interface
Improved structural characterization with Real-Time Library Search

Acquisition and interpretation of mass spectra to characterize small-molecule unknowns can be a formidable task. Sample complexity, background interferences, compound structural diversity, and the shortage of robust data processing tools can make it difficult to set up analytical experiments and interpret data.

The Orbitrap IQ-X Tribrid mass spectrometer overcomes these challenges with advanced data acquisition and processing tools that are accessed in a single powerful instrument control software, harmonized across all next-generation Thermo Scientific™ mass spectrometers.

Real-Time Library Search guides data acquisition and analysis

Using an offline version of mzCloud or a custom-built spectral library, Real-Time Library Search evaluates MS² spectra in real time to trigger additional scan events based on the search results.

- Unknowns can preferentially trigger MSⁿ or alternate fragmentation events on fragments that did not match spectral library, to obtain more structural information.
- Additional scans can be triggered on possible isomers to aid in differentiation.
- Compounds with a library match can be blocked from triggering additional scans to instead collect data on other unknowns.

Find more metabolites with less effort using Met-IQ

The Met-IQ data acquisition strategy uses Real-Time Library Search to find spectral similarities with library compounds. When an MS² spectrum is similar to a library spectrum, such as a drug-metabolite compared to the original drug, additional information is collected. This has multiple benefits:

- Only compounds with matching fragments are selected for additional scans, it also identifies them as potential targets during the data processing step.
- Limiting additional data collection to only structurally related compounds means the instrument spends more time collecting MS² spectra for a more in-depth analysis.
- Analyzing metabolized amprenavir six additional potential drug metabolites were found in a single run using Met-IQ acquisition compared to a traditional data dependent acquisition (DDA).

Sample provided by Dr. Shuguang Ma, Genentech, South San Francisco, CA
For research purposes only.
Application-specific methods are one click away.
The intuitive method editor features a drag-and-drop user-friendly interface with predefined, optimized method templates.

- Run advanced experiments effortlessly with method templates for a large range of applications.
- Edit parameters in easily accessible panels, featuring recommended defaults for each experiment.

Go from data to actionable results with a suite of software tools:

- **mzCloud™ mass spectral library**: A database with over 19,000 compounds to help annotate a wide variety of unknowns.
- **Thermo Scientific™ mzVault™ spectral library**: Curates custom libraries from known standards.
- **Thermo Scientific™ AcquireX™ intelligent data acquisition software**: Allows automatic generation of inclusion/exclusion lists and iterative sample interrogation.
- **Thermo Scientific™ Almanac™ application**: Provides remote access to instrument health and alerts to any issues.
- **Thermo Scientific™ FreeStyle™ software**: Allows for rapid and straightforward examination of chromatograms and mass spectra.
- **Thermo Scientific™ TraceFinder™ software**: Provides high speed quantitative processing of large data sets.
- **Thermo Scientific™ LipidSearch™ software**: Enables rapid high confidence analysis of lipids.
- **Thermo Scientific™ Mass Frontier™ spectral interpretation software**: Helps analyze a compound’s fragments and structure.
- **Thermo Scientific™ Compound Discoverer™ software**: Identifies unknowns and performs statistical analysis.
- **Thermo Scientific™ Xcalibur™ software**: Provides a centralized platform for instrument control and a wide variety of data processing tools.
- **Thermo Scientific™ mzLogic Algorithm**: Compares spectra against an extensive library of fragmentation data to get the highest confidence candidates for unknowns.

**AcquireX workflows**

**Real-Time Library Search**
Metabolomics like never before

The Orbitrap Tribrid IQ-X mass spectrometer offers a streamlined approach to routinely achieve comprehensive metabolome coverage with confident compound annotation through comparison against spectral libraries or by de novo structural elucidation of unknown metabolites. The power of the Orbitrap mass analyzer combined with AcquireX data acquisition workflows and Real-Time Library Search of MSn spectra redefines possibilities for small molecule research. Optional UVPD generates unique fragments for unparalleled lipid structure characterization.

Intelligent solutions to metabolomics problems

Getting comprehensive data in metabolomics is challenging. There are complex matrices and an extensive number of unknowns to be investigated. Using Real-Time Library Search, data can be collected intelligently to ensure not only comprehensive coverage, but also that the most useful structural information is being collected the first time.

Initial MS² from plasma compound

![Initial MS² from plasma compound](image)

mzCloud MS² for stachydrine

Mirror plot of stachydrine and unknown compound triggered for MSn.

Real-Time Library Search for added confidence

Static parameters do not always yield sufficient information, compounds can be under-fragmented or missing a critical fragment for confident annotation. Using Real-Time Library Search, the instrument interrogates the library in real time and collects additional data on poorly annotated compounds. For example, stachydrine yields few structural peaks using standard settings (see above). Triggering a higher normalized collision energy (NCE) scan guided by Real-Time Library Search results acquires the information needed for confident annotation.

High NCE MS² triggered by RTLS

![High NCE MS² triggered by RTLS](image)

Mirror plot of stachydrine and unknown compound triggered for additional MSn scans.

Results obtained in collaboration with Dr. Gary Patti, Washington University in St. Louis, MO. For research purposes only.
Comprehensive sample coverage with AcquireX data acquisition

AcquireX data acquisition automates generation of inclusion and exclusion lists between runs to target new compounds in subsequent runs and increase the depth of coverage. The number of unique compounds with fragmentation spectra in human plasma (NIST SRM1950) obtained using AcquireX workflows are more than doubled compared to traditional DDA.

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Auto-Ready ion source for effortless calibration

The Auto-Ready ion source simplifies calibration by integrating a dedicated pump, emitter, ion transfer tube, and container of Thermo Scientific™ Pierce™ FlexMix™ Calibration Solution inside the instrument. The mass spectrometer will calibrate itself regularly during scheduled off hours without interrupting data acquisition. During a months worth of experiments, ten metabolites showed a root mean square (RMS) of less than 1 ppm using the Auto-Ready ion source for scheduled mass and system calibrations, and EASY-IC ion source to maintain mass accuracy between calibrations.

A breakthrough in lipid structural elucidation

Using soft fragmentation techniques such as CID or HCD, it is impossible to locate double bonds in the acyl chain of lipid molecules. Optional UVPD produces structurally diagnostic information including ions indicative of double bond locations and site-specific glucuronidation.

UVPD hardware is enclosed inside the mass spectrometer with MS² fragments generated in the linear ion trap. Both the ion trap and Orbitrap mass analyzers detect these fragments to provide unambiguous characterization of various lipid classes.

HRAM UVPD MS² spectrum of [M+Li]⁺ precursor ions of TG 16:0/16:0/18:1, with two fragment ions diagnostic of the double bond location (data obtained on Thermo Scientific™ Orbitrap™ Fusion Lumos™ mass spectrometer).
Characterize and quantify small-molecule structures with greater confidence

Combined with powerful spectral library and data processing software, the Orbitrap IQ-X Tribrid mass spectrometer provides the ultimate solution for accuracy, efficiency, and overall productivity of drug impurity and metabolite identification, extractable and leachable analysis, and other related applications.

Optional UVPD allows generation of unique fragments complementary to CID and HCD to obtain detailed structural information for high-confidence identification of unknown compounds. Optional 1M adds enhanced resolution and fine isotope detection to improve determination of elemental composition and enhance stable isotope labeling experiments. Optional FAIMS Pro Duo interface increases selectivity and provides orthogonal gas-phase fractionation using differential ion mobility.

Alternate fragmentation with UVPD
Certain compounds break apart to yield fragments with minimal structural information using HCD and CID. Adding the UVPD option provides an alternate mode of fragmentation to help elucidate complex structures. For example, derivatized telmisartan yields only a non-informative fragment using HCD (top panel shown below). Using UVPD, multiple structurally significant fragments are generated and the structure can be characterized (bottom panel).

MS² spectra of derivatized telmisartan using HCD (top) and UVPD (bottom) fragmentations.
Comprehensive oligomer analysis

Nucleic acid oligomers are an emerging compound class that have shown promise as biopharmaceuticals. Using assisted CE, the Orbitrap IQ-X Tribrid mass spectrometer can determine an optimal CE for fragmentation to help achieve complete sequence coverage. Additionally, UVPD results in efficient fragmentation regardless of the charge state of the oligomer, reducing the need for lengthy method optimization.

Increased sensitivity with FAIMS Pro Duo interface

The Orbitrap IQ-X Tribrid mass spectrometer is compatible with the FAIMS Pro Duo interface option to increase the limit of quantitation for select compounds. For example, monensin analyzed in muscle meat matrix, the limit of quantitation was improved by an order of magnitude when the experiment was performed using the FAIMS Pro Duo interface, shown below.

1M resolution for fine isotope structure

Sometimes a compound can have a fine isotope structure that cannot be resolved using high resolution settings. Using optional 1M, even the most complicated isotopic fine patterns can be resolved, providing unambiguous determination of the elemental composition. For example, the compound shown in the top spectrum could belong to C_{28}H_{35}NO_{7}S and C_{30}H_{32}N_{3}O_{4}P. Using 1M, the identity is clearly determined as of C_{28}H_{35}NO_{7}S.
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