thermo scientific

Leading performance

Orbitrap Exploris 240 mass spectrometer

ThermoFisher
SCIENTIFIC

Deliver the exceptional

The Thermo Scientific™ Orbitrap Exploris™ 240 mass spectrometer provides leading performance and application versatility to drive discovery and identification, with the quantitative precision and accuracy to confidently scale up to achieve impact.

Operational simplicity, together with intelligent data acquisition, fast tracks you to confident results.

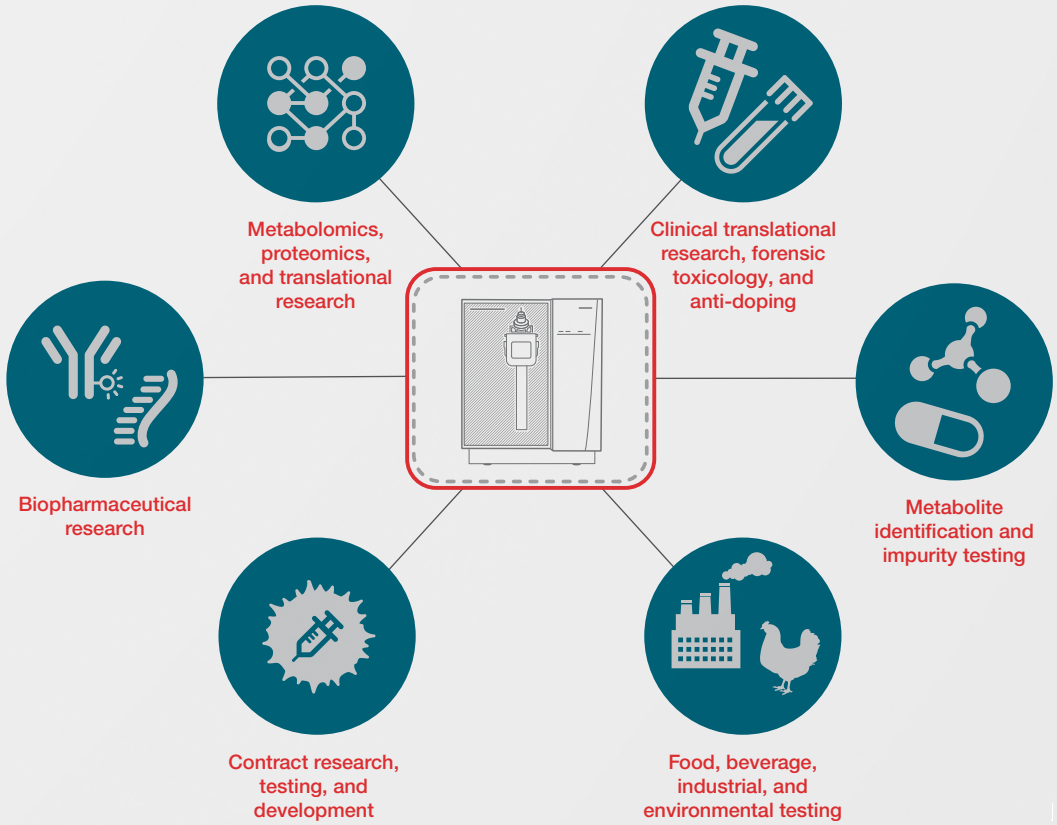
The Orbitrap Exploris 240 mass spectrometer coupled to the Thermo Scientific™ Vanquish™ Flex Duo UHPLC system for increased sample throughput.

Performance | Versatility | Operational Simplicity

More than twenty years of experience, designed into our fourth-generation quadrupole-Orbitrap mass spectrometer

Work smarter and achieve high-quality results across multiple applications

The challenges of confidently identifying small-molecule unknowns, performing comprehensive characterization of complex biotherapeutics, and undertaking impactful proteomic research shouldn't require you to work harder to find answers.
No matter what your application challenge, the Orbitrap Exploris 240 mass spectrometer delivers no-compromise, high-quality results.



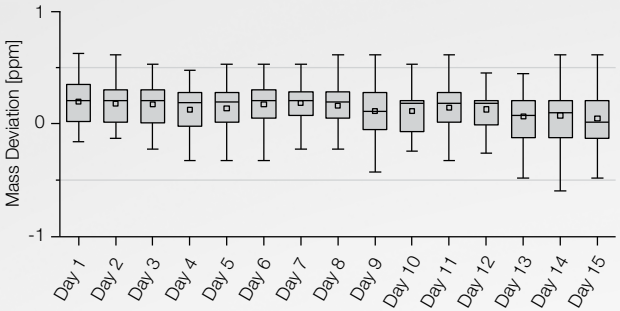
System versatility across multiple applications without compromising reliability, performance robustness, uptime, or productivity.

Enhance your science with exceptional data quality

Regardless of your application and sample complexity, the Orbitrap Exploris 240 mass spectrometer provides the highest-quality, intelligently collected high-resolution, accurate-mass (HRAM) MS data to confidently power your science.

Consistent mass accuracy

Ensure complete confidence in results with sub-ppm mass accuracy for at least five days provided by the Thermo Scientific™ EASY-IC™ (internal calibration) source and a simple, single external calibration across the entire mass range of *m/z* 40–6,000.

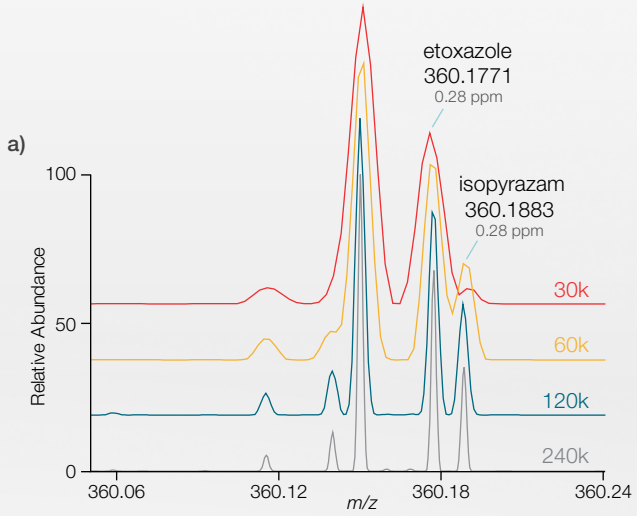


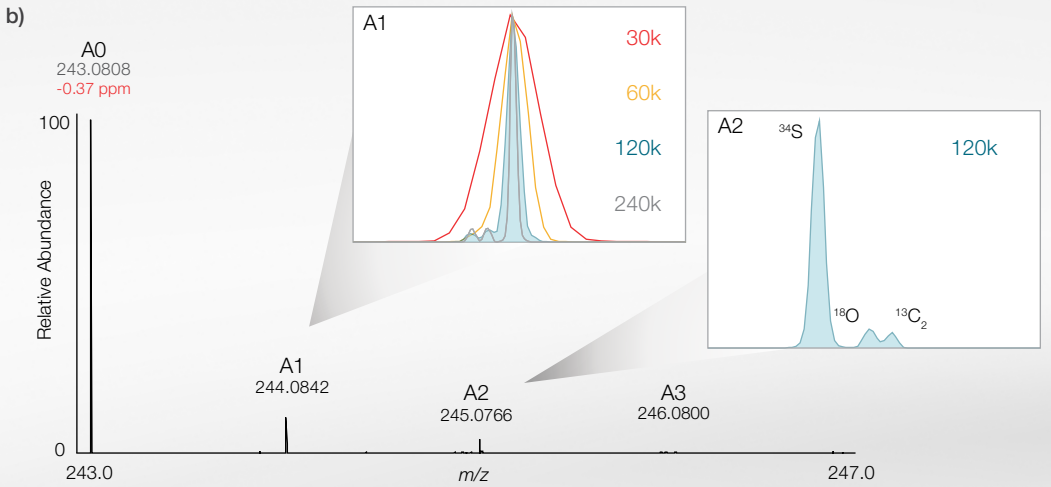
This analysis of 15 veterinary drugs spiked into meat-muscle matrix using positive/negative polarity switching over 15 days following calibration demonstrates exceptional sub-1-ppm mass accuracy providing high confidence for subsequent identification, characterization, and quantitation.

Excellent mass accuracy and resolution combine for data certainty

a) High-resolving power enables you to differentiate between matrix interferences and analytes of interest. Baseline resolution and confident identification of etoxazole (*m/z* 306.1770) and isopyrazam (*m/z* 360.1882) in olive oil matrix require a resolution greater than 120k.

b) This analysis of biotin demonstrates excellent mass accuracy, and at resolutions greater than 120k, access to isotopic pattern determination as shown for the A1 and A2 isotopic clusters. Combining these capabilities reduces the number of potential elemental compositions and provides assurance in assignments.



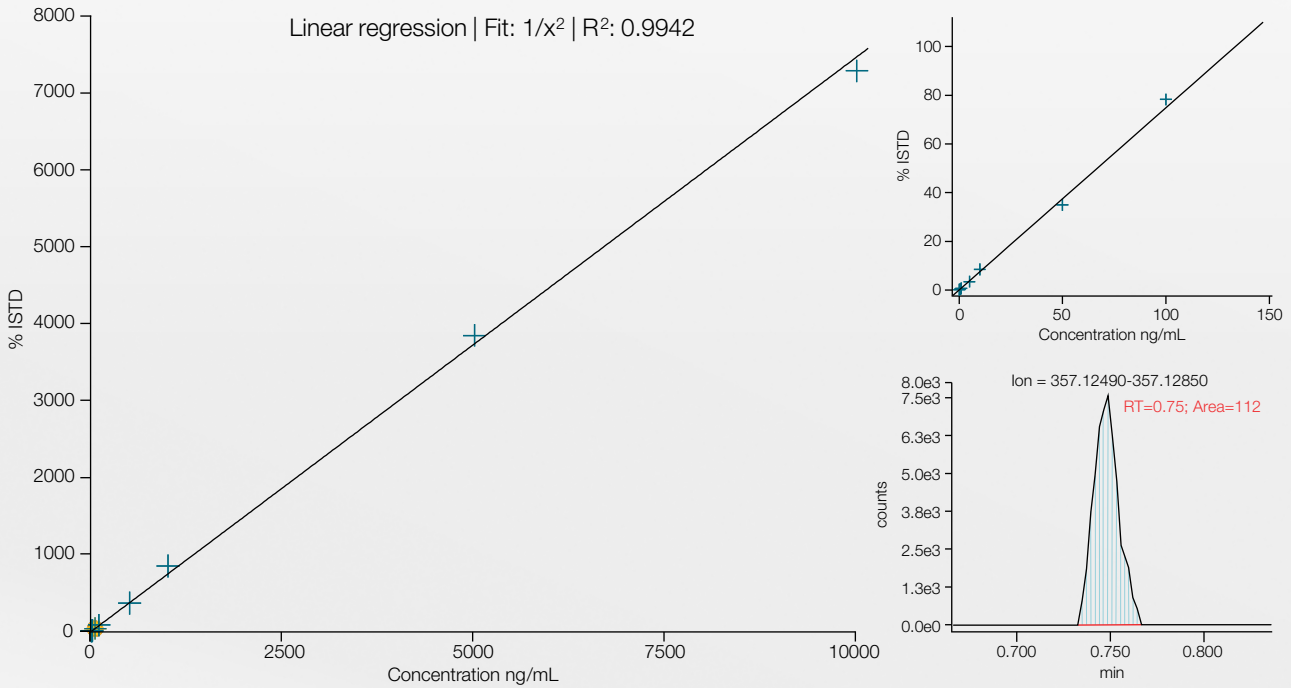


> The ability to establish and maintain mass accuracy better than sub-1-ppm using EASY-IC on the Orbitrap Exploris 240 mass spectrometer is a real game changer for non-targeted analysis; with this capability, elemental formula elucidation of unknowns is significantly more robust."
>
> Dr. Lee Ferguson, Associate Professor of Civil and Environmental Engineering, Duke University

Accurate, optimization-free quantitation

From small-molecule unknown identification to protein, peptide, and biotherapeutic applications, combining excellent mass accuracy and resolution with the ability to perform quantitation using full scan or targeted data acquisition modes, you can be sure of obtaining the highest possible sensitivity and dynamic range regardless of sample matrix complexity.

Deliver dependable sample insights with minimal effort and confidently acquire highest-quality data using the multiple data acquisition options that are easily accessed in intelligent, ready-to-run method templates.



This analysis of pioglitazone in plasma using full scan data acquisition at a resolution setting of 60k provided calibration data that was linear over five orders of dynamic range from 0.1 to 10,000 ng/mL (an expansion of 0.1 to 100 ng/mL is shown, highlighting the lower calibration points). The combination of mass accuracy and resolution allows use of narrow extraction windows to increase specificity. The lowest limit of quantitation (LLOQ) of 0.1 ng/mL (0.03 pg on-column) shown was determined using an extraction tolerance of ±5 ppm. Even at the LLOQ, there are 14 data points across the peak to ensure the highest confidence in quantitative performance.

See the complete picture: protein identification and quantitation

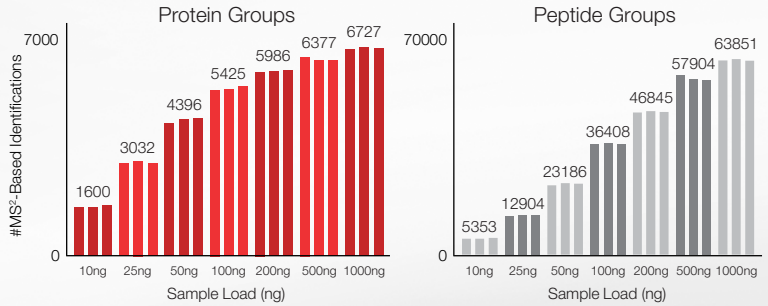
Comprehensive proteomic analyses require flexible, proven applications, and integrated workflows to address the scale and variety of proteomic projects while enabling fast time-to-results. The sensitivity, versatility, and operational simplicity of the Orbitrap Exploris 240 mass spectrometer empowers you to take discoveries beyond identification to link complex biological function with trusted, best-in-class relative and targeted quantitation.

Accelerate your discovery

For scientists looking for industry-established mass resolution, accuracy, speed, and comprehensive data acquisition workflows to expand capacity and versatility, the Orbitrap Exploris 240 mass spectrometer is a premium HRAM solution designed to accelerate discovery and provide trusted biological insights.

High-performance proteomics with confidence

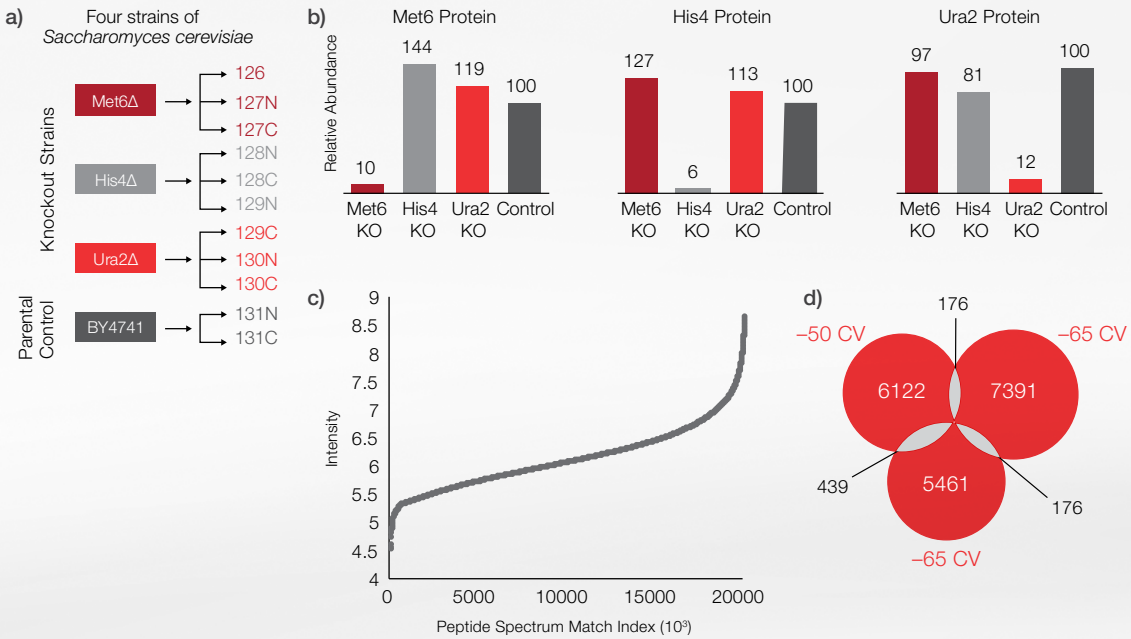
The analysis of Thermo Scientific™ Pierce™ HeLa Protein Digest Standard, using 90-minute LC-MS runs with the Thermo Scientific™ FAIMS Pro™ interface at two different compensation voltages (CV), demonstrates premium performance and sensitivity for shotgun applications.



From sample loads ranging from 10 to 1,000 ng, the number of MS²-based protein and peptide group identifications highlights the ability of the Orbitrap Exploris 240 mass spectrometer combined with gas-phase fractionation to increase proteome coverage.

Increase quantitative throughput with multiplexing

Increase quantitative performance compared to label-free quantitation approaches using multiplexing with Thermo Scientific™ Pierce™ TMT11plex™ or TMTpro™ 16plex isobaric reagents with the FAIMS Pro interface.



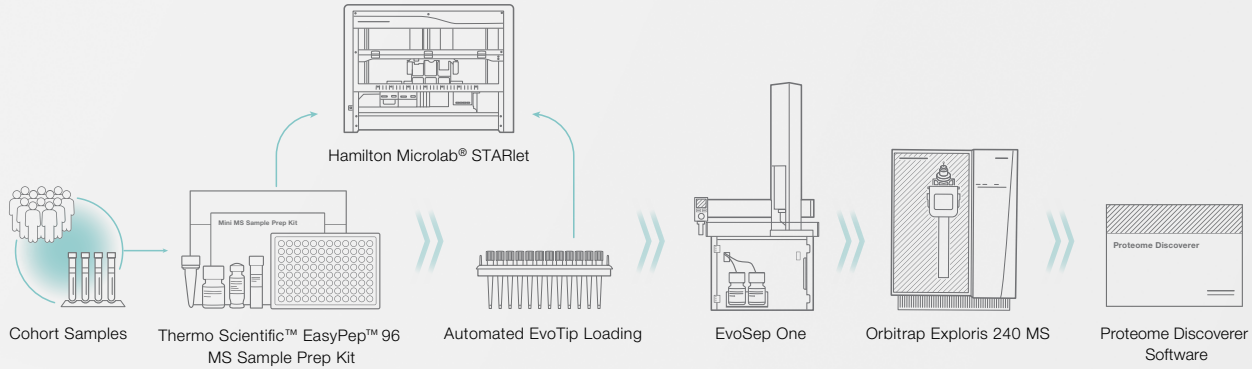
a) Quantitative experimental design for the analysis of a control and three knockout (KO) strains.
b) Quantitative ratios for each of the samples highlighting the relative abundance of the KO proteins.
c) Intensity ranking across five orders of quantitative dynamic range for the peptide spectrum matches.
d) The orthogonality of the FAIMS Pro interface improved peptide coverage using a range of CVs.

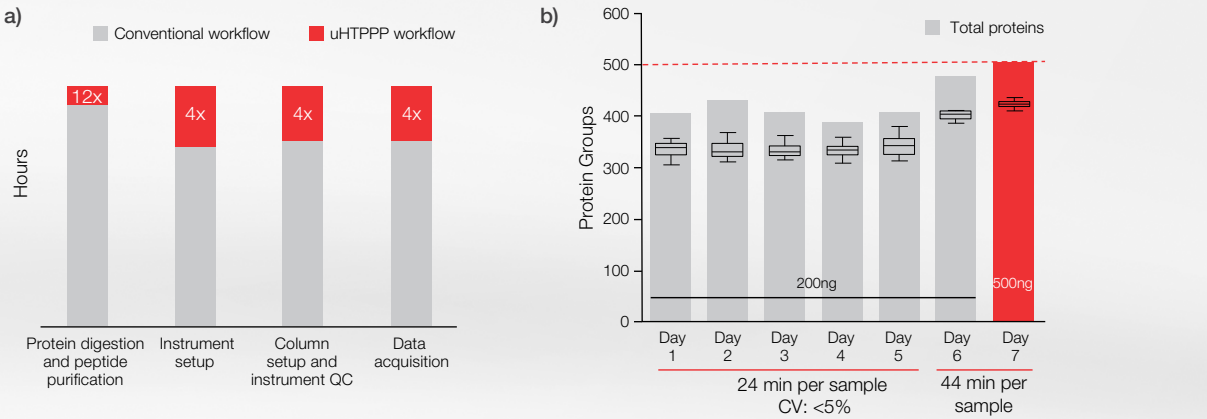
Scale translational research discoveries to reliable clinical experiments

Translational research demands scalable, standardized, and reproducible workflows. The Orbitrap Exploris 240 mass spectrometer delivers high-confidence quantitative proteome profiling of large-scale plasma and tissue sample cohorts to support your precision medicine and translational research. From integrated, automated sample preparation, sample clean-up, separations, and built-in QA/QC procedures, to industry-leading data processing, Thermo Fisher Scientific provides a complete solution that produces the rigorous and relevant results required to accelerate translation of discoveries into clinical applications.

Scale up for high-throughput protein analysis

The Ultra-High-Throughput Plasma Protein Profiling (uHTPPP) workflow provides an ideal solution for high-throughput and reproducible plasma protein analysis, while significantly reducing preparation and acquisition times, providing fast time-to-results.





a) The uHTPPP automated sample preparation workflow is high throughput—from 4- to 12-fold faster—delivering significant time savings depending upon the workflow step. b) Consistent and precise plasma protein characterization over 150 injections (130 samples and 20 QCs) is shown. The box plots show the averaged number of proteins identified with the total proteins identified and quantified highlighted. The uHTPPP workflow is reliable: for the 200 ng sample load over six days using a 24-minute analysis, the coefficient of variation was less than 5%.

Deliver qualitative and quantitative insights faster

Driven by customizable, user-friendly templates, Thermo Scientific™ Proteome Discoverer™ software addresses multiple research workflows, from complex sample analysis to large datasets, with powerful data processing and visualization capabilities. Within a single package, you can link your identification, characterization, and quantitation with an extensive and adaptable toolset that rapidly processes large and complex datasets to deliver real, actionable insights.

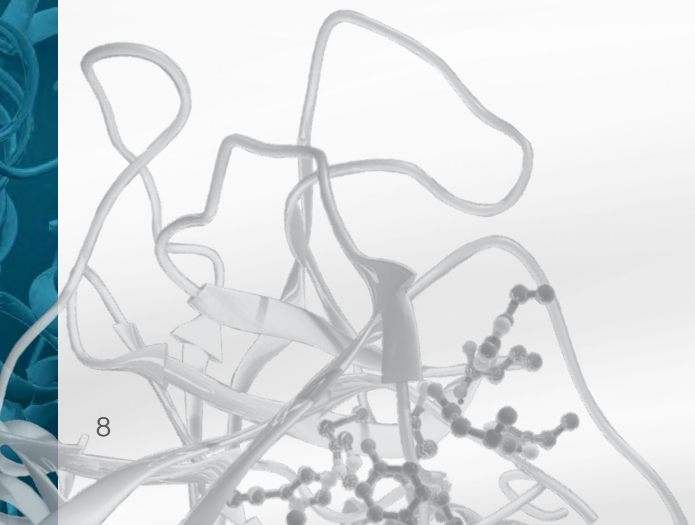
Obtain must-have high-performance biotherapeutic characterization

> The Orbitrap Exploris 240 mass spectrometer is a reliable and flexible solution for high-performance biopharmaceutical characterization. I am really impressed by the sensitivity achieved for native MS analyses. When the instrument is coupled to the Vanquish Duo UHPLC system, we don't have to wait during column equilibration. As a result, the mass spectrometer is constantly acquiring valuable data. With Chromeleon CDS software and all of its features, it is fantastic. The system is a must-have instrument for analytical and characterization labs supporting biopharmaceutical development and manufacture."

Dr. Jonathan Bones, Principal Investigator, NIBRT

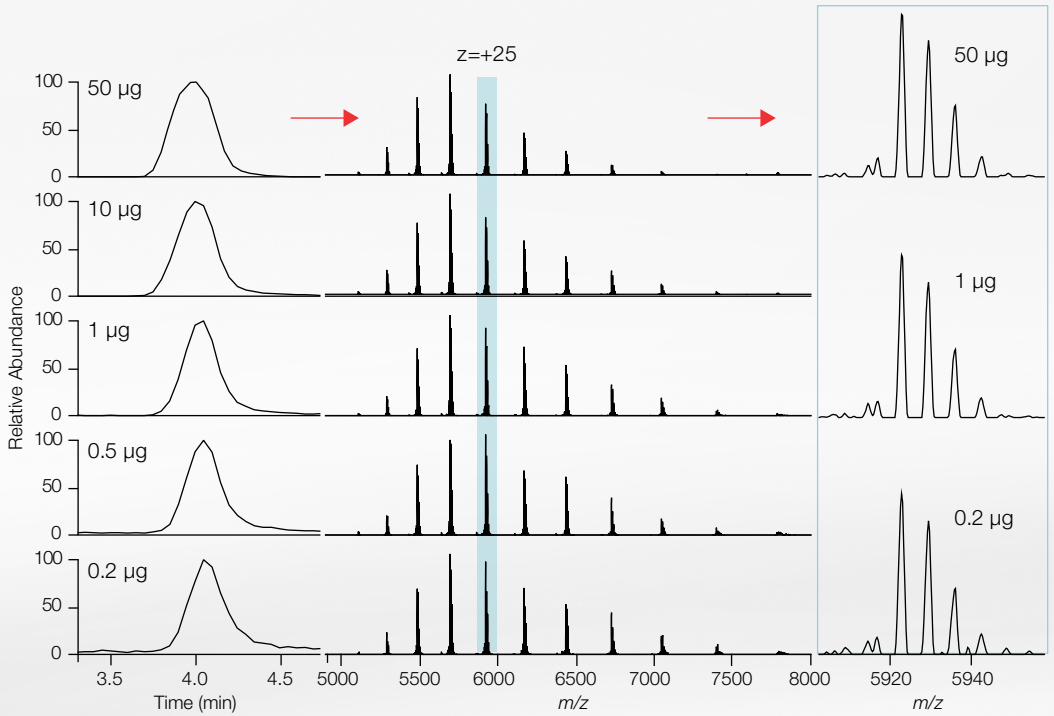
With superb spectral clarity, the Orbitrap Exploris 240 mass spectrometer delivers the high-confidence characterization required to reliably quantitate and identify biotherapeutics in both research and routine laboratory environments.

From intact mass analysis under denaturing and native conditions, to subunit analysis, middle- and top-down analysis, and peptide or disulfide bond mapping—assign more spectral features and maximize your productivity through improved flexibility, speed, dependability, and operational simplicity.



Use less sample for reliable, high-sensitivity native intact mass analysis

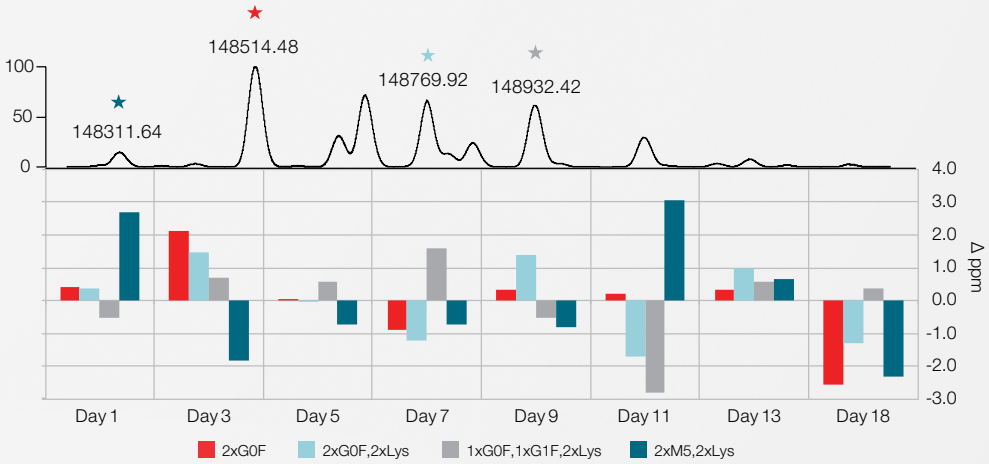
Exceptional sensitivity and mass accuracy combined with proven spectral quality for the analysis of native intact proteins at low concentration levels provide reproducible, high-confidence intact protein masses after deconvolution.



Size exclusion chromatographic (SEC) MS analysis of trastuzumab from 50 to 0.2 µg on-column using the Thermo Scientific™ BioPharma option to extend instrument mass range to *m/z* 8,000 (left). Compared to denaturing conditions, intact native analysis (center), reduces the complexity of spectral data. Consistent glycoform distributions are obtained (right), even at low sample loadings. With simplicity of operation, native MS analysis is now a routinely accessible assay.

Robust, day-to-day deconvoluted intact mass accuracy

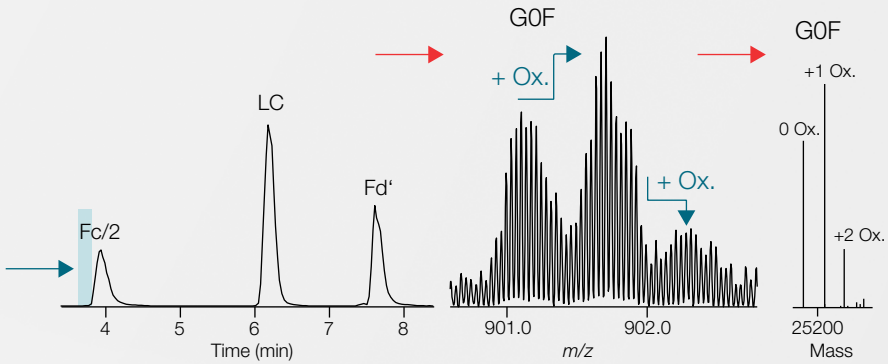
Mass stability is crucial for ensuring confident glycoform identifications and observing modifications. With a single calibration over the entire mass range (including the extended mass range provided by the BioPharma option), long-term mass precision is easily obtained, ensuring robust, superior biopharmaceutical characterization.



Under denaturing conditions, the complex glycoform distribution of infliximab is clearly observed (top). The mass stability for the four most abundant glycoforms monitored over 18 days shows exceptional accuracy for the deconvoluted masses.

Identify trace process modifications easily

High sensitivity, accurate monoisotopic mass determination, and unrivaled spectral clarity enable fast identification of post-translational modifications at intact and subunit levels with exceptional confidence.



Chromatogram showing ipilimumab subunit separation (left) with the leading edge highlighted. The leading edge contained low levels of endogenous mono- and doubly-oxidized glycoforms of the Fc/2 G0F subunit (middle). The deconvolution result determined using the Xtract algorithm in BioPharma Finder software represents unoxidized, mono- and doubly-oxidized G0F glycoforms.

Simplified protein characterization

Comprehensive, optimized workflows facilitate rapid data interpretation. Thermo Scientific™ BioPharma Finder™ software features powerful algorithms to generate easy-to-understand results for all biotherapeutic characterization analyses.

Compliance-ready protein monitoring and quantitation

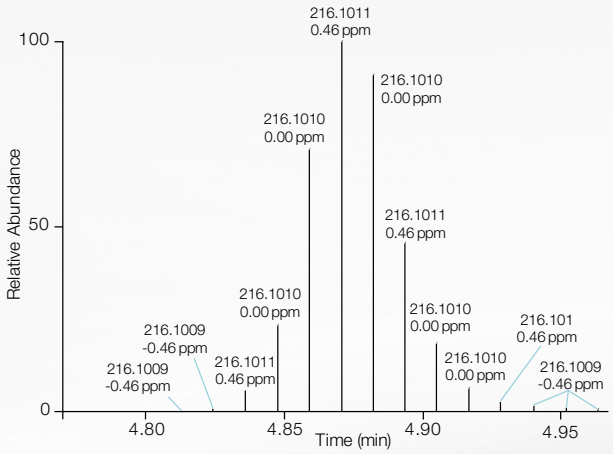
Acquisition, protein monitoring, and intact mass deconvolution are all performed in compliance-ready Thermo Scientific™ Chromeleon™ Chromatography Data System (CDS) software, ensuring data integrity and security. For advanced investigations, a single click exports your data for analysis with BioPharma Finder software.

Achieve complete confidence across multiple small-molecule applications irrespective of complexity or dynamic range

Regardless of your application, complete confidence in qualitative and quantitative data is critical for decision-making. Fast track your productivity and meet your experimental objectives with absolute certainty in your MS data.

Single-scan accuracy for absolute confidence

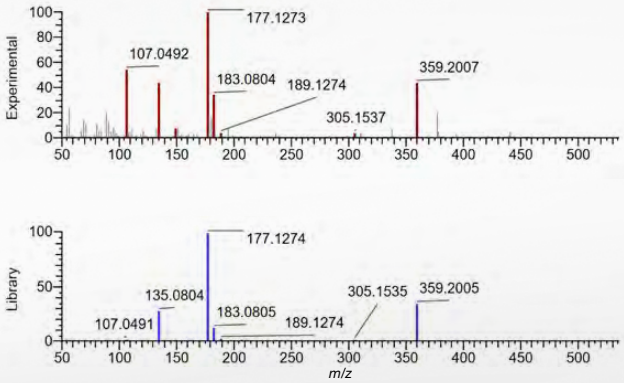
Scan-to-scan mass accuracy and stability enables greater confidence in compound assignments, even at low intensities, and the use of narrow extraction windows increases specificity and accuracy when quantifying.



As shown above for atrazine (*m/z* 216.1010), each datapoint is within ±0.5 ppm, regardless of peak intensity, which combined with high resolving power, provides the basis for robust data analysis without the need to average data acquired from multiple scans.

Rapid screening with spectral confirmation

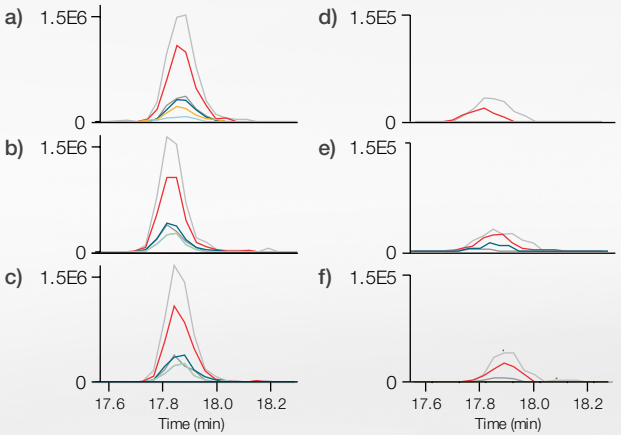
While consistent sub-ppm mass accuracy for precursor confirmation when performing targeted screening provides high levels of confidence, fast scanning and the use of high-quality mass spectral fragmentation libraries, such as the Thermo Scientific™ mzVault™ library, provide additional confidence in results.



The data above show the data-independent acquisition analysis of pesticides in olive oil. Excellent spectral fragmentation matching between the library and experimental MS^2 data for etofenprox at a concentration of 1 ppb is observed.

Leverage leading performance for cutting-edge clinical research

The complexity of plasma samples presents a challenge when quantitating proteins and identifying real changes, especially for low-abundance proteins, such as beta-actin, a low-abundance protein found in white blood cells and platelets.



The use of low centrifuge force (a–c) and high centrifuge force (d–f) shows depletion in beta-actin (×40 lower relative concentration) in properly spun out plasma, demonstrating the accuracy, sensitivity, and resolving power of Thermo Scientific™ Orbitrap™ technology in addressing this analytical challenge.

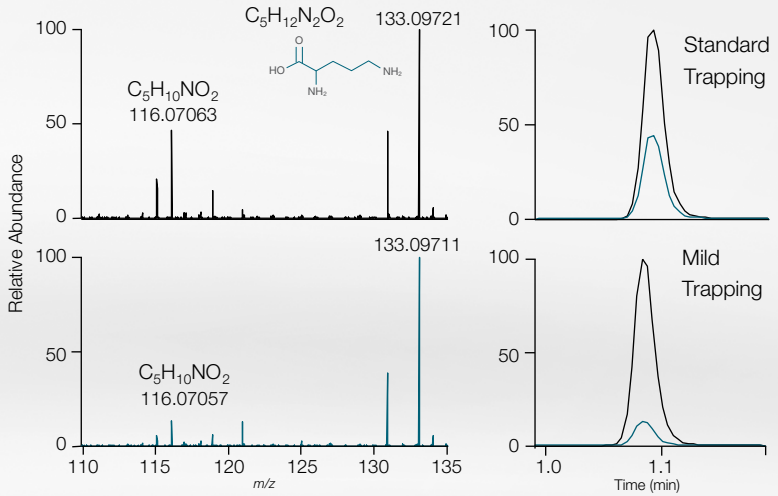
Adopt one solution for all metabolomics workflows

Obtain valuable insights from untargeted, semi-targeted, targeted, and stable isotope labeling metabolomics experiments, with relative and absolute quantitation, using a single mass spectrometer. With Thermo Scientific™ AcquireX™ intelligent data acquisition workflow to collect more meaningful data, the Orbitrap Exploris 240 mass spectrometer redefines versatility and time-to-results for both small- and large-scale studies, day after day.

With single-click calibration and ready-to-use method templates, access data of highest quality for a comprehensive range of metabolomics workflows.

Increase compound annotation confidence with mild trapping

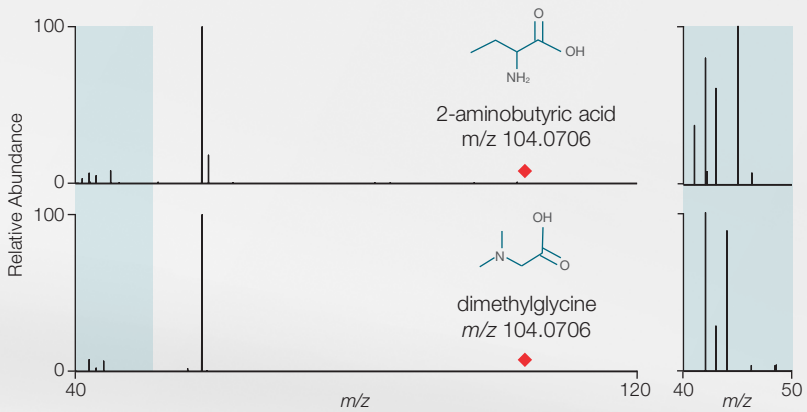
Avoid misannotated metabolites with mild trapping to reduce unintentional MS^1-level precursor ion dissociation.



The *m/z* 116.0706 product ion of ornithine found in the MS^1 spectra above could be mistaken as proline because they share the same exact mass. Compared to standard trapping (top), the fragment ion's intensity is significantly reduced (bottom) when using mild trapping.

Improve identification with extended low mass range

Extended low mass range down to *m/z* 40 enables detection of more fragment ions, increasing confidence in small-molecule identifications.



An extended low *m/z* range enables confident identification of isomers. For 2-aminobutyric acid (top) and dimethylglycine (bottom), there are five additional fragment ions detected, allowing confident differentiation between the two structural isomers.

Collect more meaningful high-quality data with ease

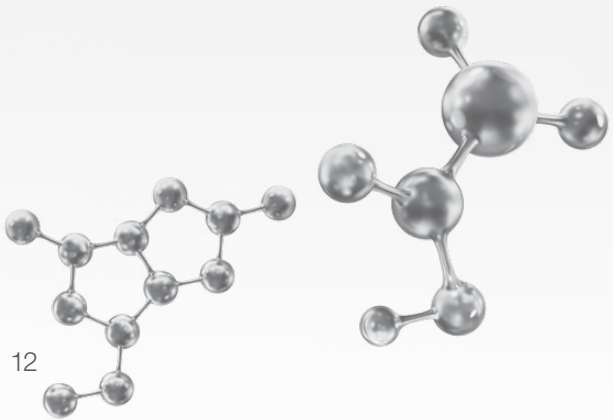
Small-molecule analysis demands reliable acquisition of high-quality MS and MS^2 data to facilitate successful compound identification and characterization. However, complex samples can limit the utility of data-dependent and independent acquisition strategies due to collection of irrelevant data from background matrices. Proven AcquireX intelligent data acquisition collects more meaningful high-quality MS^2 data, increasing profiling efficiency with minimal manual experimental setup and easier subsequent data interpretation.

The challenge of capturing "everything of interest"

AcquireX intelligent data acquisition maximizes data-dependent acquisition (DDA) effectiveness, unlocking your data's true value.

Data-dependent acquisition isolates a single precursor ion with a narrow isolation window, generating easily-interpretable fragmentation spectra. However, low-abundance species can be missed.

Data-independent acquisition (DIA) fragments all precursors for a given precursor mass window, including background ions, resulting in complex fragmentation spectra requiring deconvolution to relate fragment ions back to their precursor ion.



AcquireX intelligent data acquisition workflows

Four unique experimental workflows to generate meaningful MS^2 spectra for more sample-relevant compounds.

- Background Ion Exclusion
- Background Ion Exclusion and Component Inclusion
- Iterative Precursor Exclusion
- Deep Scan

> With greater than 90% MS^2 coverage for all detected sample-specific compounds with a few injections using the deep scan AcquireX workflow, the need to use non-DDA MS^2 is eliminated. Even in complex matrices, the AcquireX workflow provides certainty in fragmentation spectra compared to acquiring fragmentation for everything."
>
> Dr. Lee Ferguson, Associate Professor of Civil and Environmental Engineering, Duke University

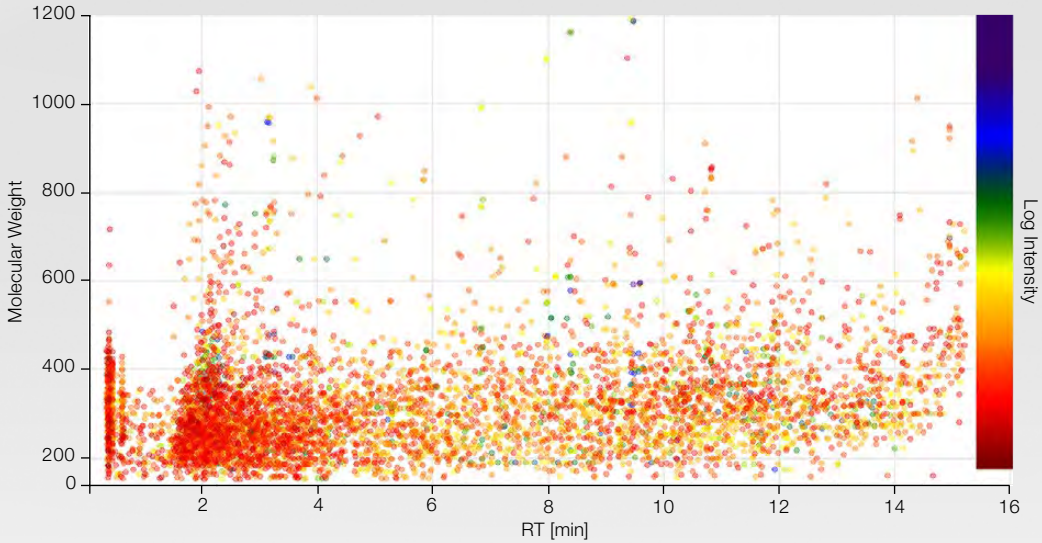
Utilize maximum instrument duty cycle and avoid fragmenting background ions and unrelated sample peaks by automatically generating an ion exclusion list.

Focus on the sample-relevant chromatographic peaks by generating an ion inclusion list from a matrix sample to further reduce uninformative fragmentation spectra by prioritizing the molecular ion.

Obtain exhaustive fragmentation information for all small molecules, while avoiding fragmenting the same ion twice with automated exclusion list updates over multiple iterative injections.

Intelligent exclusion of background ions and comprehensive fragmentation of sample-relevant compounds across iterative injections achieves ultimate sample interrogation.

Greater than 90% MS^2 coverage in three injections



Using the deep scan AcquireX intelligent data acquisition workflow to analyze river water for emerging pollutants (e.g., PFAS) generated MS^2 data for more than 90% of the approximately 7,000 compounds detected in the pooled samples from three iterative injections and a 15-minute gradient. By comparison, a standard DDA experiment generates less than 60% MS^2 coverage with less specificity for sample-specific compound fragmentation (the majority of compounds within the sample are low intensity). Because MS^2 data is acquired for a greater number of compounds, retrospective data analysis can be performed without re-analyzing samples.

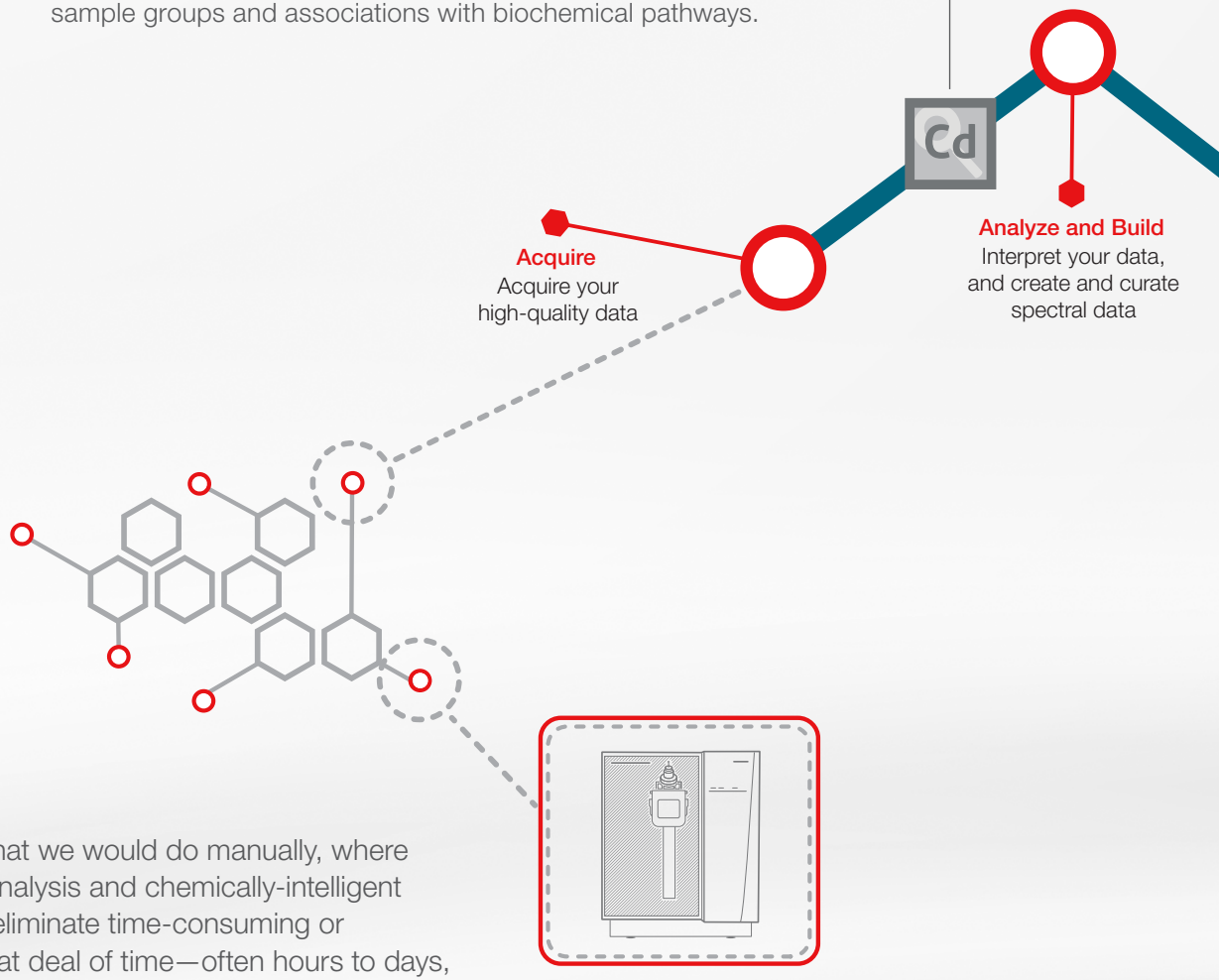
Streamline your path to small-molecule insights

Powerful software tools connect small-molecule unknown identification and characterization to screening and quantitation. Once you have acquired comprehensive, high-quality MS and MS^2 data, our software ecosystem is designed to reduce the time to high-confidence insights.

- Streamline qualitative and quantitative data analysis using template-driven data processing
- Access world-leading mass spectral fragmentation libraries to identify compounds
- Seamlessly transfer knowledge from discovery to everyday testing
- When regulatory compliance is required, Chromeleon CDS software delivers productivity with MS quantitation and targeted screening capabilities

From sample to structure, pathway to insight with Compound Discoverer software

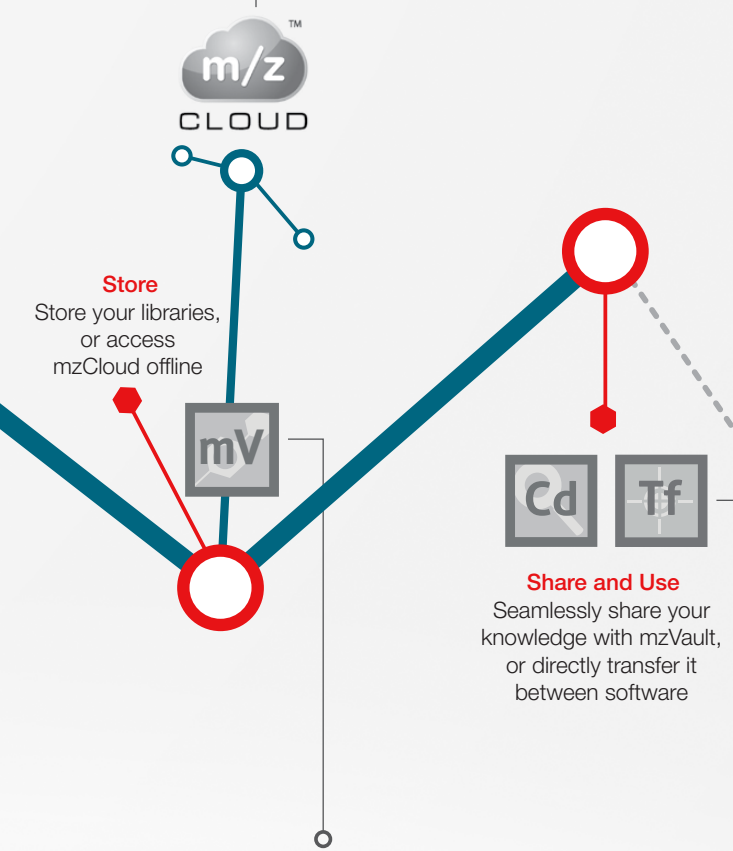
Obtain deeper insights by transforming high-quality MS and MS^2 data into known compounds. Thermo Scientific™ Compound Discoverer™ software makes it easy to confidently annotate compounds and to identify differences between sample groups and associations with biochemical pathways.



> Compound Discoverer software replicates much of what we would do manually, where its extensive suite of processing tools, and statistical analysis and chemically-intelligent software algorithms help to minimize subjectivity and eliminate time-consuming or non-value-added steps. Together, these save us a great deal of time—often hours to days, depending upon study complexity or the questions at hand—ultimately helping to drive the metabolite identification process and support drug-project decisions in a timely manner."
>
> Dr. Dan Weston, Associate Director, DMPK, Sygnature Discovery

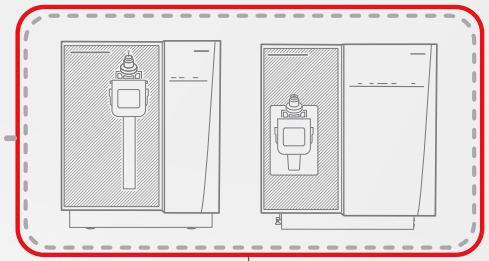
Confident compound identification with mzCloud mass spectral fragmentation library

Confidently identify sample components using the expansive, chemically diverse, high-resolution MS^n fragmentation spectra in the Thermo Scientific™ mzCloud™ mass spectral library, the world's largest LC-MS^n mass spectral fragmentation library.



Simplified high-throughput screening and quantitation with TraceFinder software

Directly transfer discovery knowledge to high-throughput screening and quantitation assays. Thermo Scientific™ TraceFinder™ software enhances laboratory productivity with fast and flexible screening and quantitation. Its customizable user interface and method templates seamlessly integrate with compound databases and mass spectral libraries for rapid method setup and increased screening confidence with spectral matching.



Store your knowledge and access the mzCloud library offline through mzVault library

Access and search MS^2-level information in the mzCloud mass spectral library offline, or curate proprietary libraries using the mzVault mass spectral library. The mzVault library also allows you to store and share mass spectral knowledge with other qualitative and quantitative software applications from Thermo Fisher Scientific.

Productivity and compliance, with Chromeleon CDS software

When regulatory compliance is required, Chromeleon CDS software provides superior MS data processing and automation capabilities for quantitation, targeted screening, and protein and peptide analyses. In addition to controlling more than 25 Thermo Scientific™ MS instruments, Chromeleon CDS software provides extensive, multi-vendor control for remote connection to more than 525 chromatography instruments (LC, IC, and GC) in an enterprise environment.

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Almanac web-based monitoring and management

Stay connected to your science. See how the Thermo Scientific™ Almanac™ application can help you get the most out of your instruments.

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Technical and online support: peak performance for your instruments

Helping you keep your instruments running at peak performance is our goal. Whether you're looking for an instrument manual or spare parts, want to submit a repair request, or check on the status of your warranty or service contract, we have every support option you're looking for.

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Protecting your investments: unparalleled laboratory services

Unity™ Lab Services provides a single source for integrated lab service, support, and supply management. Our customized service offerings and world-class service experts have the flexibility and experience to address your laboratory's needs. We provide a complete portfolio of services and support solutions designed to help you improve productivity, reduce total cost of ownership, and ensure performance throughout your laboratory.

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Thermo Scientific Data Acquisition software
thermofisher.com/InstrumentControl

Thermo Scientific Data Processing software
thermofisher.com/DataProcessing

Find out more at **thermofisher.com/OrbitrapExploris240**

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