

thermo scientific

# Productivity redefined

Orbitrap Exploris 120 mass spectrometer



**ThermoFisher**  
SCIENTIFIC

# Setting the new standard in productivity

Whether it's method development or everyday testing, accelerate your route to qualitative and quantitative confidence with consistently accurate data delivered by proven Thermo Scientific™ Orbitrap™ technology.

Designed for operational simplicity, the Thermo Scientific™ Orbitrap Exploris™ 120 mass spectrometer sets the new standard in instrument productivity and ruggedness.



The Orbitrap Exploris 120 mass spectrometer coupled to the Thermo Scientific™ Vanquish™ Core HPLC system.

**Productivity | Operational Simplicity | Ruggedness**

- **Take the fast path to high-confidence, high-resolution MS results**

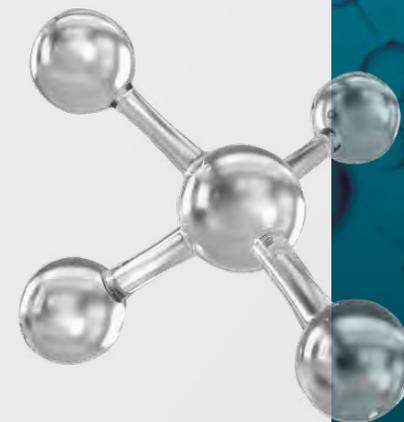
Spend less time questioning data and more time finding answers to your most pressing questions. The Orbitrap Exploris 120 mass spectrometer combines superior resolution and mass accuracy with a powerful suite of data analysis tools to provide accurate results for screening and quantitation, and to streamline method development and everyday testing.

- **Maximize return on investment**

Gain peace of mind knowing that your laboratory will keep running smoothly. The Orbitrap Exploris 120 mass spectrometer minimizes time spent on calibration of different mass ranges and on maintenance, while delivering robust performance. For laboratories testing a high volume of samples, fast scanning and polarity switching decrease sample turnaround times.

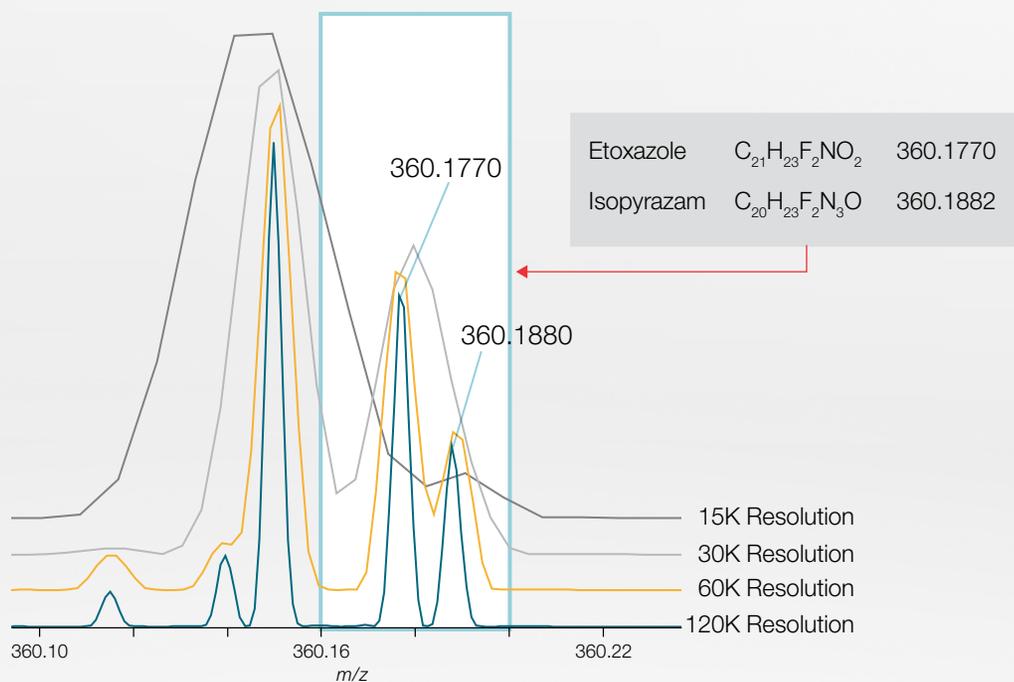
- **Reduce method set-up time**

Empower both novice and experienced staff to analyze samples using ready-to-run method templates. Minimize time spent on training using the common data-acquisition user interface shared by next-generation Thermo Scientific Orbitrap Exploris, Thermo Scientific™ TSQ™ Triple Quadrupole and Thermo Scientific™ Orbitrap Tribrid™ mass spectrometers.



# Confidently uncover more analytes of interest

High-resolution mass spectrometers are designed to resolve analytes of interest from interferences. With Orbitrap high-resolution accurate-mass (HRAM) technology, the Orbitrap Exploris 120 mass spectrometer goes further by discriminating ions of interest from interfering ions differing by only very small mass increments at mass-to-charge ratios as low as  $m/z$  40. As a result, you substantially reduce the likelihood of false positives and negatives when analyzing complex sample matrices.



Full-scan mass spectrum of etoxazole and isopyrazam, measured using the Orbitrap Exploris 120 mass spectrometer at a resolution (R) setting up to 120,000 (FWHM) at  $m/z$  200, demonstrates outstanding resolving power.

## Unknown analysis, non-targeted and targeted screening

Resolve ions of interest from interfering ions with high mass resolution up to 120,000 (FWHM) at  $m/z$  200 over the mass range  $m/z$  40–3,000.

## Confident identification using accurate mass assignments

Determine elemental compositions based on accurate  $m/z$  values.

## Analyte confirmation

Obtain correct assignment of fine isotopes for an additional dimension of information beyond MS/MS fragments, accurate masses, and retention times.

## Data mining

Answer ongoing and future questions about specific analytes or groups of new analytes by interrogating full-scan accurate-mass data at any time!

# Quantify analytes in complex matrices with maximum accuracy

## Accurate, optimization-free quantitation

The Orbitrap Exploris 120 mass spectrometer improves data accuracy for quantitation in complex matrices, reliably meeting limits of detection (LODs) with superior resolving power. Orbitrap HRAM technology delivers sub-ppm mass accuracy, enabling accurate, selective detection of target analytes over five orders of linear quantitative dynamic range without detector saturation. Once you choose a scan mode and mass range, no further compound optimization is required.

| Level | Concentration | % Diff | % Ion Ratio | % CV |
|-------|---------------|--------|-------------|------|
| Cal1  | 0.01 ng/mL    | -5.07  | pass        | 0.9  |
|       |               | -5.64  | pass        |      |
|       |               | -4.62  | pass        |      |
| Cal2  | 0.02 ng/mL    | 0.11   | pass        | 5.0  |
|       |               | 5.10   | pass        |      |
|       |               | -9.24  | pass        |      |
| Cal3  | 0.05 ng/mL    | -5.39  | pass        | 0.9  |
|       |               | -2.83  | pass        |      |
|       |               | -4.59  | pass        |      |
| Cal4  | 0.2 ng/mL     | -0.51  | pass        | 2.1  |
|       |               | 2.01   | pass        |      |
|       |               | -2.34  | pass        |      |
| Cal5  | 0.8 ng/mL     | 4.74   | pass        | 1.8  |
|       |               | 0.72   | pass        |      |
|       |               | 1.79   | pass        |      |
| Cal6  | 3.0 ng/mL     | 11.41  | pass        | 2.0  |
|       |               | 8.49   | pass        |      |
|       |               | 5.96   | pass        |      |

| Level | Concentration | % Diff | % Ion Ratio | % CV |
|-------|---------------|--------|-------------|------|
| Cal7  | 6.0 ng/mL     | 0.80   | pass        | 1.0  |
|       |               | 1.18   | pass        |      |
|       |               | -0.77  | pass        |      |
| Cal8  | 10.0 ng/mL    | -2.74  | pass        | 1.0  |
|       |               | -4.09  | pass        |      |
|       |               | -2.22  | pass        |      |
| LQC   | 0.27 ng/mL    | -2.71  | pass        | 2.3  |
|       |               | 0.21   | pass        |      |
|       |               | 2.11   | pass        |      |
| MQC   | 1 ng/mL       | -0.86  | pass        | 3.2  |
|       |               | -0.74  | pass        |      |
|       |               | -6.25  | pass        |      |
| HQC   | 6.2 ng/mL     | -0.5   | pass        | 2.9  |
|       |               | -4.44  | pass        |      |
|       |               | -5.85  | pass        |      |

## Popular scan modes

**Full Scan:** Obtain comprehensive data coverage by capturing all ions in a user-defined mass range with high mass accuracy. Extract desired  $m/z$  values immediately after data acquisition or later using retrospective data analysis.

**Targeted Selection Ion Monitoring (t-SIM):** Achieve higher sensitivity by setting a narrow mass range (quadrupole as narrow as 0.4 Da).

## Targeted-MS/MS (previously parallel reaction monitoring mode):

Gain additional selectivity in complex matrices. A high-resolution product-ion spectrum is only generated for precursor ions detected in a narrow mass range per a mandatory inclusion list.

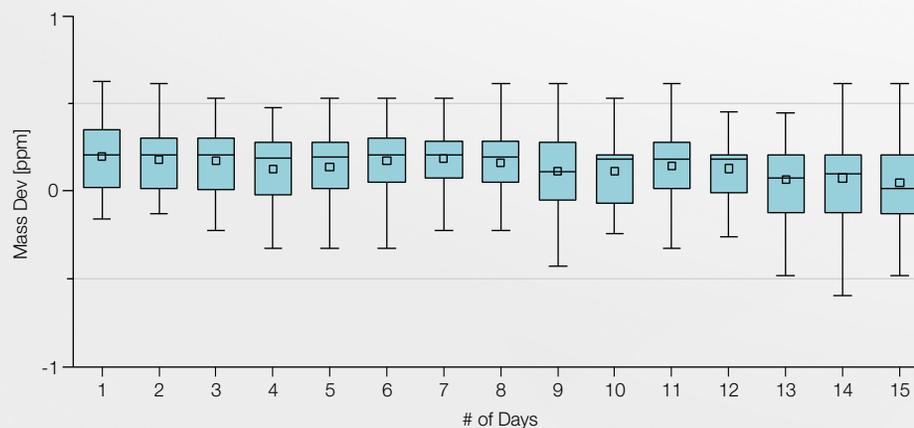
Exceptional linearity over a wide concentration range and a lower limit of quantitation (LLOQ) of 0.01 ng/mL for testosterone in serum demonstrate the ability of the Orbitrap Exploris 120 mass spectrometer to accurately quantify analytes in complex matrices with high reproducibility.

# Keep your laboratory running seamlessly

Frequent unplanned or planned downtime can impede your laboratory's ability to achieve its goals. By minimizing downtime, the Orbitrap Exploris 120 mass spectrometer ensures on-time delivery of your results.

## Single, stable calibration procedure for the entire mass range

Access sub-ppm mass accuracy for at least five days with the Thermo Scientific™ EASY-IC™ ion source. With automated internal calibrant delivery, the EASY-IC ion source saves you time so you can quickly return to running your samples. Use the Thermo Scientific™ Pierce™ FlexMix™ Calibration solution to perform a single calibration for the full mass range of  $m/z$  40–3,000, in both positive and negative modes.

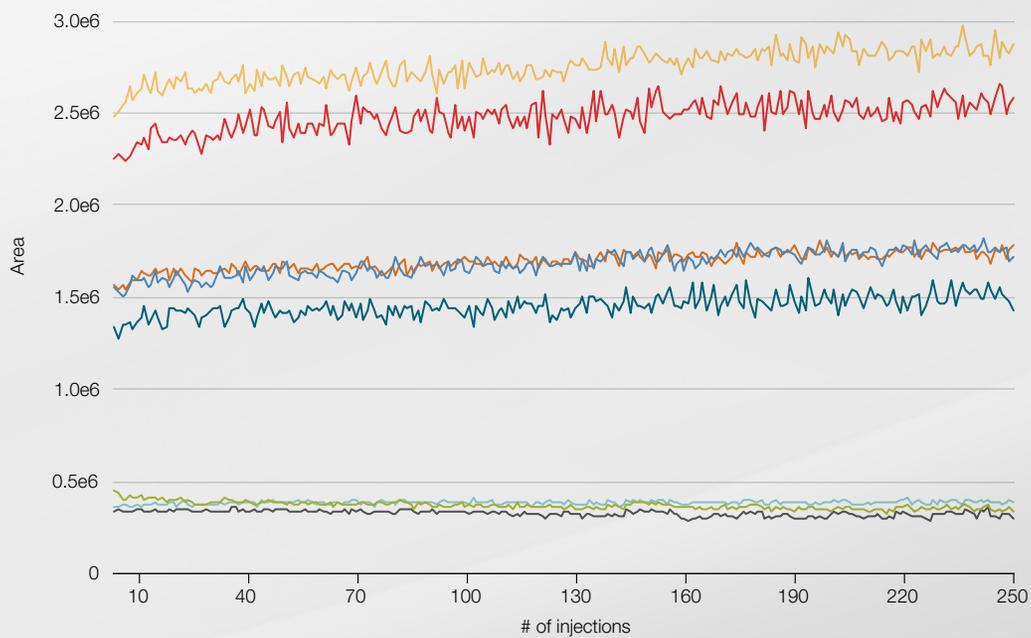


Through the use of Thermo Scientific EASY-IC ion source, sub-ppm mass accuracy is consistently delivered without user intervention for at least five days. A panel of veterinary drugs with  $m/z$  range from 160...900 was analyzed at 100  $\mu\text{g/L}$  over a 15 day period with continual polarity switching, providing exceptional mass accuracy.

## Minimal user intervention for servicing

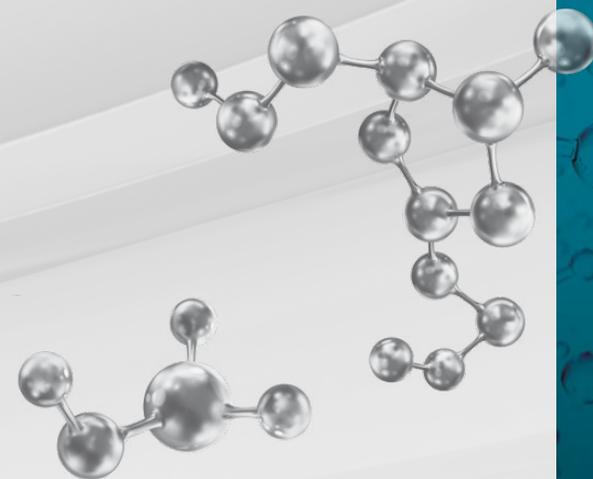
Don't limit your laboratory's productivity with lengthy scheduled maintenance procedures. The Orbitrap Exploris 120 instrument design allows easy access to mass analyzer components, reducing time spent on maintenance.

### Peak area stability over 250 injections



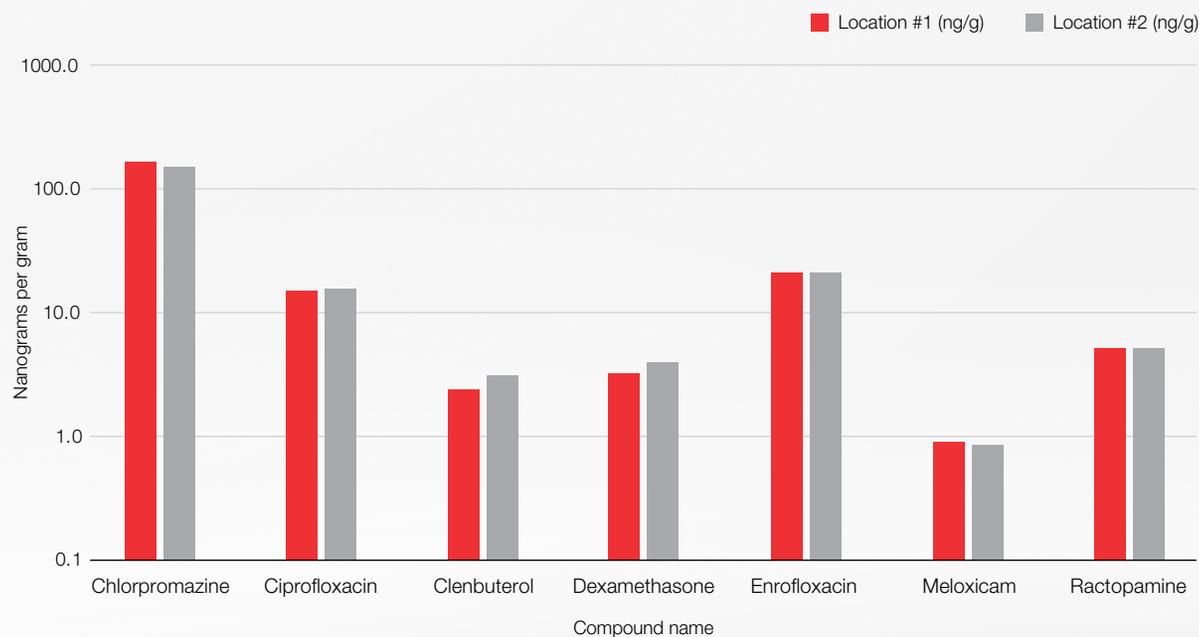
| Compound name  | Average %RSD for 250 injections |
|----------------|---------------------------------|
| Atrazine       | 1.6                             |
| Azoxystrobin   | 2.0                             |
| Bentazone neg  | 2.5                             |
| Bromoxynil neg | 1.2                             |
| Carbendazim    | 2.0                             |
| Cycluron       | 1.6                             |
| Diclotophos    | 2.2                             |
| Fluazinam neg  | 5.5                             |

Long term system robustness demonstrated for pesticides in olive oil over 250 injections with polarity switching.

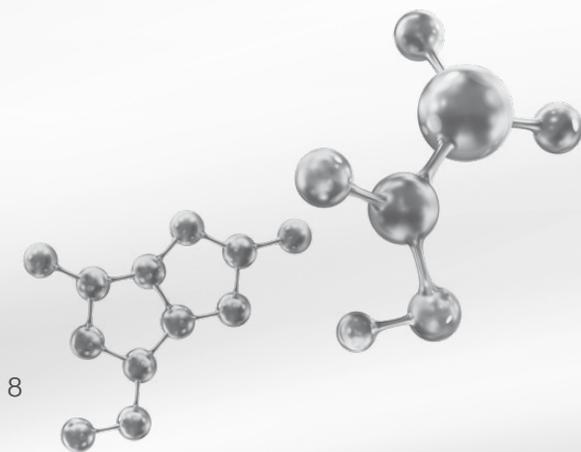


# Gain peace of mind with system-to-system consistency

For organizations that plan to have different users running more than one instrument in the same lab or in different locations, the Orbitrap Exploris 120 mass spectrometer has a demonstrated ability to deliver consistent results across multiple instruments and users.



To assess LC-HRAM MS system-to-system reproducibility, two operators at two different locations analyzed the same sample of veterinary drug residues in bovine muscle matrix on two separate systems. The minimal 5.1% average difference observed in analyte concentrations demonstrate high reproducibility across multiple Orbitrap Exploris 120 mass spectrometer systems.



# Decrease sample turnaround times

For laboratories processing a high volume of samples or facing tight deadlines to submit results, the Orbitrap Exploris 120 mass spectrometer quickly generates accurate results, enabling you to meet internal and external client expectations.

## Maximize compound coverage with fast scan rates

With a scan rate of up to 22 Hz, the Orbitrap Exploris 120 mass spectrometer triggers more precursor ions for MS/MS analyses, so you can produce results quickly and confidently. Fast scanning also enables you to run shorter UHPLC gradients with excellent resolution, sensitivity, and mass accuracy.



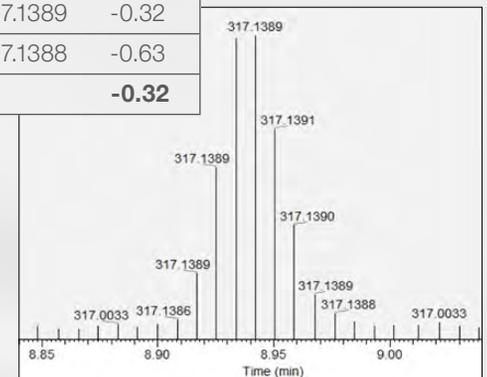
Quantitation of all compounds in bovine muscle matrix is easily achieved by fast scan speeds, even when multiple precursor ion  $m/z$  isolation windows are selected for the data-independent acquisition (DIA) experiment.

## Analyze samples twice as quickly with rapid polarity switching

Process samples faster using positive and negative mode switching in approximately 1.4 Hz cycles. In contrast to other high-resolution instruments, the mass resolution and mass stability of the Orbitrap Exploris 120 instrument does not need to recover after polarity switching, saving valuable analytical time.

| Scan           | Exact mass | Observed mass | Delta ppm    |
|----------------|------------|---------------|--------------|
| 1              | 317.1390   | 317.1386      | -1.26        |
| 2              | 317.1390   | 317.1389      | -0.32        |
| 3              | 317.1390   | 317.1389      | -0.32        |
| 4              | 317.1390   | 317.1390      | 0.00         |
| 5              | 317.1390   | 317.1389      | -0.32        |
| 6              | 317.1390   | 317.1391      | 0.32         |
| 7              | 317.1390   | 317.1390      | 0.00         |
| 8              | 317.1390   | 317.1389      | -0.32        |
| 9              | 317.1390   | 317.1388      | -0.63        |
| <b>Average</b> |            |               | <b>-0.32</b> |

Full-scan MS data acquired for 90 ng/g Zearalenone in corn feed demonstrates preservation of mass accuracy stability during polarity switching.



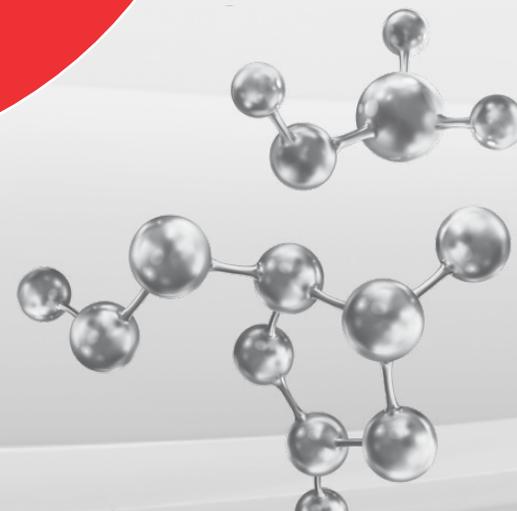
# Deploy Orbitrap HRAM technology for a variety of samples

When it comes to small molecule analysis, many industries face similar challenges. Orbitrap HRAM technology enables laboratories to use novel approaches to emerging contaminant identification, meet increasingly lower LODs, and protect their brand's reputation for product or service quality. Overall, Orbitrap HRAM data provides many industries a faster path to unambiguous answers.



“ The Orbitrap Exploris 120 mass spectrometer allows us to react to emergency testing situations in a variety of matrices without having to do a lot of method development. This enables us to provide high quality data for veterinary drug residue testing to our clients.”

Dwayne Schruck, Laboratory Manager of the Analytical Chemistry Services,  
Iowa State University



# Focus on driving results with faster method set up

The intuitive Method Editor features a drag-and-drop user-friendly interface with optimized method templates for a wide range of applications, simplifying everyday usability.

## Easy, intuitive instrument control

- Single-method control of tune and data-acquisition parameters simplifies error-free operation
- Ready-to-use application-specific templates reduce method development time
- Auto-settings enable quick startup for most experiments
- Drag-and-drop method editing with Tool Tips offers flexibility in an easy-to-visualize format

The screenshot displays the Method Editor software interface, which is divided into several sections. At the top, there are tabs for 'Global Parameters', 'Scan Parameters', and 'Summary'. Below these, a 'Method Timeline' shows a single method step with a duration of 60 minutes. To the right, there are 'Settings' for 'Infusion Mode' (Liquid Chromatography), 'Expected LC Peak Width (s)' (30), 'Miss Trapping' (checked), and 'Internal Mass Calibration' (Off). A 'System Templates' sidebar on the left lists various application-specific templates such as 'Clinical Research', 'Environmental', 'Food Safety', 'Lipidomics', 'Metabolomics', 'Pharma', and 'System Suitability'. The 'Clinical Research' and 'Steroids' templates are highlighted with red boxes. Below the sidebar, a 'Scan' table lists various compounds and their retention times. The table has columns for 'Scan', 'Compound', 'Formula', 'Adduct', 'Retention (min)', 'Precision Change (s)', 'RT Bias (min)', 'Window (min)', 'Collision Energy (V)', and 'Polarity'. The table contains 23 rows of data, including compounds like '11 deoxyepiandrosterone', '11-epiandrosterone', '11-epiandrosterone-d5', '17-OH-P', '17-OH-d5', 'Androsterone', 'Androsterone-d7', 'Androsterone-d9', 'Androsterone-d11', 'Androsterone', 'Androsterone-d3', 'Androsterone-d5', 'Corticosterone', 'Corticosterone-d3', 'Cortisol', 'Cortisol-d3', 'Cortisol-d5', 'Cortisol-d7', 'DHEA', 'DHEA-d3', 'DHEA-d5', 'DHEA-d7', 'DHEA-d9', 'DHEA-d11', 'DHEA-d13', 'DHEA-d15', 'DHEA-d17', 'DHEA-d19', 'DHEA-d21', 'DHEA-d23', 'DHEA-d25', 'DHEA-d27', 'DHEA-d29', 'DHEA-d31', 'DHEA-d33', 'DHEA-d35', 'DHEA-d37', 'DHEA-d39', 'DHEA-d41', 'DHEA-d43', 'DHEA-d45', 'DHEA-d47', 'DHEA-d49', 'DHEA-d51', 'DHEA-d53', 'DHEA-d55', 'DHEA-d57', 'DHEA-d59', 'DHEA-d61', 'DHEA-d63', 'DHEA-d65', 'DHEA-d67', 'DHEA-d69', 'DHEA-d71', 'DHEA-d73', 'DHEA-d75', 'DHEA-d77', 'DHEA-d79', 'DHEA-d81', 'DHEA-d83', 'DHEA-d85', 'DHEA-d87', 'DHEA-d89', 'DHEA-d91', 'DHEA-d93', 'DHEA-d95', 'DHEA-d97', 'DHEA-d99', 'DHEA-d101', 'DHEA-d103', 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'DHEA-d2447', 'DHEA-d24

# Report actionable results faster using powerful data analysis tools

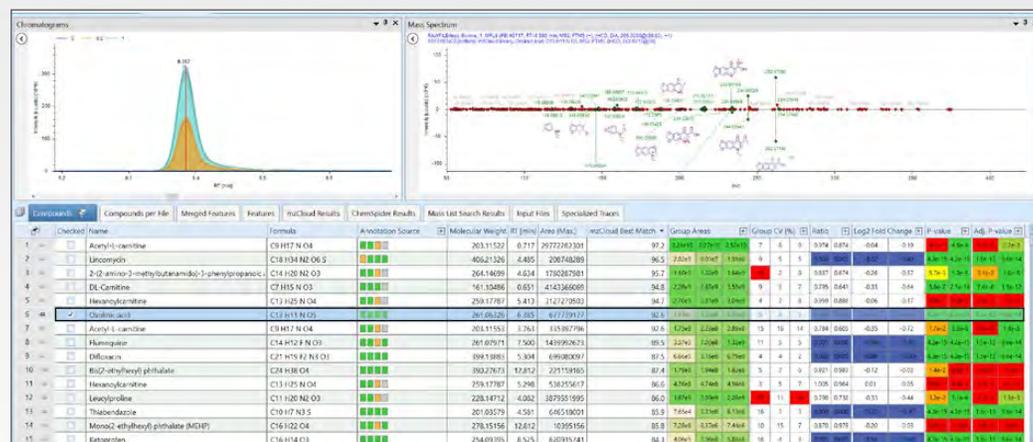


Providing reportable results in a timely manner requires access to a truly connected data processing ecosystem. Regardless of application, Thermo Scientific small-molecule data analysis solutions streamline unknown identification, screening, and quantitation using a powerful suite of tools.

## Compound Discoverer software

### Small-molecule unknown identification

- Confidently identify unknowns faster with spectral library searching using the online mzCloud mass spectral library, offline Thermo Scientific™ mzVault™ spectral libraries and searchable on-line 3rd party libraries
- Efficiently rank putative candidates with the Thermo Scientific™ mzLogic™ data analysis algorithm
- Specify desired data flows with drag-and-drop workflow nodes
- Review only data you choose with customizable data visualization



Unknown screening results shown with an integrated view in Compound Discoverer software, including raw data, chromatographic peak, and mass spectrum (including mirror plot with mzCloud match).



## Thermo Scientific™ mzCloud™ mass spectral library

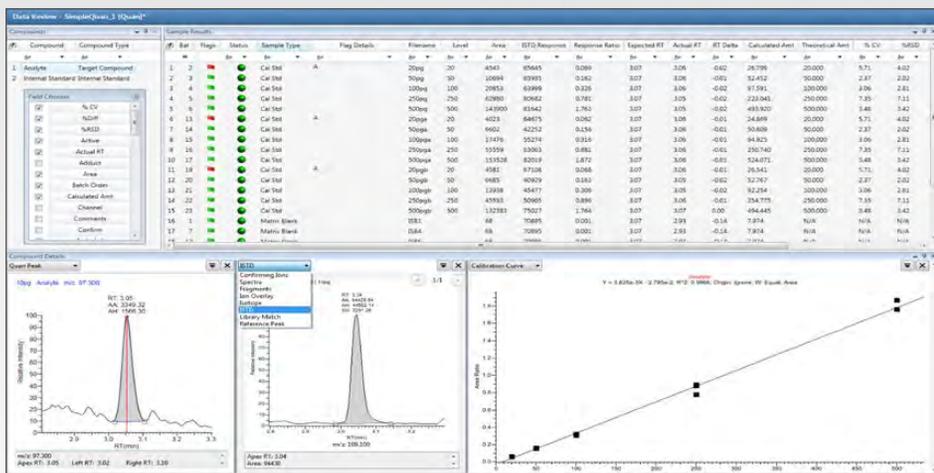
- Extensive, high-quality spectral fragmentation library
- Chemically diverse, covering all applications
- Fully integrated with Thermo Scientific™ Compound Discoverer™ software
- Available offline via mzVault for Thermo Scientific™ TraceFinder™ software



## TraceFinder software

### High-throughput screening and quantitation

- Save time training staff using a single platform for both screening and quantitation
- View only desired data parameters with a customizable user interface
- Efficiently analyze and report data with customizable flagging and report templates



Rearrange flexible data-review panes to customize columns, plot layouts, and positioning of content. Quickly and easily observe data processing status, view compound-related flags to locate compounds which need attention, and take appropriate steps to correct any problems.



## Thermo Scientific™ Chromeleon™ Chromatography Data System (CDS) software

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- Streamline chromatography and MS software training using the first CDS with quantitative MS analysis control
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# Fourth-generation quadrupole-Orbitrap mass spectrometer

The Orbitrap Exploris 120 mass spectrometer combines proven technology refined over more than 20 years with advanced performance and speed capabilities, day-to-day reliability, and a compact footprint. Now both novice and expert high-resolution MS users can efficiently deploy the instrument to obtain highly reliable and accurate results.

## OptaMax NG electrospray ion source

Positions reliably with easy-to-change probes and needles common across next-generation Thermo Scientific mass spectrometers

## EASY-IC internal calibration source

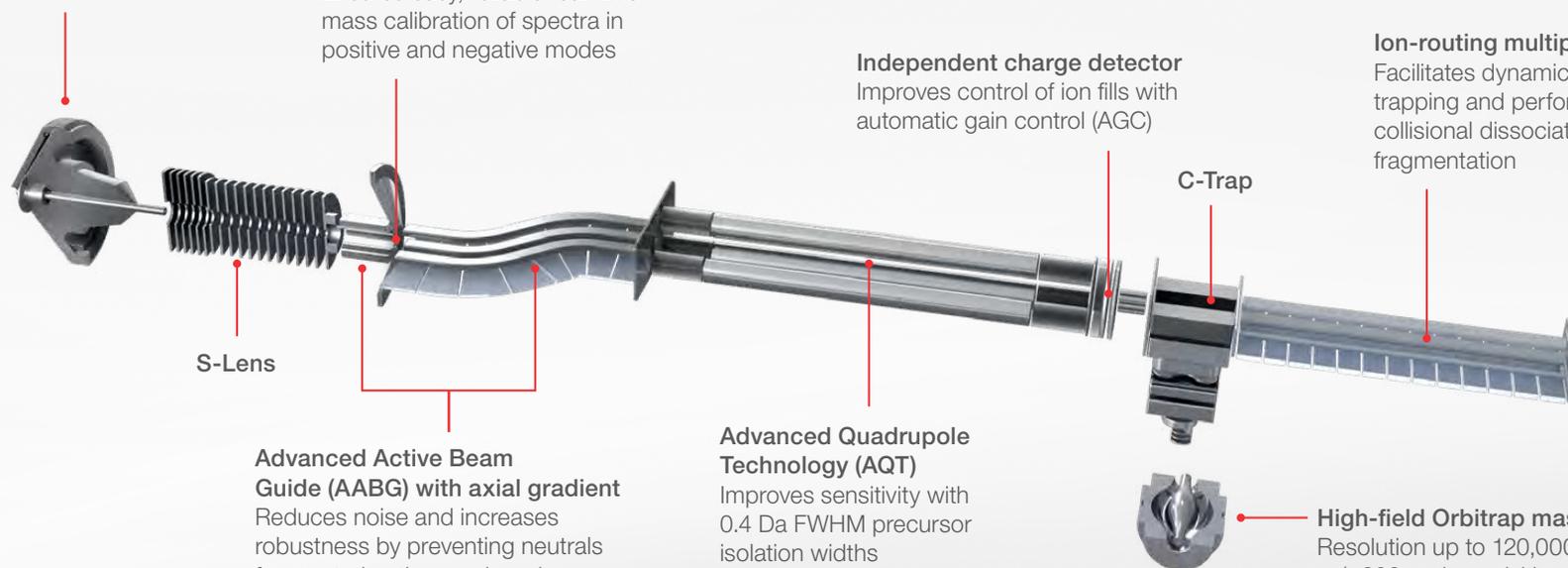
Ensures easy, reliable real-time mass calibration of spectra in positive and negative modes

## Independent charge detector

Improves control of ion fills with automatic gain control (AGC)

## Ion-routing multipole (IRM)

Facilitates dynamic, extended ion trapping and performs higher-energy collisional dissociation (HCD) fragmentation



S-Lens

## Advanced Active Beam Guide (AABG) with axial gradient

Reduces noise and increases robustness by preventing neutrals from entering the quadrupole mass filter, and by eliminating effects of local charging

## Advanced Quadrupole Technology (AQT)

Improves sensitivity with 0.4 Da FWHM precursor isolation widths

C-Trap

## High-field Orbitrap mass analyzer

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