

Mass spectrometry

Expand your analytical horizons

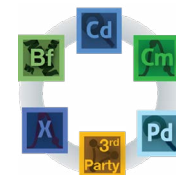
Orbitrap Excedion hybrid mass spectrometer

Orbitrap Excedion BioPharma hybrid mass spectrometer

Benefits

- Fast-scanning, high-field Thermo Scientific™ Orbitrap™ Excedion™ mass analyzer provides premium quantitative and qualitative performance from scan to scan
- Higher sensitivity with Electrodynamic Ion Funnel optimized for labile compounds
- Enhanced Dynamic Range (eDR) enables five orders of magnitude of intra-scan dynamic range
- Extended detection up to m/z 8,000 with the Thermo Scientific™ Orbitrap™ Excedion™ BioPharma Edition mass spectrometer
- Compatible with next generation Thermo Scientific™ OptaMax™ Plus and Thermo Scientific™ OptiSpray™ ion sources as well as Thermo Scientific™ FAIMS Pro Duo interface
- Instrument control software user interface with intuitive tuning, single-click calibration, drag-and-drop method setup, and predefined experiments
- In-lab upgradable to Thermo Scientific™ Orbitrap™ Excedion™ Pro mass spectrometer
- Common instrument control software user interface with Thermo Scientific™ Orbitrap™ Excedion™ Pro MS, Thermo Scientific™ Orbitrap™ Astral™ series, Thermo Scientific™ Orbitrap™ Tribrid™ series, Thermo Scientific™ Stellar™, and Thermo Scientific™ TSQ™ Triple Quadrupole mass spectrometers

Discover the Thermo Scientific™ Orbitrap™ Excedion™ mass spectrometer (MS), offering high-resolution, accurate-mass performance combined with enhanced intra-scan dynamic range (eDR). This enables simultaneous detection of both low- and high-abundance molecules in a single run, supporting applications in metabolomics, lipidomics, drug metabolite identification and quantification (DMPK), as well as environmental and food safety research. Built on the modern Orbitrap Excedion platform, the Orbitrap Excedion MS delivers everyday reliability and a clear in-lab upgrade path to the Thermo Scientific™ Orbitrap™ Excedion™ Pro hybrid mass spectrometer, unlocking advanced capabilities like electron-based fragmentation (fast and sensitive EASY-ETD), hybrid-DIA with on-the-fly adaptive retention time (RT) routine adjustment, Thermo Scientific™ TMTpro™ 32plex deuterated label reagents, and higher-speed scanning.

Thermo Scientific™ Vanquish™
Neo UHPLC SystemOrbitrap Excedion
mass spectrometerThermo Scientific™ and 3rd
party software platforms

• Start-up services

• Repair services

• Compliance services

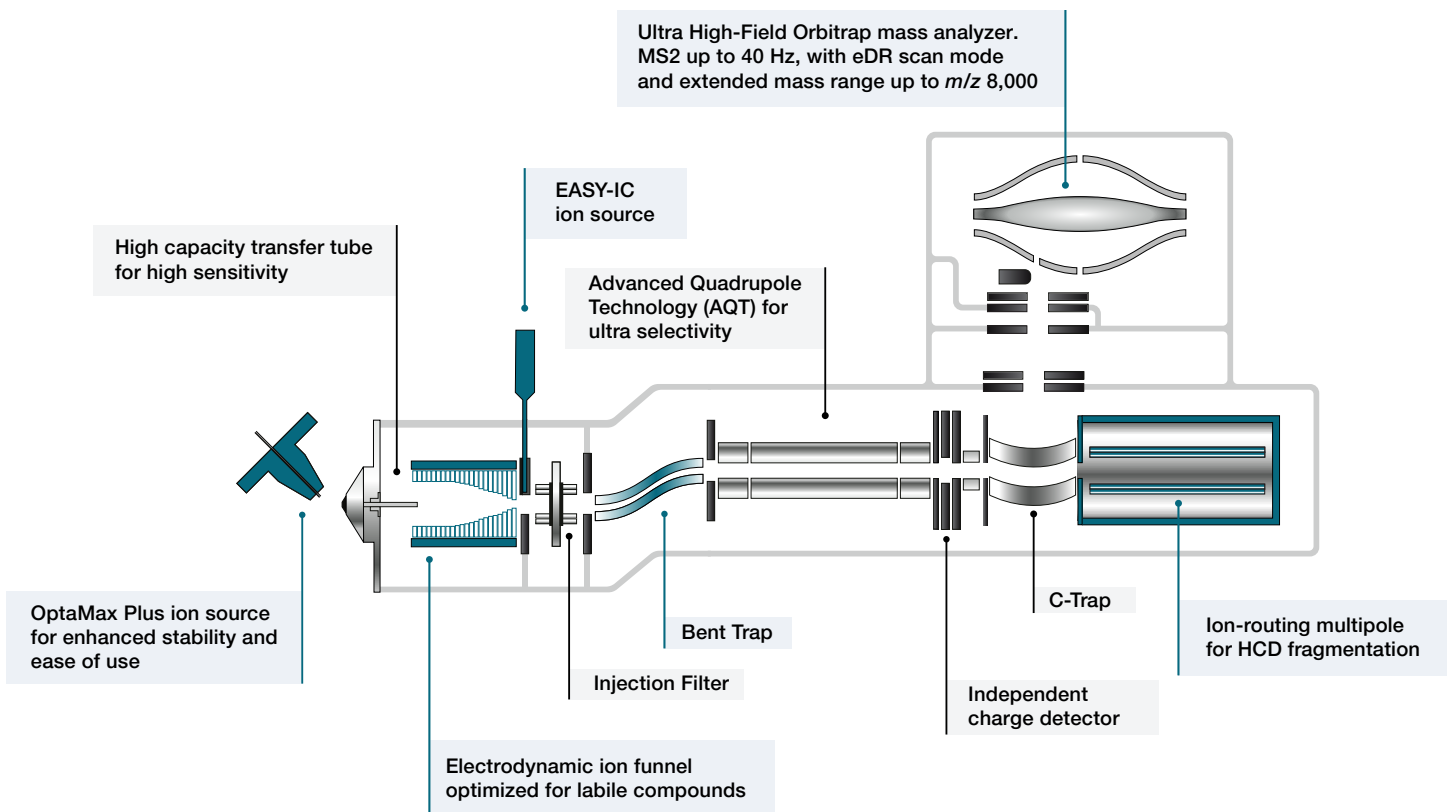


When you invest in Thermo Scientific™ instrumentation, you not only benefit from top-quality product performance, you can also enjoy world-class service solutions from Unity™ Lab Services. Our comprehensive service portfolio was designed to meet the needs of your lab. Keep focused on what matters. We've got your back.

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Key capabilities

- An enhanced, high-sensitivity atmospheric pressure interface integrates a high-capacity ion transfer tube with an electrodynamic ion funnel, optimized for labile compounds and efficient ion transmission. This design increases ion flux while ensuring gentle ion handling, enabling lower detection limits across a broader range of molecules
- Thermo Scientific™ EASY-IC™ internal calibrant source generates ions for real-time mass calibration of the Orbitrap analyzer in both positive and negative modes
- Advanced Quadrupole Technology (AQT) that includes a segmented quadrupole mass filter with hyperbolic surfaces to maximize ion transmission and achieve unprecedented levels of qualitative and quantitative performance with fast switching time
- Higher-energy Collisional Dissociation (HCD) in ion-routing multipole for detection in the Orbitrap mass analyzer
- MS and MS² acquisition rates of up to 40 Hz in the Orbitrap mass analyzer
- eDR mode enabling up to five orders of magnitude of intra-scan dynamic range
- Accurate quantification of Thermo Scientific™ TMTpro™ 18-plex reporter ions
- Maximum Orbitrap mass analyzer resolution of up to 240,000 FWHM at m/z 200
- Thermo Scientific™ Precursor Fit filter enables precursor ion selection with a defined specificity
- Advanced Peak Determination (APD) for improved precursor annotation in data-dependent experiments
- Intuitive, flexible drag-and-drop instrument method editor simplifies method development and creation of unique analytical workflows
- Extensive pre-built and optimized method templates that are fully customizable for a variety of application workflows
- Low energy-consumption instrument featuring a low-maintenance dry pump
- Orbitrap Excedion BioPharma Edition MS comes with application mode “Intact Proteins” providing enhanced performance for larger molecules including an extended mass range up to m/z 8,000 with the Orbitrap mass analyzer for comprehensive analysis
- Orbitrap Excedion BioPharma Edition MS comes with application mode “Oligonucleotide”, providing optimum transmission for mRNA mapping
- Option to switch pressure modes in the ion-routing multipole during acquisition (BioPharma Edition only)



Orbitrap Excedion mass spectrometer ion path

Hardware features

Ion sources

OptaMax Plus ion source

- Enhanced stability—the new heater and sprayer design significantly enhances heat transfer, ensuring superior electrospray stability across a broad temperature range
- User-friendly design—experience enhanced ease of use with easily adjustable and reproducible movement, simplifying your workflow
- Versatile flow rate compatibility—supports a wide range of flow rates from 1–2,000 $\mu\text{L}/\text{min}$, providing flexibility for various applications
- Optional atmospheric pressure chemical ionization (APCI) probe—the optional APCI probe is compatible with flow rates of 100–2,000 $\mu\text{L}/\text{min}$ and can be upgraded with atmospheric pressure photoionization (APPI) capabilities for expanded functionality

EASY-IC ion source

Provides <0.2 ppm root mean squared (RMS) mass accuracy under defined conditions

Generates optional internal reference ions for real-time mass correction of spectra in both positive and negative ionization mode

Ion optics

The atmospheric pressure ionization (API) interface consists of:

High-capacity ion transfer tube (HCTT)

- Improved sensitivity and desolvation with increased ion flux into the vacuum system
- Vent-free maintenance

Electrodynamic ion funnel (EDIF)

- A radio frequency (RF) device, optimized for labile compounds, efficiently captures ions as they leave the HCTT
- Automatic tuning results in broad ion transmission curves with reduced ion losses, increasing sensitivity

Bent trap

- Reduces noise by preventing neutrals and high-velocity clusters from entering the quadrupole mass filter using a double-bent design geometry
- Axial field along the length of the rods improves ion transfer robustness

Advanced quadrupole technology (AQT)

- Segmented quadrupole mass filter for precursor ion selection with variable precursor isolation width from m/z 0.4 to m/z 2,000
- MS^2 precursor ion selection with high transmission from m/z 40 to 2,500
- Prolonged uptime due to patented configuration switching mode

Ion-routing multipole (IRM)

- Robust ion trapping for MS scans and higher energy collisional dissociation (HCD)
- Nitrogen collision gas

Automatic gain control (AGC)

Reliable AGC measurements for controlled injection of the number of ions are ensured by the Independent Charge Detector

Orbitrap mass analyzer

- Ultra high-field Orbitrap mass analyzer with 4 kV central electrode voltage
- Low noise detection pre-amplifier

Vacuum system

- A compact, single, six-stage turbomolecular pump design regulates the adequate vacuum in six stages for the aluminum high-vacuum analyzer chambers
- Advanced vacuum technology reduces pressure in the ultra-high vacuum regions, enhancing transmission of ions to the Orbitrap mass analyzer

Analog inputs

Channel 1 analog input (± 10 V), Channel 2 analog (± 10 V)

Optional hardware

OptiSpray ion source

- Maximum low-flow electrospray ionization performance and reproducibility using automated spray optimization with integrated sheath gas control
- Simple installation, use, and usage tracking of cartridge nano and capillary columns
- Enhanced robustness with exchangeable emitters and inactive spray position between injections
- Supports OptiSpray cartridge columns
- Compatible with flow rates from 50 to 10,000 nL/min

Easy-Spray ion source

- Maximum nanoelectrospray performance with minimum adjustment
- Easy-to-use nano-ESI source
- Supports Thermo Scientific™ Easy-Spray™ ion source and Thermo Scientific™ μ PAC™ NEO HPLC columns
- Compatible with flow rates from 50 to 4,000 nL/min

Thermo Scientific™ NanoSpray Flex™ ion source

- High nano-ESI flexibility and probe position adjustment
- Supports a wide range of column formats and static and dynamic electrospray ionization
- Compatible with flow rates from 50 to 4,000 nL/min

FAIMS Pro Duo interface

- Performs online gas-phase fractionation based on differential ion mobility
- Reduces noise and substantially increases system robustness

Data acquisition system

Instrument control and data acquisition PC

- High-performance PC with Intel™ microprocessor
- High-resolution LED color monitor
- Microsoft™ Windows™ 11 Enterprise (Long Term Service version) operating system

Orbitrap Hybrid series instrument control software

- Tune application for instrument calibrations and checks, diagnostics, and manual data acquisition
- Method editor application with a comprehensive application-specific template library, method setup supported by tooltips, and a drag-and-drop user interface to facilitate method development

Thermo Scientific™ Xcalibur™ Data Acquisition and Interpretation software

- Xcalibur software is the control software for the Thermo Scientific mass spectrometer portfolio
- Shared instrument control software interface with Thermo Scientific™ Orbitrap™ Astral™ MS, Thermo Scientific™ Orbitrap™ Tribrid MS, Thermo Scientific™ Orbitrap Exploris™ MS, and Thermo Scientific™ TSQ MS platforms to accelerate familiarization and reduce training needs

Thermo Scientific™ AcquireX™ Intelligent Data Acquisition Workflow

- AcquireX data acquisition workflows provide comprehensive small molecule sample profiling on an LC timescale using automated, logic-based sample re-injection with inter-run inclusion and exclusion lists

Optional data acquisition and analysis software

Thermo Scientific™ Proteome Discoverer™ software

- Flexible, expandable software for the qualitative and quantitative analysis of proteomics data
- Simplifies a wide range of proteomics workflows, from protein and peptide identification to post-translational modification (PTM) analysis to isobaric mass tagging and label-free quantitation with both data-dependent acquisition (DDA) and data-independent acquisition (DIA) data
- Optional CHIMERYS™ intelligent search algorithm to enhance DDA, DIA, tandem mass tag (TMT), and phosphoproteomics data analysis

Thermo Scientific™ ProSightPD™ software

- Processing node within Proteome Discoverer software that allows execution of ProSight searches of top-down and middle-down data

Thermo Scientific™ BioPharma Finder™ software

- Offers complete workflows for peptide mapping, host cell protein analysis, and multi-attribute method (MAM) development, ensuring high-confidence identification and quantification
- Powerful visualization tools for quality attributes, sequence variants, and post-translational modifications
- Simplifies and automates data processing, reducing manual intervention and increasing throughput for both expert and non-expert users

Thermo Scientific™ Compound Discoverer™ software

- Connects with the Thermo Scientific™ Ardia™ platform
- Streamlines small molecule unknown identification, determination of differences between samples, and elucidation of biological pathways with an integrated suite of data analysis tools

Thermo Scientific™ Chromeleon™ Chromatography Data System (CDS)

- Connects with the Ardia platform
- Streamlined chromatographic and MS targeted screening and quantitative workflows within an enterprise and compliance-ready single software application

Thermo Scientific™ TraceFinder™ software

- Acquire and process high-throughput screening and quantitation with built-in intelligence, driving productivity gains from data acquisition and processing to reporting

Operation modes

Application-specific operation modes and system templates

Sets optimal default instrument parameters and manages application-specific system templates for easy method development and execution. Available modes are:

- Small molecule
 - 'Mild Trapping' is available with application mode 'Small Molecule' and is optionally applicable for particularly labile compounds
- Peptide
 - With application mode 'Peptide', singly charged (+1) ions are filtered out, prioritizing multiply charged species that are more characteristic of peptides for improved data quality in proteomics analyses
- Intact protein (included with BioPharma Edition mass spectrometer)
 - With application mode 'Intact Protein', pressure regimes (low, standard, and high) can be selected and scheduled in the experiment for best performance with native and denaturing conditions
- Oligonucleotide (included with BioPharma Edition mass spectrometer)
 - With application mode 'Oligonucleotide', pressure regimes (low, standard, and high) can be selected and scheduled in the experiment for best performance across a range of oligonucleotide and mRNA samples

General

- Supports Xcalibur AcquireX workflows
- Multiple experiments can be set up within one method
- One experiment can contain combinations of scans
- 'Collision Energy Type' can be selected: 'Normalized (NCE)' and 'Absolute (CE)'

High Resolution-Data Independent Acquisition (HR-DIA)

- Acquisition logic in which the scan event execution follows a predetermined pattern set by the experimental settings

Data-Dependent Acquisition (DDA)

- Acquisition logic in which a decision for a scan event execution is made in real-time, based upon certain criteria being met in a master scan
- Top speed: maximizes the number of high-quality MS² spectra in each cycle by intelligently scheduling MS and data dependent MS² scans based on a user-defined time between adjacent survey spectra
- TopN: enables a user-defined maximum number of high-quality MS² spectra from each cycle

Enhanced Dynamic Range (eDR)

- The full MS mass range is dissected into two Orbitrap subscans, each performing multiplexed isolation and overall MS¹ acquisition of equidistant or customizable *m/z* sub-ranges with efficient ion delivery to the Orbitrap analyzer. Stitching of two Orbitrap subscans is achieved automatically and fully embedded in the data structure. The number of windows within each Orbitrap subscan can be adjusted according to individual needs

Advanced Peak Determination (APD)

- Precursor annotation algorithm for improved charge state assignment to increase the number of precursors available for data-dependent analysis
- APD is available with all application modes and can be checked for improved determination of a) charge states and b) monoisotopic *m/z* values of isotopic envelopes. APD is automatically switched on for eDR scans

Automatic gain control

- Ensures that the optimum number of ions are utilized within a given ion injection time range for any acquisition type

Filters for data-dependent experiments

Filters guide data-dependent (discovery and confirmational) decisions on the fly and in real time. To achieve optimum results when applying application-dependent filter settings, the user is guided with the appropriate application-dependent default parameter settings and tool-tip text

Filters can be selected as follows:

- Dynamic Exclusion
- Intensity
- Precursor Fit
- Charge State
- Targeted Mass Inclusion
- Targeted Mass Exclusion
- Monoisotopic Precursor Selection (MIPS)
- Precursor Selection Range
- Apex Detection
- Isotope Exclusion

Targeted mass trigger

- Performs data-dependent scans upon the detection of a defined product ion for targeted, confirmational experimental set-ups

Scan functions

- Unique scan types are available:
- Full MS, including eDR scans
- All-Ions Fragmentation (AIF)
- Targeted Selected Ion Monitoring (tSIM)
- DIA
- Targeted MS² (tMS²)

Unique scan types are combinable within one single experiment, such as:

- Full Scan Data-Dependent MS² (ddMS²)
- Full Scan Data-Dependent Selected Ion Monitoring (ddSIM)

Both with 'Number of Scans' (= TopN), 'Cycle Time', or 'Scans per Outcome' (branching)

In addition, multiple experiments can be created combining all the scan types listed above

Installation requirements

Power

208–240 Vac single phase, 15 A, 50/60 Hz, with earth ground for instrument

200–230 Vac single phase, 15 A, 50/60 Hz, with earth ground for dry forepump

100–240 Vac single phase, 15 A, 50/60 Hz, with earth ground for the data system

Gas

Source gas: high-purity nitrogen gas supply (>99% pure at 600 ± 50 kPa [6.0 ± 0.5 bar, 87 ± 7 psi])

A pre-regulator might be required to keep the source gas pressure within the required limits

Collision and EASY-IC gas: ultra-high-purity nitrogen (UHP > 99.999% pure*) at 600 ± 50 kPa [6.0 ± 0.5 bar]

Weight

110 kg (242 lb.) without data system, vacuum rough pump
78 kg (172 lb), and optional items

Environment

System averages 2,000 W (6,820 Btu/h) output when considering air conditioning needs

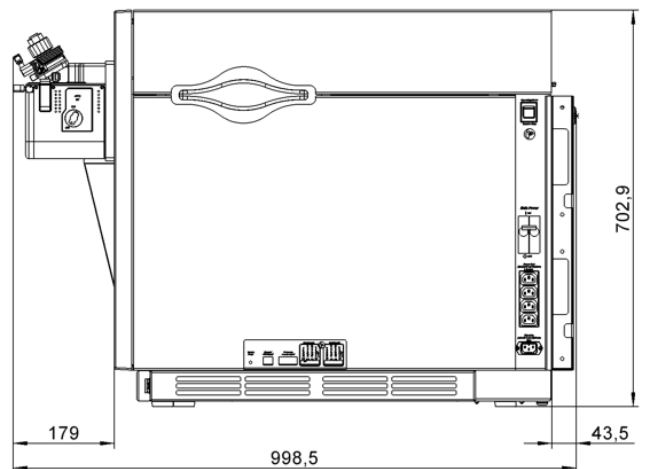
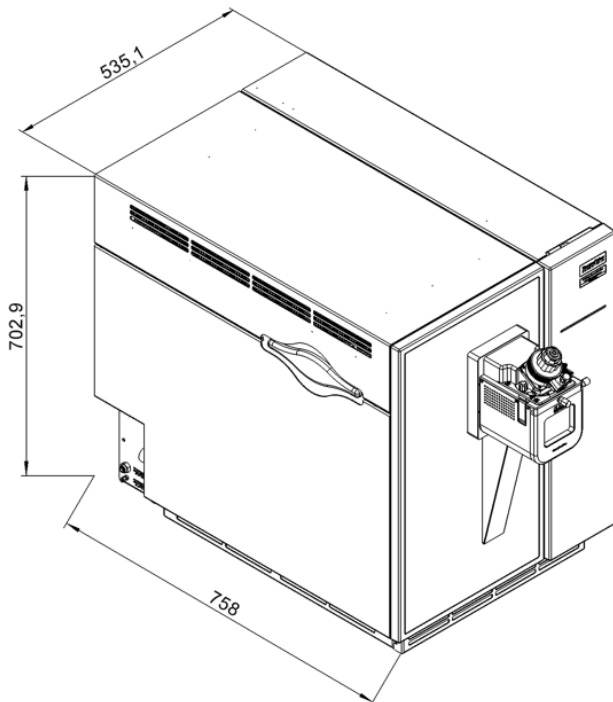
Operating environment must be 18–27 °C (64–81 °F). Relative humidity must be 20–80% with no condensation

Designed for indoor use at an altitude of up to 3,000 m (10,000 ft) above sea level

The Orbitrap Excedion mass spectrometer comes with a single rough dry pump, reducing noise, heat, and energy consumption by 30% compared to two oil rough pumps

Dimensions (width x length x height)

534 x 763 x 703 mm (21 x 30 x 27.7 in.)



Performance specifications

Mass range	Standard mass range m/z 40–6,000 BioPharma Edition mass range up to m/z 8,000 The following mass range limitation applies: set last mass $\leq 15 \times$ first mass. For first mass $> 2,500$, the actual ion collection range is m/z 2,500–last mass.
Orbitrap mass analyzer resolution	Up to 240,000 at m/z 200
Scan rate**	Up to 40 Hz
Instrument detection limit	Full Scan: < 1.5 fg reserpine on column MS ² : < 1.5 fg reserpine on column SIM: < 0.8 fg reserpine on column
Mass accuracy**	External calibration achieves < 3 ppm RMS Internal calibration achieves < 1 ppm RMS
Mass stability	External calibration achieves < 3 ppm mass drift over 24 hours Internal calibration achieves < 1 ppm mass drift over 24 hours EASY-IC (scan-to-scan lock mass correction) achieves < 1 ppm mass drift for at least 5 days 1-point mass calibration achieves < 3 ppm mass drift over 4 weeks
Mass accuracy, single mass**	Internal calibration achieves < 0.2 ppm RMS for m/z 262.63612 [MRFA ²⁺] in positive mode Internal calibration achieves < 0.2 ppm RMS for m/z 362.96962 [Perfluoroheptanoic acid] in negative mode
Intra-scan dynamic range**	5 orders of magnitude within an eDR mode scan Orbitrap mass analyzer spectrum
Polarity switching	One Full Scan cycle [†] < 700 ms equals > 1.4 Hz One tSIM Scan cycle [‡] < 600 ms equals > 1.6 Hz
Multiplexing	Up to 20 precursor ions per scan
Fragmentation	Higher collisional dissociation (HCD)

* With less than one ppm each water and oxygen

** Under defined conditions

[†]One cycle consists of acquiring one Full Scan in positive mode and one Full Scan in negative mode at resolution setting 60,000

[‡]One tSIM Scan in positive mode and one tSIM Scan in negative mode at resolution setting 60,000

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