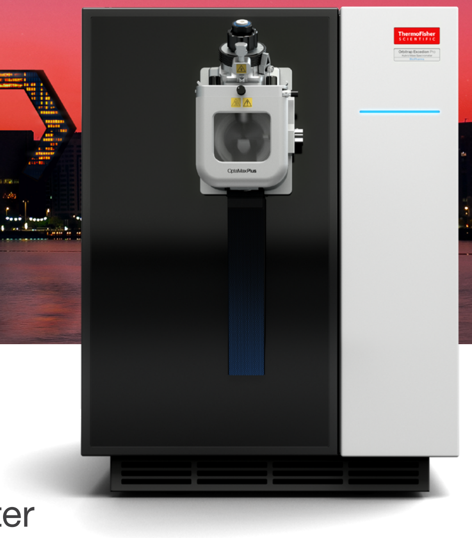
Mass spectrometry



Discover. Innovate. Exceed.

Orbitrap Excedion Pro hybrid mass spectrometer
Orbitrap Excedion Pro BioPharma hybrid mass spectrometer

Welcome to the next generation of mass spectrometry with the Thermo Scientific™ Orbitrap™ Excedion™ Pro Hybrid Mass Spectrometer. Building on our outstanding legacy quadrupole-Orbitrap hybrid mass spectrometry technology, the Orbitrap Excedion Pro hybrid mass spectrometer delivers enhanced sensitivity, dynamic range, fast and sensitive electron-based fragmentation and innovative capabilities, transforming everyday analysis into exceptional results.

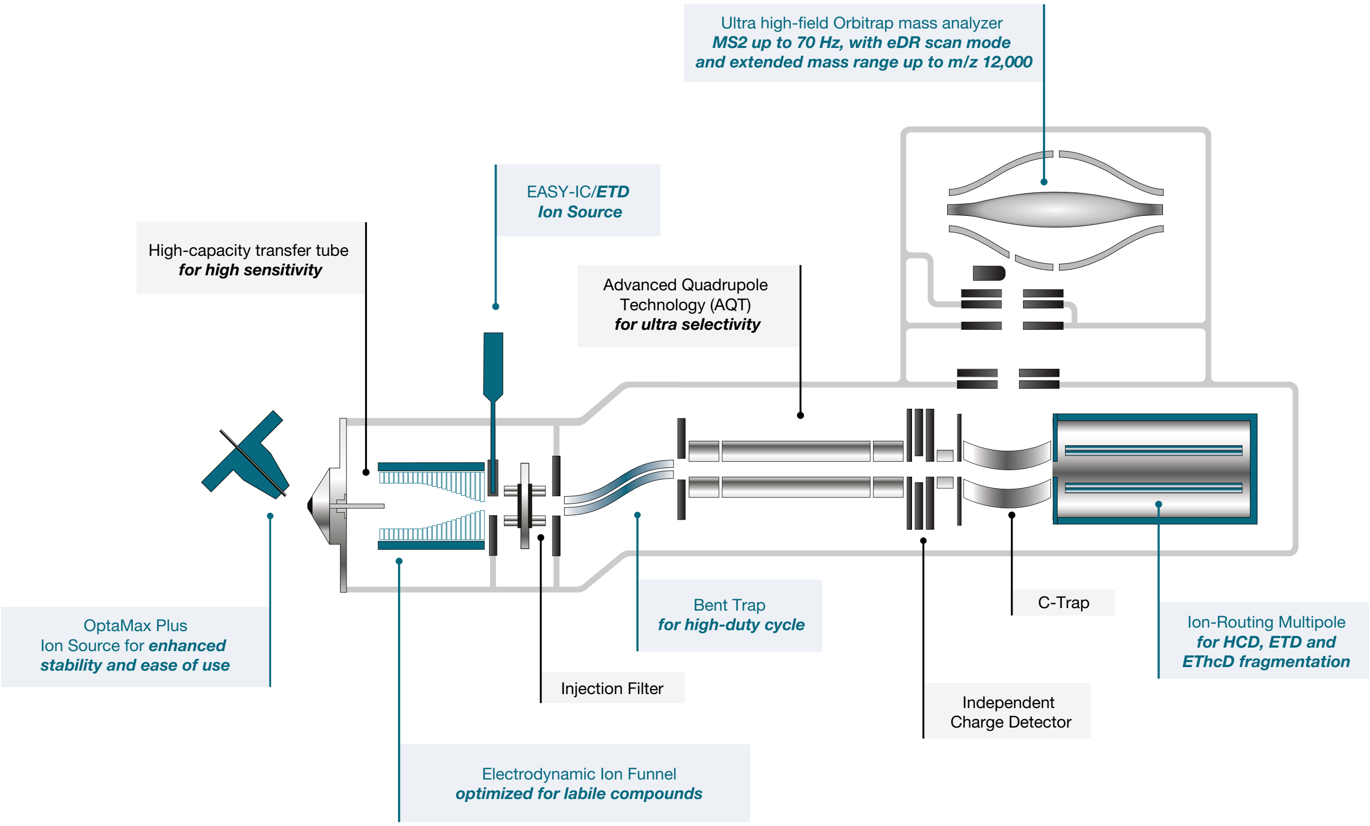
Designed for biopharma characterization, higher-order structure characterization, sensitive metabolomics analysis and proteomics research applications, this advanced benchtop hybrid mass spectrometer sets a new standard in analytical performance, empowering you to make groundbreaking discoveries.

Benefits

- Fast-scanning High-Field Thermo Scientific™ Orbitrap™ mass analyzer provides premium quantitative and qualitative performance from scan to scan
- Fast and sensitive alternative fragmentation with Electron Transfer Dissociation (ETD) combined with Higher-Energy Collisional Dissociation (HCD) fragmentation delivers distinct Electron-Transfer/Higher-Energy Collision Dissociation (EThcD) fragmentation data on a hybrid benchtop platform
- Higher sensitivity with Electrodynamic Ion Funnel (EDIF) optimized for labile compounds
- Enhanced Dynamic Range (eDR) enabling up to 5 orders of magnitude of intra-scan dynamic range
- Hybrid-DIA, supported by the adaptive retention time (RT) routine, combines Parallel Reaction Monitoring (PRM) and Data-Independent Acquisition (DIA) into one experiment for discovery and highly sensitive, targeted analysis
- Extended detection up to *m/z* 12,000 with the Thermo Scientific™ Orbitrap™ Excedion™ Pro BioPharma Hybrid Mass Spectrometer
- Adaptive RT routine provides on-the-fly RT adjustment in the LC timescale, enabling the use of narrow triggering windows for targeted MS^2
- Compatible with next-generation Thermo Scientific™ OptaMax™ Plus and OptiSpray™ technology 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 pre-defined experiments
- Common instrument control software user interface with:
  - Thermo Scientific™ Orbitrap™ Astral™ series mass spectrometers
  - Thermo Scientific™ Orbitrap™ Tribrid™ series mass spectrometers
  - Thermo Scientific™ Stellar™ mass spectrometers
  - Thermo Scientific™ TSQ™ Triple Quadrupole mass spectrometers

Key capabilities

- Improved high-sensitivity atmospheric pressure interface combines a high-capacity ion transfer tube and an EDIF optimized for labile compounds and efficient ion transfer, providing an increased ion flux and gentle transfer of ions—and enabling lower limits of detection for a wider range of molecules
- Thermo Scientific™ EASY-IC™ internal calibrant source generates ions for real-time and scheduled one-point 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
- HCD in ion routing multipole for detection in the Orbitrap mass analyzer
- Fast and sensitive alternative fragmentation with Thermo Scientific™ EASY-ETD™ ion source, available as an option
- EThcD fragmentation as a combination of ETD with optional HCD fragmentation to deliver complementary fragments and additional structural information
- MS and MS/MS acquisition rates of up to 70 Hz in the Orbitrap mass analyzer
- eDR mode enabling up to 5 orders of magnitude of intra-scan dynamic range
- Adaptive RT routine for dynamic adjustment of chromatographic monitoring windows, helping ensure reproducible measurements with sensitivity and specificity to achieve comprehensive coverage of targeted compounds across large sample cohorts
- Hybrid-DIA combines the sensitivity and specificity of targeted experiments with the unbiased discovery of DIA-based shotgun proteomics in a single experiment
- TurboTMT processing supporting the Orbitrap Excedion Pro hybrid mass spectrometer for accurate quantification of Thermo Scientific™ TMTpro™ 32-plex reporter ions
- Maximum Orbitrap mass analyzer resolution of up to 480,000 (FWHM) at *m/z* 200
- Thermo Scientific™ Precursor Fit filter enables precursor ion selection for 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 customized 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
- The Orbitrap Excedion Pro BioPharma hybrid mass spectrometer comes with Application Mode 'Intact Proteins' with enhanced performance for larger molecules including an extended mass range up to *m/z* 12,000 with the Orbitrap mass analyzer for comprehensive analysis



Orbitrap Excedion Pro hybrid mass spectrometer ion path

Hardware features

Ion sources

OptaMax Plus ion source

- Enhanced stability—the new heater and sprayer design significantly enhances heat transfer, offering superior electrospray stability across a broad temperature range
- User-friendly design—experience enhanced ease of use with adjustable and reproducible movement, simplifying your workflow
- Versatile flow rate compatibility—supports a wide range of flow rates from 1 to 2,000 µL/min, providing flexibility for various applications
- Optional Atmospheric Pressure Chemical Ionization (APCI) probe—the optional APCI probe is compatible with flow rates from 100 to 2,000 µL/min and can be upgraded with Atmospheric Pressure Photoionization (APPI) capabilities for expanded functionality

EASY-IC ion source

- Provides <1 ppm Root Mean Square (RMS) mass accuracy under defined conditions with minimum effort
- Generates optional internal reference ions for real-time mass correction and scheduled one-point mass calibration spectra in both positive and negative ionization modes

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
- Automatic gain control (AGC) modulates the pre-accumulation of ions when needed to increase duty cycle and sensitivity

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/MS precursor ion selection with high transmission from *m/z* 40 to 2,500
- Prolonged uptime with patented configuration switching mode

Ion-routing multipole (IRM)

- Robust ion trapping for MS scans, HCD and next generation in high-sensitivity ETD
- Nitrogen collision gas

Automatic gain control (AGC)

- Reliable AGC measurements for controlled injection of the number of ions is enabled 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 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 the transmission of ions to the Orbitrap mass analyzer

Analog inputs

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

Optional hardware

OptiSpray technology

- 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-ETD option

- Factory installed next generation in high sensitivity ETD
- Field upgradable next generation in high sensitivity ETD

Easy-Spray ion source

- Easy-to-use nano-ESI source
- Supports Thermo Scientific™ Easy-Spray™ and µPAC™ columns
- Compatible with flow rates from 50 to 4,000 nL/min

Thermo Scientific™ NanoSpray Flex™ NG ion source

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

Thermo Scientific 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™ 10 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™ software

- Xcalibur software is the control software for the Thermo Scientific mass spectrometer portfolio
- Shared instrument control software interface with Orbitrap Astral MS, Orbitrap Tribrid MS, Thermo Scientific™ Orbitrap Exploris™ MS and TSQ MS platforms to accelerate familiarization and reduce training needs
- Integrates with the Thermo Scientific™ Ardia™ Platform for automated data transfer and secure central storage

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

Ardia Platform

The Ardia Platform is highly recommended for use with Orbitrap Excedion Pro hybrid mass spectrometers.

It is designed for chromatography and mass spectrometry users with an intuitive web-based interface that enables them to work with their instruments and data, both in and out of the lab.

- Automatically stores data in a secure, central location for all connected Thermo Scientific chromatography and mass spectrometry systems
- Enhances connected Thermo Scientific and third-party data processing software with additional capabilities such as automation and connectivity to streamline processing and simplify data sharing
- Delivers core functionality that enables online scheduling of instruments, visualization and electronic recording of instrument-related activities, viewing MS and chromatography data in a single location and dashboarding to provide key lab insights

The Ardia Platform is delivered pre-installed on a dedicated appliance to support on-premises central data storage with transfer, archival and backup capabilities and CHIMERYS™ intelligent search algorithm.

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™ BioPharma Finder™ software

- Connects with the Ardia Platform
- Offers complete workflows for peptide mapping, host cell protein analysis and Multi-Attribute Method (MAM) development, supporting 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 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™ Proteome Discoverer™ software

- Connects with the Ardia Platform
- 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 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™ 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
- Intact protein (included with the Pro BioPharma mass spectrometer)
- With Application Mode 'Intact Protein,' pressure regimes (low, standard and high) can be selected for best performance with native and denaturing conditions

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 MS^2 spectra in each cycle by intelligently scheduling MS and data-dependent MS^2 scans based on a user-defined time between adjacent survey spectra
- TopN: Enables a user-defined maximum number of high-quality MS/MS 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 MS^1 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 improves 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.

Adaptive RT routine

Adaptive RT routine for dynamic adjustment of chromatographic monitoring windows enables reproducible measurements with sensitivity and specificity to achieve comprehensive coverage of targeted compounds across large sample cohorts.

Hybrid-DIA

Hybrid-DIA combines the sensitivity and specificity of targeted PRM (proteomics) experiments with the unbiased discovery of DIA-based shotgun proteomics in a single experiment

TurboTMT intelligent data acquisition mode (TMT-32plx)

Unique processing mode powered by the Phased Spectrum Deconvolution Method (PSDM), TurboTMT is specifically designed to improve the acquisition rate of TMT-32plex experiments.

Automatic gain control (AGC)

AGC helps ensure 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 and targeted loss trigger

Performs data-dependent scans upon the detection of defined product ion(s)/defined mass loss(es) for targeted, confirmational experimental setups.

Scan functions

Unique scan types are available:

- Full MS scan, including eDR scans
- All-Ions Fragmentation (AIF)
- Targeted Selected Ion Monitoring (tSIM)
- DIA
- Targeted MS/MS (tMS2)

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

- Full Scan Data-Dependent MS/MS (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 (243 lb.) without data system, vacuum rough pumps and optional items

Environment

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

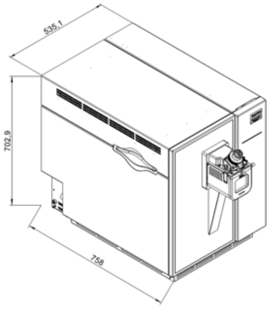
Operating environment must be 18–27°C (64–81°F). Relative humidity must be 20–80% with no condensation.

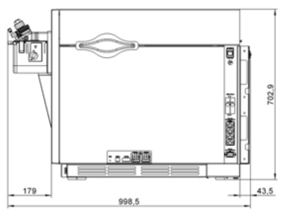
Designed for indoor use at an altitude of up to 3,000 m (10,000 ft.) above sea level

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

Dimensions (W x D x H)

535 x 758 x 703 mm (21 x 29.8 x 27.7 in.)





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*With less than one ppm each water and oxygen

Performance specifications

Mass range	Standard mass range *m/z* 40–6,000 BioPharma Edition mass range up to *m/z* 12,000
Orbitrap mass analyzer resolution	Up to 480,000 (FWHM) at *m/z* 200
Scan rate**	Up to 70 Hz
Mass accuracy**	1-point calibration achieves <3 ppm RMS drift over at least 4 weeks Internal lock mass calibration achieves <1 ppm RMS drift over 24 hours EASY-IC achieves <1 ppm RMS drift for at least 5 days
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
Intra scan dynamic range**	5 orders of magnitude of intra-scan dynamic range within an eDR mode scan Orbitrap mass analyzer spectrum
Polarity switching	1 Full Scan cycle[†] <700 ms equals >1.4 Hz
	1 tSIM Scan cycle[†] <600 ms equals >1.6 Hz
Multiplexing	Up to 20 precursor ions per scan
Fragmentation	HCD ETD[‡]-fast and sensitive ETD reaction of precursor ion with fluoranthene radical anions (*m/z* 202) injection into the IRM to generate a series of *c/z*-fragment ions EThcD fragmentation enabled by reaccelerating ETD fragment ions into IRM for HCD fragmentation

**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

[‡] ETD is an option either in field or factory installed

Learn more at **thermofisher.com/orbitrapexcedionpro**