

Orbitrap Exploris 240 Mass Spectrometer

Leading performance

Benefits

- Premium quantitative and qualitative performance with the fast-scanning High-Field Thermo Scientific™ Orbitrap™ mass analyzer
- Compatible with Thermo Scientific next-generation ion sources including the Thermo Scientific™ FAIMS Pro™ interface
- Comprehensive, automated sample profiling with Thermo Scientific™ AcquireX™ data acquisition workflow
- Set up and forget with at least five days of maximum mass accuracy provided, using built-in Thermo Scientific™ EASY-IC™ ion source internal reference mass
- Extended mass transmission and detection up to m/z 8,000 with the Thermo Scientific™ BioPharma option

The Thermo Scientific™ Orbitrap Exploris™ 240 mass spectrometer is a Thermo Scientific™ quadrupole-Orbitrap™ mass spectrometer, which is based on proven hardware and instrument control software designs of the next-generation Thermo Scientific mass spectrometers.¹

The Orbitrap Exploris 240 mass spectrometer provides the performance and versatility needed to drive discovery and identification, and the quantitative precision and accuracy to confidently scale up for impact. Operational simplicity with intelligent acquisition of high-resolution accurate-mass data (HRAM) provides the fast path to high-quality results for users of all skill levels in a range of applications including small molecule, peptide, and intact protein analyses.

Hardware features

Ion source

Thermo Scientific™ OptaMax™ NG ion source

- Adjustable heated electrospray ionization (H-ESI II) probe for ultimate sensitivity
- Additional non-heated low-flow calibrant sprayer for optimal mass and system calibration
- Designed for maximum performance with minimum adjustment
- Enhanced ruggedness and reduced chemical noise with sweep gas
- Flow rates from 1 $\mu\text{L}/\text{min}$ to 1,000 $\mu\text{L}/\text{min}$; OPTON-30139 (low-flow needle; 1–10 $\mu\text{L}/\text{min}$), OPTON-30694 (high-flow needle; 5–1,000 $\mu\text{L}/\text{min}$)

Ion optics

The atmospheric pressure ionization (API) interface consists of:

Round bore transfer tube

- Removable, heated ion transfer tube
- Vent-free maintenance

S-lens

S-lens stacked-ring radio frequency (RF) ion guide captures and efficiently focuses the ions into a tight beam. Large variable spacing between electrodes allows for better pumping efficiency and improved ruggedness.

Advanced active beam guide (AABG)

Axial field and injection filtering reduce noise by preventing neutrals and high-velocity clusters from entering the quadrupole mass filter using double bent design geometry

Advanced quadrupole technology (AQT)

- Segmented quadrupole mass filter for precursor ion selection with variable precursor isolation width from 0.4 to 1,200 Da
- MS/MS precursor ion selection with high transmission from m/z 40 to 2,500

Ion-routing multipole (IRM)

- Robust ion trapping for MS scans and higher energy collisional dissociation (HCD)
- Selection of absolute collision energy (CE) or normalized collision energy (NCE) for precursor fragmentation
- Nitrogen collision gas

Automatic gain control (AGC)

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

Thermo Scientific Orbitrap mass analyzer

- High-Field Orbitrap mass analyzer
- Low noise detection pre-amplifier
- 4kV central electrode voltage

Vacuum system

- A compact single turbo pump design providing 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

Thermo Scientific EASY-IC ion source

- Provides <1 ppm RMS mass accuracy under defined conditions with minimum effort for at least five days
- Generates internal calibrant ions for real-time mass calibration of spectra in both positive and negative modes

Optional hardware

BioPharma option

- Analysis of large molecules including intact proteins and large complexes sprayed under denatured or native conditions
- Includes mass transmission and detection up to m/z 8,000

Thermo Scientific™ Nanospray Flex™ NG ion source

- Supports static and dynamic electrospray experiments
- Compatible with liquid flow rates of 50 nL/min to 2 $\mu\text{L}/\text{min}$

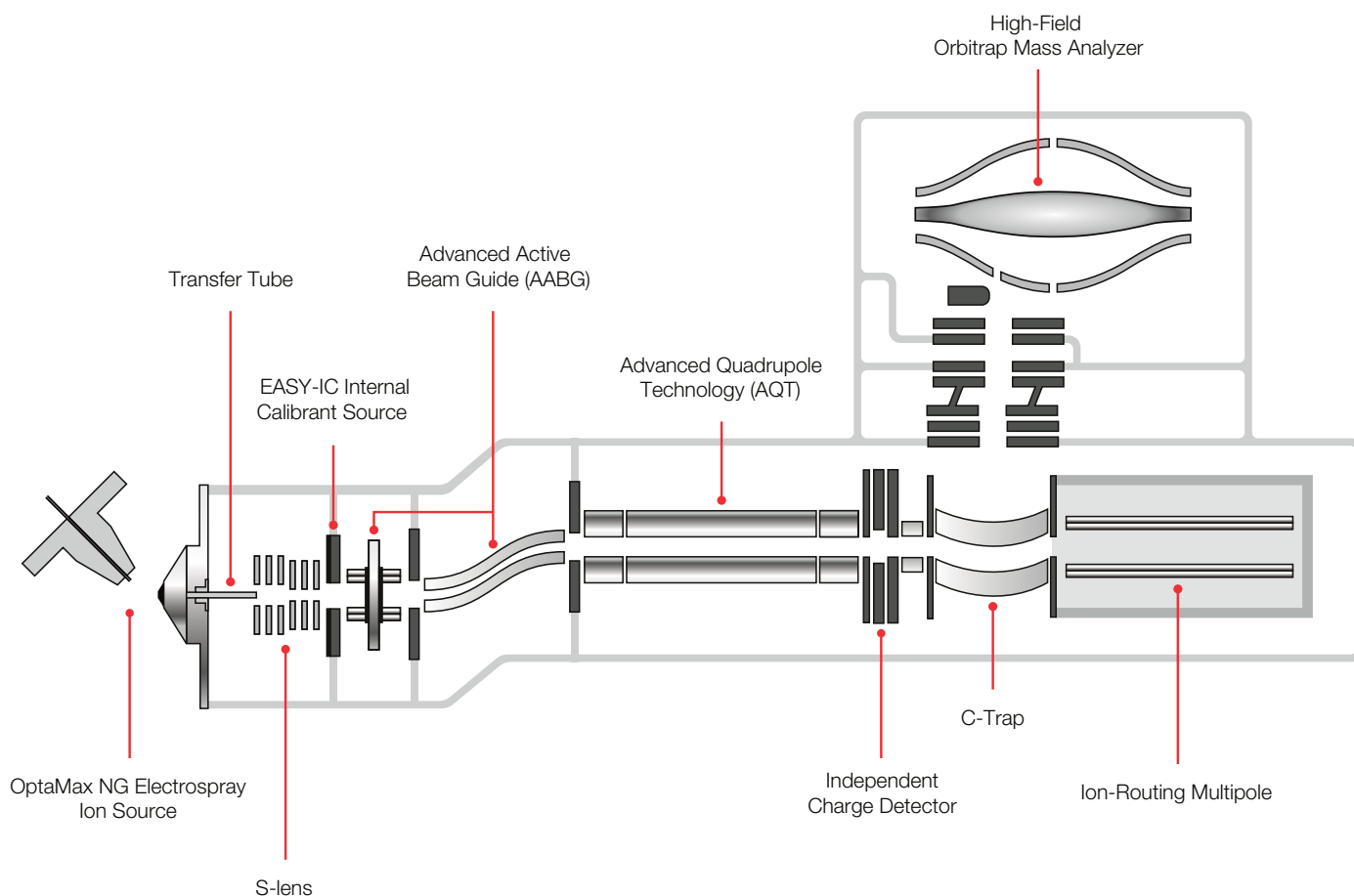
APCI probe for OptaMax NG ion source

- Compatible with flow rates from 50 $\mu\text{L}/\text{min}$ to 1,000 $\mu\text{L}/\text{min}$ without splitting
- The APCI probe can be upgraded to APPI

Thermo Scientific FAIMS Pro interface

- FAIMS Pro interface (high field asymmetric ion mobility spectrometry) augments analytical selectivity, enabling identification and quantitation of more proteins while reducing time-consuming sample preparation
- Performs online gas-phase fractionation based on differential ion mobility
- Optimized for 100–1,000 nL/min flow rates

Orbitrap Exploris 240 mass spectrometer ion path



Performance specifications

Mass Range	Standard mass range m/z 40–6,000, up to m/z 8,000 with BioPharma option
Orbitrap mass analyzer Resolution	Up to 240,000 at m/z 200
Scan Rate*	Up to 22 Hz at resolution setting 15,000 at m/z 200
Mass Accuracy*	External calibration achieves <3 ppm RMS drift over 24 hours; Internal lock mass calibration achieves <1 ppm RMS drift over 24 hours; EASY-IC achieves <1 ppm RMS drift for at least 5 days
Sensitivity	MS/MS: 200 fg reserpine on column S/N 100:1 tSIM: 200 fg reserpine on column S/N 250:1
Dynamic Range	>5,000 within a single 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 precursors per scan
Analog Inputs	Channel 1 analog input (± 10 V), Channel 2 analog input (± 10 V)

* 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

Data acquisition system

Data System

- High-performance PC with Intel® microprocessor
- High-resolution LED color monitor
- Microsoft® Windows® 10 Enterprise (Long Term Service version) operating system
- High-speed real-time data acquisition and instrument control
- Automatic calibration of all ion transfer and analysis parameters via instrument control software

Thermo Scientific AcquireX Data Acquisition Workflow

Automated and intelligent MS and MS/MS acquisition for complete, in-depth sample analysis

Thermo Scientific Orbitrap Exploris instrument control software

- Tune application for instrument mass and system calibrations and checks, diagnostics, and manual data acquisition
- Method Editor with a comprehensive application-specific template library, method setup supported by tooltips, and a drag-and-drop user interface to facilitate method development
- Consistent instrument control software whether using Thermo Scientific™ Xcalibur™ or Thermo Scientific™ Chromeleon™ Chromatography Data Systems (CDS) for data acquisition

Data acquisition and optional analysis software

Thermo Scientific Xcalibur software

- Xcalibur software is the control software for the next-generation Thermo Scientific mass spectrometer portfolio
- Accelerates familiarization and reduces training needs

Thermo Scientific Chromeleon Chromatography Data System (CDS)

Streamlined chromatographic and MS screening and quantitative workflows within an enterprise and compliance-ready single software application

Optional software

Thermo Scientific™ Proteome Discoverer™ software

Simplifies a wide range of proteomics workflows, from protein and peptide identification to PTM analysis to isobaric mass tagging, and SILAC and label-free quantitation

Thermo Scientific™ BioPharma Finder™ software

Provides complete protein characterization, including intact protein mass analysis, top- and middle-down analysis, peptide mapping or multi-attribute method (MAM) workflows

Thermo Scientific™ ProSightPC™ software

Stand-alone software for analyzing top-down, middle-down, and bottom-up data

Thermo Scientific™ Compound Discoverer™ software

Streamlines small molecule unknown identification, determination of real differences between samples, and elucidation of biological pathways with an integrated suite of data analysis tools

Thermo Scientific™ TraceFinder™ software

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

Operation modes

Resolution settings

Ranging from 15,000 to 240,000 at m/z 200

Advanced Peak Determination (APD)

Precursor annotation algorithm for improved charge state assignment to increase the number of precursors available for data-dependent analysis

Application Modes

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

- Small molecule
- Peptide
- Intact Protein (included with BioPharma option)

Scan functions

Full scan

MS² by Data-Dependent Acquisition (DDA) following a master scan (i.e., a Full MS scan or a tSIM scan):

- With up to Top100 ddMS²
- With Targeted Mass Filter
- 'Number of Scans' (TopN) and 'Cycle Time' (Top Speed) option
- Isolation Width: 0.4 u to 5 u
- HCD Collision Energy set value is definable per compound
- By performing a dependent scan on the most intense ion, if no target mass is found (optional)

tMS²

- Targeted MS² with Mass List Table
- Isolation Width, HCD Collision Energy, RF Lens, Resolution, Polarity, Microscans set values are definable compound-dependent (w/o msx)
- Isolation Width: 0.4 u to 5 u
- Multiplexing for up to 20 compounds
- Isolation Width set values can be defined compound-dependent (w/ msx)

SIM by Data-Dependent Acquisition (DDA) following a master scan (i.e., a Full MS scan or tSIM scan):

- With up to Top100 for ddSIM
- With Targeted Mass Filter
- 'Number of Scans' (TopN) and 'Cycle Time' (Top Speed) option
- Isolation Width: 0.4 u to 50 u
- By performing a dependent scan on the most intense ion, if no target mass is found (optional)

tSIM

- Targeted SIM with Mass List Table
- With Targeted Mass Filter for ddMS²
- Isolation Width, RF Lens, Resolution, Polarity, Microscans set values are definable compound-dependent (w/o msx)

- Isolation Width: 0.4 u to 50 u
- Multiplexing for up to 20 compounds
- MSX ID, multiplexing groups definable
- Isolation Width set values is definable compound-dependent (w/ msx)

AIF

- All Ion Fragmentation

DIA

- Data-Independent Acquisition (DIA) as MS²
- Isolation Width minimum: 0.4 u; with max 800 u; fixed for a given experiment
- Number of scan events defined via isolation width
- Multiplexing for up to 20 DIA windows
- MSX ID, multiplexing groups definable

General

- Application Modes 'Small Molecule', 'Peptide', 'Intact Protein' are available
- With Application Mode 'Small Molecules', a method can apply to Xcalibur AcquireX workflows (optional); it is a global setting and applies to the entire run
- 'Mild Trapping' is available with Application Mode 'Small Molecule' and can be applied optionally for particularly labile compounds; it is a global setting and applies to the entire run
- With Application Mode 'Intact Protein', pressure regimes (low, standard and high) can be selected for best performance with native and denaturing conditions
- APD is available optionally with all Application Modes. APD can be checked for improved determination of a) charge states and b) monoisotopic *m/z* values of isotopic envelopes
- Multiple experiments can be set up within one method
- One experiment can contain combinations of scans
- 'Collision Energy Type' can be selected: 'Normalized' and 'Absolute'
- 'Collision Energy Mode' can be selected: 'Fixed' and 'Stepped'

Filters

Filters guide data-dependent (discovery and confirmational) decisions on the fly and in real time. To achieve optimum results when applying application- and sample-dependent filter settings, the user is guided with appropriate application-dependent parameter settings and tool tips with tailored recommendations and detailed 'learn more' sections.

Filters can be selected as follows:

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

Installation requirements

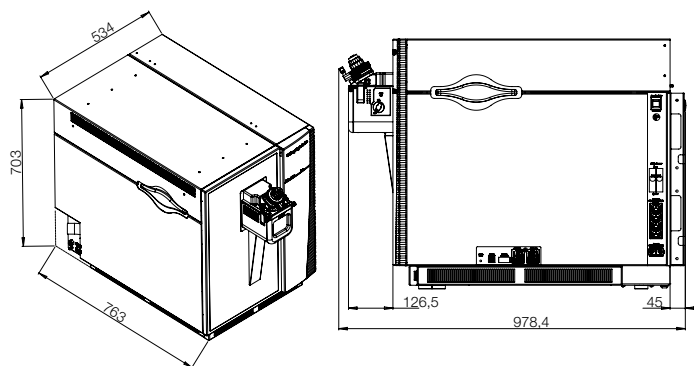
Power

- 2×208–240 Vac single phase, 15 A, 50/60 Hz, with earth ground for instrument and source vacuum pump
- 208–240 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 stable within the required limits
- HCD collision gas: ultra-high-purity nitrogen
- With EASY-IC: ultra-high-purity nitrogen (UHP > 99.999% pure†) at 600 ±50 kPa [6.0 ±0.5 bar]

† with less than one ppm each water and oxygen



Dimensions (w, d, h)

- 534 × 763 × 703 mm (21 × 30 × 27.7 in)

Weight

- 120 kg (265 lb) without data system, vacuum rough pumps, and optional items

Environment

- System averages 3440 W (11,730 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

Reference

1. Thermo Scientific™ Orbitrap™ Tribid™ mass spectrometers, Thermo Scientific™ TSQ Altis™ triple quadrupole mass spectrometer, Thermo Scientific™ TSQ Quantis™ triple quadrupole mass spectrometer, Thermo Scientific™ TSQ Fortis™ triple quadrupole mass spectrometer, and Thermo Scientific™ Orbitrap Exploris™ mass spectrometers

Find out more at

thermofisher.com/OrbitrapExploris240