

Orbitrap Exploris 480 Mass Spectrometer

Extraordinary simplified

Benefits

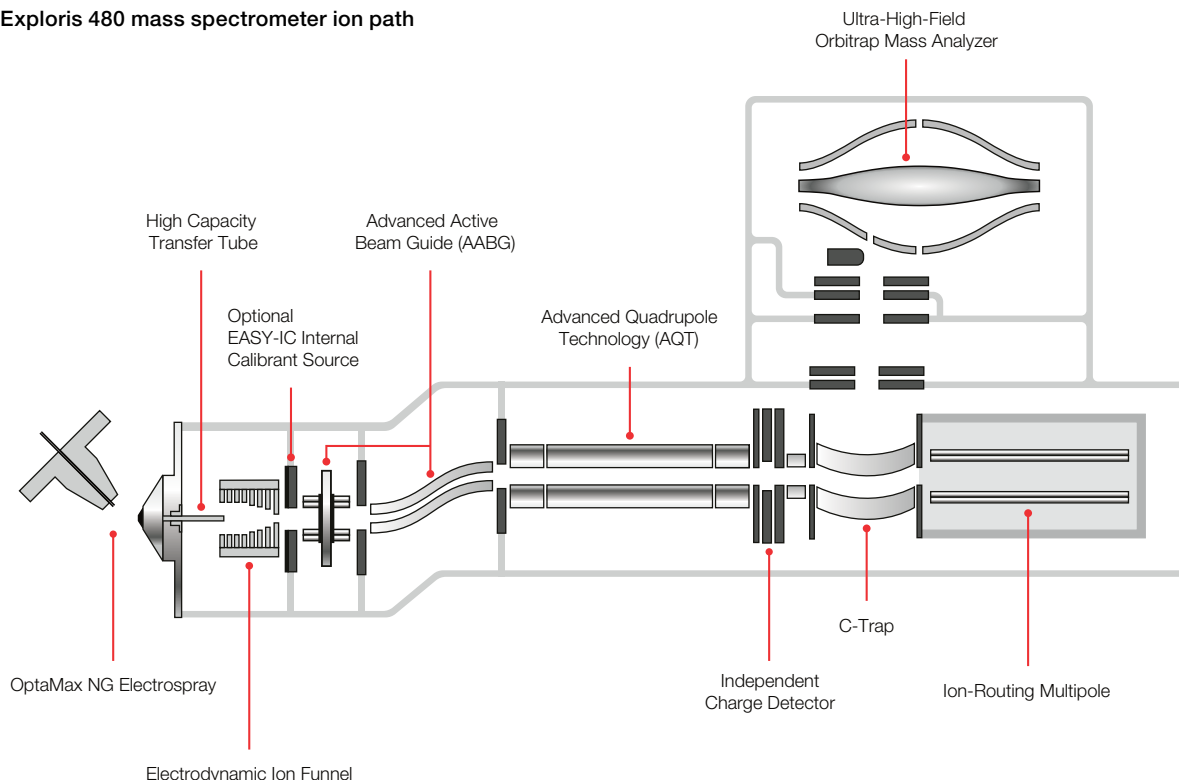
- High-performance featuring ultra-high-field Orbitrap mass analyzer technology
- Next-generation software with intuitive tuning, single-click calibration, drag-and-drop method setup, and pre-defined experiments
- Prolonged robustness and improved serviceability increase uptime
- Hardware and software shared with next-generation Thermo Scientific™ mass spectrometers¹ streamlines method transfer and familiarization
- Compatible with Thermo Scientific™ next generation ion sources including FAIMS Pro interface
- Enhanced peptide quantitation with advanced operating modes
- Thermo Scientific™ BioPharma option for analysis of large biomolecules

The Thermo Scientific™ Orbitrap Exploris™ 480 mass spectrometer is a Thermo Scientific™ quadrupole-Orbitrap™ mass spectrometer, based on the hardware and instrument control software designs of the next-generation Thermo Scientific™ mass spectrometers.¹

Built on the guiding principle of ease-of-use and reliable hardware, robust system performance boosts sample throughput. Soundness of data is assured with high-resolution accurate-mass (HRAM) selectivity, high scan speed and best-in-class mass spectral quality, all within a compact footprint to conserve bench space.

Simplified operation, smart scheduling and execution of user selected scan types deliver rich, high-confidence sample insights for users of all skill levels in a wide range of applications from small molecules to peptides and intact proteins.

Orbitrap Exploris 480 mass spectrometer ion path



Hardware features

Ion source

Thermo Scientific™ OptaMax™ NG ion source

- Adjustable heated electrospray ionization (HESI) 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 1000 $\mu\text{L}/\text{min}$;
OPTON-30139 (low-flow needle; 1–10 $\mu\text{L}/\text{min}$),
OPTON-30694 (high-flow needle; 5–1000 $\mu\text{L}/\text{min}$)

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, efficiently captures ions as they leave the HCTT
- Automatic tuning results in broad ion transmission curves with reduced ion losses, increasing sensitivity

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 1200 u
- MS/MS precursor ion selection with high transmission from m/z 40 to 2500
- Prolonged uptime due to patented configuration switching mode

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

Orbitrap mass analyzer

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

Vacuum system

- Pump controlling vacuum in six regions
- 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

Optional hardware

Thermo Scientific™ 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 8000

Thermo Scientific™ EASY-IC™ ion source

- Generates internal calibrant ions for real-time mass calibration of spectra in both positive and negative modes
- Provides <1 ppm RMS mass accuracy under defined conditions with minimum effort
- Available as field-upgrade or factory-installed option

Thermo Scientific™ EASY-Spray™ NG ion source

Maximum nanoelectrospray performance with minimum adjustment

Thermo Scientific™ NanoSpray Flex™ NG ion source

- Supports static and dynamic electrospray experiments
- Compatible with liquid flow rates of 50 nL/min to 2 μ L/min

APCI probe for OptaMax NG ion source

- Compatible with flow rates from 50 μ L/min to 1000 μ L/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 100–1000 nL/min flow rates

Performance specifications

Mass Range	Standard mass range m/z 40–6000, up to m/z 8000 with BioPharma option
Orbitrap mass analyzer Resolution	Up to 480,000 at m/z 200
Scan Rate*	Up to 40 Hz at resolution setting 7500 at m/z 200
Mass Accuracy (Orbitrap mass analyzer)*	External calibration achieves <3 ppm RMS drift over 24 hours, measured with Flex Mix; Internal calibration achieves <1 ppm RMS drift over 24 hours, measured with Flex Mix
Sensitivity	MS/MS: 50 fg reserpine on column S/N 100:1 SIM: 50 fg reserpine on column S/N 150:1
Dynamic Range	>5000 within a single Orbitrap mass analyzer spectrum
Polarity Switching	One full experimental cycle acquired in at >1.4 Hz where the cycle consists of acquiring one full scan MS in positive and negative polarity at a resolution setting of 60,000
Multiplexing	Up to 20 precursors per scan
Analog Inputs	Channel 1 analog input (\pm 10 V), Channel 2 analog (\pm 10 V)

* Under defined conditions

Software features

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™ 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™ Orbitrap Exploris™ instrument control software

- Tune application for instrumental 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 and drag-and-drop user interface to facilitate method development

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

Operation modes

Resolution settings

Ranging from 7500 to 480,000 at m/z 200

TurboTMT intelligent data acquisition mode

Novel processing mode powered by Phased Spectrum Deconvolution Method (ΦSDM) specifically designed to improve the acquisition rate of TMT experiments

Advanced peak determination (ADP)

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

Application mode

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
- SIM scan: Selected Ion Monitoring
 - in DDA* manner (discovery)
 - in targeted SIM manner based upon a sample-dependent, user-defined mass list
 - with Targeted Mass Filter applied (confirmation)
- AIF scan: All Ion Fragmentation
- MS² scan by Data Dependent Acquisition (DDA**) following a master scan (e.g., a Full scan):
 - in TopN or Top Speed manner (discovery)
 - with Targeted Mass Filter applied (confirmation)
 - by combining discovery and conformation manner
- MS² scan: targeted MS² (Parallel Reaction Monitoring), based upon a sample-dependent, user-defined mass list
- MS² scan by Data Independent Acquisition (DIA***)
 - w/ or w/o interspersed, data independent Full scan (e.g.)
 - with isolation widths settable per experiments

** a Data Dependent Acquisition (DDA) is an acquisition manner in which a decision for a scan execution is based upon certain criteria met in a fore-running master scan

*** a Data Independent Acquisition (DIA) is an acquisition manner in which the scan execution is independent from any criteria met in a fore-running scan; there is no need for a fore-running scan.

Filters

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 Inclusion
- Targeted Exclusion
- MIPS (Monoisotopic Precursor Selection)
- Precursor Selection Range
- Apex Detection

Targeted mass trigger

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

Installation requirements

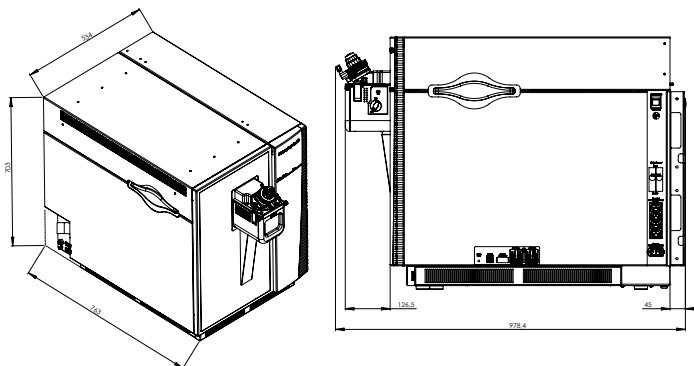
Power

- 2×208–240 Vac single phase, 15 A, 50/60 Hz, with earth ground for instrument and source vacuum pump
- 115 or 230 Vac single phase, 15 A, 50/60 Hz, with earth ground for auxiliary forepump
- 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 within the required limits
- HCD collision gas: ultra-high-purity nitrogen (UHP > 99.999% pure*) at 600 ±50 kPa [6.0 ±0.5 bar]
- For EASY IC option: ultra-high-purity nitrogen (UHP > 99.999% pure****)

**** 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 3000 m (10,000 ft) above sea level

Reference

1. Thermo Scientific™ Tribrid™ mass spectrometers, Thermo Scientific™ TSQ Altis™ mass spectrometer, Thermo Scientific™ TSQ Quantis™ mass spectrometer, and Thermo Scientific™ TSQ Fortis™ mass spectrometer.

Find out more at

thermofisher.com/OrbitrapExploris480