



Orbitrap Eclipse Tribrid Mass Spectrometer

Go beyond today's discovery

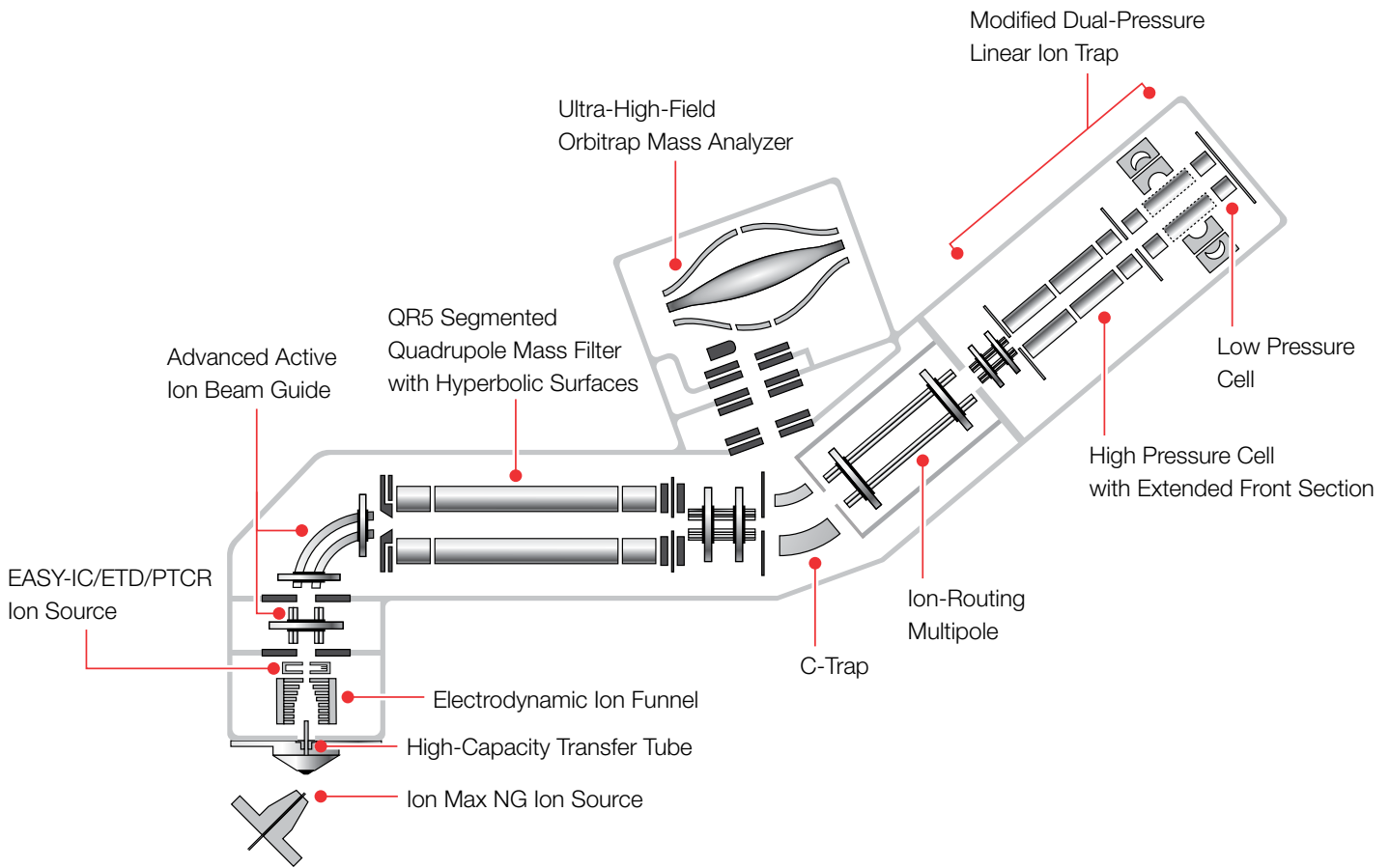
Benefits

- Exceptional precursor selectivity and sensitivity with the next-generation quadrupole mass filter
- Unmatched depth and accuracy of TMT analysis with novel Real-Time Search
- High Mass Range MSⁿ (HMRⁿ) option for comprehensive analysis of native protein complexes
- Unique Proton Transfer Charge Reduction (PTCR) option for simplifying complex top-down spectra
- Full experimental flexibility with revolutionary instrument control
- A wide range of optional functionalities for unprecedented versatility
- Common user interface with Thermo Scientific™ Orbitrap Exploris™ 480 and TSQ™ triple quadrupole mass spectrometers

The Thermo Scientific™ Orbitrap Eclipse™ Tribrid™ mass spectrometer combines industry-leading versatility and usability with the exceptional performance afforded by its built-in intelligence and revolutionary Thermo Scientific™ Tribrid™ architecture to deliver an instrument designed to address the most difficult analytical challenges. This newest Tribrid platform includes Advanced Ion Management Technology (AIM+) with the new QR5 segmented quadrupole mass filter, Real-Time Search, Enhanced Vacuum Technology, optional Proton Transfer Charge Reduction (PTCR), and optional High Mass Range MSⁿ (HMRⁿ) mode. Collectively, these features make this instrument uniquely suited for accurate and high-throughput full-proteome quantitation, characterization of complex mixtures of protein or small molecule-based pharmaceuticals, and deciphering higher-order protein structures. The Orbitrap Eclipse Tribrid MS makes it easy to tackle these difficult analyses and collect the high-quality data required to drive the right decisions, pushing your science beyond today's discovery.

Key capabilities

- **Active Ion Management (AIM+) Technology** that includes the QR5 segmented quadrupole mass filter with hyperbolic surfaces, maximizes ion transmission to achieve unprecedented levels of qualitative and quantitative performance
- **Real-Time Search** enables faster data acquisitions and improved specificity, significantly increasing analytical performance of TMT-based quantification experiments
- **Thermo Scientific™ TurboTMT mode** improves HRAM MSⁿ acquisition rates in TMT experiments
- **Thermo Scientific™ Precursor Fit filter** enables precursor ion selection for a defined specificity
- **Enhanced Vacuum Technology** improves Thermo Scientific™ Orbitrap™ mass analyzer performance
- **Improved accumulation and transmission of high molecular weight ions** to the ion trap and Orbitrap mass analyzers
- **Optional Proton Transfer Charge Reduction (PTCR)** simplifies MSⁿ spectra of multiply charged analytes
- **Optional High Mass Range MSⁿ (HMRⁿ) mode** provides expanded mass range capabilities for comprehensive MSⁿ characterization of intact proteins and protein complexes
- Unique Tribrid architecture includes a quadrupole mass filter, and dual-pressure linear ion trap and Orbitrap mass analyzers, allowing for high acquisition rates to provide maximum experimental flexibility for dissociation and detection of fragment ions
- Improved high-sensitivity atmospheric pressure interface combines a high capacity transfer tube and electrodynamic ion funnel, providing an increased ion flux and lower limits of detection for a wide range of molecules
- Advanced active ion beam guide (AABG) prevents neutrals and high velocity clusters from entering the resolving quadrupole
- Ultra-high-field Orbitrap mass analyzer provides ultra-high resolution and highest acquisition rates
- Acquisition rates of up to 40 and 45 Hz for Orbitrap mass analyzer and linear ion trap MSⁿ experiments, respectively
- Orbitrap resolution up to 500,000 FWHM at m/z 200; optional resolution up to 1,000,000 FWHM
- Large surface area ion trap detector for significantly improved robustness and lifetime
- Full parallelization of MS and MSⁿ analyses with Dynamic Maximum Injection Time
- Synchronous Precursor Selection (SPS) for MSⁿ experiments
- Optional Compact Electron Transfer Dissociation (ETD)/PTCR ion source based on Townsend discharge with extremely stable anion flux for improved usability and reagent longevity
- Multiple fragmentation techniques: collision-induced dissociation (CID), higher-energy collisional dissociation (HCD), optional ETD (including electron-transfer higher-energy collision dissociation, or ETHcD, and electron-transfer collision-induced dissociation, or ETciD) and optional ultraviolet photodissociation (UVPD), available at any stage of MSⁿ with detection in the Orbitrap mass analyzer or linear ion trap analyzer
- Advanced Peak Determination (APD) for improved precursor annotation in data-dependent experiments
- Universal Method maximizes peptide identifications without method optimization when sample concentration is unknown
- Intuitive, flexible drag-and-drop instrument method editor simplifies method development and creation of unique analytical workflows
- Extensive method template library
- Thermo Scientific™ AcquireX data acquisition provides all-inclusive, automated small molecule sample profiling on an LC timescale
- Streamlined calibration routines with improved Orbitrap calibration for ions with $m/z < 200$



Orbitrap Eclipse Tribrid mass spectrometer ion path

Hardware features

Active Ion Management (AIM+) Technology

AIM+ technology maximizes ion transmission, from injection to detection, using a novel hardware design for precise management of electrical fields and removal of noise to achieve unprecedented levels of quantitative performance

Ion source

Thermo Scientific™ Ion Max NG™ ion source

- Adjustable heated electrospray ionization (HESI) probe provides ultimate sensitivity
- Flow rates from 1 to 2000 $\mu\text{L}/\text{min}$
- Designed for maximum performance for a broad range of molecular ions
- Enhanced ruggedness
- Sweep gas reduces chemical noise
- Optional APCI probe compatible with liquid flow rates of 50 to 2000 $\mu\text{L}/\text{min}$ without splitting; the APCI probe can be upgraded to optional APPI capability

Generation V ion optics

The new API interface consists of a High-Capacity Transfer Tube (HCTT) and an Electrodynamic Ion Funnel (EDIF)

High-capacity ion transfer tube (HCTT)

- The HCTT increases ion flux into the vacuum system for improved sensitivity
- Vent-free maintenance

Electrodynamic ion funnel (EDIF)

- 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 ion beam guide (AABG)

AABG with an axial field and low-pass filter prevents neutrals and high-velocity clusters from entering the quadrupole mass filter

QR5 segmented quadrupole mass filter with hyperbolic surfaces

Next generation quadrupole mass filter with 5.25 mm field radius delivers industry leading ion transmission across m/z 50–2000 range for efficient precursor selection with 0.4–1200 m/z isolation width

Ion-routing multipole

- Ion storage capabilities
- Higher-energy collisional dissociation (HCD)
- Variable pressure control from 0.5 to 20 mTorr with HMRⁿ option, for small and large molecule workflows
- Efficient and reliable ion transfer between the ion-routing multipole, Orbitrap mass analyzer and linear ion trap mass analyzer

Orbitrap mass analyzer

- Next-generation ultra-high-field Orbitrap mass analyzer
- Low noise detection pre-amplifier
- Automatic calibration of all ion transfer parameters

Modified dual-pressure linear ion trap

- Extended front section of the high-pressure cell for improved ETD and PTCR reaction control
- For precursors between m/z 50 and 1800, isolation widths range from 0.2 to 3000 m/z
- Minimum precursor isolation width for ions with $m/z > 1800$ between 2 m/z at m/z 1800 and up to 100 m/z at m/z 8000, with a maximum precursor isolation width of 4000 m/z
- Collision-induced dissociation (CID)
- ETD/ET_hcD/ET_icD and UVPD fragmentation techniques
- PTCR ion-ion reaction
- Low pressure cell for improved scan rates, resolving power, and mass accuracy
- Dual-dynode detector with high linear dynamic range for improved quantification, and a large surface area for increased lifetime and robustness

Vacuum system

- Split-flow turbomolecular pump provides vacuum in three regions
- Stainless steel and aluminum high-vacuum analyzer chambers
- Enhanced vacuum technology reduces the pressure in the ultra-high vacuum region to $<10^{-10}$ Torr
- Improved Orbitrap mass analyzer performance at a wider range of collision gas settings

Analog inputs

Channel 1 analog input (0–10 V); Channel 2 analog (0–2 V)

Optional hardware

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

Thermo Scientific™ EASY-Spray™ ion source

Maximum nanoelectrospray performance with no need for adjustments

Thermo Scientific™ EASY-ETD™ ion source

- Generates fluoranthene anions for ETD
- Townsend discharge provides extremely stable and robust ionization
- Compact size, located entirely within the footprint of the instrument
- Active reagent ion filtering using the quadrupole mass filter
- Charge-state dependent calibration of reaction time to maximize spectral quality
- Improved dynamic range and signal-to-noise ratio (S/N) for fragments using high dynamic range EASY-ETD HD

Thermo Scientific™ PTCR ion source

- Extension of the EASY-ETD ion source
- Generates perfluoroperhydrophenanthrene (PFPP) ions for subsequent gas-phase ion-ion reactions
- Simplifies interpretation of complex spectra by decreasing the charge state of precursors and/or product ions

Thermo Scientific™ EASY-IC™ ion source

- Generates internal calibrant ions for real-time mass calibration of spectra in positive and negative modes
- Provides <1 ppm RMS drift over 24 hours, measured with Flex Mix

Thermo Scientific™ UVPD ion source

- Includes a Class 1, 213 nm CryLaS laser system with 2.5 kHz repetition rate, delivering >1.2 μJ per pulse
- Performs dissociation of precursors at any stage of MSⁿ, with detection in either the ion trap or Orbitrap mass analyzers
- Compact size, located entirely within the footprint of the instrument

Thermo Scientific™ 1M

Enables mass measurements at ultra-high resolution of 1,000,000 FWHM at m/z 200

Thermo Scientific™ FAIMS Pro™ interface

- Performs online gas-phase fractionation based on differential ion mobility
- Optimized performance for 100 to 1000 nL/min flow rates

High Mass Range with MSⁿ (HMRⁿ)

- Extends the mass range to m/z 8000 for detection of precursor and product ions in the Orbitrap mass analyzer
- Precursor ion isolation from m/z 2000 to 8000 using the linear ion trap
- MSⁿ, n = 1 through 10 using any available fragmentation technique

Software features

Data system

- High-performance PC with Intel® microprocessor
- High-resolution LED color monitor
- Microsoft® Windows® 10 operating system

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

Orbitrap Eclipse MS instrument control software

- Tune application for instrument 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

Optional software

Thermo Scientific™ Proteome Discoverer™ software

Flexible, expandable platform for the qualitative and quantitative analysis of proteomics data

ProSightPD™ software

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

Thermo Scientific™ ProSightPC™ software

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

Thermo Scientific™ BioPharma Finder™ software

Integrated solution for protein-based biotherapeutic analysis through molecular and sub-structural data processing utilizing deconvolution and predictive fragmentation pattern algorithms

Thermo Scientific™ Compound Discoverer™ software

Platform for small-molecule structural identification, qualitative, and quantitative data analysis

Operation modes

Top Speed mode

Maximizes the number of high-quality MSⁿ spectra in each cycle by intelligently scheduling MS and data-dependent MSⁿ scans based on a user-defined time between adjacent survey spectra

TopN mode

Enables a user-defined maximum number of high-quality MSⁿ spectra from each cycle

Dynamic maximum injection time

Maximizes the amount of high-quality data acquired by synchronizing operation of the quadrupole mass filter, ion-routing multipole, and linear ion trap and Orbitrap mass analyzers

Advanced Peak Determination (APD)

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

Exclusive technologies

Dynamic scan management

Enables intelligent, real-time scheduling, parallelization, and prioritization of acquisition events, and selection, sorting, and routing of precursors to different fragmentation modes and analyzers based on user-selected parameters, including precursor m/z , intensity, and/or charge

Multiple dissociation options

Precursor dissociation can be performed in the ion-routing multipole (HCD), the linear ion trap (CID, optional ETD/ETciD, optional UVPD) or both (optional EThcD), with product ion detection in the linear ion trap or Orbitrap mass analyzers at any stage of MS^n analysis

Automatic gain control

Ensures that the ion-routing multipole is always filled with the optimum number of ions for any acquisition type

Proton transfer charge reduction option

Performs ion-ion reaction to reduce charge states of selected precursors or product ions and can be applied at any stage of MS^n analysis

Real-Time Search

Searches user-defined database in real time to then select identified/or not identified precursors for further MS^n experimentation.

Example: Selection of identified precursors for SPS MS^3 quantitation increases the accuracy and proteome coverage of TMT experiments.

TurboTMT mode

Novel processing mode powered by Phase-Constrained Spectrum Deconvolution Method (ϕ SDM) designed to improve the acquisition rate of TMT experiments

Precursor Fit filter

Allows selection of precursors with defined specificity

Advanced data-dependent experiments

TMT SPS MS^3 aided by Real-Time Search

TMT SPS MS^3 experiment with real-time protein database search to perform SPS MS^3 only on identified precursors

Universal method

Powered by Dynamic Maximum Injection Time, ensures the best results from samples with unknown concentrations

Product ion triggered- MS^n

Fragment ion or neutral loss-triggered MS^n experiment, including at the same MS^n level

Isolation offset

Custom centering of the precursor isolation window, optimized for broad isotopic distributions

Quanfirmation workflow

Synchronous acquisition of HRAM SIM with full scan MS/MS in the linear ion trap for precursor identity confirmation

SureQuant internal standard (IS) targeted protein quantitation workflow

Novel PRM experiment that leverages internal standards to guide and automatically maximize outcomes and data quality for real-time targeted proteomics analysis

Performance specifications

Orbitrap Mass Range	Standard mass range m/z 50–2000, mid-mass range m/z 200–6000, and HMR ⁿ mass range m/z 500–8000
Orbitrap Resolution	Standard resolution settings range from 7500 to 500,000 (FWHM) at m/z 200, with isotopic fidelity up to 240,000 FWHM; up to 1,000,000 (FWHM) at m/z 200 with isotopic fidelity up to 240,000 FWHM with 1M option
Acquisition Rate*	Orbitrap MS ⁿ acquisition rates up to 40 Hz when measured using a data-dependent experiment with Flex Mix, MS and HCD MS/MS resolution setting of 7500, with a maximum ion fill time of 11 milliseconds; linear ion trap MS ⁿ acquisition rates up to 45 Hz using a data dependent experiment with Flex Mix, Orbitrap mass analyzer resolution of 240,000 and HCD MS/MS ion trap detection range of m/z 200–1400, with a MS/MS maximum ion fill time of 10 milliseconds
Orbitrap Mass Accuracy*	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
MS/MS Electrospray Ionization (ESI) Ion Trap Sensitivity	2 μ L of a 50 fg/ μ L solution of reserpine (100 femtograms total) injected at a flow rate of 500 μ L/min produces a minimum S/N ratio of 200:1 for the transition of the isolated protonated molecular ions at m/z 609 to the largest two product ions, m/z 397 and m/z 448, when the mass spectrometer is operated at unit resolution in the full scan MS/MS mode, m/z 165–615; the test requires the HESI II probe
Dynamic Range	>5000 within a single Orbitrap mass spectrum
MS Scan Power	Collects MS ⁿ , for $n = 1$ through 10, detected in either the Orbitrap or linear ion trap mass analyzers
Synchronous Precursor Isolation	Samples up to 20 precursors per MS ⁿ scan
Precursor Multiplexing	Up to 10 precursors can be multiplexed using the quadrupole mass filter and ion-routing multipole to perform selected ion monitoring or tandem MS
Polarity Switching	One full experimental cycle acquired in <1.1 seconds where the cycle consists of acquiring one full MS scan in positive and negative polarity at a resolution setting of 30,000
ETD Option Efficiency	Reaction with ETD anions dissociates the isolated 2 ⁺ MRFA precursor (m/z 262) to generate a series of fragments that have a summed relative abundance \geq 15% to the precursor measured in the linear ion trap, using Flex Mix solution infused at 6 μ L/min
UVPD Option Efficiency	Exposure of 100 ms dissociates the isolated Caffeine molecular ion (m/z 195) to generate the m/z 138 product ion with a relative abundance of \geq 25% to the precursor measured in the linear ion trap, using Flex Mix solution infused at 6 μ L/min
PTCR Option Efficiency	Reaction time of 100 ms causes isolated MRFA 2 ⁺ molecular ion (m/z 262) to convert to a charged reduced ion at m/z 524, with a relative abundance of \geq 25% to the precursor measured in the linear ion trap, using Flex Mix solution infused at 6 μ L/min

* Under defined conditions

Installation requirements

Power

- 230 Vac \pm 10% single phase, 50/60 Hz, with ground, 3x outlets at 15 A each
- 120 or 230 Vac single phase with earth group for the data system

Gas

- Ultra-high purity Helium (99.999%) with less than 1 ppm each of water, oxygen, and total hydrocarbons
- High purity Nitrogen (99.5% pure, flow rate 15 L/min) gas supply for the API source and ion routing multipole (IRM)

Dimensions (w, d, h)

- 1270 × 767 × 703 mm (50 × 30.2 × 27.7 in)

Weight

- 180 kg (400 lb) without data system, vacuum rough pumps and optional items

Environment

- System averages 2800 W (10,000 Btu/hr) output when considering air conditioning needs
- Operating environment must be 16–26°C (59–78°F) and relative humidity must be 50–80% with no condensation
- Optimum operating temperature is 18–21°C (65–70°F)

IC/ETD/PTCR ion source options

- Nitrogen supply for IC/ETD ion source options: Ultra-high purity nitrogen (UHP, 99.999%) with less than 1 ppm each water and oxygen

FAIMS Pro interface option

- Nitrogen supply for FAIMS Pro interface is 99.5% pure nitrogen at >20 L/min (100 psi)

Find out more at thermofisher.com/OrbitrapEclipse