



Orbitrap Eclipse Tribrid Mass Spectrometer

## Go beyond today's discovery

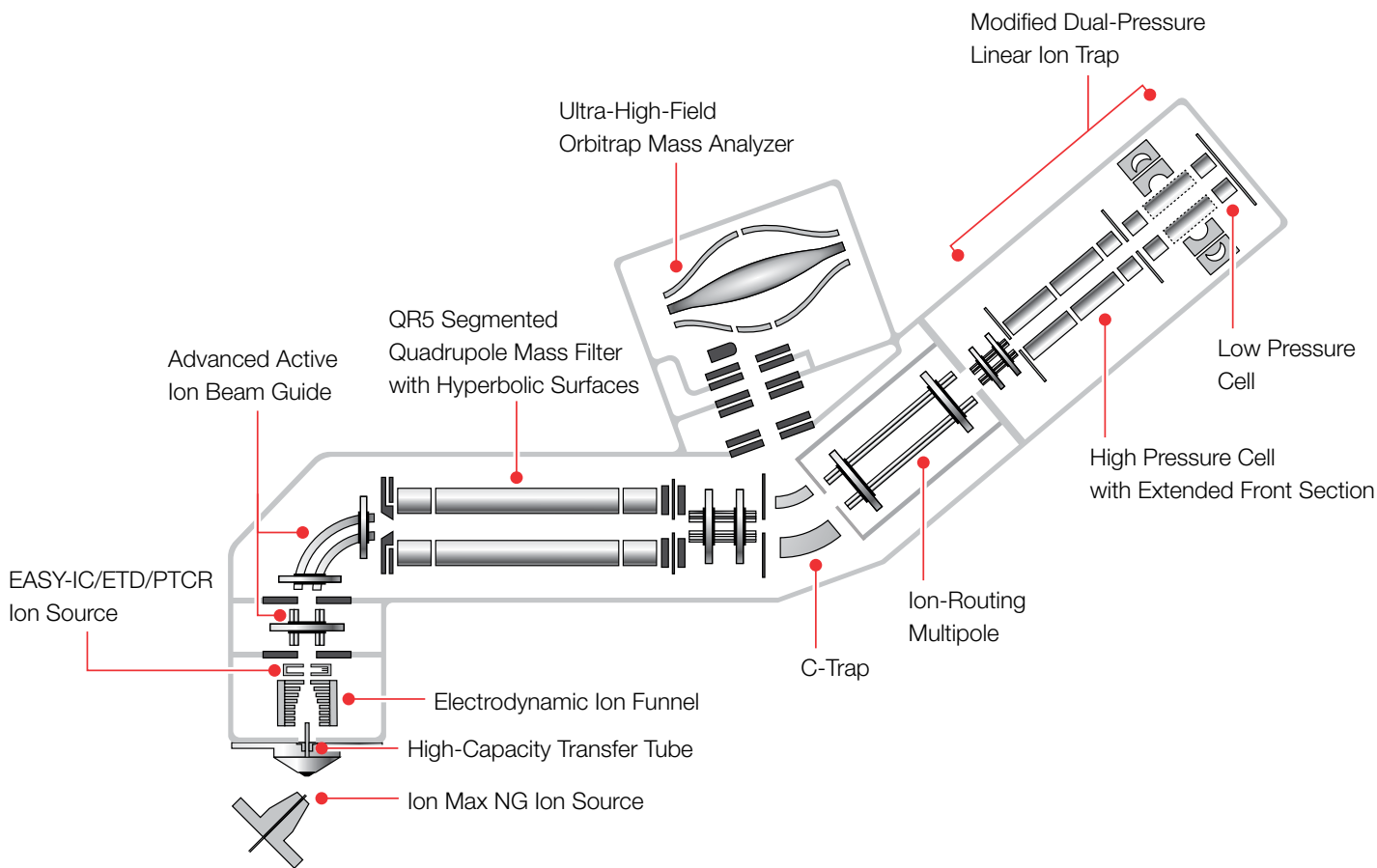
### Benefits

- 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 MS<sup>n</sup> (HMR<sup>n</sup>) 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 MS<sup>n</sup> (HMR<sup>n</sup>) 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 MS<sup>n</sup> 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 MS<sup>n</sup> spectra of multiply charged analytes
- **Optional High Mass Range MS<sup>n</sup> (HMR<sup>n</sup>) mode** provides expanded mass range capabilities for comprehensive MS<sup>n</sup> 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 MS<sup>n</sup> 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 MS<sup>n</sup> analyses with Dynamic Maximum Injection Time
- Synchronous Precursor Selection (SPS) for MS<sup>n</sup> 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 MS<sup>n</sup> 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 HMR<sup>n</sup> 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 PTRC 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<sub>h</sub>cD/ET<sub>i</sub>cD and UVPD fragmentation techniques
- PTRC 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  $\mu$ 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™ PTRC 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 MS<sup>n</sup>, 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 MS<sup>n</sup> (HMR<sup>n</sup>)

- 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
- MS<sup>n</sup>, 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 MS<sup>n</sup> spectra in each cycle by intelligently scheduling MS and data-dependent MS<sup>n</sup> scans based on a user-defined time between adjacent survey spectra

### TopN mode

Enables a user-defined maximum number of high-quality MS<sup>n</sup> 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 ( $\phi$ 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 <sup>n</sup> 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 <sup>n</sup> 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 <sup>n</sup> 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 $\mu$ L of a 50 fg/ $\mu$ L solution of reserpine (100 femtograms total) injected at a flow rate of 500 $\mu$ 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 <sup>n</sup> , 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 <sup>n</sup> 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 <sup>+</sup> 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 $\mu$ 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 $\mu$ L/min
PTCR Option Efficiency	Reaction time of 100 ms causes isolated MRFA 2 <sup>+</sup> 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 $\mu$ 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](https://thermofisher.com/OrbitrapEclipse)