



## Mass spectrometry

# Rethink what is possible

## Orbitrap Astral mass spectrometer

### Benefits

- Faster throughput with shorter gradients due to higher HRAM MS/MS sensitivity, dynamic range, and acquisition rate
- Deeper coverage due to higher HRAM MS/MS sensitivity, dynamic range, and faster acquisition rate
- Higher sensitivity measurements with the Astral mass analyzer for low sample input, including single cell experiments
- Accurate and precise quantitation for label-free quantitation (LFQ) and Tandem Mass Tag™ (TMT™) analyses across a broader dynamic range
- BioPharma option for comprehensive analysis of native protein complexes
- Full experimental flexibility with revolutionary instrument control software
- Common user interface with Thermo Scientific™ Orbitrap Exploris™, Thermo Scientific™ Orbitrap Tribrid™, and Thermo Scientific™ TSQ™ Triple Quadrupole mass spectrometers

The Thermo Scientific™ Orbitrap™ Astral™ mass spectrometer combines faster throughput, deeper coverage, and higher sensitivity while delivering accurate and precise quantitation over a high dynamic range. Powered by the synergy of the high resolution quadrupole mass filter, Thermo Scientific™ Orbitrap™ mass analyzer and the novel Thermo Scientific™ Astral™ mass analyzer, this revolutionary new instrument achieves unsurpassed performance with industry leading usability. The combination of these three mass analyzers enables the rapid acquisition of exceptional quality high resolution accurate mass (HRAM) data with high sensitivity and dynamic range. The performance characteristics of this instrument make it ideally suited for accurate and precise quantitation at an unprecedented depth of coverage and higher throughput from single cells to bulk samples.

## Key capabilities

- Improved high-sensitivity atmospheric pressure interface combines a high capacity ion transfer tube and an electrodynamic ion funnel, providing an increased ion flux and lower limits of detection for a wider range of molecules
- Thermo Scientific™ EASY-IC™ internal calibrant source generates ions for real-time mass calibration of Orbitrap analyzer and automated calibration of the Astral 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 a faster switching time
- Higher-energy Collisional Dissociation (HCD) in ion routing multipole for detection in the Orbitrap mass analyzer or in the ion processor for detection in the Astral mass analyzer
- MS/MS acquisition rates of up to 200 Hz in the Astral mass analyzer with 80,000 resolution at  $m/z$  524
- Astral mass analyzer utilizes a novel high dynamic range (HDR) detector with significantly improved sensitivity, dynamic range and longevity
- Maximum Astral mass analyzer resolution up to 80,000 FWHM at  $m/z$  524 enabling resolution of TMTpro™ 18-plex reporter ions
- MS/MS acquisition rates of up to 40 Hz with 7,500 resolution at  $m/z$  200 for the Orbitrap mass analyzer
- Maximum Orbitrap mass analyzer resolution of up to 480,000 FWHM at  $m/z$  200
- Enhanced Vacuum Technology improves Orbitrap mass analyzer performance
- 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 unique analytical workflows
- Extensive pre-built and optimized method templates that are fully customizable for a variety of application workflows
- Streamlined calibration routines with improved transmission for ions with  $m/z$  <200 to Orbitrap and Astral mass analyzers
- Low energy consumption instrument featuring a low maintenance dry pump
- Optional Thermo Scientific™ BioPharma option provides expanded mass range capabilities with the Orbitrap mass analyzer for comprehensive characterization of native proteins and complexes

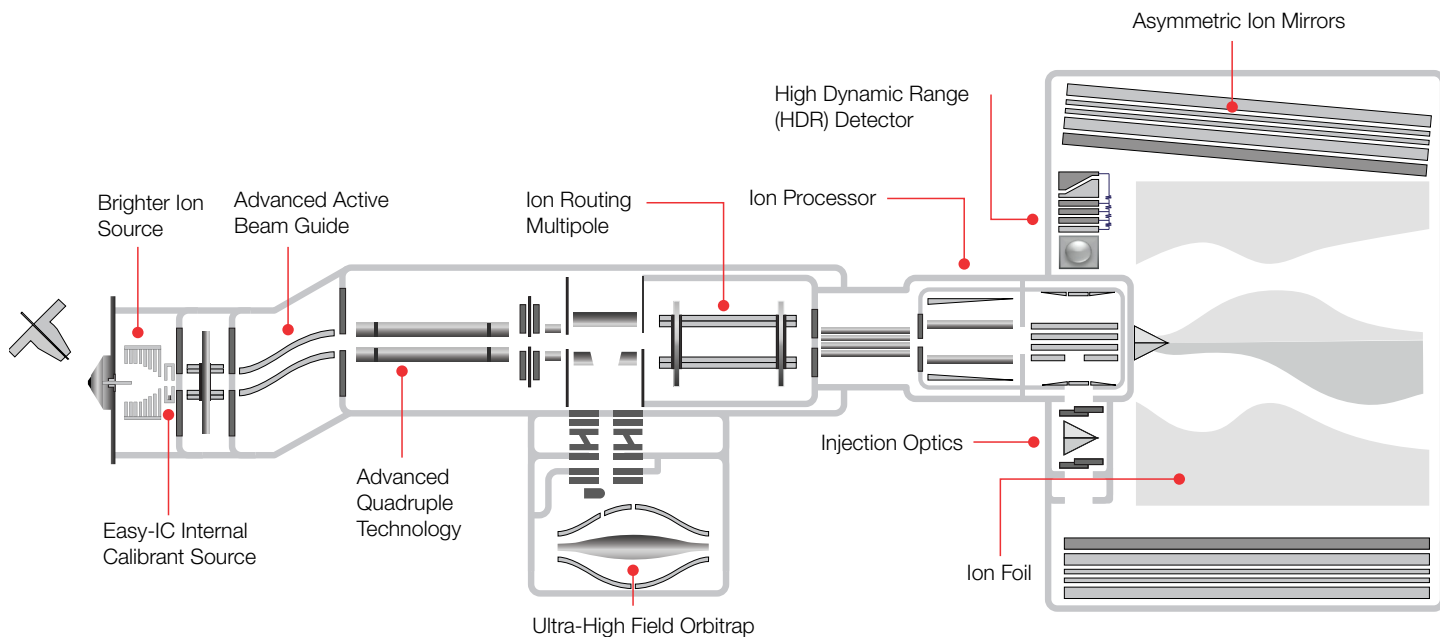
## Hardware features

### Novel instrument design

- Unique architecture includes a quadrupole mass filter, Orbitrap, and Astral mass analyzers, allowing for high acquisition rates to provide maximum experimental flexibility for dissociation and detection of fragment ions
- Full parallelization of Orbitrap mass analyzer MS and Astral mass analyzer MS<sup>2</sup> analyses to handle 5 ion packages simultaneously and maximize instrument utilization

### Active Ion Management (AIM+) Technology

AIM+ 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



Orbitrap Astral mass spectrometer ion path

## Ion source

### Thermo Scientific™ OptaMax NG™ ion source

- Adjustable heated electrospray ionization (HESI) probe provides ultimate sensitivity and ease of use
- Flow rates 1–1,000  $\mu\text{L}/\text{min}$
- Designed for maximum performance for a broad range of molecular ions
- Enhanced ruggedness
- Reduced chemical noise with sweep gas
- Optional APCI probe compatible with liquid flow rates of 50–1,000  $\mu\text{L}/\text{min}$  without splitting; the APCI probe can be upgraded to optional APPI capability

## Ion optics

### The atmospheric pressure ionization (API) interface consists of:

#### High-capacity ion transfer tube (HCTT)

- Increased ion flux into the vacuum system for improved sensitivity and desolvation
- Vent-free maintenance

### Electrodynamic ion funnel (EDIF)

- A radio frequency (RF) device that efficiently captures and transmits ions as they leave the HCTT
- Automatic tuning results in broad ion transmission curves with reduced ion losses, increasing sensitivity

### EASY-IC internal calibrant source

- Generates internal calibrant ions for real-time lock mass calibration in positive and negative modes for the Orbitrap mass analyzer
- Provides <1 ppm RMS drift over 24 hours, measured with FlexMix Calibration Solution for the Orbitrap mass analyzer
- Automatic single point recalibrations for the Astral mass analyzer to reduce mass drift.

### Advanced active beam guide (AABG)

- Axial field and low-pass ion filtering reduces noise by preventing neutrals and high-velocity clusters from entering the quadrupole mass filter using a double bent geometry

### Advanced quadrupole technology (AQT)

- Segmented quadrupole mass filter for precursor ion selection with variable precursor isolation width from 0.4 to 1,200 u
- MS/MS precursor ion selection with high transmission from  $m/z$  40 to 2,500
- Improved robustness with unique RF-switching mode
- Faster quadrupole isolation switching of 1 ms for ion selection

### ***Ion-routing multipole (IRM)***

- Efficient ion trapping and storage
- Performs higher-energy collisional dissociation (HCD) with nitrogen collision gas for acquisition of Orbitrap MS<sup>2</sup> spectra
- Selection of absolute collision energy (CE) or normalized collision energy (NCE) for precursor fragmentation
- Efficient and reliable ion transfer between the ion-routing multipole, Orbitrap mass analyzer, and Astral mass analyzer
- Variable pressure control with BioPharma option, optimizing performance for small and large molecule workflows

### ***Automatic Gain Control (AGC)***

- Dynamic adjustment of ion injection time based on real-time measurement of ion flux

### ***Orbitrap mass analyzer***

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

### ***Astral mass analyzer***

Next generation high-resolution accurate mass analyzer

- Ion processor with dual pressure regions to efficiently trap, fragment ions with HCD, and prepare ion packet for Astral MS<sup>2</sup> acquisition at rates of up to 200 Hz
- Injection optics maximize ion transmission and alignment to minimize losses
- Asymmetric ion mirrors direct ions into transversal asymmetric oscillations
- Ion foil shapes and maintains ion packet to maximize transmission and resolution and provide a higher space-charge capacity
- HDR detector assembly aligns and post-accelerates ion packet for high sensitivity HRAM ion detection over a wide  $m/z$  range
- High linear dynamic range two-channel detection system
- Isolated pressure cell for low noise and increased lifetime of the detector

### **Vacuum system**

- Three turbomolecular pumps and a single dual-stage oil-free roughing pump for reduced energy consumption
- Two split-flow turbomolecular pumps for ultra-high vacuum in Orbitrap and Astral mass analyzers
- Stainless steel and aluminum high-vacuum analyzer chambers
- Enhanced vacuum technology reduces the pressure in the ultra-high vacuum region of the Orbitrap mass analyzer 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**

### **BioPharma option**

- Analysis of large molecules including intact proteins and large complexes introduced under denatured or native conditions
- Includes mass transmission and detection up to  $m/z$  8,000 in the Orbitrap mass analyzer

### **Thermo Scientific™ Ardia™ Advanced Tower Server**

- Server hardware that delivers the Thermo Scientific™ Ardia™ platform cloud architecture on-premise
- Integrates and automates Thermo Scientific™ Proteome Discoverer™ software processing, including support for on-premise processing with the CHIMERY™ intelligent search algorithm
- Provides central data management and storage with transfer, archival and backup capabilities

### **EASY-Spray ion source**

- Maximum nanoelectrospray performance with minimum adjustments and high ease of use
- Supports static and dynamic electrospray experiments
- Compatible with liquid flow rates of 50 to 2,000 nL/min

### **Thermo Scientific™ NanoSpray Flex NG™ ion source**

- Maximum nanoelectrospray flexibility and probe position adjustment
- Supports static and dynamic electrospray experiments
- Compatible with liquid flow rates of 50 to 2,000 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
- Optimized performance for 100 nL/min to 1 mL/min flow rates

### APCI probe for OptaMax NG ion source

- Compatible with flow rates of 50–100  $\mu\text{L}/\text{min}$  without splitting
- The APCI probe can be upgraded to APPI

## Software features

### Orbitrap Astral 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

### Data system

- High-performance PC with Intel® microprocessor
- High-resolution LED color monitor
- Microsoft® Windows® 10 Enterprise (Long Term Service version) operating system

### Thermo Scientific™ Xcalibur™ software

- Xcalibur software is the control software for the next-generation Thermo Scientific mass spectrometer portfolio
- Shared instrument control software interface with Orbitrap Tribrid MS, Orbitrap Exploris MS and TSQ MS platforms to accelerate familiarization and reduce training needs
- Optional automated data transfer and data processing using the Ardia platform and Proteome Discoverer software

## Operation modes

### Resolution settings

- Orbitrap mass analyzer ranging from 7,500 to 480,000 resolution at  $m/z$  200
- Astral mass analyzer is operated at a single resolution setting of 80,000 at  $m/z$  524

### High Resolution-Data Independent Acquisition (HR-DIA)

- Acquisition logic in which the scan event execution follows a predetermined pattern set by the experimental settings.
- Enables acquisition of user-defined full scan using the Orbitrap analyzer and parallel acquisition of Astral DIA MS<sup>2</sup> scans

### 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<sup>2</sup> spectra in each cycle by intelligently scheduling MS and data-dependent MS<sup>2</sup> scans based on a user-defined time between adjacent survey spectra
- TopN: Enables a user-defined maximum number of high-quality MS<sup>2</sup> spectra from each cycle

### Advanced Peak Determination (APD)

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

### Dynamic scan management

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

### Automatic gain control

Ensures that the optimum number of ions are utilized within a given ion injection time range for any acquisition type

### Thermo Scientific™ SureQuant™ internal standard (IS) targeted protein quantitation workflow

Enhanced targeted MS<sup>2</sup> (tMS<sup>2</sup>) experiment that leverages internal standards to guide and automatically maximize outcomes and data quality for real-time targeted proteomics analysis

### Precursor Fit filter

Allows selection of precursors with defined specificity



## 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:

- Peptide
  - Extensive pre-built method templates for data-dependent acquisition (DDA), data-independent acquisition (DIA), TMT, and SureQuant for multiple application areas including plasma and single cell proteomics
- Intact protein (included with BioPharma option) with native and denaturing conditions using the Orbitrap mass analyzer
  - Pressure regimes (low, medium, and high) can be selected for best performance with native and denaturing conditions
- Small molecule analysis
  - Pre-built method templates for small molecule analysis including the option to enable 'Mild Trapping' as a global setting that applies to the entire run for Orbitrap mass analyzer scan events to reduce unwanted fragmentation of particularly labile compounds

## Scan event functions

- Full MS using Orbitrap mass analyzer
- Selected Ion Monitoring (SIM)
  - in DDA experiment (discovery)
  - in targeted SIM experiment based upon a sample-dependent, user-defined mass list
  - with Targeted Mass Filter applied (confirmation)
- MS<sup>2</sup> using Orbitrap or Astral mass analyzers in DDA experiments following a master scan (e.g., a Full scan):
  - using TopN or Top Speed logic (discovery)
  - using Targeted Mass Filter (confirmation)
  - by combining TopN or Top Speed and a Targeted Mass Filter to include confirmation in discovery experiments

- Parallel Reaction Monitoring MS<sup>2</sup> using Orbitrap or Astral mass analyzers, based upon a sample dependent, user defined target mass list
- MS<sup>2</sup> scan using Orbitrap or Astral mass analyzer by Data Independent Acquisition (DIA)
  - With full MS scan using the Orbitrap mass analyzer (e.g., parallel acquisition of Full MS scan in Orbitrap mass analyzer with simultaneous acquisition of DIA MS<sup>2</sup> scans in the Astral mass analyzer)
  - with adjustable, experiment dependent widths
- All Ion Fragmentation (AIF)

## Filters for data-dependent experiments

Filters are used to optimize data-dependent decisions in real time based on the goals of the experiment. To achieve optimum results when applying application-dependent filter settings, the user is guided by the application-dependent default parameter settings and tool-tip text.

Below are some of the available filters that can be used in a data-dependent experiment:

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

## Other method capabilities

### Alternate precursor sorting

Modifies the logic in which precursor order is selected for fragmentation

### Targeted mass trigger

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

### Isolation offset

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

### Quantification workflow

Synchronous acquisition of HRAM SIM in the Orbitrap mass analyzer with MS<sup>2</sup> in the Astral mass analyzer for precursor identity confirmation

## Optional data acquisition and analysis software

### Ardia Platform

Provides instrument management, scheduling, electronic logbooks and data storage capabilities for all connected chromatography and mass spectrometry systems controlled by Xcalibur 4.7 software or higher. It facilitates the organization, sharing, and archiving of raw and processed data through integrated tools.

### Proteome Discoverer software

Flexible, expandable platform for the qualitative and quantitative analysis of proteomics data. Simplifies a wide range of proteomics workflows, from protein and peptide identification to PTM analysis to isobaric mass tagging and label-free quantitation with both DDA and DIA data. Includes the CHIMERYS™ intelligent search algorithm to enhance DDA, DIA, TMT, and phosphoproteomics data analysis.

### ProSightPD™ software

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

### Thermo Scientific™ BioPharma Finder™ software

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

### Thermo Scientific™ Compound Discoverer™ software

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™ TraceFinder™ software

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

## Installation requirements

### Power

- 2 × 208V/230V 15/16A for the instrument, separately fused (tripping characteristics C)
- 1 × 200V/230V 16A for the Edwards nXL110iDE pump (fuse tripping characteristics C)
- 1 × 100V/240V 15/16A for Instrument Control PC and accessories

### Gas

- 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)

- 952 × 1963 × 1394 mm

### Weight

- 680 kg without data system, vacuum rough pump, and optional items

### Environment

- System averages power consumption of 1,400 W for low-flow and 1,500 W for high-flow operation
- Heat output of approximately 5,200 Btu/hr
- Operating environment must be 18–27°C and relative humidity must be 20–80% with a non-condensing and non-corrosive atmosphere
- Maximum temperature fluctuation of 0.5°C/10 min
- Designed for indoor use at an altitude of up to 3,000 m (10,000 ft) above sea level

### Optional EASY-Spray ion source

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

### Optional FAIMS Pro Duo interface

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

## Performance specifications—Orbitrap analyzer

Orbitrap mass range	Standard mass range $m/z$ 40–6,000, $m/z$ 40–8,000 with BioPharma option
Orbitrap resolution	Standard resolution settings range from 7,500 to 480,000 (FWHM) at $m/z$ 200, with isotopic fidelity up to 240,000 FWHM
Acquisition rate*	Orbitrap MS <sup>n</sup> acquisition rates up to 40 Hz when measured using a data-dependent experiment with FlexMix calibration solution, MS and HCD MS/MS resolution setting of 7,500 @ $m/z$ 200
Orbitrap mass accuracy*	External calibration achieves <3 ppm RMS drift over 24 hours, measured with Pierce™ FlexMix™ Calibration Solution; internal calibration achieves <1 ppm RMS drift over 24 hours, measured with FlexMix Calibration Solution
MS/MS Electrospray Ionization (ESI) Orbitrap sensitivity	MS/MS: 50 fg reserpine on column S/N 100:1 SIM: 50 fg reserpine on column S/N 150:1
Dynamic range	>5,000 within a single microscan Orbitrap mass spectrum

## Performance specifications—Astral analyzer

Astral mass range	Standard mass range $m/z$ 40–6,000
Astral resolution*	80,000 FWHM at $m/z$ 524
Acquisition rate*	Astral MS <sup>2</sup> acquisition rates up to 200 Hz with a maximum injection time of 3 ms
Astral mass accuracy*	External calibration achieves <5 ppm RMS drift over 24 hours, measured with FlexMix Calibration Solution
Dynamic range	>1,000 within a single microscan Astral mass spectrum

\* Under defined conditions

 Learn more at [thermofisher.com/OrbitrapAstral](https://thermofisher.com/OrbitrapAstral)

**For Research Use Only. Not for use in diagnostic procedures.** © 2023 Thermo Fisher Scientific Inc. All rights reserved. All trademarks are the property of Thermo Fisher Scientific and its subsidiaries unless otherwise specified. Intel is a registered trademark of Intel Corporation. Microsoft and Windows are registered trademarks of Microsoft Corporation. ProSightPD is a registered trademark of Proteinaceous, Inc. Tandem Mass Tag and TMT are trademarks of Proteome Sciences. CHIMERYS is a registered trademark of MSAID, GmbH. This information is presented as an example of the capabilities of Thermo Fisher Scientific products. It is not intended to encourage use of these products in any manners that might infringe the intellectual property rights of others. Specifications, terms and pricing are subject to change. Not all products are available in all countries. Please consult your local sales representatives for details. **PS001797-EN 0623M**