Thermo Scientific Orbitrap Fusion Lumos Tribrid Mass Spectrometer

Breakthrough Gains for Quantitative Biology Sensitivity Transformed

The Thermo Scientific™ Orbitrap Fusion™ Lumos™
Tribrid™ mass spectrometer is the industry-leading
high-performance mass spectrometer with enhanced
sensitivity facilitated by a new High Capacity Transfer
Tube, Electrodynamic Ion Funnel, Advanced Quadrupole
Technology, Advanced Vacuum Technology, and ETD HD.



Novel Orbitrap Fusion Lumos MS Features

- Novel high-sensitivity API interface combines a High Capacity Transfer Tube and an Electrodynamic Ion Funnel for increased ion flux and lower limits of detection
- Advanced Active Beam Guide (AABG) prevents neutrals and high velocity clusters from entering the resolving quadrupole
- Advanced Quadrupole Technology (AQT) combines high selectivity and efficiency of transfer for the selected ions symmetrically across the isolation window
- Advanced Vacuum Technology for improved transmission of high molecular weight ions to the Orbitrap analyzer
- Novel ETD HD—high dynamic range ETD providing significantly increased fragment ion coverage

Established Tribrid Features

- Tribrid architecture includes quadrupole mass filter, linear ion trap and Orbitrap mass analyzers
- Ultra high-field Orbitrap analyzer for ultra-high resolution and the fastest Orbitrap acquisition rates
- Resolving power up to 500,000 FWHM, with isotopic fidelity up to 240,000 FWHM at m/z 200
- Large surface area ion trap detector for significantly improved robustness and life span
- Full parallelization of MS and MSⁿ analyses with intelligent ADAPT™ (All Dynamically Available Parallelizable Time) technology
- Synchronous Precursor Selection (SPS) for MS and MSⁿ experiments
- Multiple fragmentation techniques: CID, HCD and optional ETD and EThcD available at any stage of MSⁿ with detection in either the Orbitrap or linear ion trap detector
- . Unique Tribrid architecture allows for

- high acquisition rates in Orbitrap and linear ion trap analyzers and maximum flexibility for dissociation and detection of fragment ions
- Compact ETD ion source based on Townsend discharge with extremely stable anion flux for improved usability and reagent longevity
- Acquisition rates of up to 20 Hz for both Orbitrap and linear ion trap MSⁿ analyses
- Universal Method provides maximal peptide identifications without method optimization for samples of unknown concentration, reducing sample and instrument time requirements for routine peptide identification experiments
- Intuitive and flexible drag-and-drop user interface simplifies method development and enables unique and complex workflows



Hardware Specifications

Ion Source

Thermo Scientific™ Ion Max NG™ Ion Source

- Adjustable heated electrospray ionization (HESI) probe for ultimate sensitivity
- Flow rates from 1 μL/min up to 2.000 μL/min
- Designed for maximum performance with no need for adjustments
- · Enhanced ruggedness
- Sweep Gas[™] reduces chemical noise
- Optional APCI probe compatible with liquid flow rates of 50 µL/min to 2,000 µL/min without splitting

Generation IV 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

- The HCTT increases ion flux into the vacuum system for improved sensitivity and desolvation
- 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 transmission curves and reduces ion losses, increasing sensitivity

Advanced Active Beam Guide

 Advanced Active Beam Guide with an axial field and low pass filtering reduces noise by preventing neutrals and high-velocity clusters from entering the quadrupole mass filter

Advanced Quadrupole Technology

- Segmented Quadrupole Mass Filter for precursor ion selection with variable precursor isolation width from 0.4 u to 1,200 u
- Superior ion transmission across isolation widths up to 1,200 u
- MS/MS precursor ion selection with high transmission from 50 to 3,000 *m/z*

Ion-Routing Multipole

- IRM for ion storage
- Higher-energy collisional dissociation (HCD) cell
- Efficient, reliable ion transfer between the ion-routing multipole and the Orbitrap and linear ion trap mass analyzers

Orbitrap Mass Analyzer

- Next-generation, ultra high-field Orbitrap analyzer
- New low noise detection pre-amplifier

- High-speed real-time data acquisition and instrument control system
- Automatic calibration of all ion transfer and analysis parameters via instrument control software

Dual-Pressure Linear Ion Trap

- High-pressure cell for MSⁿ precursor ion isolation from 0.2 u to 600 u
- Collision-induced dissociation (CID) and optional electron-transfer dissociation (ETD)
- Low-pressure cell for improved scan speed, resolving power, and mass accuracy
- Dual-dynode detector with high linear dynamic range for improved quantitation and a large surface area for increased lifespan and robustness

Vacuum System

- Split-flow turbomolecular pump controlling vacuum in three regions
- Aluminum high-vacuum analyzer chambers
- Advanced Vacuum Technology reducing the pressure in the ultra-high vacuum region to <2 × 10¹⁰ and enhancing transmission of the ions to the Orbitrap mass analyzer

Options

Thermo Scientific™ NanoSpray Flex NG™ Ion Source

- Supports static and dynamic nanoelectrospray experiments
- Compatible with liquid flow rates of 50 nL/min to 2 µL/min

Thermo Scientific™ EASY-Spray™ Ion Source

 Maximum nanoelectrospray performance with no need for adjustments

Thermo Scientific™ EASY-ETD Ion Source

- Improved dynamic range and S/N for ETD fragments using Easy ETD HD™
- Generates fluoranthene anions for electron transfer dissociation (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
- The ion sorting routines and charge state dependent calibration of the ETD reaction time maximize ETD spectral quality

Thermo Scientific™ EASY-IC™ Ion Source

- Generates internal calibrant ions for real-time mass calibration of MS scans in both positive and negative modes
- Provides <1 ppm RMS mass accuracy under defined conditions and minimizes effort

Performance Characteristics

Mass Range

m/z 50–2,000 *m/z* 200–4.000

up to m/z 6,000 without precursor ion selection (OTMS only)

Resolution OTMS

15,000-500,000 (FWHM) at *m/z* 200

Scan Rate*

OTMSⁿ up to 20 Hz ITMSⁿ up to 20 Hz

Mass Accuracy OTMS*

< 3 ppm RMS using external calibration < 1 ppm RMS using internal calibration

MS/MS Electrospray Ionization (ESI) Ion Trap sensitivity:

 $2~\mu L$ of a 50 fg/ μL solution of reserpine (100 femtograms total) injected at a flow of 500 μL /min will produce a minimum signal-to-noise 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 HESI III probe.

Dvnamic Range

> 5,000 within a single OTMS spectrum

MS Scan Power

 MS^n , for n = 1 through 10

Synchronous Precursor Isolation

Up to 20 precursors per MSⁿ scan

Multiplexing Using the Ion Routing Multipole

Up to 10 precursors per scan using the quadrupole mass filter

Polarity Switching

One full cycle in < 1.1 sec (one full scan positive mode and one full scan negative mode at resolution setting of 30,000)

ETD Efficiency

ETD fragmentation efficiency of >15%, (infusion of 1 pmol/μL angiotensin at 3 μL/min)

Analog Inputs

Channel 1 analog input (0-10 V), Channel 2 analog (0-2 V)

*Under defined conditions

Software Features

Data System

- High-performance PC with Intel® microprocessor
- High-resolution LCD color monitor
- Microsoft® Windows® 7 operating system
- Microsoft Office 2010 software
- Thermo Scientific™ Xcalibur™ processing and instrument control software
- Tune editor for system calibration, diagnostics, and manual data acquisition
- Method editor with comprehensive application-specific template library and drag-and-drop user interface to facilitate method development

Operation Modes

- Top-speed mode maximizes the number of high-quality MSⁿ spectra from each cycle by intelligently scheduling MS and data-dependent MSⁿ scans based on a user-definable time between adjacent survey scans
- Dynamic parallelization using ADAPT™ technology maximizes the amount of high-quality data acquired by synchronizing operation of the quadrupole mass filter, ion-routing multipole, linear ion trap and Orbitrap mass analyzers

Exclusive Technologies

- Dynamic Scan Management allows for intelligent, real-time scheduling, parallelization, and prioritization of the scan events. It also enables 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
- Precursor fragmentation can take place in the ion-routing multipole (HCD), in the ion trap (CID, ETD) or both (EThcD) with fragment detection in the linear ion trap or Orbitrap mass analyzers at any stage of MSⁿ analysis
- All Dynamically Available Parallelizable Time (ADAPT™) technology determines in real time the most efficient parallelization of quadrupole mass filter, Orbitrap and linear ion trap operations
- Automatic gain control (AGC) ensures that the ion routing multipole is always filled with the optimum number of ions for any acquisition type

Advanced Data-Dependent Experiments

- Universal Method powered by ADAPT technology always ensures the best results from the samples with unknown concentrations
- Fragment ion or neutral-loss-triggered MSⁿ experiments including at the same MSⁿ level

- Synchronous MS³ precursor selection significantly increases the number of peptides accurately quantified in isobaric mass tagging experiments
- Data-dependent neutral-loss experiment triggers an MS³ scans only for product ions with a predefined neutral loss
- Isolation offset allows for custom centering of the window when working with broad isotopic distributions
- Quanfirmation experiment uses synchronous HRAM SIM for quantitation with full-scan MS/MS in the linear ion trap for precursor identity confirmation

Optional Application-Specific Software

- Thermo Scientific™ Proteome Discoverer™ software—flexible, expandable platform for the analysis of qualitative and quantitative proteomics data
- Thermo Scientific™ Protein Deconvolution software—intact-protein analysis platform
- Thermo Scientific™ ProSightPC™ software—stand-alone software for analyzing top-down intact-protein data, as well as middle-down and bottom-up data
- Thermo Scientific™ Compound Discoverer™ software—integrated solution for small-molecule structural identification
- Thermo Scientific™ SIEVE™ software label-free, semi-quantitative differential analysis of highly complex data sets

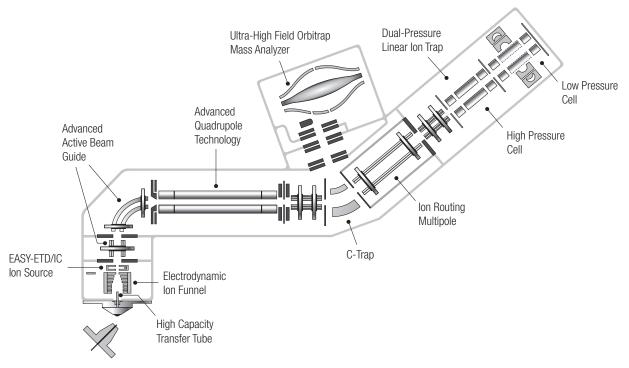


Figure 1. Orbitrap Fusion Lumos MS ion path.

Installation Requirements

Power

- 230 Vac ± 10% single phase, 15 Amp, 50/60 Hz, with earth ground for the instrument
- 120 or 230 Vac single phase with earth ground 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 the ion routing multipole (IRM)

Size

 $1270 \times 767 \times 703$ mm (w, d, h)

Weight

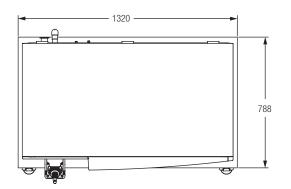
180 kg (400 pounds) without data system, vacuum rough pumps and optional items

Environment

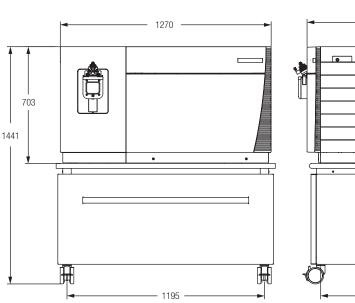
- System averages 2,800 W (10,000 Btu/hr) output when considering air conditioning needs
- Operating environment must be 16–26 °C (59–78 °F) and relative humidity must be 50–80% with no condensation
- Optimum operating temperature is 18–21 °C (65–70 °F)

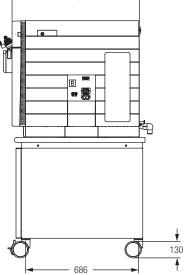
IC/ETD Options

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



All dimensions in millimeters





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Figure 2. Orbitrap Fusion Lumos MS dimensions

www.thermoscientific.com/lumos

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