IET | International Equipment Trading Ltd.
www.IetLtd.com | *Proudly serving laboratories worldwide since 1979*
CALL +847.913.0777 for Refurbished & Certified Lab Equipment

LTQ Orbitrap XL with ETD
Hybrid FT Mass Spectrometer
Performance Specifications

Installation Requirements:

Power
230 Vac ±10% 3 phase, 16 Amps, 50/60 Hz, with earth ground for the instrument

120 or 230 Vac single phase with earth ground for the data system

120 or 230 Vac single phase, 15 Amps, with earth ground for the water chiller

Gas
One high purity nitrogen gas supply (99.5% pure, flow rate 15 L/min) for the API source

One ultra-high purity helium gas supply (99.998%) with less than 1 ppm each of water, oxygen, and total hydrocarbons for the linear ion trap

One ultra-high purity nitrogen gas supply (99.999% or higher) is required for ETD operation

Environment
System averages 2800 W (10,000 Btu/hr) output when considering air conditioning needs

Operating environment must be 15-26 °C (59-78 °F) and relative humidity must be 40-70% with no condensation Optimum operating temperature is 18-21 °C (65-70 °F)

Weight
~700 kg

Dimensions
141.4 × 91.3 × 170.6 cm
(H × W × D)

The Comprehensive Proteom Three Complementary Fragm

The Thermo Scientific LTQ Orbitrap XL ETD is the most powerful instrument for proteomics analyses, combining three different and complementary fragmentation techniques - CID, HCD, and ETD -with the proven benefits of Orbitrap™ technology. It is the most comprehensive solution for complex PTM analysis, intelligent sequencing of peptides, top-down and middle-down analysis, and protein quantitation via stable isotope labeling such as TMT®, iTRAQ™ or label-free quantitation.

LTQ Orbitrap XL ETD offers

➢ Highly confident peptide identification using multiple activation types and Data Dependent Decision Tree
➢ High-throughput sequencing applications with parallel acquisition capabilities
➢ Identification of unexpected PTMs using high resolution and accurate mass
➢ Quantitation over a wide dynamic range, including low abundance peptides

Large Peptides and Protein Analysis

➢ High resolution and high mass accuracy for complex ETD spectra analysis
➢ Unambiguous charge state determination of precursor and fragment ions
➢ ProSightPC™ software suite for automated data mining

Data Dependent Decision Tree for Peptide Sequencing by LC/MS

➢ Increasing the number of identified peptides without increasing the experiment time
➢ Automatic selection of optimal fragmentation technique based on peptide properties (charge state, *m/z* etc.) for highest fragmentation efficiencies
➢ Proteome Discoverer Software Platform for qualitative and quantitative data analysis
➢ Complementary ETD, CID, and HCD spectra for unambiguous *de novo* sequencing

PTM Analysis

➢ ETD for labile PTM analysis such as phosphorylation and glycosylation
➢ Unambiguous PTM site determination
➢ High mass accuracy and high resolution for differentiation between phosphorylation and sulfation
➢ Combination of ETD, CID, and HCD for glycosylation site determination and glycan structure elucidation
➢ Supplemental activation of the charge reduced species for high ETD efficiencies

Xcalibur™ data system

Stable operating platform

Xcalibur is the versatile, easy-to-use data system that controls all Thermo Scientific MS systems. Xcalibur's Home Page offers easy navigation through the process of instrument setup, sequence setup, and data acquisition. The XReport package simplifies custom reporting with drag-and-drop functionality.

Protein Calculator

Protein Calculator performs *in silico* digestion on specified peptide sequences with post-translational modifications. The proteolytic fragment spectra can be saved as RAW data files for comparison with acquired spectra.

Xtract
Xtract deconvolutes isotopically resolved data, simplifying complex MS/MS spectra acquired in top-down, intact protein analysis. Specify the mass range, mass resolution, and S/N criteria for deconvolution and display in one of four modes: monoisotopic masses, isotopic pattern, or approved or disapproved signals. The results can be exported as RAW or ASCII file formats.

Proteome Discoverer
Mass informatics platform for protein scientists
Proteome Discoverer is a new, workflow-based, proteomics data processing software for in depth data mining of complex LC-MSn data sets. With the ability to exploit data from different dissociation techniques (CID, HCD, IRMPD, ETD and ECD), Proteome Discoverer provides extra certainty for peptide and protein identifications. Optional inclusion of multiple search algorithms increases analytical flexibility, and results can now be merged into a single report for easier interpretation.

ProSightPC™
ProSightPC was developed to address the specific requirements of a top-down and middle-down proteomics strategy. The fragmentation spectra of multiply-charged, intact proteins are exceedingly complicated. ProSightPC processes high resolution, accurate mass data from the Thermo Scientific LTQ Orbitrap XL ETD to produce a list of neutral fragment masses and performs comparisons to proteome databases to identify and characterize proteins.