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Thermo Finnigan LTQ **Specifications**

The Finnigan LTQ is a high precision linear ion trap mass spectrometer that delivers unparalleled sensitivity and fast scanning.

- Unparalleled Sensitivity
- Universal Ion Max Source
- Dual Detectors
- Increased Scan Speed
- Advanced Data Dependent Suite

System Specifications

MS/MS Sensitivity Electropray Ionization (ESI) – A loop injection of 2 μL of a 125 fg/ μL solution of reserpine (250 femtograms, 0.375 femtomoles total sample) at a flow of 400 $\mu\text{L}/\text{min}$ of 50% isopropyl alcohol/50% water will produce a minimum signal-to-noise ratio of 50:1, for the transition of the isolated protonated molecular ion at m/z 609 to the largest two product ions, when the mass spectrometer is operated at unit resolution in the full-scan MS/MS mode, scanning the product ion spectrum from m/z 165 – 615.

Atmospheric Pressure Chemical Ionization (APCI) – A loop injection of 2 μL of a 125 fg/ μL solution of reserpine (250 femtograms, 0.375 femtomoles total sample) at a flow of 400 $\mu\text{L}/\text{min}$ of 50% isopropyl alcohol/50% water will produce a minimum signal-to-noise ratio of 50:1, for the transition of the isolated protonated molecular ion at m/z 609 to the largest two product ions, when the mass spectrometer is operated at unit resolution in the fullscan MS/MS mode, scanning the product ion spectrum from m/z 165 – 615.

Installation Requirements

Power

- One 230 Vac $\pm 10.0\%$, 15 Amps, 50/60 Hz, single phase, with earth ground dedicated to the instrument
- 120 or 230 Vac single phase, with earth ground for the data system

Gas

- One high-purity (99% pure, flow rate 15 L/min) nitrogen gas supply for the API source
- One ultra high-purity helium gas supply (99.998% pure) with less than 1 ppm each of water, oxygen, and total hydrocarbons for the mass analyzer

Environment

- System averages 2300 W (8000 Btu/h) output when considering air conditioning needs
- Operating environment must be 15-27°C (59-80°F) and relative humidity must be 4-80% with no condensation
- Optimum operating temperature is 18-21°C (65-70°F)

Dimensions/Weight

- MS: 56 cm × 79 cm × 59 cm (h × w × d)
- MS: ~120 kg
- Two roughing pumps: 38.6 kg each

Performance Specifications

Mass Range

- m/z 50 – 2000

Scan Power

- MS_n, for n = 1 through 10
- Contact Closure
- Start In/Out
- Start Out is programmable

Analog Inputs

- One (1) analog Input (0-1 V)
- One (1) analog Input (0-10 V)

The Finnigan LTQ is the latest innovation in the well-established Finnigan ion trap mass spectrometers. Based on novel design features including a hyperbolic segmented linear ion trap, dual detectors, radial ion ejection, and state-of-the-art electronics, the Finnigan LTQ redefines performance. The culmination of these features enables more experiments, leading to greater coverage on less sample in less time. The Finnigan LTQ incorporates the rugged Ion Max™ source, allowing simple toolless switching of ionization probes. The exceptional ion transmission achieved with the Ion Max source, combined with the increased ion storage capacity of the linear ion trap, novel ion ejection and detection technology, makes the Finnigan LTQ the most sensitive LC/MS_n instrument available today.

Unrivalled sensitivity and fast scanning serve to maximize the power of the advanced Data Dependent™ suite within the cross platform data acquisition software, Xcalibur.® These technology improvements deliver the performance and easy-to-use features that accelerate the identification and quantification of analytes at low levels in applications such as proteomics, metabolism, and environmental studies.

Hardware Features

Ion Max API Source

- Enhanced sensitivity and ruggedness
- Sweep Gas™ reduces chemical noise
- 60° interchangeable ion probe orientation
- Removable metal ion capillary tube provides vent-free maintenance

Transfer Ion Optics

- Advanced multipole ion guides
- Split voltage quadrupole lens reduces noise
- High stability and ion transmission efficiency

2D Linear Quadrupole Ion Trap Mass Spectrometer

- Analyzer dimensions optimized for ultimate performance
- Regulated helium flow for stable performance
- Automatic system calibration and optimization
- Radial ion ejection

Vacuum System

- Differentially-pumped vacuum system to 10⁻⁵ Torr
- Split-flow turbomolecular pump controls vacuum in three regions
- Dual rotary vacuum pump configuration
- High-vacuum machined aluminum analyzer chamber

Detection System

- Patented dual conversion dynode detector
- Two off-axis continuous dynode electron multipliers with extended dynamic range
- Digital electronic noise discrimination
- High-efficiency radial ion ejection

Integrated Divert Valve

- Fully-automated data system control enables user to switch the solvent front, gradient end point and any other portion of the HPLC run to waste
- User-definable default state of the valve, either “to waste” or “to source”

Integrated Syringe Pump

- Syringe Pump allows automated infusion under data system control

Options

- ESI source compatible with liquid flow rates of <1 µL/min to 1 mL/min, without splitting
- APCI/APPI source compatible with liquid flow rates of 50 µL/min to 2 mL/min, without splitting
- APCI source compatible with liquid flow rates of 50 µL/min to 2 mL/min, without splitting
- Metal needle option for high and low-flow analyses
- 96-position sample plate AP MALDI for automated and manual data acquisition
- NanoSpray source supports both static and dynamic nanospray experiments, compatible with liquid flow rates of 50 nL/min* to 2 µL/min

*Lower limit is dependent on gauge of needle used

Software Features

Data System

- Xcalibur processing and instrument control software
- LCQUAN™ quantification package

- Microsoft® Office XP software package
- Microsoft Windows® XP operating system
- High-performance PC with Intel® Pentium® microprocessor
- High-resolution LCD color monitor

Scan Functions

- Full-scan feature provides full-scan mass spectra for sensitive analyses and produces spectra for rapid screening of unknown compounds
- Selected Ion Monitoring (SIM) monitors selected ions for target compound analysis
- Full-scan MS/MS produces full-scan product ion spectra at sensitivities higher than any ion trap mass spectrometer
- Selected Reaction Monitoring (SRM) for a traditional LC/MS/MS quantitative analytical experiment
- MS_n for multi-stage MS experiments to probe the structure of ions
- ZoomScan,[™] a high-resolution, full-range scan to resolve isotopic envelopes which is often used for charge state determination of peptides and ionization state determination of organometallics
- Ultra ZoomScan for ultimate resolution
- TurboScan,[™] an ultra-fast scan to improve signal-to-noise and sampling rate

Exclusive Technologies

- Unique, patented Automatic Gain Control (AGC) ensures that the ion trap is always filled with the optimum number of ions for any scan type
- Dynamic Exclusion[™] allows acquisition of MS/MS and MS_n spectra from lower intensity ion species
- WideBand Activation[™] fragments the water loss ion within an MS/MS spectrum, generating more structurally informative spectra
- Normalized Collision Energy[™] compensates for the mass-dependent energy deposition characteristics of ion trap mass spectrometers in MS/MS experiments, providing reproducible data from instrument to instrument

Advanced Data Dependent Experiments

- Data Dependent features trigger acquisition of MS_n spectra only when a compound of interest is detected
- Isotopic Data Dependent scanning software triggers MS/MS scanning only when a specified isotopic pattern is detected. Performs MS/MS only when a user-defined isotopic pattern is detected
- Triple Play determines the charge state and MS/MS scan range of a multiply charged ion
- Nth Order Triple Play allows the number of ions undergoing a Triple Play to be defined
- Ion Mapping[™] automatically generates a 3-dimensional MS/MS map, yielding product ion, precursor ion, and neutral loss information.
- Ion Mapping Browser software for viewing data generated by Ion Mapping experiments
- Data Dependent Ion Tree performs MS_n experiments on up to 25 species
- Data Dependent Zoom Map generates sequential MS/MS experiments using a ZoomScan for charge state determination prior to each MS/MS experiment

- MSn Browser software for viewing data generated by Data Dependent Ion Tree and Ion Mapping experiments

Optional Application-Specific Software

- BioWorks™/SEQUEST®/TurboSEQUEST™ –protein identification tools
- Mass Frontier™ – spectral interpretation and classification software to identify unknowns
- Metabolite ID – rapid review and reporting of drug metabolism data
- DeNovoX™ – automatically sequences unknown peptides.



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