

Thermo Scientific LTQ Velos Dual-Pressure Linear Ion Trap



*World's fastest and most sensitive ion trap
mass spectrometer*

The Instrument for the Most Demanding Sample Analyses

The Thermo Scientific LTQ Velos is the latest evolution in the award winning LTQ family of linear ion trap mass spectrometers. Building on a tradition of innovation, the LTQ Velos™ provides the analyst with significantly enhanced performance for complex sample analyses.

The innovative dual-pressure ion trap and S-Lens ion optics combine to deliver increased ion transmission along with better trapping and fragmentation efficiency. The result is the fastest and most sensitive ion trap for all applications.

Continuing a commitment to providing researchers with the latest in high-performance mass spectrometers, the LTQ Velos is fully upgradeable with electron transfer dissociation (ETD) and Orbitrap™ technology to extend its capabilities even further.

- **Unique dual-pressure linear ion trap technology provides superior scan speed and resolution**
- **Faster scanning and greater ion transmission improve identification of low-level analytes**
- **Simultaneous identification and quantification of even complex samples increases throughput**
- **Upgradeable to accurate mass and ultra-high resolution Orbitrap™ technology**



Increased Performance Through Innovative Technology

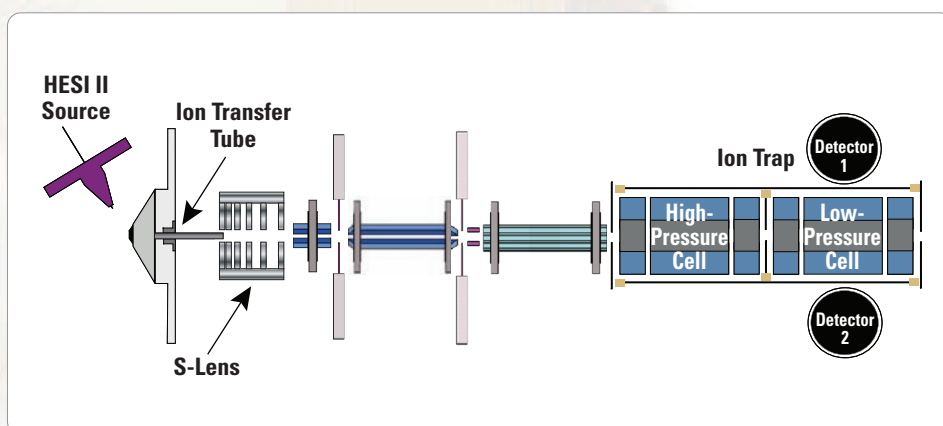
The LTQ Velos excels at quantitative, as well as qualitative, analyses. With high-transmission ion optics and a fast scanning dual-pressure trap, the LTQ Velos is capable of simultaneously analyzing multiple low-level components at speeds compatible with U-HPLC systems.

The S-lens is a significant advance over high-pressure, skimmer-based ion optics designs. The superior ion transmission of the S-lens enables faster scan times and increases overall instrument sensitivity.

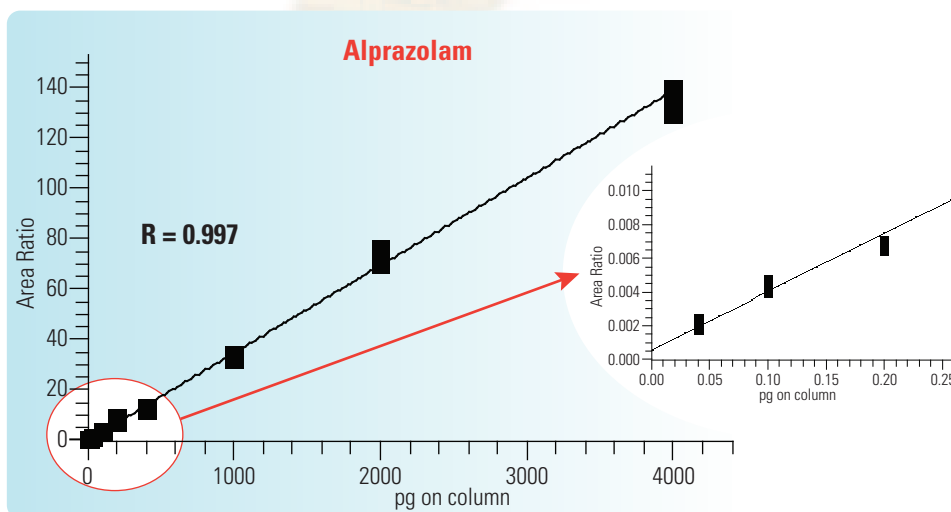
Typically ion traps are operated at single pressure, a compromise between the optimum pressures for ion manipulation and ion detection. The revolutionary

LTQ Velos dual-pressure ion trap features a high-pressure cell that increases ion trapping efficiency to over 90%. It also increases fragmentation efficiency, allowing fragmentation times to be cut to one third. The low-pressure cell increases scan speed by a factor of 2—to 33,300 u/s—while simultaneously improving mass resolution by 0.1 u FWHM.

The LTQ Velos merges all these innovations and more into an ion trap mass spectrometer with unrivaled performance, including ultra-fast 10 Hz acquisition rate and low femtogram sensitivity.



Innovative S-lens ion optics and dual-pressure linear ion trap make the LTQ Velos the fastest, most sensitive ion trap commercially available



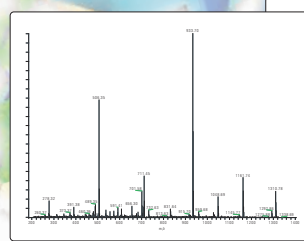
Quantitation of Alprazolam in plasma yields an LOQ of 40 fg on column and demonstrates excellent linearity over 5 orders of magnitude

Unprecedented Performance Generates Greater Insight into Complex Samples

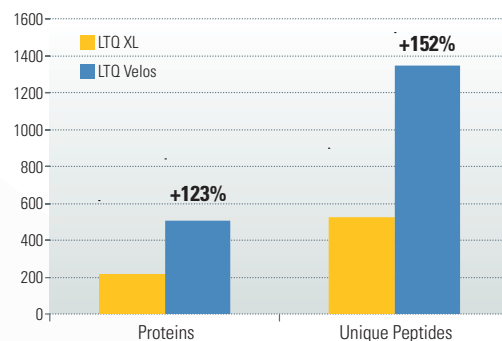
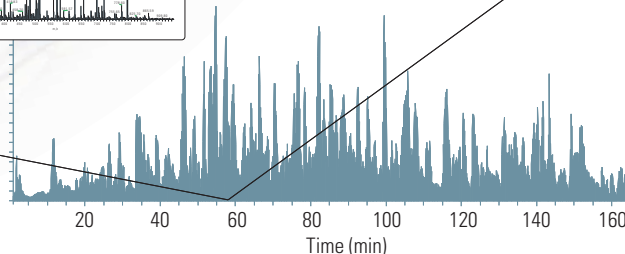
Routine analysis of complex proteomics samples is often confounded by the inability to adequately detect low-abundance proteins, by the large number of post-translational modifications (PTMs) possible, and because of the dynamic nature of the proteome. Ion trap-based mass spectrometry, however, has demonstrated a superior ability to rapidly identify and characterize low-abundance proteins, and determine their relative expression levels. It has become an essential tool in proteomics labs.

The LTQ Velos enables a new level of proteomics sample interrogation, made possible by improvements in acquisition rates, MSⁿ sensitivity, and selective accumulation of low-abundance ions. Predictive Automatic Gain Control (P-AGC) ensures that while the scan speed is increased, sensitivity is not compromised. Increased scan speed on the LTQ Velos also facilitates ultra-fast LC separation for high-throughput analysis.

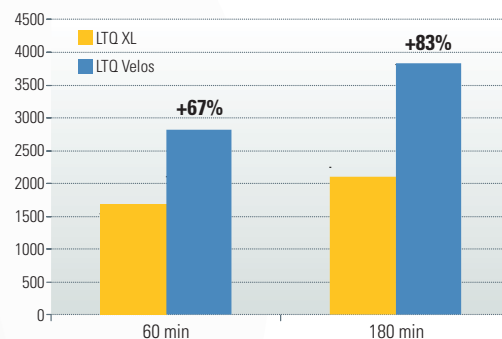
Data-dependent acquisition by the LTQ Velos at 7 Hz - more than 2X the rate of the LTQ XL - producing high-quality MS/MS data



Five consecutive MS/MS spectra in 0.7 s



LTQ Velos doubles the number of proteins and unique peptides identified by a 60-minute, data-dependent LC-MS/MS analysis of a 20 ng digest of *C. elegans*



LTQ Velos linear ion trap identified more peptides and proteins in a 60 min LC/MS run than an LTQ XL did in a 180 min run (1 µg digest of *C. elegans*)

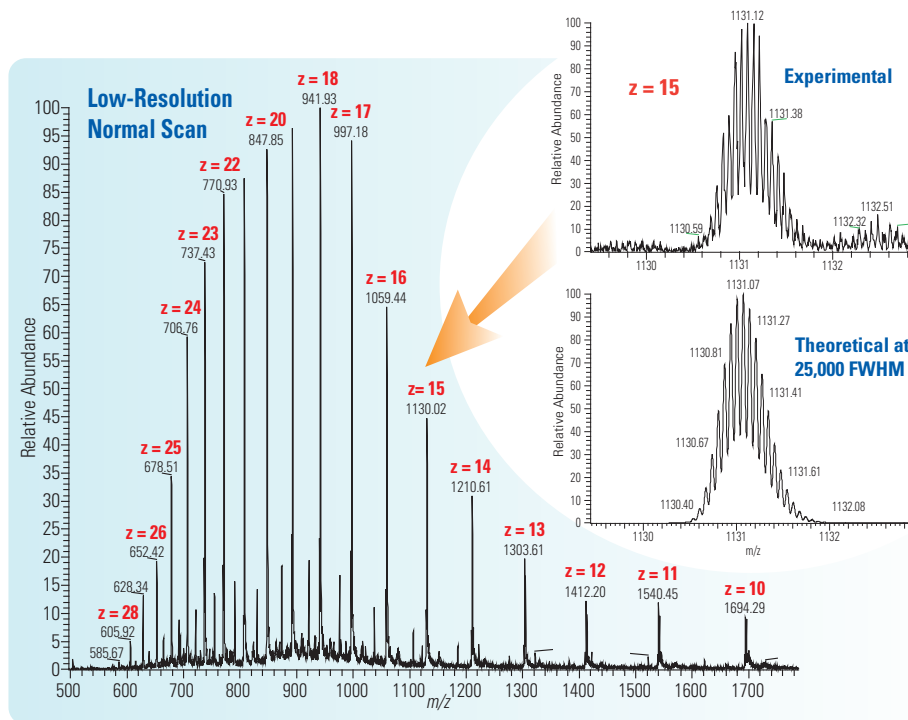
Facilitating our Understanding of Systems Biology

- Identify low-abundance proteins to extend information about cellular processes
- Determine protein expression changes with faster-scanning PQD for more quantifiable peptides
- Characterize the most complex PTMs using multiple dissociation techniques and MSⁿ capabilities
- Analyze intact proteins and perform N-terminal sequencing with ETD
- Annotate results with information from public databases such as GO to illuminate biological context

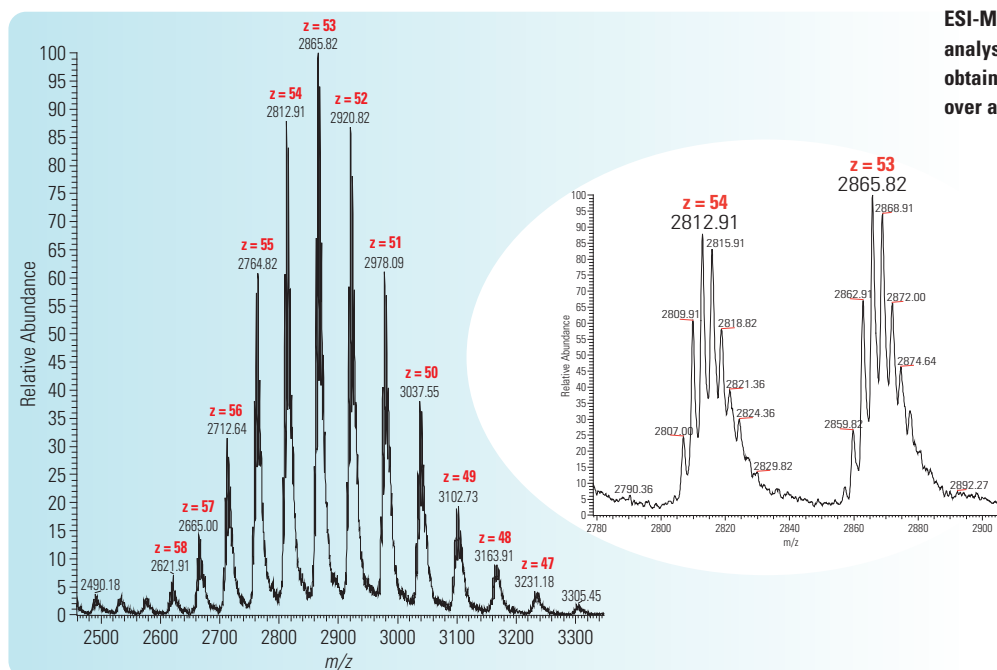
Ultimate Resolution and Sensitivity for Protein Characterization

The LTQ Velos offers resolving power rivaling that of many commercial Q-TOF mass spectrometers to aid in top-down characterization of proteins. Additional

improvements in the efficiency of detection in extended mass ranges provide unmatched sensitivity for large macromolecules, such as intact antibodies.



LTQ Velos Ultra ZoomScan analysis of intact equine myoglobin (~17 kDa), 15+, demonstrates isotopic resolution greater than 25,000 FWHM



ESI-MS envelope from LTQ Velos analysis of intact IgG (152 kDa), obtained by averaging spectra over a 1-minute wide LC peak

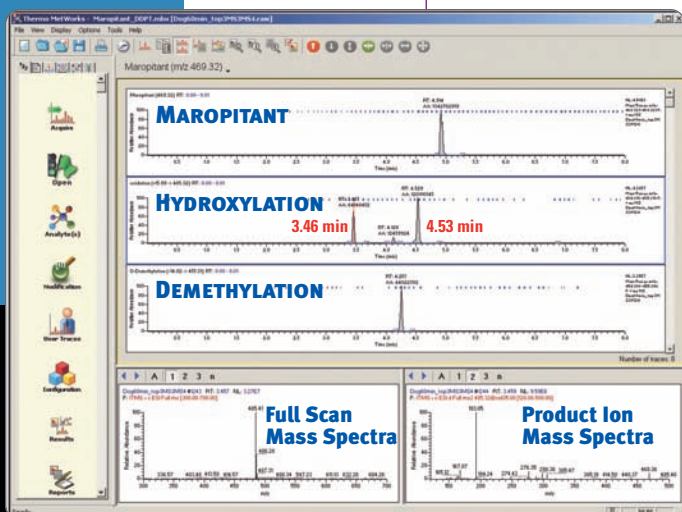
Comprehensive Compound Identification and Quantitation of Complex Samples

The characterization of drug metabolites plays a pivotal role in pharmaceutical discovery and development. Parent drug and metabolites need to be identified in a variety of biological matrices over a wide range of concentrations for both *in vivo* and *in vitro* studies. When used together, Thermo Scientific MetWorks and Mass Frontier software and the LTQ Velos create a robust, sensitive, integrated workflow for identification, characterization, and quantitation of drugs and drug metabolites in biological matrices.

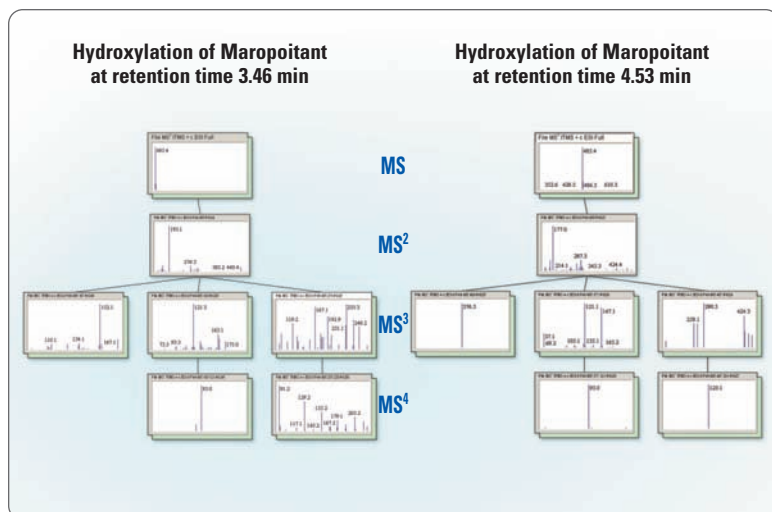
The rapid scan speed of the LTQ Velos allows simultaneous qualitative and quantitative metabolite analysis to be carried out easily for both *in vivo* and *in vitro* studies. The faster scan rates of the LTQ Velos allow more MSⁿ experiments to be carried out in shorter chromatographic runs. This, along with improved sensitivity, results in more high-quality ion trees for qualitative metabolite analysis and characterization. The use of Data Dependent™ acquisition coupled with Dynamic Exclusion™ provides a methodology for the analysis of both predicted and unexpected metabolites. Multiple dissociation methods provide the analyst with more approaches to structural elucidation.

Processing of metabolism data is supported with both MetWorks and Mass Frontier software

- MetWorks™ software uses MSⁿ spectral trees for unambiguous structural elucidation; e.g. differentiation of structural isomers and identification of the site(s) of biotransformation.
- MetWorks metabolite identification software integrates acquisition, processing and reporting capabilities.
- Mass Frontier™ facilitates the spectral interpretation by predicting fragmentation pathways and automated assignments of structures to spectral trees.



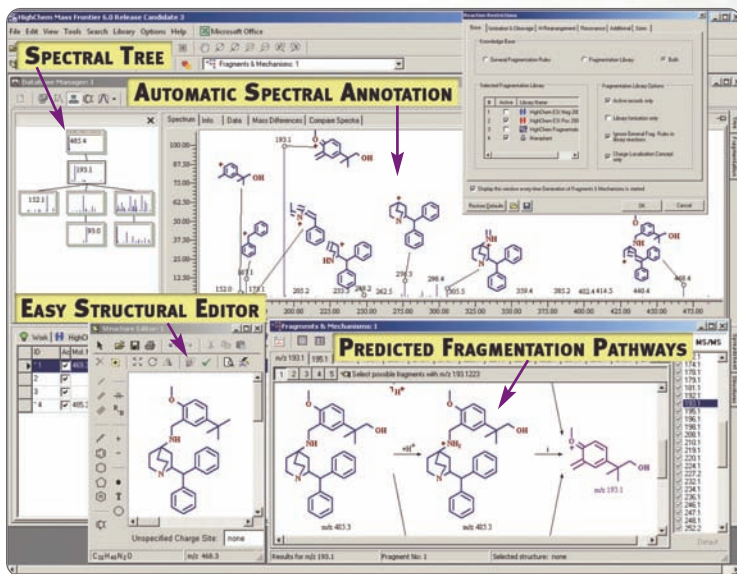
Modifications View from MetWorks software



Two ion trees of two isomeric mono-hydroxylated metabolites

High-Quality Data for Metabolomics Analyses

Feature segregation and identification are key components of all metabolomics workflows. While software packages such as SIEVE discriminate components of interest as potential markers of a condition, feature identification relies on the quality of the data generated by the mass spectrometer. The LTQ Velos greatly extends the performance of the groundbreaking, robust and sensitive LTQ linear ion trap, producing more high-quality MSⁿ data from smaller amounts of sample. Mass Frontier is a pivotal component of the metabolomics workflow. It melds the acquisition speed, sensitivity and information-rich MSⁿ spectra generated by the new LTQ Velos with the power of spectral trees and library or database searching. The combination of mass spectrometric performance, advanced feature detection, powerful metabolite identification and intuitive/integrated software solutions simplifies problem solving.



Mass Frontier software provides tools for automated MSⁿ spectral tree deconvolution, fragmentation prediction and spectral annotation

ACQUIRE

- Acquire nominal-mass or accurate-mass LC/MS

DISCOVER

- Differentially Expressed Small Molecules
- SIEVE, SIMCA-P (Umetrics)
- Genedata Expressionist

IDENTIFY

- Endogenous Metabolites
- Database Search and Mass Frontier

QUANTIFY

- Routinely Quantify Sets of Identified Metabolites in Large Sample Populations

Specifications

Software Features

Data System

- Thermo Scientific Xcalibur processing and instrument control software
- Microsoft® Office XP software package
- Microsoft Windows® XP operating system
- High-performance PC with Intel® 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 selected reaction monitoring (SRM) for a traditional LC-MS/MS quantitative analytical experiment
- MSⁿ 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 MSⁿ spectra from lower intensity ion species
- WideBand Activation™ generates more structurally informative spectra
- Normalized Collision Energy™ provide reproducible data from instrument to instrument

System Specifications

MS/MS Sensitivity

Electrospray Ionization (ESI) –2 µL 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 100:1, for the transition of the isolated protonated molecular ion 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, scanning the product ion spectrum from m/z 165 – 615.

Atmospheric Pressure Chemical Ionization (APCI) – 2 µL 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 100:1, for the transition of the isolated protonated molecular ion at m/z 609 to the largest two product ions, 397 and 448, 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.

Installation Requirements

Power

- One 230 Vac ±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 40-80% 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
- Roughing pumps: 38.6 kg

Performance Specifications

Mass Range

- m/z 15 – 200
- m/z 50 – 2000
- m/z 200 – 4000

Resolution

- 0.05 FWHM (full width half maximum) with Ultra ZoomScan

Scan Power

- MSⁿ, for n = 1 through 10

Analog Inputs

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

In addition to these offices, Thermo Fisher Scientific maintains a network of representative organizations throughout the world.

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