QUADRUPOLE ION TRAP MASS SPECTROMETER

LCQ Advantage

The World's Most Rugged Ion Trap Mass Spectrometer

Thermo Finnigan

The Most Rugged Quadrupole Ion Trap Mass Spectrometer on the Market

LCQ™ Advantage

Built on the proven LCQ platform, the LCQ Advantage features a completely redesigned orthogonal API source with Ion Sweep™ technology. This gives the LCQ Advantage the increased sensitivity and ruggedness to tackle today's demanding applications. Patented Automatic Gain Control™ and Normalized Collision Energy™ features ensure reproducible generation of highly precise, library-searchable data. The power of MS/MS to generate important structural information is enhanced by superior Data Dependent™ functions, including Dynamic Exclusion,™ for extraction of the most information from a single experiment. These intelligent software tools maximize productivity by minimizing the time spent in method development.

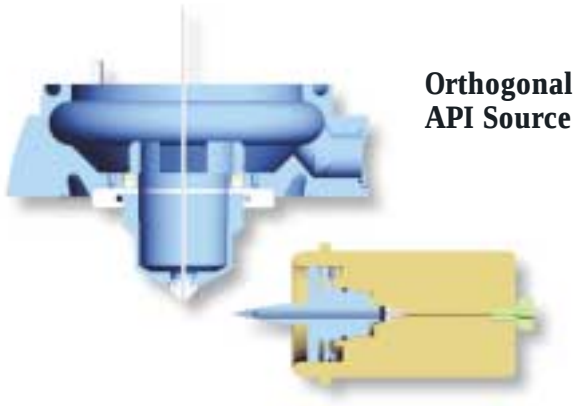
- *Ion Sweep* technology and the orthogonal API source combine to create the most rugged ion trap mass spectrometer available
- Automated full-scan MS/MS delivers detailed compound structures
- Proprietary Xcalibur™-based application-specific software enables rapid and intuitive data analysis
- Exceptional reproducibility ensures high quality data
- Seamless integration with the Surveyor™ LC System facilitates automated LC/MS analysis
- Full-scan MS^n available to permit detailed probing of ion dissociation pathways

New Source Technology

With a new orthogonal API source, the LCQ Advantage provides unsurpassed ruggedness to maximize productivity

Orthogonal Geometry Reduces Chemical Noise

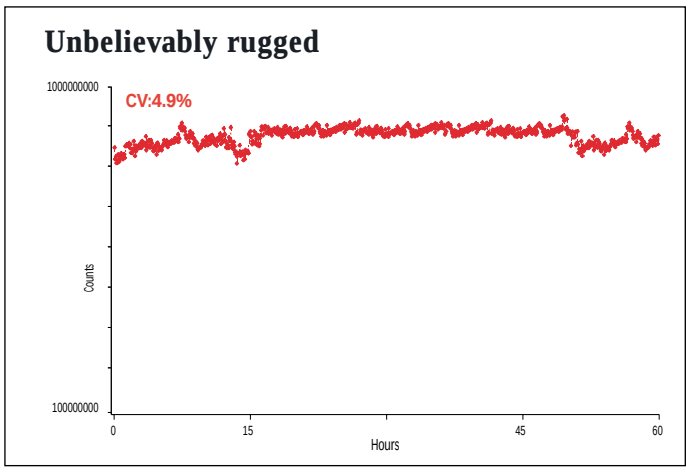
The completely redesigned orthogonal API source introduces ions into the trap while leaving solvent and neutrals behind. This results in reduced chemical noise, improved quantitative precision and increased ruggedness. Two-dimensional spray head mobility adds the flexibility necessary to easily optimize signal for a wide variety of applications.



Orthogonal API Source

Enhanced Ruggedness and Sensitivity

Orthogonal geometry combined with a novel, wide-bore ion capillary tube and *Ion Sweep* technology permit the analysis of extremely dirty matrices for extended periods of time. The *Ion Sweep* cone keeps salts and impurities from biological matrices away from the ion path so the face of the ion capillary tube stays clean. When the source needs to be cleaned, the ion capillary tube is removed and a vent prevent mechanism automatically activates. Breaking vacuum is not necessary to clean the source! Additionally, the wide-bore ion capillary tube allows more analyte to enter the trap, leading to a dramatic increase in sensitivity. The combination of orthogonal geometry, ion capillary tube and *Ion Sweep* technology ensure that even the dirtiest matrices can be sprayed effectively, providing the utmost in ruggedness and sensitivity.



Analysis of reserpine in 10 mM sodium phosphate buffer. Data shows over 1000 injections in 60 hours with no decrease in signal.

Solutions for Low-Flow Analyses

Nanospray is the ionization technique of choice when sample amounts are limited and ultimate sensitivity is required. The state-of-the-art nanospray source is easily installed on the versatile source platform. Both static and dynamic nanospray experiments are possible, providing the flexibility to make even the most difficult low-flow analyses routine.

For high-throughput low-flow analyses requiring less sensitivity, a microflow electrospray ionization source is available. This source provides a rugged and practical solution for the routine user.

Nanospray Ionization Source

Advanced Technologies Give You The Advantage

Patented, cutting-edge techniques allow precise control of the
LCQ Advantage instrument conditions, generating the highest quality data

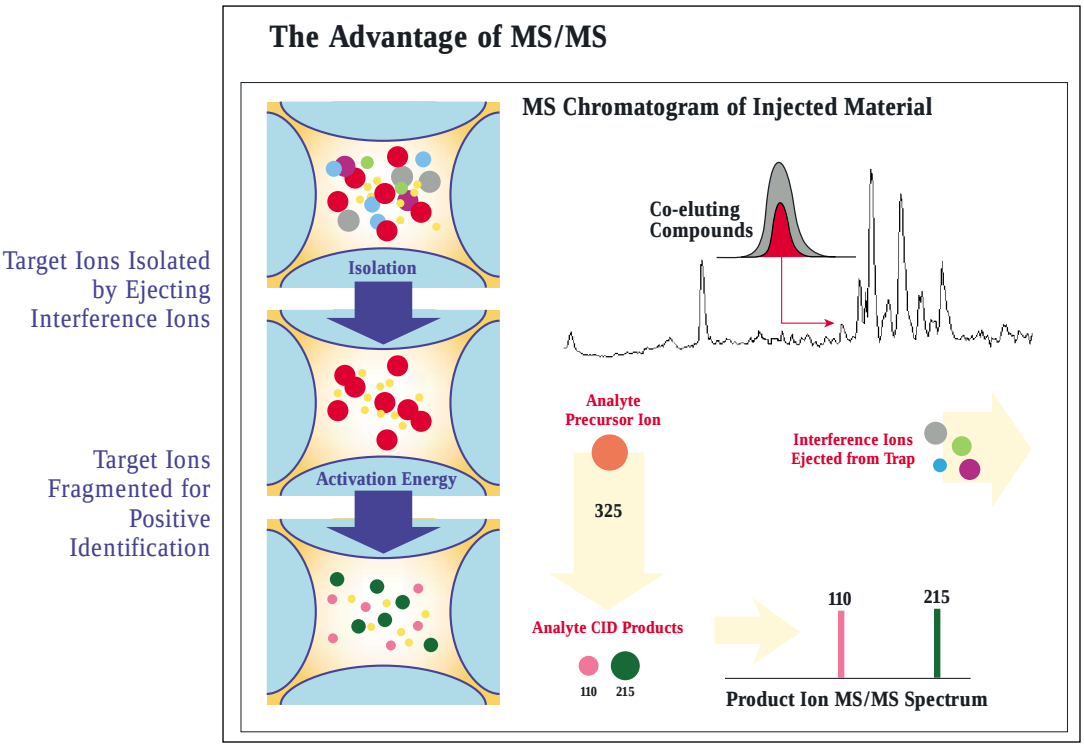
Structural Elucidation Made Routine: The Advantage of MS/MS and MS^n

The flexibility of the LCQ Advantage allows MS, MS/MS and MS^n experiments to be performed, either manually, or with Xcalibur's powerful *Data Dependent* suite of tools.

In an MS-only experiment, the molecular weight and abundance of all compounds eluting from an LC column are obtained. A single MS experiment, however, cannot completely confirm the identity of a compound in the majority of cases because multiple compounds in a complex matrix may have the same molecular weight. The lack of specificity resulting from a single MS experiment implies that co-eluting compounds and background ions can disguise or 'contaminate' the determination of an analyte.

The problems resulting from co-eluting compounds can be overcome using MS/MS. The LCQ Advantage can isolate a target ion, known as a 'precursor' ion, by ejecting all other ions from the ion trap. The ion of interest remaining in the trap is then automatically dissociated, producing a highly selective MS/MS (product ion) spectrum. Because of this isolation and dissociation process, the spectrum becomes a molecular 'fingerprint', reproducible and uniquely characteristic of the compound of interest.

When additional structural specificity is required, the LCQ Advantage has the ability to perform MS^n experiments. In an MS^n experiment, multiple stages of MS/MS are performed, providing unequivocal compound identification.

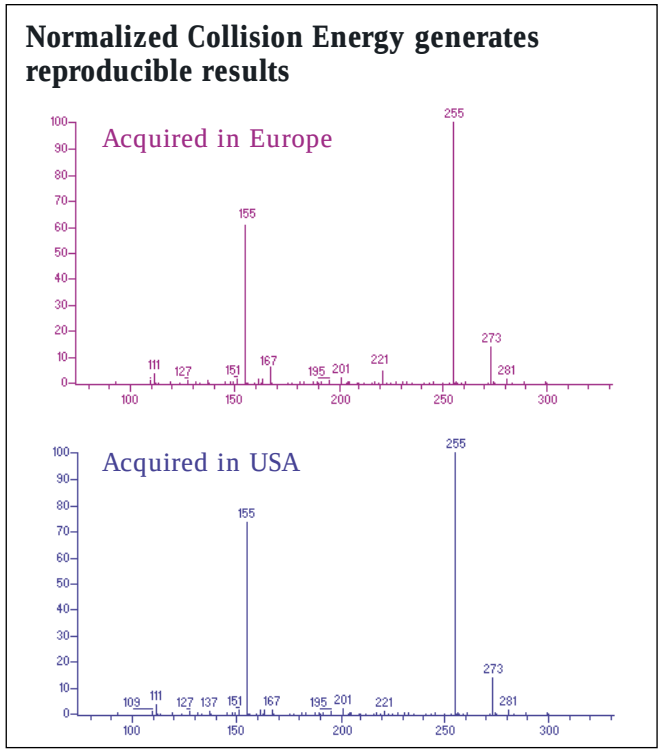


MS/MS provides product ion spectra, which quantify and distinguish analytes in complex matrices. This process is accomplished automatically in an HPLC experiment on the LCQ Advantage.

High Precision Ensures Reproducible Results

Resolution and precision in an ion trap are dependent upon the charge density of ions in the trap. Thermo Finnigan's patented *Automatic Gain Control (AGC)* is the most accurate method of automatically controlling the charge density in an ion trap, ensuring that the trap is always filled with the optimum number of ions during any type of experiment. *AGC* allows the instrument to compensate for rapidly changing signal intensities in an LC/MS experiment, eliminates guesswork when switching between scan modes and enables the consistent generation of highly precise data.

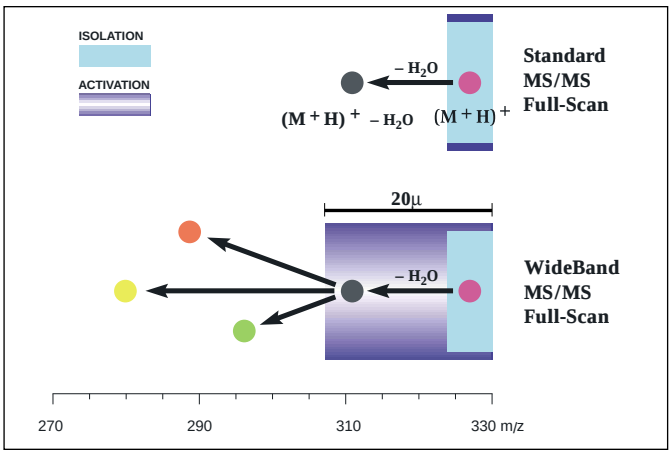
Extremely reproducible, library-searchable MS/MS spectra are generated with the help of *Normalized Collision Energy*. This feature automatically applies the optimum amount of dissociation energy to each ion. Day to day, instrument to instrument, and site to site reproducibility allows for the creation of worldwide structural databases that all users can search confidently. *Normalized Collision Energy* eliminates spectral anomalies due to instrument operating conditions.



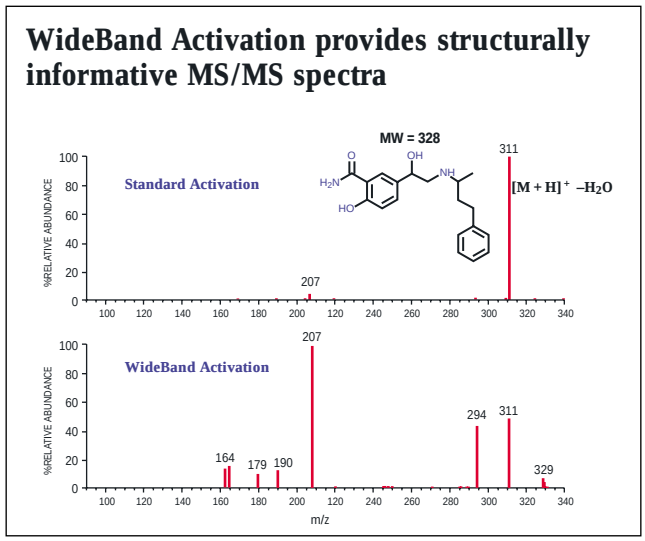
MS/MS spectra acquired from two different instruments, one in Europe the other in the USA. These spectra show the power of Normalized Collision Energy to create reproducible spectra suitable for databases and libraries.

Enhanced Structural Elucidation

Complex molecules often dissociate via loss of small neutrals (i.e. H_2O and CH_3), providing very little structural information in MS/MS experiments. Extensive fragmentation is achieved under these conditions using *WideBand Activation*.™ This feature allows the activation and isolation energies to be decoupled so that the parent ion can be isolated. Subsequently, both the precursor ion and the dehydrated or demethylated product can be fragmented in one step using a single waveform.



WideBand Activation applies resonance energy over a mass range that extends 20µ lower than the selected ion.



MS/MS spectra of labetalol acquired with and without WideBand Activation. Standard activation conditions, even with high collision energy, show only the water loss ion. In contrast, WideBand Activation generates extensive and meaningful fragmentation data in qualitative applications.

Xcalibur Data System

Xcalibur provides fully automated control of the LCQ Advantage and Surveyor LC System, accelerating methods development with intelligent data acquisition tools that increase productivity

Data Dependent Experiment Design

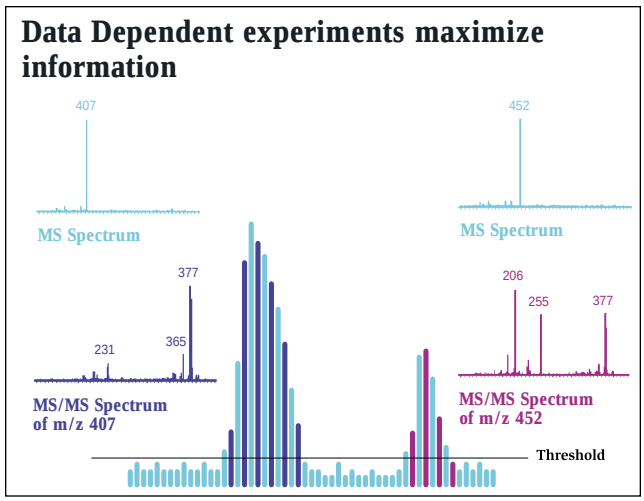
LC/MS/MS analyses of complex mixtures can be problematic because a number of different experiments must be performed to obtain detailed structural information for closely eluting, multiply-charged compounds. By automating the decision-making process, *Data Dependent* functions significantly increase the amount of quality information available from these analyte mixtures. The powerful on-board microprocessor interrogates mass spectra during the chromatographic run and switches to MS/MS mode only when user-defined criteria are met.

Using the *Isotope Ratio Data Dependency* feature, *Data Dependent* scanning is triggered if user-defined isotope mass difference and intensity ratio criteria are satisfied. Whether compounds are radio-labeled or labeled with a stable isotope, triggering the acquisition of MS/MS spectra only upon the detection of isotopically-labeled compounds can reduce the amount of data generated and facilitate the analysis of isotopically-labeled trace compounds in complex biological matrices.

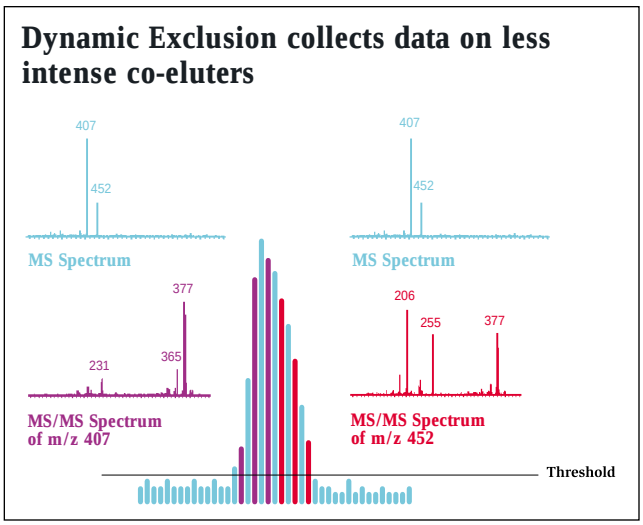
Analysis of extremely complex mixtures is challenging because many analytes can co-elute. The *Dynamic Exclusion* feature of the LCQ Advantage affords the automated analysis of less intense, co-eluting ions by temporarily putting a mass onto an exclusion list after its spectrum has been acquired. Structural information is then obtained for ions of reduced intensity by sequentially excluding more intense ions after their mass spectra have been acquired. *Dynamic Exclusion* allows MS/MS data to be easily obtained, even for co-eluting ions with very low signal intensity.

Multi-Vendor Support

The LCQ Advantage seamlessly interfaces with the Surveyor LC System, as well as many third-party instruments, such as HPLC pumps, autosamplers and UV detectors. The cross-platform software suite allows Xcalibur to directly control these instruments, eliminating the use of multiple programs and computers.



Data Dependent MS and MS/MS generate the maximum amount of information from a single run.

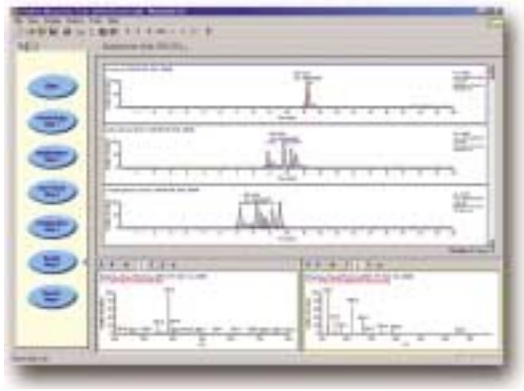


Two compounds with molecular ions at m/z 407 and m/z 452 co-elute. Using Dynamic Exclusion, after MS/MS scans of m/z 407 have been acquired, the ion is placed on the exclusion list and MS/MS spectra of the minor component at m/z 452 are collected.

Application-Specific Software

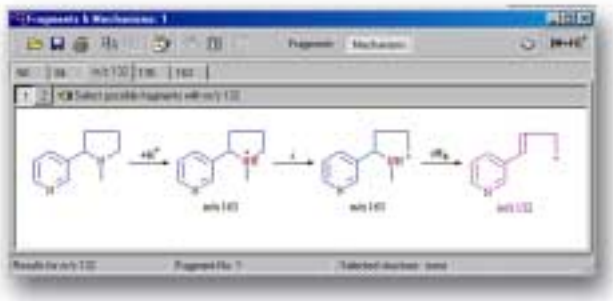
Metabolite ID: Metabolite Structural Identification

Metabolite ID software streamlines the review of data generated from drug metabolism LC/MS and LC/MS^n experiments. It simplifies the process of creating reconstructed ion chromatograms, mass spectra and summary reports for the hundreds of MS/MS scans acquired during the typical metabolic experiment. Metabolite ID harnesses the comprehensive power and flexibility of Xcalibur software, rapidly increasing compound search throughput with an intuitive, easy-to-use interface.



Mass Frontier™: Mass Spectral Prediction and Structural Elucidation

Mass Frontier virtually eliminates the often tedious process of manually interpreting mass spectra for small molecule analysis. Its *Fragments and Mechanisms* module quickly generates "bar code" mass spectra from structures and compares theoretical fragments to the actual data. Unique *Spectra Classifier* and *Spectra Projector* modules are used to rapidly compare large groups of compounds and distinguish structural similarities, aiding in compound identification.

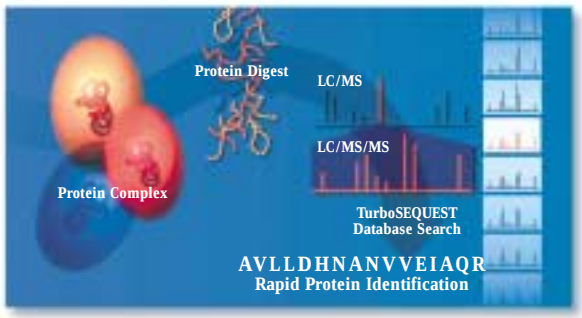


LCQUAN™: High-Throughput Quantitation

LCQUAN makes quantitation fast and intuitive by reducing the calculation and review time for quantitation data from hours to seconds. It offers a powerful solution to data processing for all quantitative LC/MS and LC/MS^n experiments. Integrated with the versatile Xcalibur software, LCQUAN enables high-throughput quantitation using a step-by-step process of sample identification, calibration level set-up, data processing, quantitative review and reporting. With a single click you can automatically generate peak integrations, component calibration reports and Excel® summaries.

TurboSEQUEST®: Protein/Peptide Sequencing

TurboSEQUEST accurately and automatically identifies proteins in mixtures without requiring time-intensive protein separation procedures. The software is used to rapidly compare and correlate acquired MS/MS spectra of peptides, typically generated by enzymatic digestion of proteins, with predicted MS/MS spectra generated from protein or nucleotide sequence databases.



Thermo Finnigan
A Thermo Electron business

Thermo Finnigan is a Thermo Electron business that designs, manufactures and supports chromatography and mass spectrometry instruments, systems and data management solutions for the analytical industry. All of our products are built to the highest quality standards to provide unmatched reliability. In virtually every scientific endeavor, researchers and analysts worldwide depend upon our systems for demanding applications. Both through our products and our people, we expect to provide you with superior performance and experienced support. We are listening to you, to understand your needs, and ensure our products meet your exacting professional standards. As innovators in the world of science for over 30 years, we bring knowledge, understanding and expertise to meet the challenges you face in your laboratory. It is our dedication, both in business and in science, that makes Thermo Finnigan unique. We invite you to learn more about Thermo Finnigan, and to experience the difference.

For more information on our products and services, please visit our website at: www.thermofinnigan.com

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