PSB 120

Advanced Data Dependent Analysis for Ion Trap Mass Spectrometers

Data Dependent™ acquisition using Thermo Scientific ion trap mass spectrometers allows automated real-time decisions for subsequent MS^n analysis. This enables mass spectrometers to acquire data selectively without any user intervention, which is important for automated structural identification, sequence determination and unknown compound confirmation.

Intelligent Data Dependent experiments were pioneered on Thermo Scientific TSQ™ triple quadrupole mass spectrometers in 1980,[1] when the TSQ was used to collect the structural information for the 50 most intense parent ions in the full-scan mass spectrum automatically. This exclusive Data Dependent technology is also particularly well-suited to ion trap mass spectrometers due to the:

- inherent capability to perform MS^n analysis
- exceptional MS/MS sensitivity of ion traps compared to other types of mass analyzers
- high quality MS/MS spectra independent of the precursor mass (using Thermo Fisher Scientific's proprietary Normalized Collision Energy™)
- simplicity of switching between MS and MS^n analysis modes

Data Dependent scanning uses specified criteria to select one or more ions of interest for subsequent analysis, such as MS/MS or a high resolution ZoomScan™ As an example, Figure 1 describes a strategy for exhaustive metabolite profiling using automated Data Dependent scanning on a Thermo Scientific ion trap mass spectrometer. This particular experiment involves six separate scan events. The mass spectrometer is set to perform a full-scan and subsequently an MS/MS scan on the most intense ion in the full-scan spectrum with Dynamic Exclusion™ [2] enabled. Dynamic Exclusion temporarily puts a mass into an exclusion list after its MS^n spectrum is acquired, providing the opportunity to collect MS^n information on less intense components that may otherwise not be examined. Then, MS^3 spectra are acquired for the two most intense ions in the MS/MS spectrum. Finally, from the MS^3 spectrum of the most intense MS/MS product ion, the first and second most intense product ions are subjected to MS^4 analysis. This acquisition scheme allows identification and characterization of not only the major metabolites but also several low-level metabolites.

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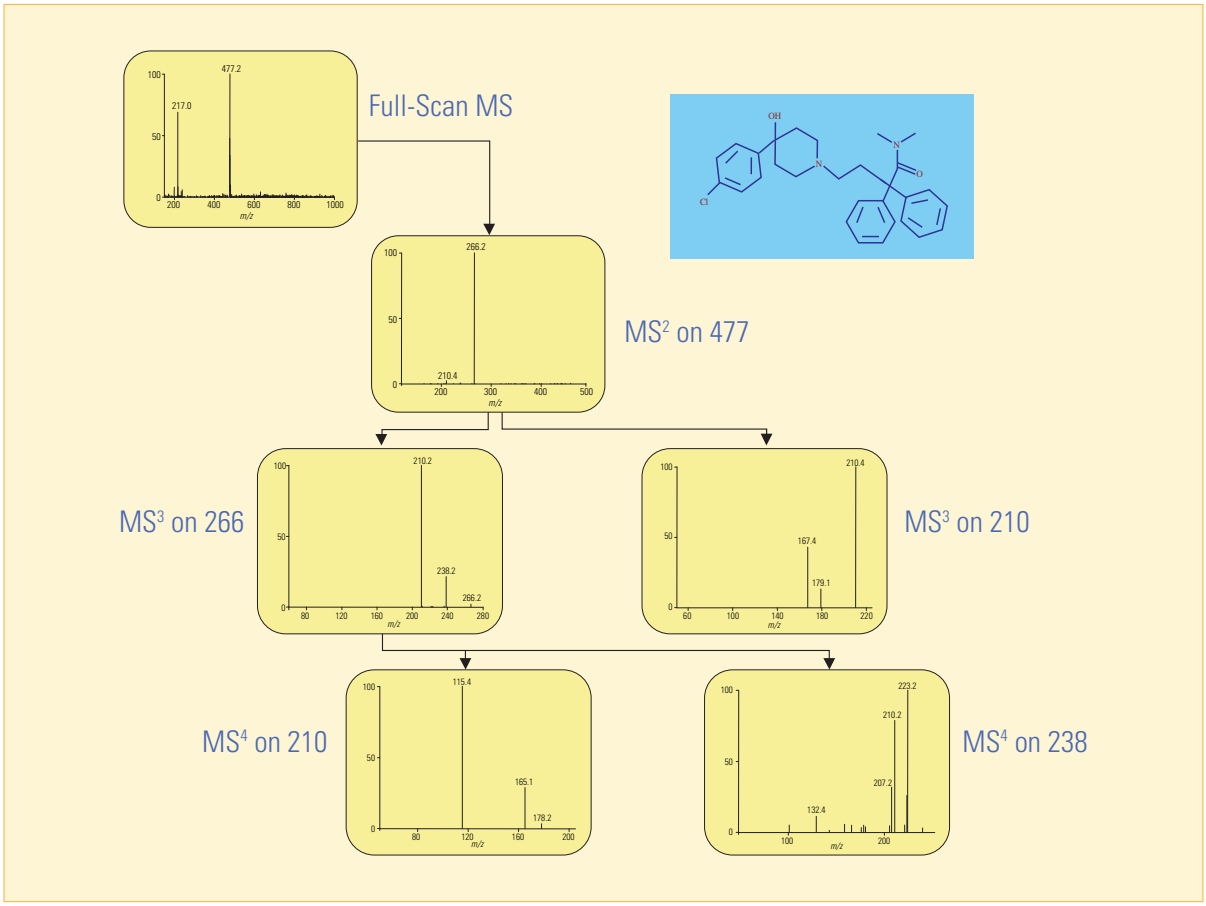

Figure 1: Structural characterization of Loperamide (MW = 476) using automated Data Dependent acquisition

A variety of Data Dependent experiments are supported by Xcalibur™ software. A summary of the available Data Dependent experimental features is listed in Table 1. These experiments are similar in that they all perform an initial full-scan MS analysis. The differences arise in how the information from the full-scan MS is used to automatically set up subsequent dependent scans. These user-friendly features simplify data capture and analysis for a wide range of desired applications.

Combined with other exclusive features of Thermo Scientific ion trap mass spectrometers, such as Automatic Gain Control (AGC), Normalized Collision Energy,[3] Stepped Normalized Collision Energy,[4] Multi-stage activation,[5] and Pulsed Q Dissociation (PQD),[6] a Data Dependent experiment produces comprehensive data from a single sample analysis with minimal user input and interaction. This powerful capability allows automated real-time decision making and therefore provides more information with less sample in less time.

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Experimental Features	*Descriptions*	*Applications*
Data Dependent MS/MS	Full-scan MS followed by MS/MS of the most intense ion	Identify low-level impurities in high-purity compounds; identify metabolites in a complex mixture
Data Dependent Triple Play	Full-scan MS followed by ZoomScan and MS/MS of the most intense ion	Determine the charge state of precursor ion and scan range for Data Dependent MS/MS
Nth Order Double Play	Perform Data Dependent MS/MS on the top "N" (up to 199) most intense ions detected in the independent scan event	Perform MS/MS on multiple ions with intensities above threshold automatically
Nth Order Triple Play	Perform Triple Play experiment on the top "N" most intense ions detected in the independent scan event	Determine the charge state and perform MS/MS on multiple ions
Data Dependent NL MS^3	Trigger MS^3 scan on only the MS/MS product ions with the pre-defined neutral loss	Identify and characterize metabolites and post-translational modifications
Isotopic Data Dependent Scan	Trigger a Data Dependent scan if isotope mass difference and intensity ratio criteria are satisfied	Detect ions containing elements with special isotopic mass difference and intensity ratio such as halogens
Data Dependent Zoom Map	Perform MS/MS on the precursor ions with intensities above the pre-selected threshold in an independent MS ZoomScan	Map all product ions in a specified mass range that are obtained from precursor ions having ZoomScan ions above a minimum signal
Data Dependent Ion Tree	Perform MS^n on up to 25 species to any level between MS^2 and MS^{10}	Build a custom library of composite MS^n spectra
Ion Mapping	Automatically generate a 3-D MS/MS map, yielding product ion, precursor ion, and neutral loss information	Provide 3-D relationship in the fragmentation pathways; extract parent ion spectra and neutral loss spectra; Identify compound classes
Dynamic Exclusion	Prevent an ion from triggering a subsequent Data Dependent scan for a pre-selected length of time after it has already triggered a Data Dependent scan	Characterize ions with relatively low abundances in complex mixtures
Charge State Screening Data Dependent Scan	Specify the charge state of the ion of interest from the MS spectra for MS/MS scan or to be rejected as precursors for Data Dependent scan	Perform or prevent MS/MS scan on ions with certain charge states

Table 1: Summary of Data Dependent Features for Thermo Scientific Ion Trap Mass Spectrometers

(1) Finnigan Topic, Number FT8004.
(2) Dynamic Exclusion, see Thermo Fisher Scientific PSB 105.
(3) Normalized Collision Energy, see Thermo Fisher Scientific PSB 104.
(4) Stepped Normalized Collision Energy, see Thermo Fisher Scientific PSB 121.
(5) Using MultiStage Activation in an Ion Trap Mass Spectrometer, see Thermo Fisher Scientific PSB 122.
(6) Pulsed Q Collision Induced Dissociation (PQD) on Linear Ion Trap Mass Spectrometers, see Thermo Fisher Scientific PSB 124.