Grant application resource: Thermo Scientific Orbitrap ID-X Tribrid mass spectrometer for metabolomics, lipidomics and structural elucidation

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Metabolomics, metabolome, untargeted, nontargeted, metabolite identification, metabolite ID, compound identification, compound annotation, profiling, unknown metabolites, targeted quantification, high throughput, fluxomics, stable isotope labeling, isotope fine structure, sub-structure analysis, lipidomics, lipids, high resolution, accurate mass, mass accuracy, mass spectrometry, Orbitrap, Orbitrap ID-X, Tribrid, AcquireX, MS^n, mzLogic, mzCloud, high resolution, data dependent acquisition, DDA, grant, precursor ion fingerprinting

Goal
This document is intended to provide conclusive reasons to justify upgrading from a Thermo Scientific™ Q Exactive™ mass spectrometer series or earlier generation of Thermo Scientific™ Orbitrap™ Hybrid™ mass spectrometer series to a Thermo Scientific™ Orbitrap ID-X™ Tribrid™ mass spectrometer dedicated to significantly augment untargeted metabolite annotation and structural elucidation capabilities in untargeted metabolomics and lipidomics research.

Summary
Thermo Scientific Orbitrap Tribrid mass spectrometers are an essential tool for high-end life science research. Equipped with a quadrupole mass filter, high-field Orbitrap and linear ion trap mass analyzers, this unique hardware combination provides superior analytical performance that enables multiple modes of analysis due to the parallel isolation and detection mechanisms not available with previous generation Orbitrap Hybrid mass spectrometer series. The most difficult analyses including identification of low-abundance metabolites in human plasma, isotopomer mixture analysis, characterization

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of isomeric flavonoid or lipid species in biological extracts, and obtaining high quality MS^n spectral reference libraries are fully achieved on the versatile Orbitrap ID-X Tribrid mass spectrometer. The Orbitrap ID-X Tribrid mass spectrometer is optimized for small molecules and can perform multiple fragmentation techniques (higher energy collision dissociation (HCD) in a high pressure collision cell or collisional induced dissociation (CID) in an ion trap plus stepwise MS^n) for annotating unknown metabolite structures in untargeted metabolomics and lipidomics experiments. The Orbitrap ID-X Tribrid mass spectrometer provides up to 500,000 resolution at m/z 200, high sensitivity, and rapid acquisition rates needed for obtaining high quality data for demanding applications such as isotopic tracer studies. The Orbitrap ID-X Tribrid mass spectrometer system extends the dynamic range for metabolite detection, compound annotation and quantitation needed to achieve a broad range of metabolome coverage, by combining the versatility of Tribrid architecture, selectivity of Orbitrap technology and high-quality MS^n spectra. The integration of Thermo Scientific™ AcquireX intelligent data dependent acquisition methods and the use of advanced scan filters to target specific compound classes provide unparalleled flexibility in designing experiments that meet the real-world challenges in metabolomics and lipidomics today.

Introduction

Untargeted metabolomics is a demanding application[1] that is challenging due to: 1) a wide range of potential analytes (from very polar to non-polar molecular species), 2) the need to identify commonly present metabolites with high confidence, and 3) the need to distinguish a host of unknown compounds as unrelated chemical background or perhaps interesting metabolites. Identification of hundreds to thousands of metabolites in complex matrices such as human plasma is one of the most difficult challenges faced by metabolomics scientists[2]. One of the main strategies employed in metabolomics is to reduce this complexity by applying several different chromatographic methods prior to analysis with a high-resolution accurate mass (HRAM) Orbitrap mass spectrometer[3]. Unambiguous identification of metabolites requires a combination of mass spectrometric tools including high mass accuracy and precision, ultra-high resolution (isotopic fine structure), multiple dissociation techniques, and a high-resolution spectral fingerprint consisting of high-quality MS^n spectral trees[4].

HRAM LC-MS metabolomics datasets contain many thousands of features that may be related to the biological sample or may be unrelated chemical background[5]. Data reduction and false positives are a major roadblock in these experiments. A recent publication reported the optimized experimental conditions for a Thermo Scientific™ Orbitrap™ Fusion™ Tribrid™ mass spectrometer operated at 500,000 resolution at m/z 200 to reliably separate and measure ^{13}C and ^{18}O ratios in metabolites thereby substantially reducing the number of possible elemental formulas.[6]

The Orbitrap ID-X Tribrid mass spectrometer was specifically developed with all of these analytical challenges in mind. This versatile LC-MS^n instrument is optimized to obtain the highest quality information from metabolite and lipid samples. High resolution, robust mass accuracy ensures that every full MS and MS^n scan is used effectively for obtaining comprehensive metabolite identification. Intelligent acquisition methods provide robust profiling of precious samples, deeper characterization of known and unknown compounds, and real-time interrogation of specific compound classes using highly selective scan filters.

Hardware benefits

The Orbitrap ID-X Tribrid mass spectrometer (Figure 1) has the following capabilities:

- Ultra-high resolution, consistent mass accuracy and mass precision to achieve in-depth metabolome and lipidome coverage with very high confidence

- Intelligent acquisition of high-quality LC-MS and MS^n spectra for robust detection, structure characterization and confident annotation of metabolites and lipids

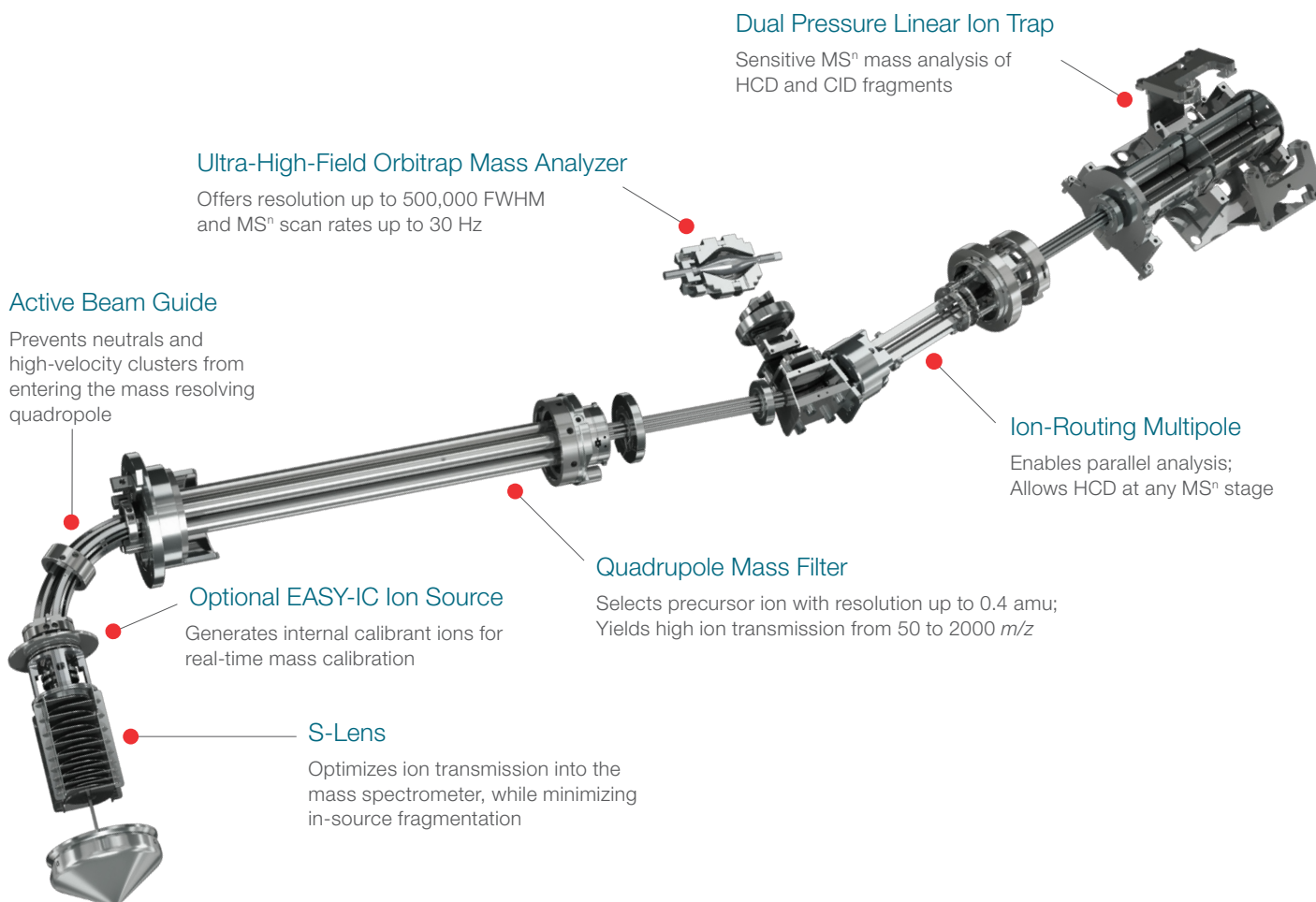- Selective and sensitive high-field Orbitrap for confident detection and quantitation

Dual Pressure Linear Ion Trap
Sensitive MS^n mass analysis of HCD and CID fragments

Ultra-High-Field Orbitrap Mass Analyzer
Offers resolution up to 500,000 FWHM and MS^n scan rates up to 30 Hz

Active Beam Guide
Prevents neutrals and high-velocity clusters from entering the mass resolving quadropole

Ion-Routing Multipole
Enables parallel analysis; Allows HCD at any MS^n stage

Optional EASY-IC Ion Source
Generates internal calibrant ions for real-time mass calibration

Quadrupole Mass Filter
Selects precursor ion with resolution up to 0.4 amu; Yields high ion transmission from 50 to 2000 *m/z*

S-Lens
Optimizes ion transmission into the mass spectrometer, while minimizing in-source fragmentation

Figure 1. Orbitrap ID-X Tribrid mass spectrometer instrument schematic.

Table 1. Novel features and performance benefits of the Orbitrap ID-X Tribrid mass spectrometer.

Features	Benefits
OptaMax NG Ion Source	Increased usability and robustness, and enhanced APCI performance
Streamlined mass calibration and optional internal calibration	Improved mass accuracy and stability across the entire mass range
Default parameters	Parameter settings optimized for small molecule analyses
AcquireX data acquisition mode using automatic reinjection logic	Automated sample profiling enables LC-MS^n analysis and comprehensive compound interrogation by sampling of blank and matrix to prioritize compounds of interest and exclude background
Templates for small molecule application-specific methods	Easy-to-use, pre-defined methods for metabolomics, lipidomics, metabolite annotation, and characterization of unknown compounds
MS^n library builder method	Enables collection of high-quality MS^n spectra for library creation (infusion and LC-MS)
Assisted collision energy	Provides real-time collision energy optimization for building libraries
Data-dependent HCD and CID MS^n experiments with advanced scan filters including targeted neutral losses, product ions, and isotope ratios	Combine untargeted profiling with data dependent experiments that are triggered only when a specific compound class is detected. Adds confidence in annotation of compound classes such as flavonoids or triacylglycerol lipids that require more sophisticated experiments for complete structural analysis

The Orbitrap ID-X Tribrid mass spectrometer is configured specifically for small-molecule applications. Key improvements for metabolomics and lipidomics include: 1) pre-defined method templates specifically designed for metabolites, lipids and MS^n spectral library building, 2) streamlined mass calibration procedures and, 3) intelligent acquisition methods for automating the entire acquisition workflow. Instrument specifications for the Orbitrap ID-X Tribrid mass spectrometer are summarized in Table 2.

Top reasons for selecting the Orbitrap ID-X Tribrid mass spectrometer for metabolomics and lipidomics

- Be more confident in metabolite annotations with high quality HCD MS^n and CID MS^n data

- Use AcquireX data acquisition methods to obtain higher LC-MS^n coverage and annotation of more real metabolites

- Obtain LC-MS^n spectra to provide more complete structure information for isomeric species

Solution and benefits
Untargeted metabolomics—workflow improvements
*Mass calibration procedure*

With the implementation of an improved and easy-to-use calibration procedure along with the use of the built-in internal calibrant option, the Orbitrap ID-X Tribrid mass spectrometer achieves mass measurements with less than 1 part-per-million (ppm) mass accuracy, as illustrated by the example of endogenous creatine from reference material NIST SRM 1950 (Figure 2, left panel). Excellent mass accuracy can be achieved for every scan across the chromatographic peak of creatine, even at low intensity, without the need of averaging several scans. Similarly, robust measurements with excellent mass accuracy were achieved for a mixture of small molecule standards, representing various endogenous metabolites ranging in molecular weight from 74–780 Da, over a period of 3 days of continuous operation (Figure 2, right panel).

Table 2. Instrument specifications of the Orbitrap ID-X Tribrid mass spectrometer.

Features	Orbitrap ID-X Tribrid mass spectrometer
OptaMax Ion Source	Improved HESI/APCI probes for stable and robust operation
S-Lens Ion Optics	Stacked-ring ion guide for ion focusing and transmission
Active Beam Guide	Reduces noise by preventing neutrals from entering quadrupole
Quadrupole Mass Filter	Efficient precursor ion selection and transmission for *m/z* 50–2000
Ion-Routing Multipole	Enables parallel analysis, HCD fragmentation at any MS^n stage
Dual-Pressure Linear Ion Trap	Provides ion trap CID MS^n up to MS^{10} mass analysis
Optional EASY-IC Ion Source	Generates internal calibrant ions for real-time mass calibration
Orbitrap Mass Analyzer	Resolution from 7,500–500,000 FWHM at *m/z* 200
Scan Rate	Orbitrap up to 30 Hz; Ion trap up to 40 Hz
Mass Accuracy	<3ppm RMS external calibration; <1ppm RMS internal calibration
Dynamic Range	>5,000 in a single scan
Multiplexing	Up to 10 different precursor ions for targeted MS^2 or SIM
Polarity Switching	One positive ion and one negative ion MS scan (30,000 resolution at *m/z* 200) in 1.1 sec
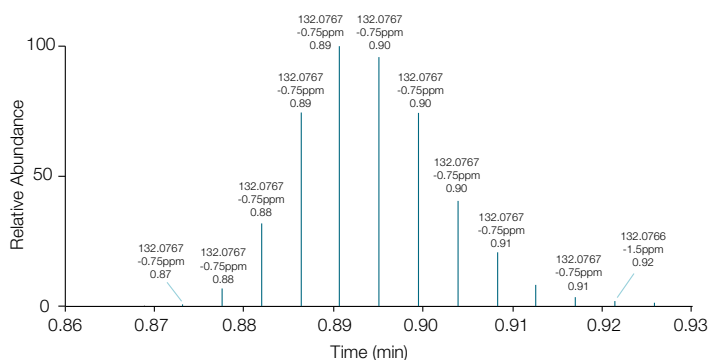
Sub-ppm scan-to-scan mass measurement accuracy. Sub-ppm mass measurement accuracy for Creatine (exact [M+H]$^+$ m/z 132.0768) detected over the LC-MS elution profile.
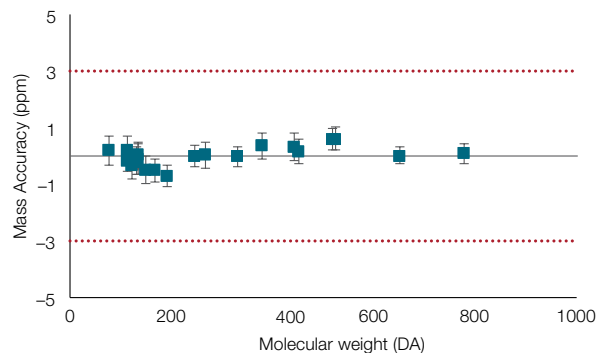
Run-to-run mass measurement accuracy. LC-MS mass measurement accuracy for a mixture of 24 small molecule standards conducted over a 72-hour period.

Figure 2. Excellent scan-to-scan and run-to-run mass measurement accuracy obtained with the Orbitrap ID-X Tribrid mass spectrometer.

The value of ultra-high resolution MS data

The capability of Orbitrap ID-X Tribrid mass spectrometer to acquire full scan MS data at up to 500,000 mass resolution at m/z 200 provides clear benefits in terms of compound annotation (Figure 3). Using Compound Discoverer software, the protonated molecular ion of $C_5H_{11}NO_2S$ (m/z 150.05844) found in human plasma is automatically grouped with the sodium adduct (m/z 172.04042) and the protonated species minus NH_3 (m/z 133.03198). The isotope fine structure at m/z 151 allows the assignment of a sulfur containing species due the presence of the ^{33}S isotope. In this example, at 160,000 actual resolution the ^{15}N and ^{33}S isotopes are easily separated. The accurate mass MS^2 spectrum matches the library spectrum of methionine and the structure of the product ions are all annotated with the expected fragment ion structures. Thus, automated data reduction and confident annotation are enabled by the use of sufficiently high resolution MS and MS^2 data.

AcquireX acquisition workflow

The AcquireX intelligent data acquisition workflow significantly improves the number of confident annotations using fully automated iterative exclusion and inclusion lists to obtain fewer redundant/irrelevant data dependent MS^n spectra.[7] The workflow allows the user to specify different sample types that includes a solvent (experimental) blank and a pooled sample matrix, prepared from a small portion of each individual biological sample. The workflow also specifies different experimental methods—full scan MS for acquiring blank and pooled reference samples and data dependent MS^n for iterative sample injection. The AcquireX process is shown in Figure 4.
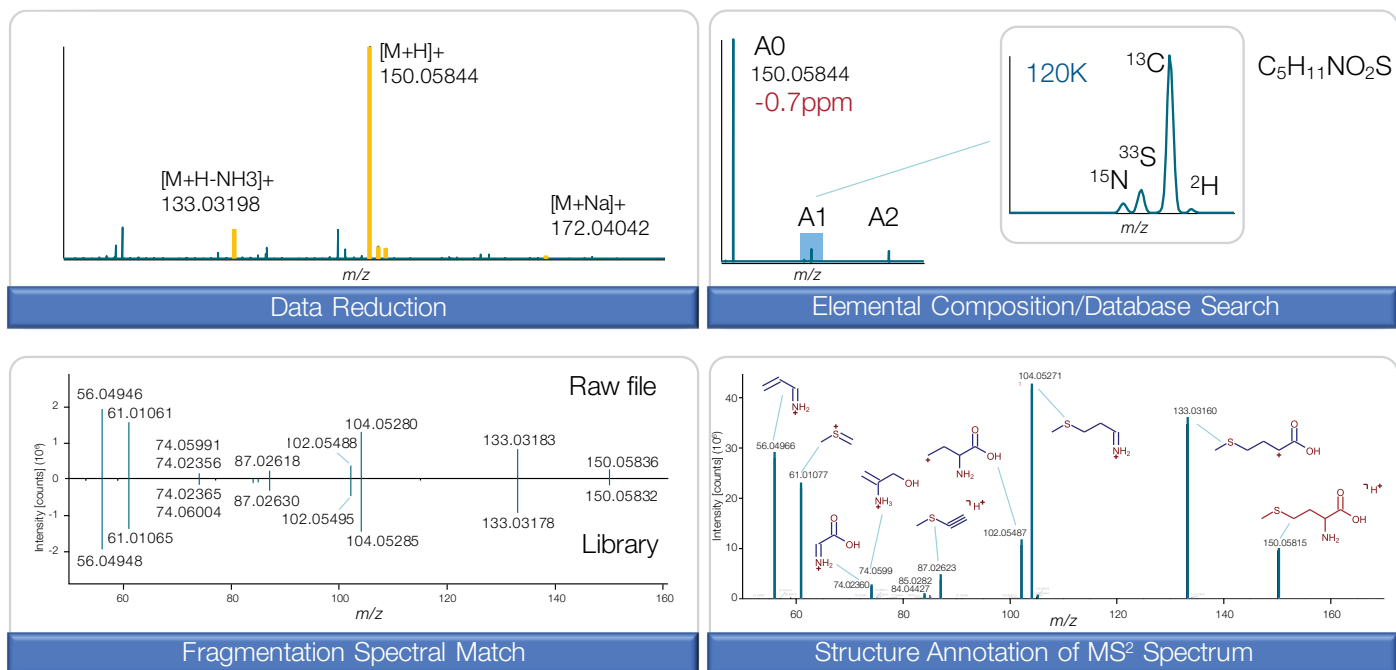

Figure 3. Ultra-high resolution MS and MS^2 data for annotation of methionine in human plasma.
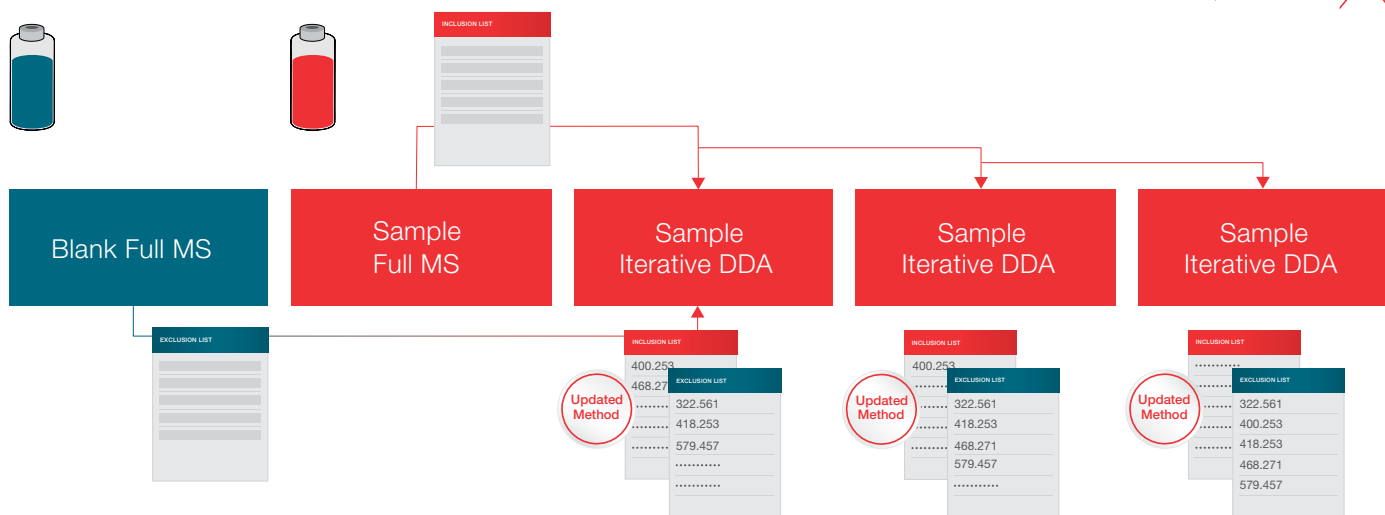
Figure 4. AcquireX data dependent workflow for improved compound annotation.

The workflow consists of a fully automated sequence designed to obtain comprehensive LC-MS^n analysis of a pooled sample by the iterative process described below.

- First, the AcquireX process obtains the LC-MS data for the blank and a pooled sample

- The AcquireX process creates an exclusion list from the blank and inclusion list from the sample data

- The first data dependent MS^2 run is acquired and the inclusion/exclusion lists are updated after the run

- On the second injection, MS^2 spectra are acquired for compounds remaining on the inclusion list

- This process is repeated for a user-specified number of injections

The AcquireX process is illustrated by the repeated injection of NIST SRM 1950 human plasma extract and analysis using the Orbitrap ID-X Tribrid mass spectrometer[7]. LC-MS analysis of the solvent blank and automated data analysis generated an exclusion list of more than 4000 features (Figure 5). Similarly, LC-MS of the plasma extract generated an inclusion list with more than 5000 features. Next, the first LC-MS^2 acquisition and data analysis was performed and the inclusion and exclusion lists were updated prior to a second LC-MS^2 acquisition. As expected, with each repeated sample injection, the number of entries on the inclusion list decreased while the number of exclusion list entries increased until the maximum number of injections was reached.
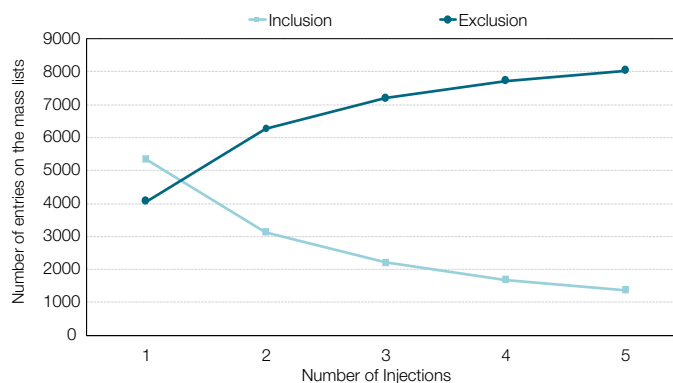

Figure 5. AcquireX updating of inclusion and exclusion lists.

During data-dependent MS^2, ions are selected based on abundance, without any knowledge of biological relevance or ion type. Often, irrelevant spectra, resulting from fragmentation of solvent clusters and other background ions dominate the duty cycle, limiting the capacity of the instrument to acquire informative spectra. With traditional data dependent analysis (DDA) 76% of the MS^2 spectra are obtained on background ions, whereas using the AcquireX process background ion MS^2 spectra were practically eliminated, allowing for analysis of more relevant sample components (Figure 6).

Small molecules form multiple adducts and cluster ions during electrospray ionization. Selection of highly abundant compounds, in the form of a parent ion or its accompanying isotopes and adducts, may prevent the fragmentation of metabolites of lower abundance. By populating the inclusion list with the preferred adduct ion

for each metabolite, more compounds can be sampled by MS^2 in a single run. Automatically updating inclusion and exclusion lists after each injection during analysis ensures that compounds not selected for MS^2 will be prioritized during a subsequent injection. The number of compounds of interest that have MS^2 spectra acquired is compared (Figure 7) for traditional DDA vs. AcquireX process. The graphs illustrate that the iterative process is far more efficient in obtaining more MS^2 spectra on relevant compounds of interest.

In the traditional DDA workflow, each injection is independent of the previous one, resulting in redundant fragmentation spectra. With the AcquireX method, inclusion and exclusion lists are automatically updated after each injection, minimizing redundant fragmentation and allowing for more analytes of lower abundance to be sampled with subsequent injections. Figure 8 shows deeper interrogation of samples with subsequent injections using the AcquireX method compared to traditional DDA by acquiring: a) lower intensity precursor ions and b) fewer redundant MS^2 spectra.
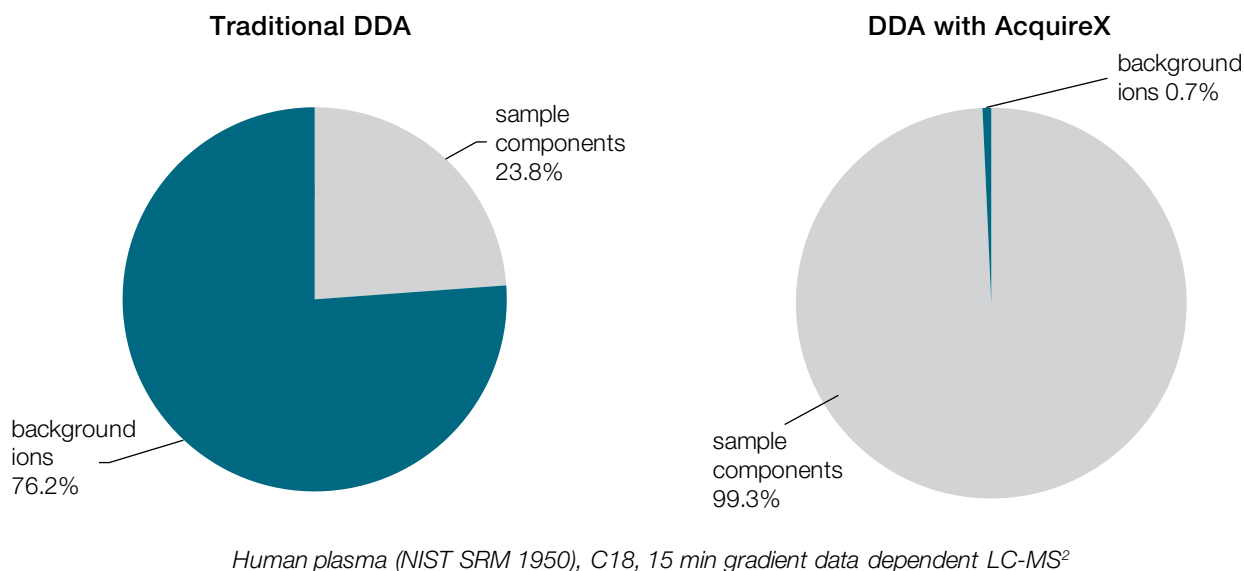

Human plasma (NIST SRM 1950), C18, 15 min gradient data dependent LC-MS^2

Figure 6. Obtaining MS^2 information on compounds vs. background: AcquireX vs. traditional DDA.

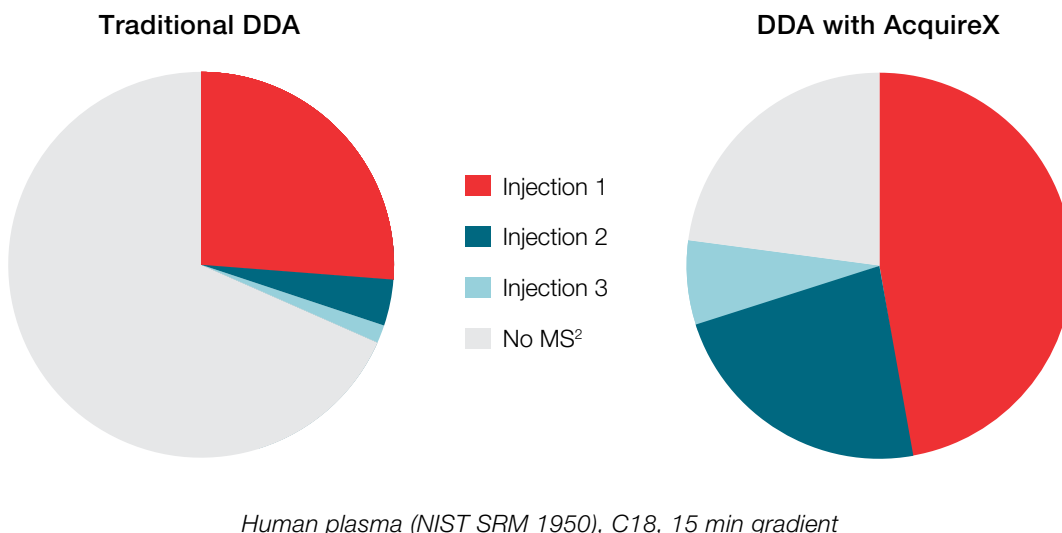*Human plasma (NIST SRM 1950), C18, 15 min gradient*

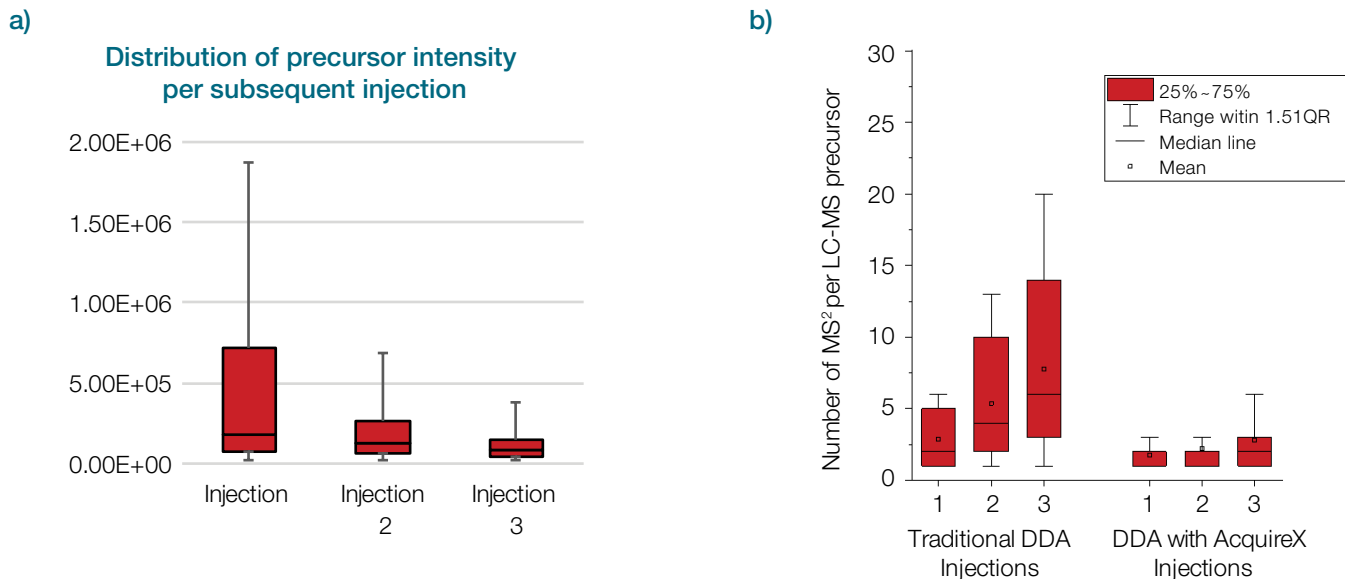**Figure 7. Comparison of MS^2 on compounds of interest: traditional DDA vs. AcquireX.**

Figure 8. Deeper interrogation of samples by: a) Lower abundance precursors and b) Less redundancy.

The cumulative result of these improvements is that, compared to traditional DDA, the AcquireX data acquisition method obtains more MS^2 spectra; this significantly increases the number of mass spectral library matches (Figure 9) against mzCloud, a very high-quality, HRAM MS^n spectral library[4]. The number of matches were defined as: *Identity match*—the precursor mass and MS^2 spectrum closely matches a reference compound or *Similarity match*—the MS^2 spectrum is similar to a reference compound but has a different precursor mass. After 3 injections, the total number of *Identity plus Similarity* matches for AcquireX data increased by more than *2-fold* over the spectral matches obtained from DDA alone. A 50% increase was observed for the identity matches.
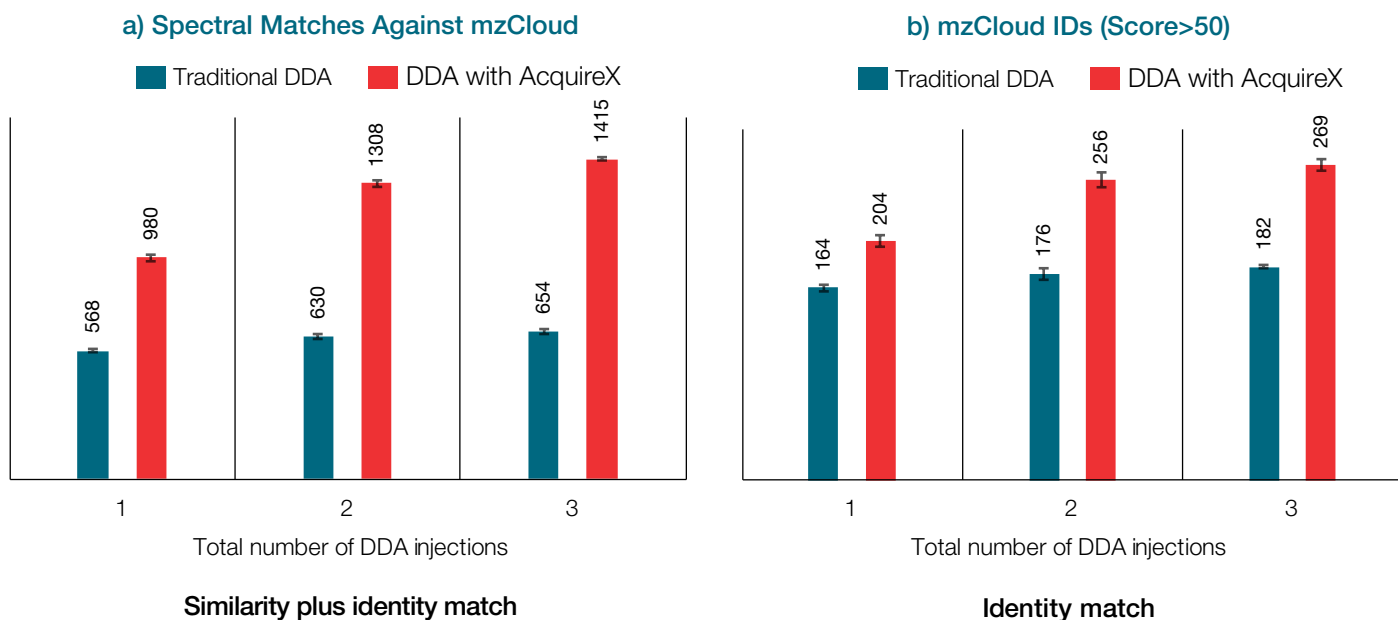

Figure 9. AcquireX data acquisition improves mzCloud library matches vs. traditional DDA:
a) Similarity plus identity match, and b) Identity match only.

LC-MS^n for more confident structural annotation of isomers

The LC-MS^n capabilities of the Orbitrap ID-X Tribrid mass spectrometer for improved structure annotation are illustrated in Figure 10 by the analysis of two flavonoid isomers—Kaempferol-3-O-β-rutinoside and Luteolin 7-rutinoside[8]. While the LC-MS^2 spectra of *m/z* 595.1650 show the same two product ions (*m/z* 449 and 287, loss of one and two sugars, respectively) although with different abundances (Figure 10), the LC-MS^3 spectra from the *m/z* 287.0546 product ions are clearly different with several unique product ions for each isomer. This illustrates the concept of precursor ion fingerprinting[4]: the *m/z* 287 ion has a different sub-structure, due to the difference in the flavonoid precursors and this is reflected in the MS^3 spectra.

Structure-based analysis of isomers

There are many examples of metabolites and lipids that are amenable to a structure-based experimental approach—for example, acylcarnitine, flavonoid,

phosphatidylcholine and triglyceride isomers are related to each other by common neutral losses or product ions. The LC-MS^n analysis of structurally-related species such as flavonoids is enabled by a data dependent workflow that is selective for the neutral loss of sugar (Table 3) from the flavonoid core structure (Figure 11)[8]. The neutral losses of the various sugars observed in the fragmentation of flavonoids is provided as a pre-defined template (Structure specific MS^4 monosaccharide loss) in the Orbitrap ID-X Tribrid mass spectrometer method editor. For flavonoids below *m/z* 420, an HCD MS^2 experiment is performed, whereas, above *m/z* 420, a more selective CID MS^2 experiment is performed to maximize the loss of a single sugar, which in turn is the precursor ion for a CID MS^3 experiment. Additional sequential sugar losses lead to CID MS^4 and CID MS^5 experiments. The value of this novel workflow is that the MS^n spectral tree is completely acquired, thus extensively characterizing the flavonoids in a real sample, and the MS^n trees can then be searched for related flavonoid sub-structures present in a reference library.
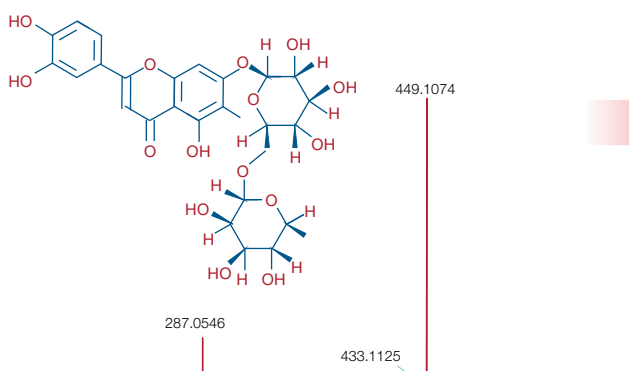
MS^2 595.1650
Kaempferol 3-O-β-rutinoside
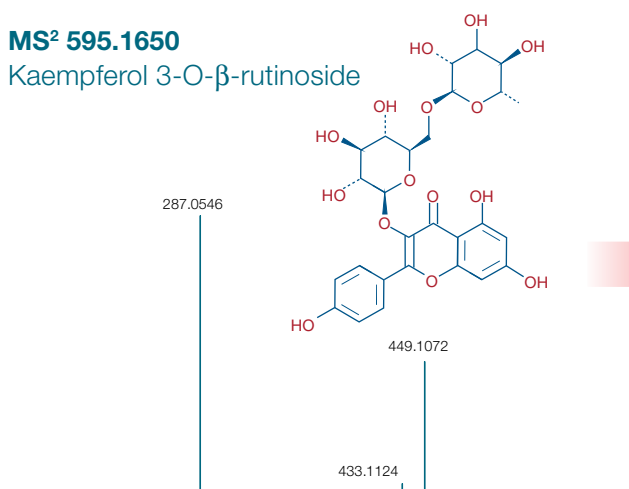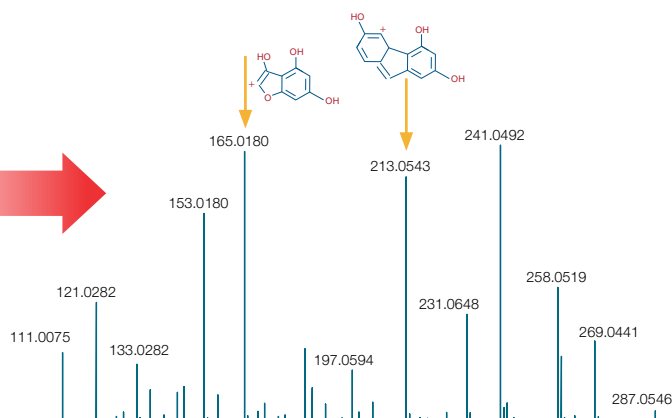
MS^3 287.0546

MS^2 595.1650
Luteolin 7-rutinoside

MS^3 287.0546
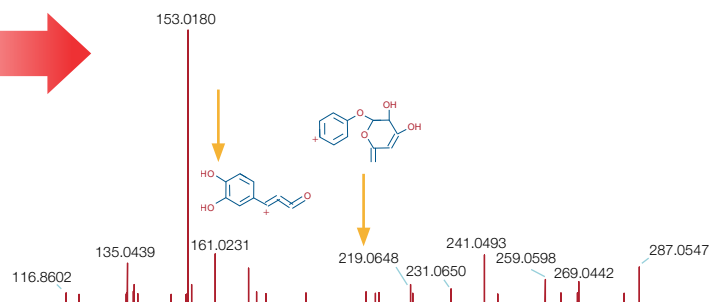
Figure 10. LC-MS^2 and MS^3 spectra of two isomeric flavonoids.
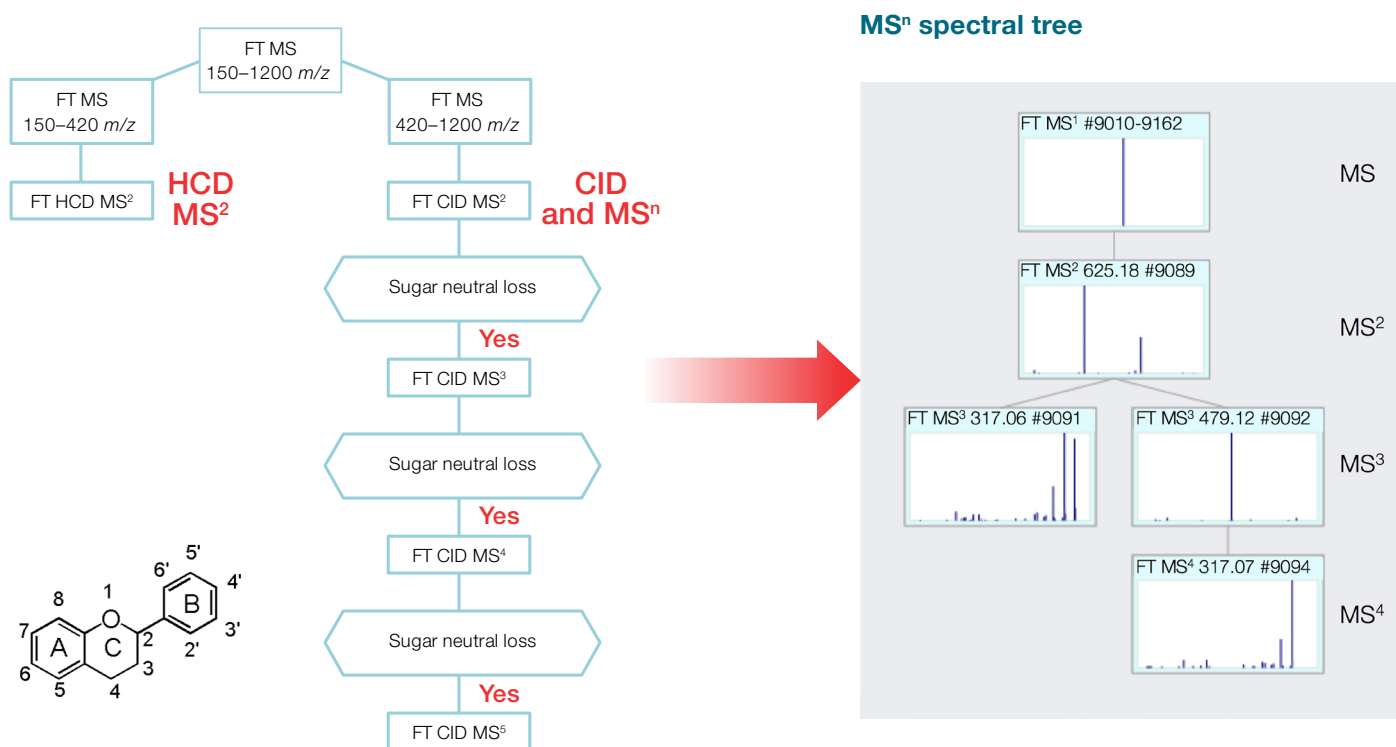
MS^n spectral tree

Figure 11. Neutral loss dependent LC-MS^n acquisition method for flavonoids.

Table 3. Sugar neutral losses from protonated flavonoid precursor ions.

Saccharide	Neutral Loss	Composition
Pentose (xylose, arabinose)	132.04226	$C_5H_8O_4$
Deoxyhexose (rhamnose)	146.05791	$C_6H_{10}O_4$
Hexose (glucose, galactose)	162.05282	$C_6H_{10}O_5$
Glucuronide	176.03209	$C_6H_8O_6$
Glucuronic acid	194.04265	$C_6H_{10}O_7$

Lipid structure annotation using LC-dd MS^2 and targeted MS^3 using a neutral loss scan filter

Advanced scan filters are employed during data dependent analysis to provide further characterization of specific compounds classes[9]. For example, during LC-MS analysis triglyceride (TG) lipids often elute as a mixture of isomers and thus, their MS^2 spectra consist of a mixture that requires additional information for annotation[10]. Using the targeted loss trigger on the Orbitrap ID-X Tribrid mass spectrometer, MS^3 scans are acquired only when a characteristic loss of fatty acid and ammonia is observed during the data-dependent MS^2 experiment. As shown in Figure 12, the MS^2 spectrum of TG 48:1 is a mixture of at least two isomeric lipids. The MS^3 spectra from three neutral losses gives confident annotation of TG 14:0-16:0-18:1 and TG 16:0-16:0-16:1.
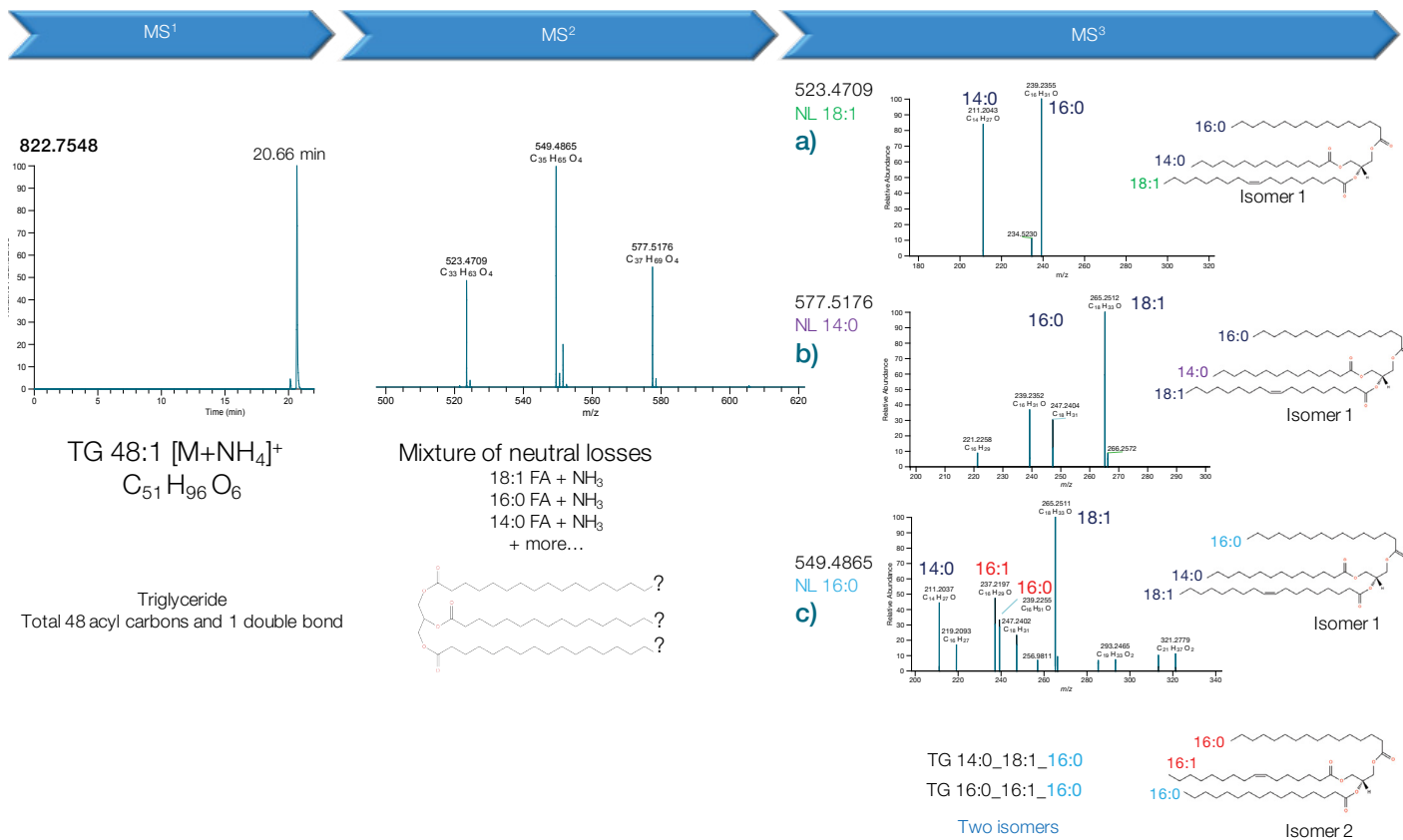
Figure 12. LC-MS² and targeted MS³ spectra of two isomeric triglycerides from insect larvae.

Detailed resources for the Orbitrap ID-X Tribrid mass spectrometer can be found:
thermofisher.com/orbitrapID-X
planetorbitrap.com/orbitrap-id-x#

For sole source specifications, kindly contact your local sales representative or contact us at: Grant Central.

Why choose the Orbitrap ID-X Tribrid mass spectrometer?

State-of-the-art research is the engine that drives advances in mass spectrometry innovation. Mass spectrometers must be equipped with superior performance such as higher resolution, mass accuracy, dynamic range and scan efficiency to fulfil more rigorous experimental demands and complexity. MS instruments must have the flexibility to handle qualitative and quantitative experiments while being extremely robust for high-throughput analysis. In addition, for small molecule identification the combination of features available on the Orbitrap ID-X Tribrid mass spectrometer (see Table 4 for comparison to other Orbitrap-based instruments) provides tools that offer a unique combination of multiple proven technologies for obtaining structural information (high resolution, accurate mass measurement, HCD MS² and linear ion trap MSⁿ) along with the real-time decision-making capability to obtain more definitive characterization of metabolites, lipids and novel compounds with unknown structures. The exceptional value of the Tribrid Orbitrap-based mass spectrometers in delivering uncompromised analytical benefits while achieving superior results are well recognized by the scientific community. The Orbitrap ID-X Tribrid mass spectrometer is designed for scientists that need higher confidence in their compound structure annotations and their metabolomics studies.

Table 4. Which Orbitrap system is right for my metabolomics research?

Instrument Attributes	Q Exactive Series Mass Spectrometer				Orbitrap Tribrid Mass Spectrometer
	Q Exactive	Q Exactive Plus	Q Exactive HF	Q Exactive HF-X	Orbitrap ID-X
Mass Analyzer	Orbitrap	Orbitrap	High Field Orbitrap	High Field Orbitrap	Tribrid–ion trap and Orbitrap
Mass Range	m/z 50–6000	m/z 50–6000	m/z 50–6000	m/z 50–6000	m/z 50–2000
Maximum Resolution at m/z 200	140,000	140,000	240,000	240,000	500,000
Enhanced Resolution	N/A	280,000 (option)	N/A	N/A	N/A
Scan Speed (Orbitrap -OT, ion trap -IT)	12 Hz	12 Hz	18 Hz	40 Hz	30 Hz $OTMS^2$ 40 Hz $ITMS^2$
Top NMS^2	Top 10 $ddMS^2$	Top 10 $ddMS^2$	Top 20 $ddMS^2$	Top 20 $ddMS^2$	
Top Speed MS^n					Up to 20 MS^n, n = 1 to 10
Mass Accuracy Internal Calibration	<1ppm	<1ppm	<1ppm	<1ppm	<1ppm
Polarity Switching	<1 sec	<1 sec	<1 sec	<1 sec	1.1 sec
Multiplex	Yes, up to 10 precursors	Yes, up to 10 precursors	Yes, up to 10 precursors	Yes, up to 10 precursors	Yes, up to 10 precursors
Dissociation	HCD	HCD	HCD	HCD	CID, HCD
AcquireX Intelligent Acquisition	No	No	No	No	Yes
Performance Features	**Q Exactive**	**Q Exactive Plus**	**Q Exactive HF**	**Q Exactive HF-X**	**Orbitrap ID-X**
Resolution	✔✔	✔✔✔ (option)	✔✔✔	✔✔✔	✔✔✔✔
Sensitivity	✔✔✔	✔✔✔	✔✔✔✔	✔✔✔✔	✔✔✔✔
Speed	✔✔✔	✔✔✔	✔✔✔✔	✔✔✔✔	✔✔✔✔
Dynamic Range	✔✔✔✔	✔✔✔✔	✔✔✔✔	✔✔✔✔	✔✔✔✔
Mass Accuracy	✔✔✔✔	✔✔✔✔	✔✔✔✔	✔✔✔✔	✔✔✔✔
HCD and CID MS^n					✔✔✔✔
Application	**Q Exactive**	**Q Exactive Plus**	**Q Exactive HF**	**Q Exactive HF-X**	**Orbitrap ID-X**
Untargeted Metabolomics	✔✔	✔✔	✔✔✔	✔✔✔	✔✔✔✔
Untargeted Lipidomics	✔✔	✔✔	✔✔✔	✔✔✔	✔✔✔✔
Stable Isotope Studies	✔✔	✔✔	✔✔✔	✔✔✔	✔✔✔✔
Structure Elucidation	✔✔	✔✔	✔✔✔	✔✔✔	✔✔✔✔
Targeted Analysis (PRM)	✔✔	✔✔	✔✔✔✔	✔✔✔✔	✔✔✔✔

Least Fit ✔✔   ✔✔✔   ✔✔✔✔   Best Fit

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10. Software Utilizing Positive and Negative Ion MS[2]/MS[3] HCD and CID Spectra for Improved MS[n] Lipid Identification, David A Peake, Reiko Kiyonami, Daniel Gachotte, Gavin E Reid, Yasuto Yokoi, and Andreas Hühmer, Scientific Poster #65257.

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Easy, Fast, and Reproducible Quantification of Cholesterol and Other Lipids in Human Plasma by Combined High Resolution MSX and FTMS Analysis, Sandra F Gallego, Kurt Højlund, Christer S. Ejsing, *J Am Soc Mass Spectrom (2018) 29, 34-41*.

https://link.springer.com article/10.1007%2Fs13361-017-1829-2

Description: Untargeted lipidomics, infusion, PRM, MSX (multiplexed MS/MS), human plasma

MS-Based Metabolomics for the Investigation of Neuro-Metabolic Changes Associated with BDE-47 Exposure in C57BL/6 Mice, Fenfen Ji, Hemi Luan, Yingyu Huang, Zongwei Cai, Min Li, *J Anal Test (2017) 1:233–244*

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Description: Untargeted metabolomics, LC-MS, Quantitation, Neuro-metabolic changes

Quantitative lipidomics reveals age-dependent perturbations of whole-body lipid metabolism in ACBP deficient mice, Sandra F. Gallego, Richard R Sprenger, Ditte Neess, Josch K. Pauling, Nils J Færgeman, Christer S Ejsing, *Biochimica et Biophysica Acta 1862 (2017) 145-155*

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Description: Untargeted lipidomics, MS[ALL], liver, nano-infusion, plasma/skeletal muscle lipids, quantitation

Comprehensive Analysis of Acylcarnitine Species in db/db Mouse Using a Novel Method of High-Resolution Parallel Reaction Monitoring Reveals Widespread Metabolic Dysfunction Induced by Diabetes, Li Xiang, Juntong Wei, Xiao Yu Tian, Bei Wang, Wan Chan, Shangfu Li, Zhi Tang, Hongsong Zhang, Wai San Cheang, Qian Zhao, Hongzhi Zhao, Zhiyi Yang, Yanjun Hong, Yu Huang, and Zongwei Cai, *Anal. Chem., 2017, 89 (19), pp 10368–10375.*

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Description: Untargeted lipidomics, human plasma, dd MS^2/ targeted MS^3, quantitation, LC-MS, Compound Discoverer, TraceFinder

Positional stable isotope tracer analysis reveals carbon routes during ammonia metabolism of Aedes aegypti mosquitoes, Thomas D. Horvath, Shai Dagan, Philip L. Lorenzi, David H. Hawke and Patricia Y. Scaraffia, *FASEB J. 2017 Sep 25. 466-477.*

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Description: Semi-targeted metabolomics, TraceFinder, glucose role in ammonia detoxification, mosquitoes

Characterization of Lipid A Variants by Energy-Resolved Mass Spectrometry: Impact of Acyl Chains, Christopher M. Crittenden, Lucas D. Akin, Lindsay J. Morrison, M. Stephen Trent, Jennifer S. Brodbelt, *J. Am. Soc. Mass Spectrom. (2017) 28, 1118-1126.*

http://link.springer.com/article/10.1007/s13361-016-1542-6

Description: Untargeted Lipidomics, Infusion, 193 nm UVPD, Lipid A, HCD and CID MS^2

Oxidized arachidonic and adrenic PE s navigate cells to ferroptosis, Valerian E Kagan Gaowei Mao, Feng Qu, Jose Pedro Friedmann Angeli, Sebastian Doll, Claudette St Croix, Haider Hussain Dar, Bing Liu, Vladimir A Tyurin, Vladimir B Ritov, Alexandr A Kapralov, Andrew A Amoscato, Jianfei Jiang, Tamil Anthonymuthu, Dariush Mohammadyani, Qin Yang, Bettina Proneth, Judith Klein-Seetharaman, Simon Watkins, Ivet Bahar, Joel Greenberger, Rama K Mallampalli, Brent R Stockwell, Yulia Y Tyurina, Marcus Conrad & Hülya Bayır, *Nat Chem Biol (2017) 13, 81-90.*

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Description: Untargeted Lipidomics, LC-dd MS^2 and targeted MS^3

Vertical sleeve gastrectomy reverses diet-induced gene-regulatory changes impacting lipid metabolism, Juan Du, Jingyan Tian, Lili Ding, Candi Trac, Brian Xia, Siming Sun, Dustin E. Schones and Wendong Huang, *Scientific Reports 7, 5274 (2017).*

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Description: Untargeted lipidomics, LC-dd MS^2, LipidSearch, Vertical sleeve gastrectomy (VSG)

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Description: Lipidomics, LC-MS, cardiolipin, cardiac fatty acid metabolism in early T2DM

Plasma metabolomics reveals membrane lipids, aspartate/asparagine and nucleotide metabolism pathway differences associated with chloroquine resistance in Plasmodium vivax malaria, Karan Uppal, Jorge L. Salinas, Wuelton M. Monteiro, Fernando Val, Regina J. Cordy, Ken Liu, Gisely C. Melo, Andre M. Siqueira, Belisa Magalhaes, Mary R. Galinski, Marcus V. G. Lacerda , Dean P. Jones, *PLoS ONE 2017, 12(8)e0182819.*

http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0182819

Description: Untargeted metabolomics, LC-MS, human plasma, LC-dd MS^2 annotation, mzCloud

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Metabolic Phenotypes of Response to Vaccination in Humans, Shuzhao Li, Nicole L. Sullivan, Nadine Rouphael, Tianwei Yu, Sophia Banton, Mohan S. Maddur, Megan McCausland, Christopher Chiu, Jennifer Canniff, Sheri Dubey, Ken Liu, ViLinh Tran, Thomas Hagan, Sai Duraisingham, Andreas Wieland, Aneesh K. Mehta, Jennifer A. Whitaker, Shankar Subramaniam, Dean P. Jones, Alessandro Sette, Kalpit Vora, Adriana Weinberg, Mark J. Mulligan, Helder I. Nakaya, Myron Levin, Rafi Ahmed, Bali Pulendran, *Cell (2017) 169, 862-877.*

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Description: Untargeted metabolomics, LC-MS, Plant metabolites

Soluble factors from stellate cells induce pancreatic cancer cell proliferation via Nrf2-activated metabolic reprogramming and ROS detoxification, Yuan Seng Wu, Chung Yeng Looi, Kavita S. Subramaniam, Atsushi Masamune and Ivy Chung, Oncotarget, 2016, 7(24) 36719-36732.

http://www.oncotarget.com/index.php? journal= oncotarget&page=article&op= view&path%5b%5d=9165 &path%5b%5d= 28075%22%20http://www.impact journals.com /oncotarget/index.php?journal= oncotarget &page=article&op=view&path[]= 9165&path[]= 28075

Description: Untargeted metabolomics, LC-MS, quantitation, pancreatic cancer

Comprehensive Lipidome Analysis by Shotgun Lipidomics on a Hybrid Quadrupole-Orbitrap-Linear Ion Trap Mass Spectrometer, Reinaldo Almeida, Josch Konstantin Pauling, Elena Sokol, Hans Kristian Hannibal-Bach, Christer S. Ejsing, J. Am. Soc. Mass Spectrom. (2015) 26:133-148.

http://link.springer.com/article/10.1007%2Fs 13361-014-1013-x

Description: Untargeted lipidomics, MSALL / targeted MS^3, nano-infusion, quantitation, mouse brain tissue lipids

An Artifact in LC-MS/MS Measurement of Glutamine and Glutamic Acid: In-Source Cyclization to Pyroglutamic Acid, Preeti Purwaha, Leslie P. Silva, David H. Hawke, John N. Weinstein, and Philip L. Lorenzi, Anal. Chem., 2014, 86 (12), pp 5633–5637.

http://pubs.acs.org/doi/abs/10.1021/ac501451v

Description: Targeted metabolomics, $LC-MS^2$ method development, in-source formation of pyroglutamic acid

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