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Unique Benefits Delivered by Orbitrap GC Technology for Non-Targeted Analysis

Jason Cole
Orbitrap GC/MS Product Manager

Presentation Overview

- Thermo Scientific™ Orbitrap™ GC/MS Systems Overview
- Orbitrap GC/MS System for Targeted Screening and Confirmation
- Orbitrap GC/MS System for Known Unknowns Identification
- Orbitrap GC/MS System for True Unknowns Identification

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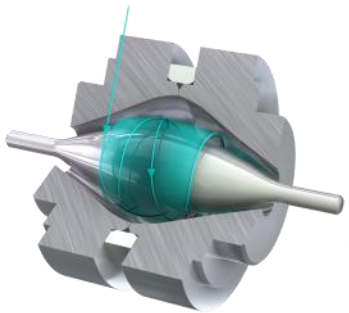
Multi-Award-Winning Orbitrap GC-MS Technology

unknowns
discovery
research



Thermo Scientific™ Q Exactive™ GC Orbitrap™ GC-MS/MS System

Unprecedented Depth in Analysis

RP 120,000 (FWHM @ *m/z* 200)

EI/CI; Full-scan, timed-SIM

MS/MS capability

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New Thermo Scientific Exactive GC Orbitrap GC-MS System

Redefining Routine GC-MS

RP 60,000 (FWHM @ *m/z* 200)

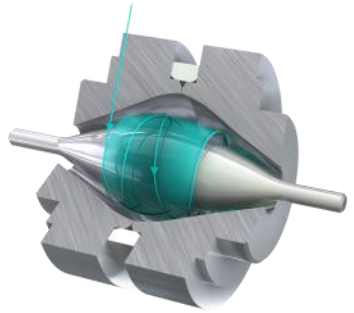
EI/CI; Full-scan; Timed-SIM

Thermo Scientific™ Exactive™ GC Orbitrap™ GC-MS System

knowns
routine
screening

Food & Beverage

Environmental



Industrial

Clinical & Toxicology

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New Addition to the Thermo Scientific Orbitrap GC-MS Family

Redefining Routine GC-MS

RP 60,000 (FWHM @ *m/z* 200)

EI/CI; Full-scan; Timed-SIM

Thermo Scientific™ Exactive™ GC Orbitrap™ GC-MS System

Thermo Scientific™ Q Exactive™ GC Orbitrap™ GC-MS/MS System

Unprecedented Depth in Analysis

RP 120,000 (FWHM @ *m/z* 200)

EI/CI; Full-scan, Timed-SIM

MS/MS capability

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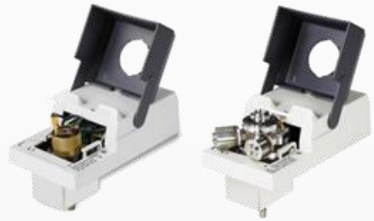
Thermo Scientific Orbitrap GC-MS Systems: The Technology Inside

Orbitrap mass analyzer

Incredible HRAM performance

Highly regarded Q Exactive GC system platform



Thermo Scientific™ TRACE™ 1310 GC System

Unique modular injector and detector design

Rapid heat cycling

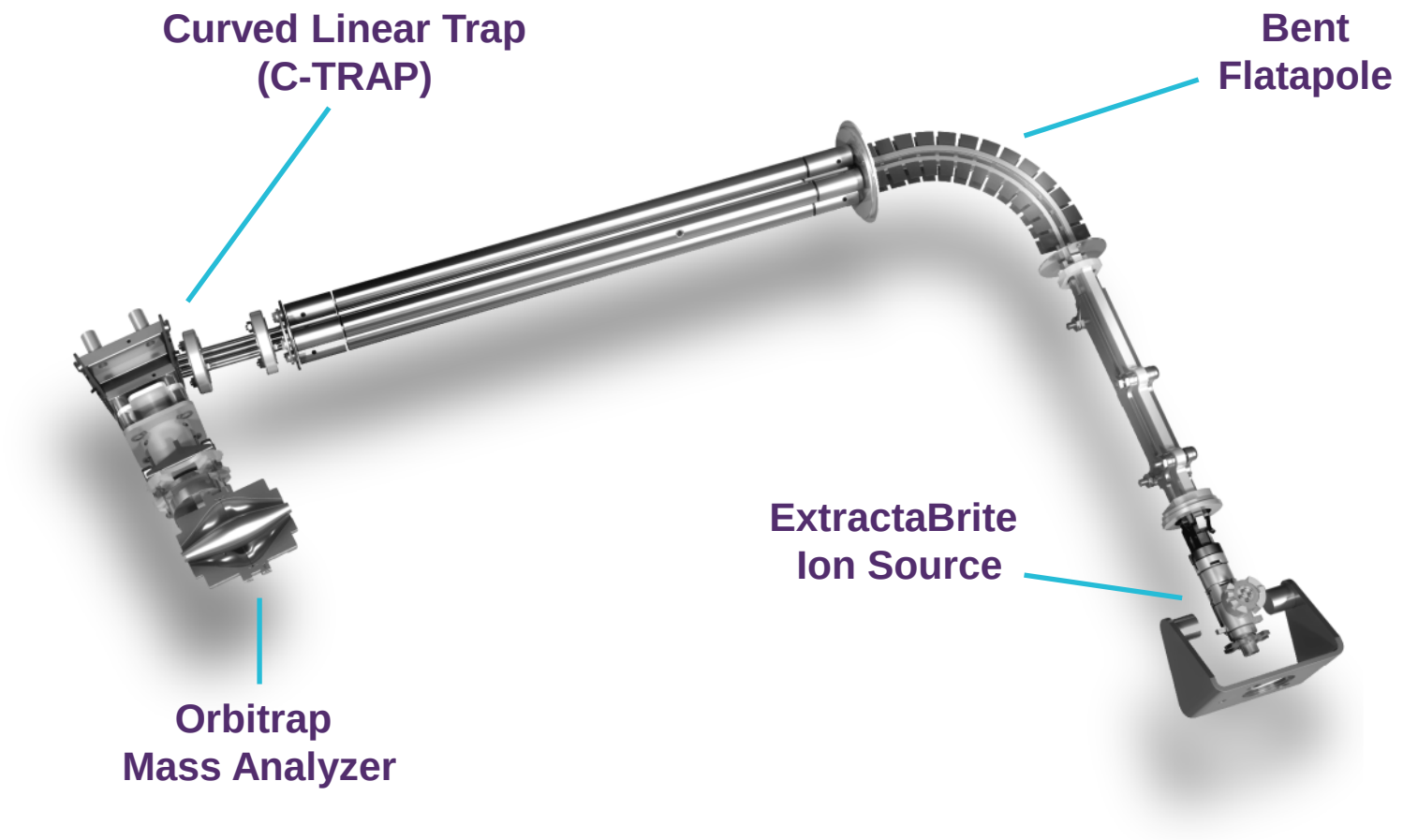
Thermo Scientific™ ExtractaBrite ™ Ion Source technology

Routine grade robustness

Patented RF lens

Removable without breaking vacuum

Thermo Scientific Exactive GC Orbitrap GC-MS System: The Technology Inside



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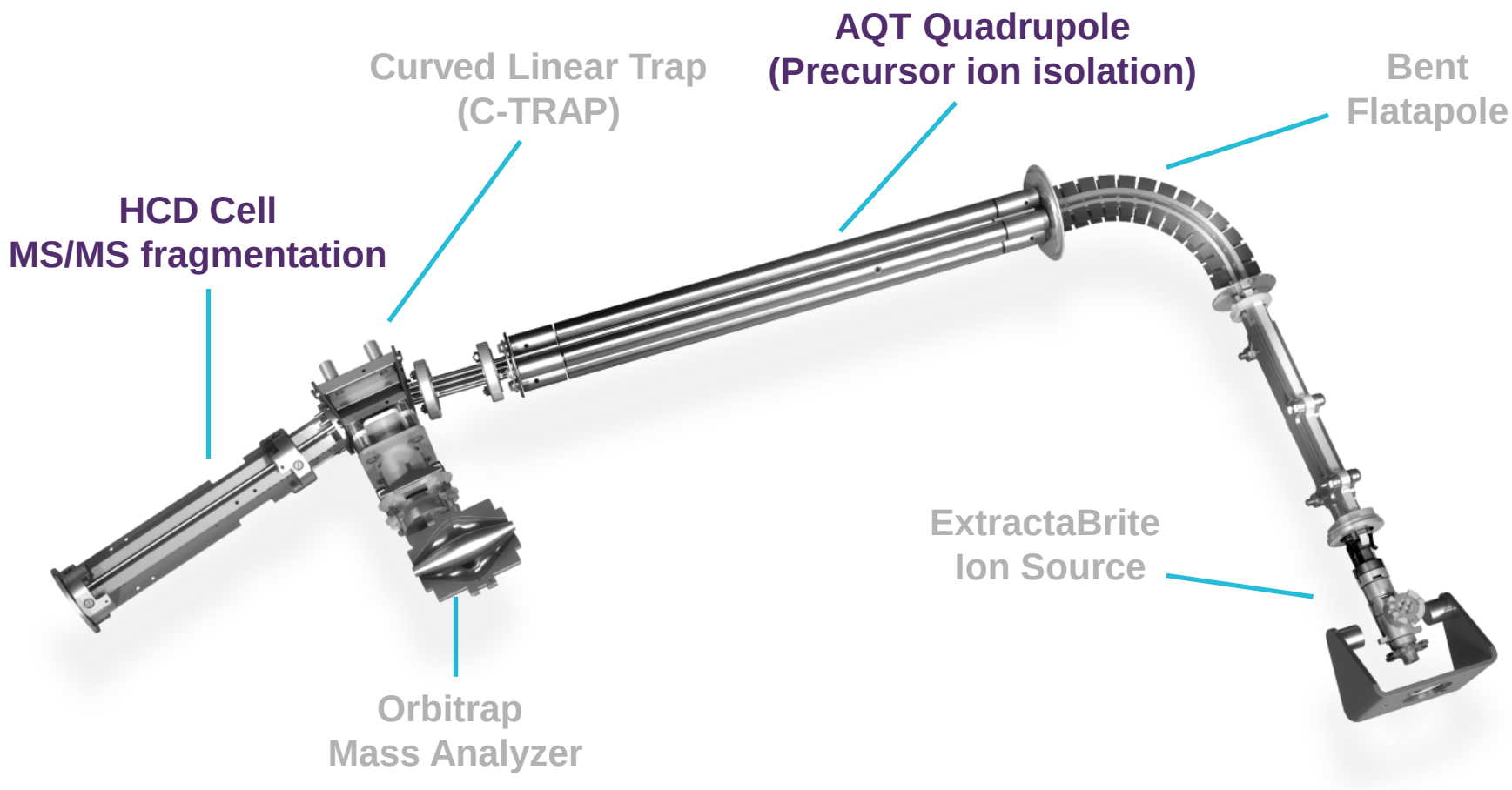
Thermo Scientific Q Exactive Orbitrap GC-MS/MS System: The Technology Inside



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Definitions

- **Mass accuracy:** The accuracy to which the mass is measured by the mass spectrometer.

$$mass\ error = \left(\frac{exact\ mass - measured\ mass}{exact\ mass}\right) * 10^6$$

- **Resolution:** Ability of a mass spectrometer to distinguish between ions of nearly equal m/z ratios (isobars).

$$R = \frac{m}{\Delta m}$$

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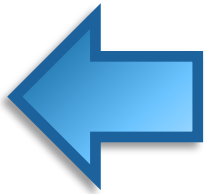
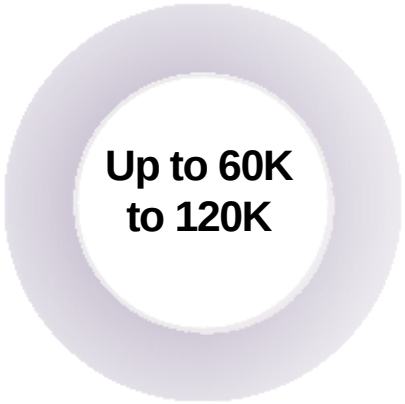
- Orbitrap GC/MS System for Targeted Screening and Confirmation 
- Orbitrap GC/MS System for Known Unknowns Identification
- Orbitrap GC/MS System for True Unknowns Identification

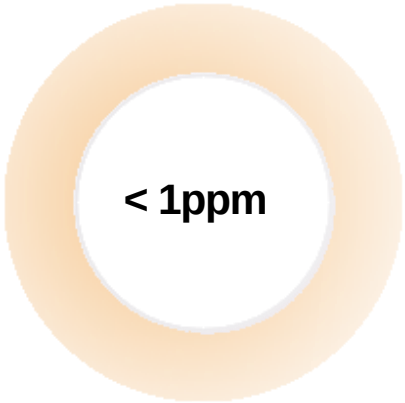
Thermo Scientific Orbitrap GC/MS System Highlights

Resolving Power



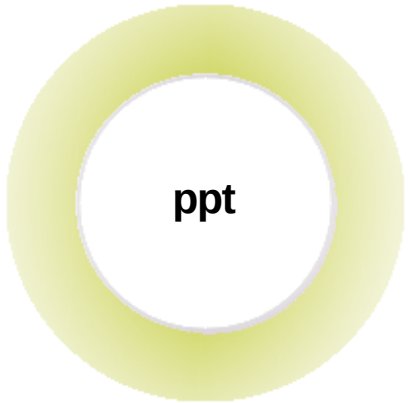
- Maximum selectivity
- Fast enough for GC

Mass Accuracy



- Every scan
- All concentrations
- In complex matrix
- Across the mass range
- Everyday!

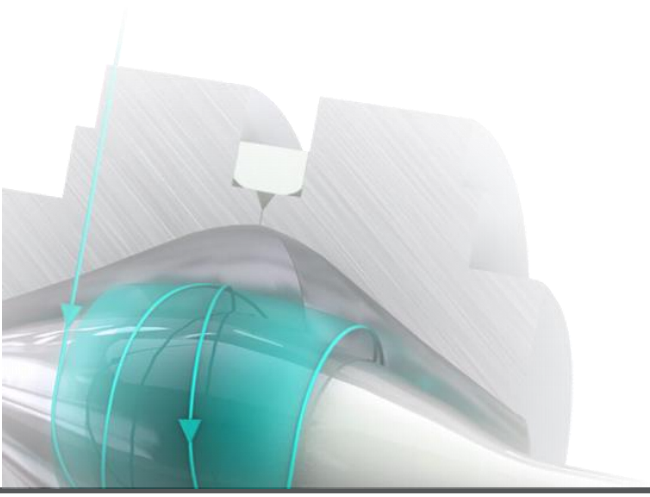
Sensitivity



- In full-scan
- High selectivity
- High spectral fidelity

Dynamic Range

- Excellent coverage in sample profiling
- “Triple quad grade” quantitation in full-scan



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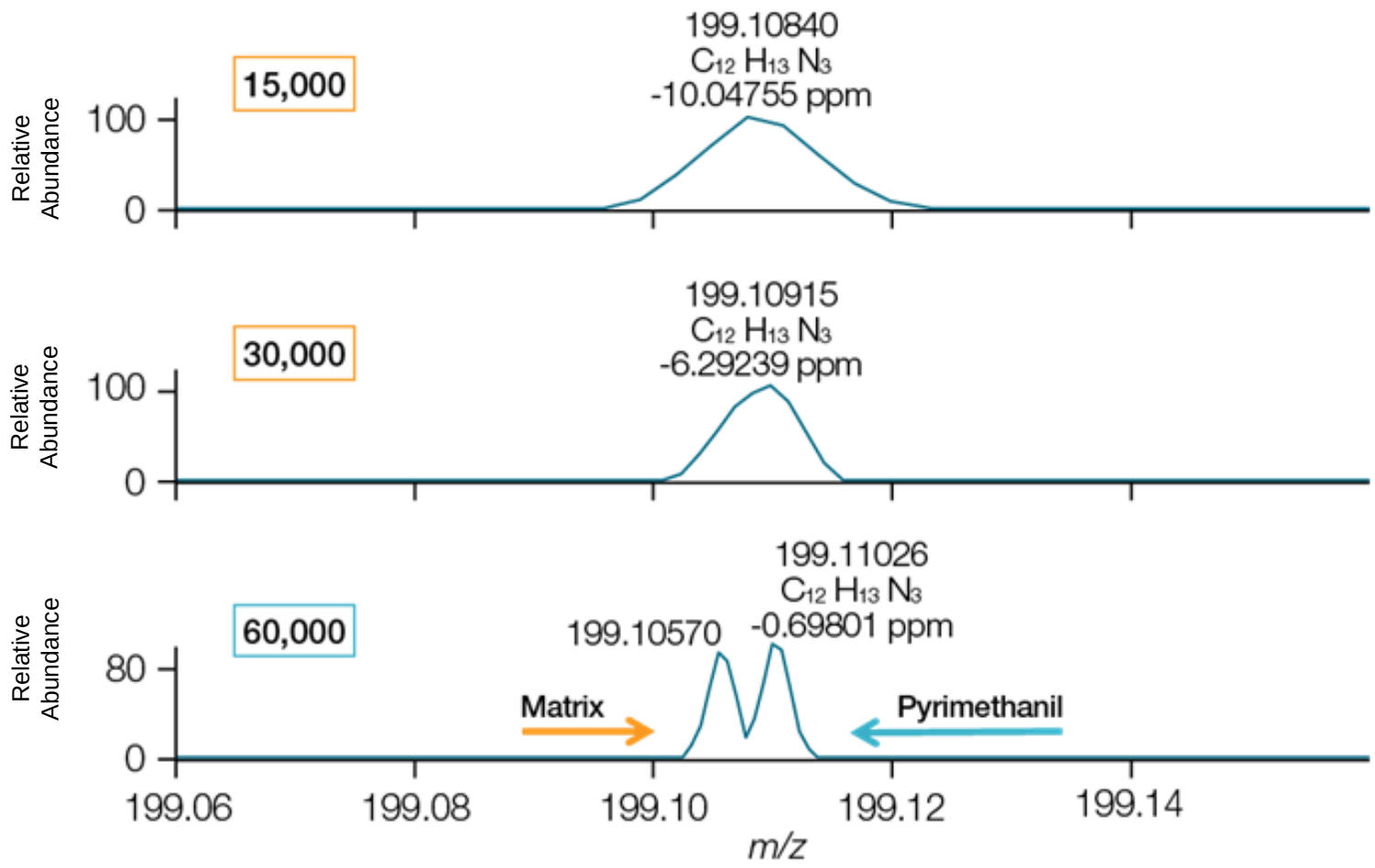
Requirements for High Resolution Targeted Screening or Quantitation

Requirement	Required for…
High Enough Resolution (Selectivity)	Good Mass Accuracy Low Level Detection

Resolving Power: Selectivity

Pyrimethanil in leek at 10 µg/Kg



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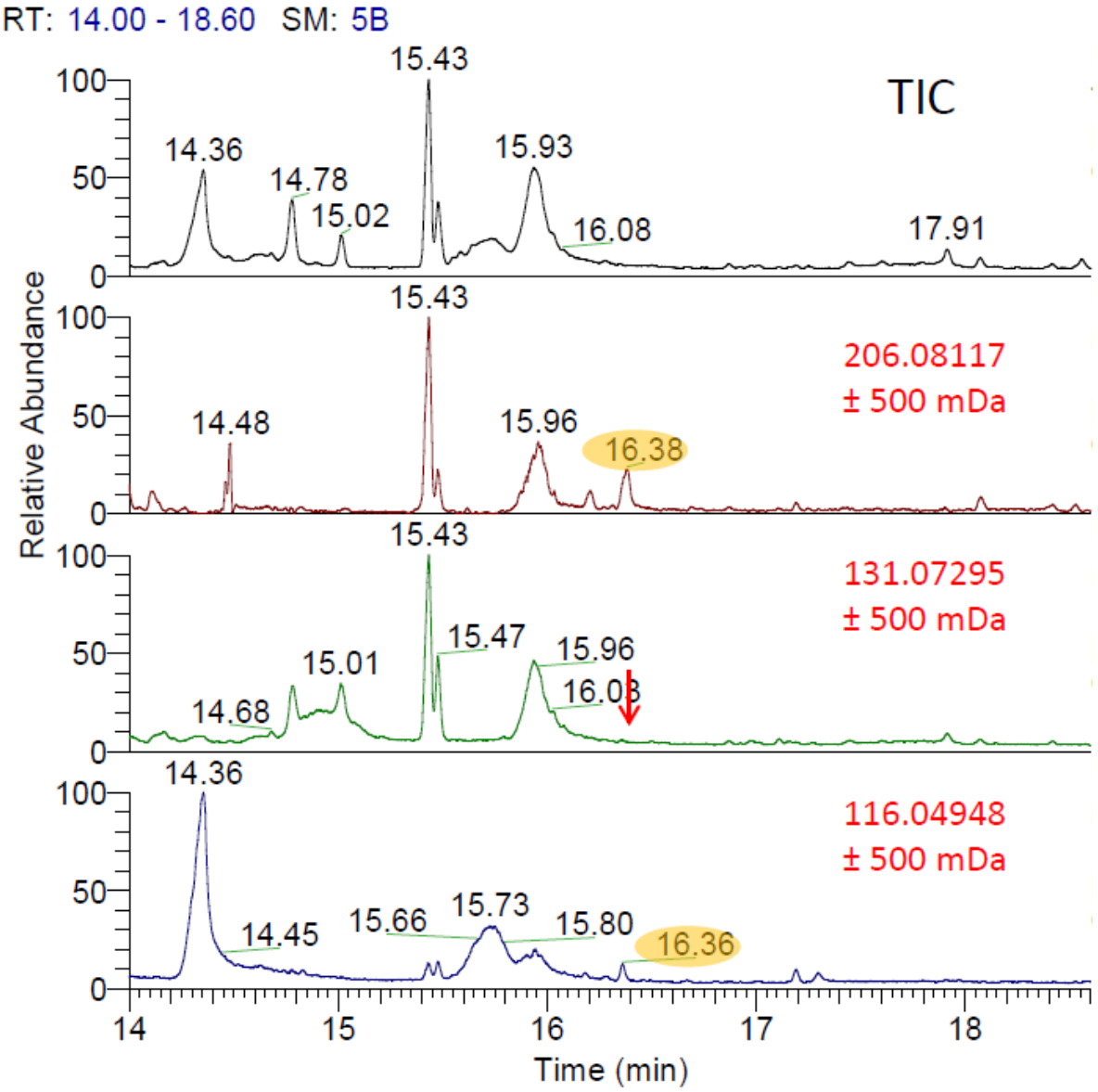
Simulated Unit Resolution MS: ± 500 mDa Extraction Window



1 µL inj. GC-Orbitrap MS
Leek spiked @ 10 ppb,
Full-scan *m/z* 50-500; Res = 60,000

Courtesy of Hans Mol,
RIKLT, The Netherlands

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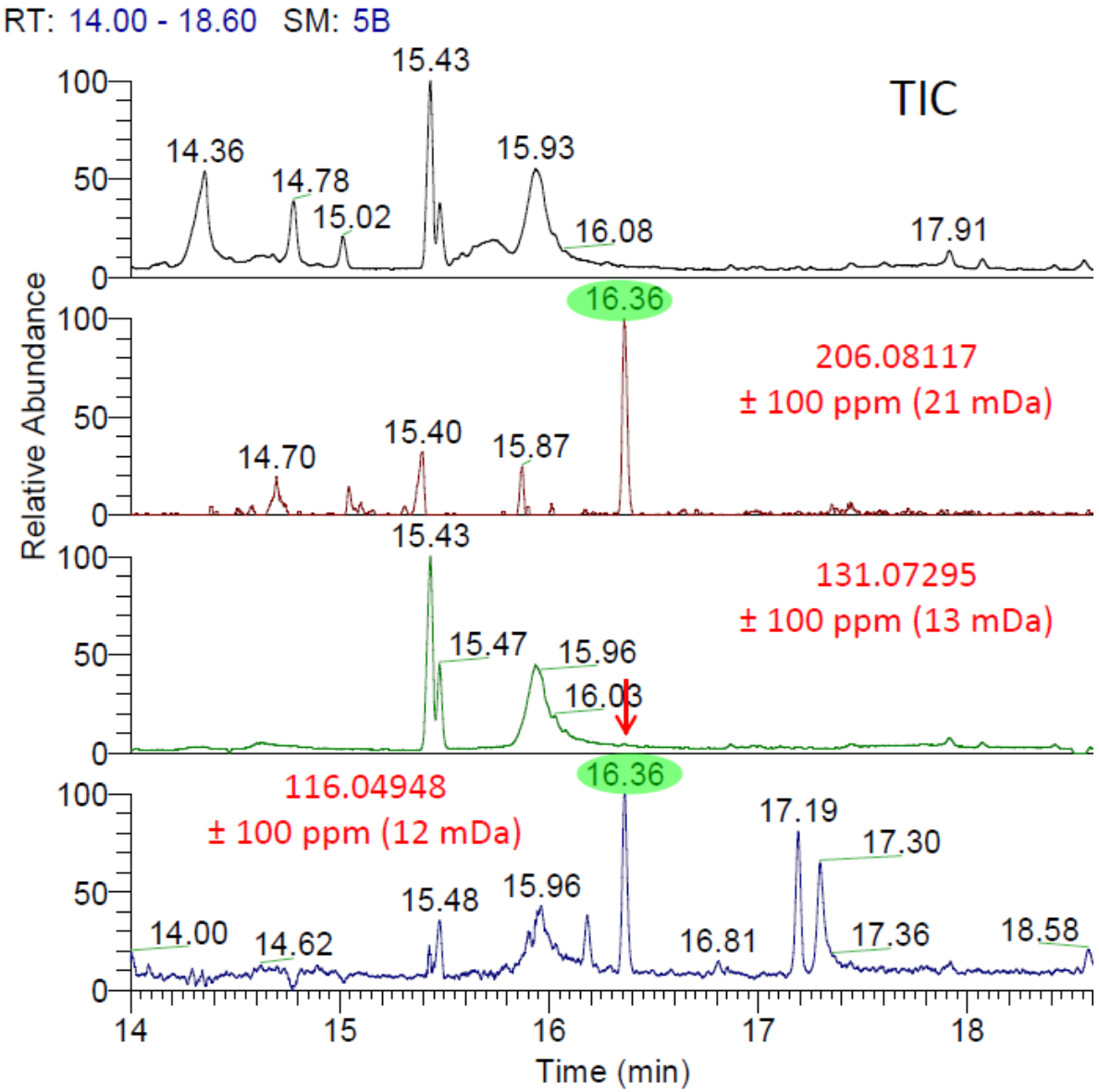
± 100 mDa Extraction Window



1 µL inj. GC-Orbitrap MS
Leek spiked @ 10 ppb,
Full-scan *m/z* 50-500; Res = 60,000

Courtesy of Hans Mol,
RIKLT, The Netherlands

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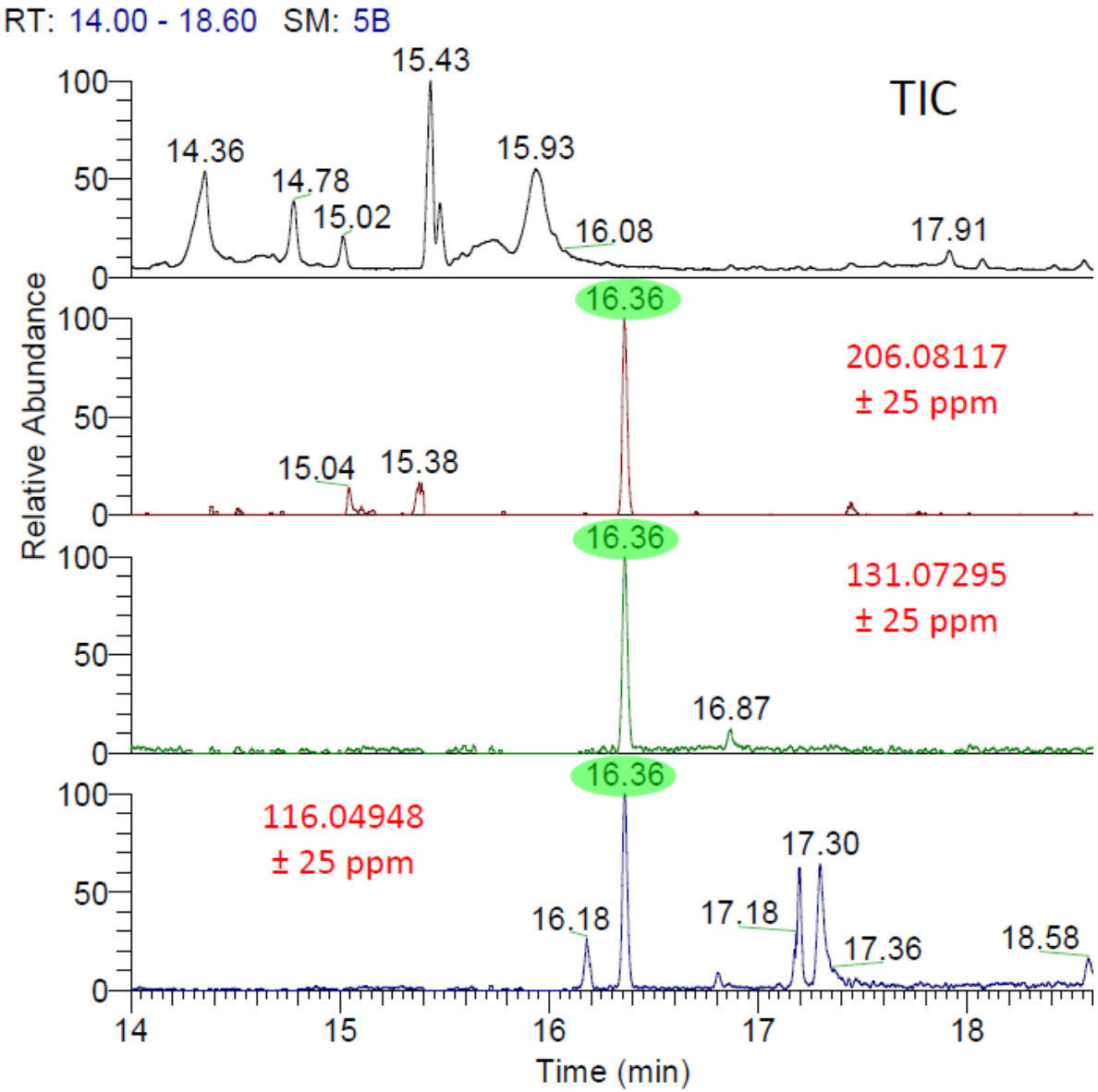
± 25 mDa Extraction Window



1 µL inj. GC-Orbitrap MS
Leek spiked @ 10 ppb,
Full-scan *m/z* 50-500; Res = 60,000

Courtesy of Hans Mol,
RIKLT, The Netherlands

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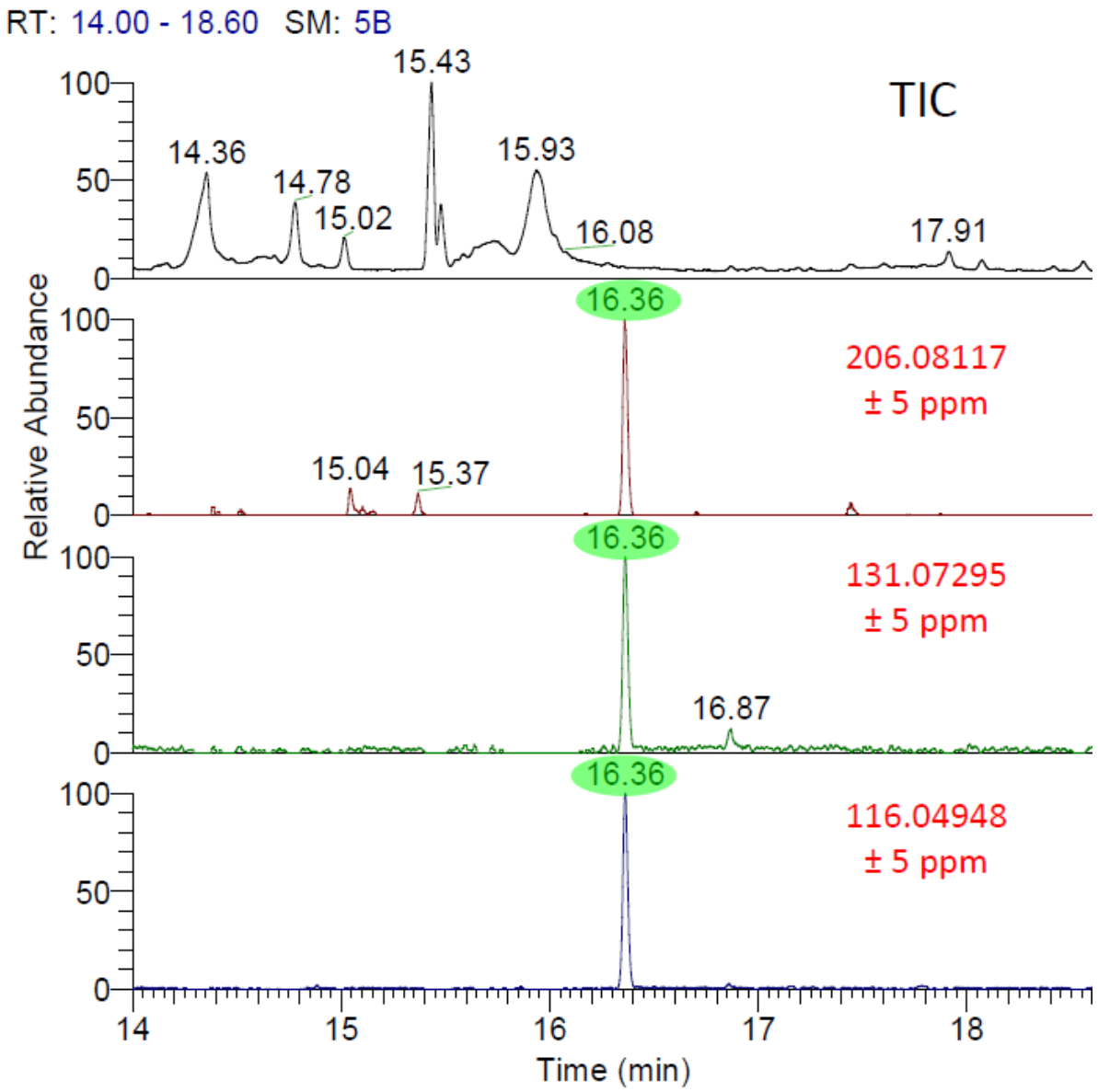
± 5 mDa Extraction Window



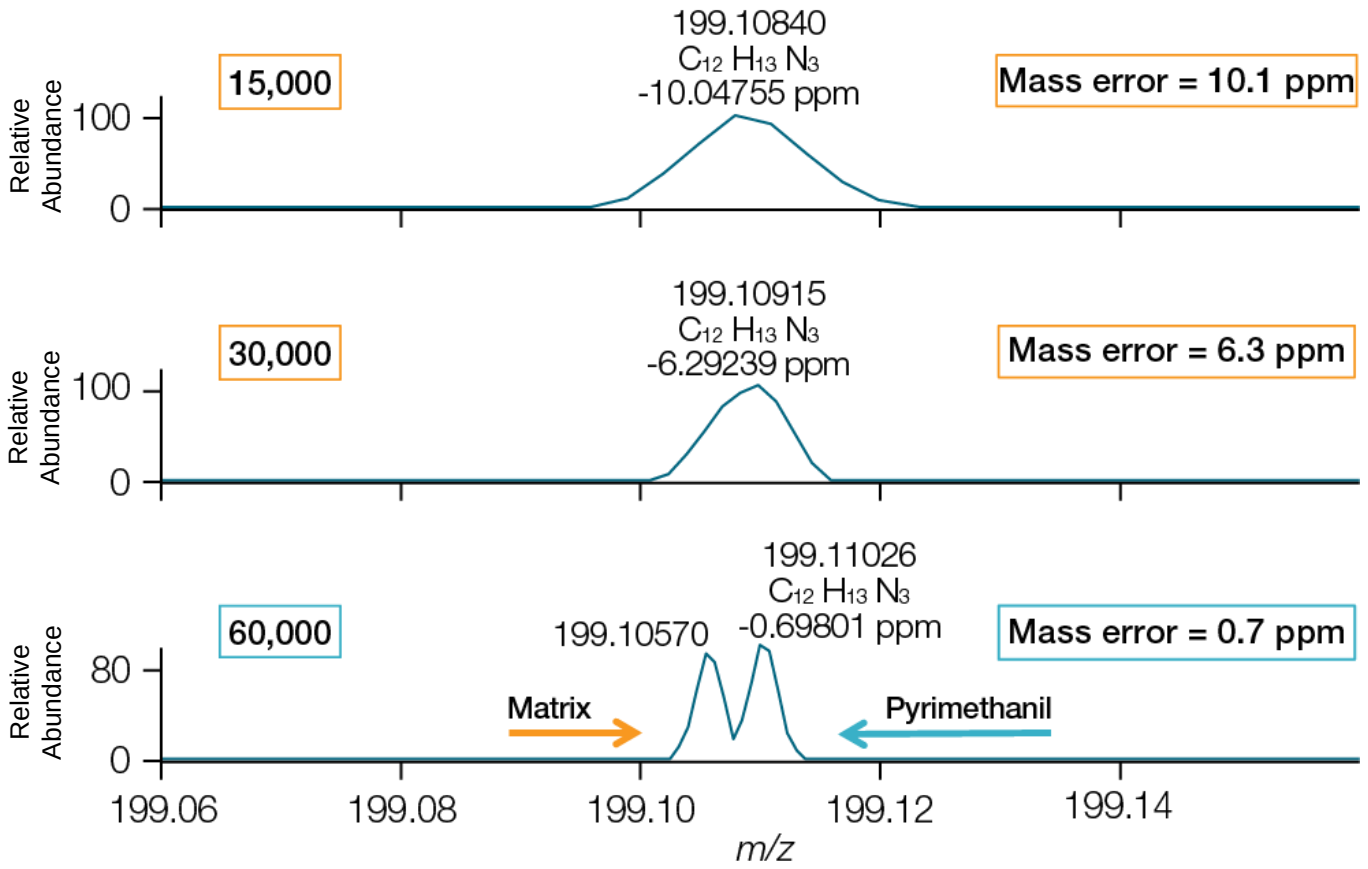
1 µL inj. GC-Orbitrap MS
Leek spiked @ 10 ppb,
Full-scan *m/z* 50-500; Res = 60,000

Courtesy of Hans Mol,
RIKLT, The Netherlands

Resolving Power: Selectivity

Pyrimethanil in leek at 10 µg/Kg

< 5 ppm ID criteria



False negative

False negative

Positive Detection

High Selectivity ∴ high sensitivity *and* confidence in identification

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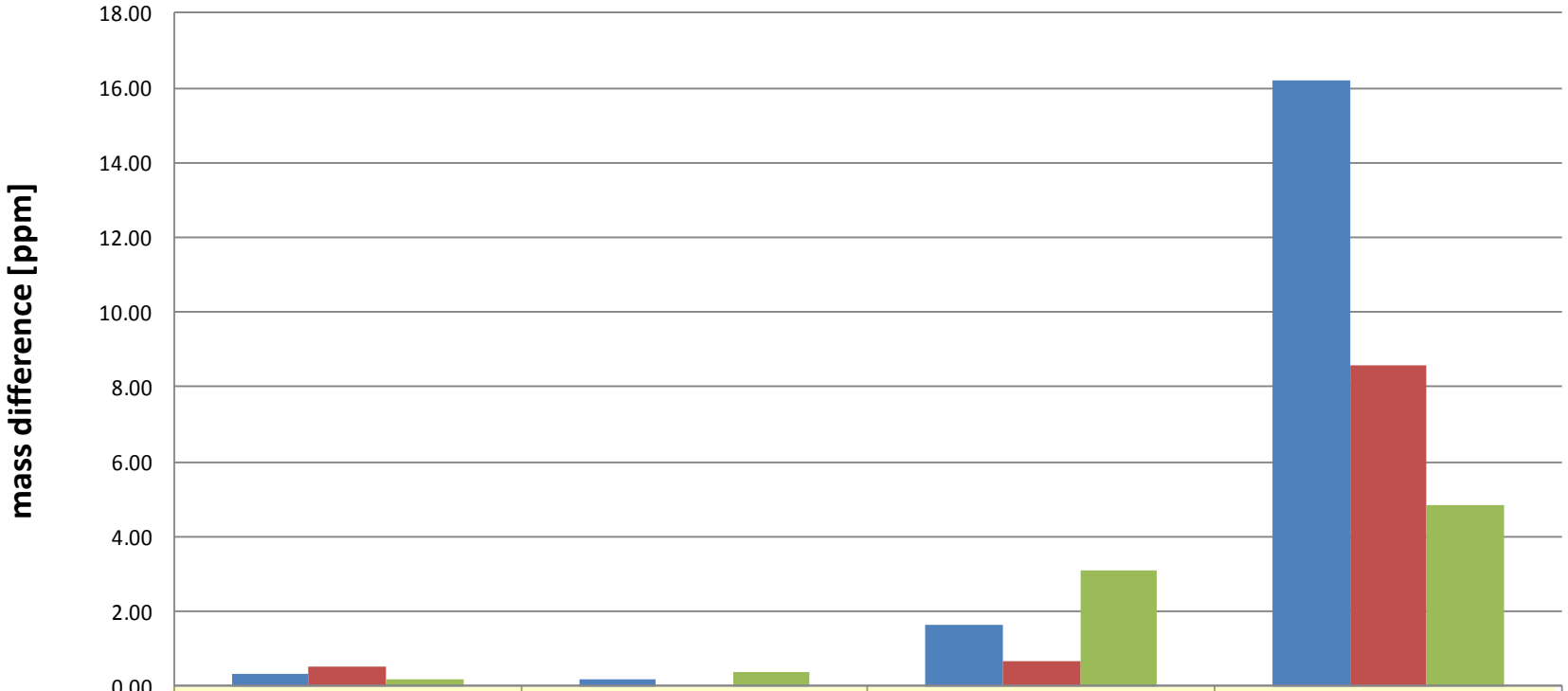
The Effect of Resolution on Accurate Mass Measurements

- Chlorpropham, procymidone and iprodione in a leek sample (10 ppb o.c.)
- A resolving power **>30k** required to completely separate these pesticides from the interfering matrix ions and to deliver **<1 ppm** mass accuracy
- <5 ppm expected mass accuracy



	120k	60k	30k	15k
chlorpropham	0.31	0.16	1.65	16.20
Procymidone	0.50	0.00	0.67	8.58
Iprodione	0.19	0.39	3.11	4.86

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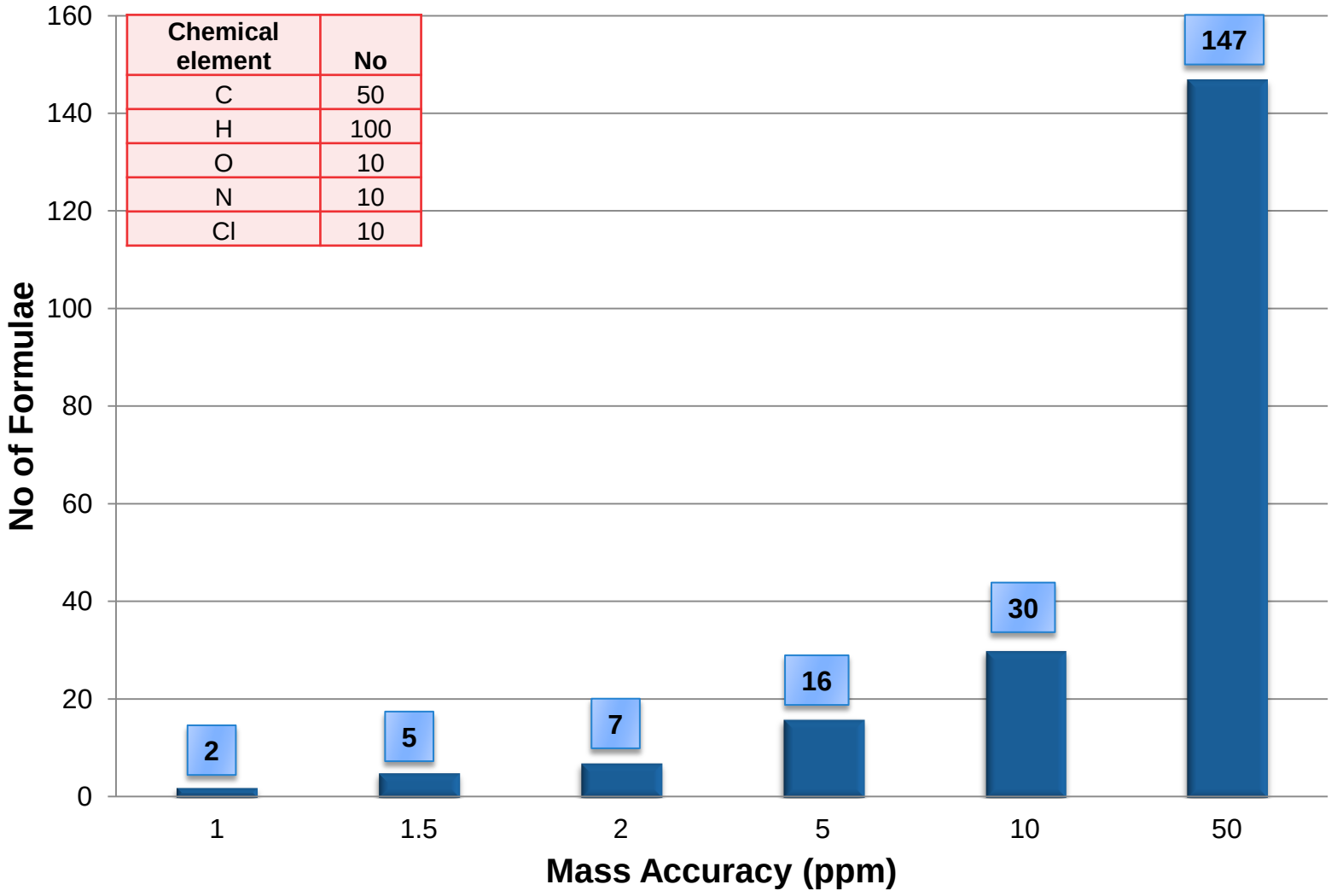
Requirements for High Resolution Targeted Screening or Quantitation

Requirement	Required for…
High Enough Resolution (Selectivity)	Good Mass Accuracy Low Level Detection
High Mass Accuracy	Confident Confirmation of Identity

Compound ID confirmation

Chemical element	No
C	50
H	100
O	10
N	10
Cl	10



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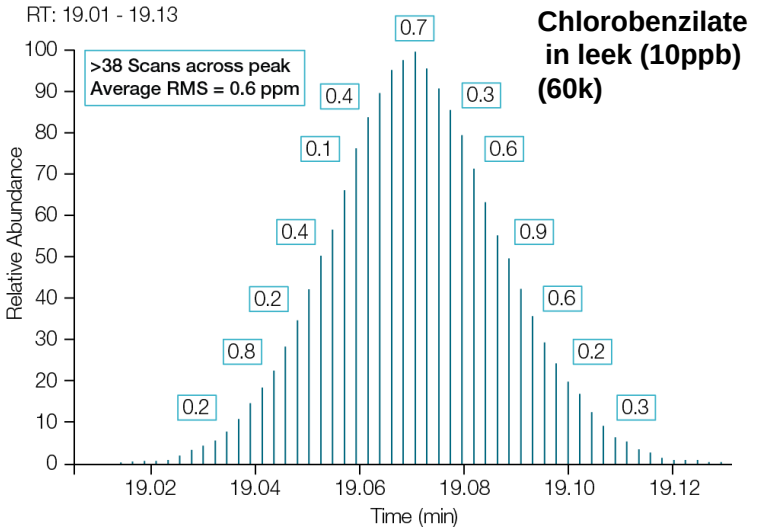
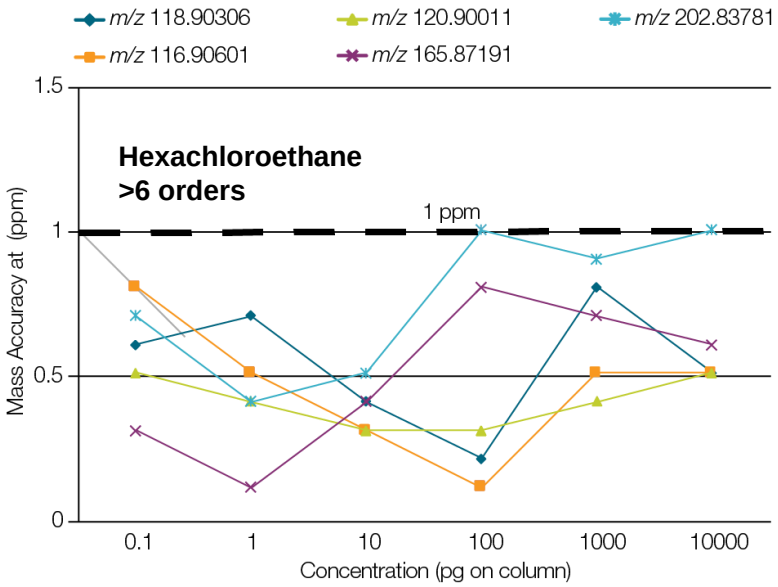
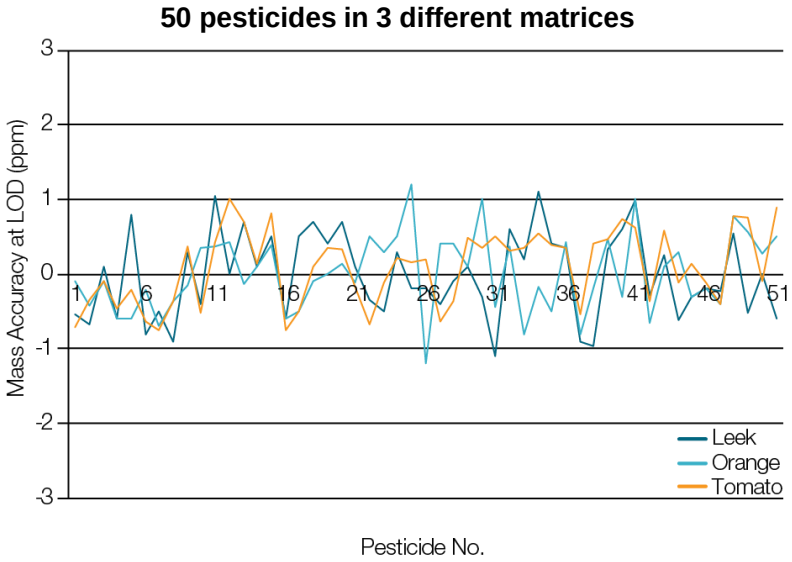
High Mass Accuracy





- Typically <1 ppm
- Across the peak
- Across the concentration range
- In matrix



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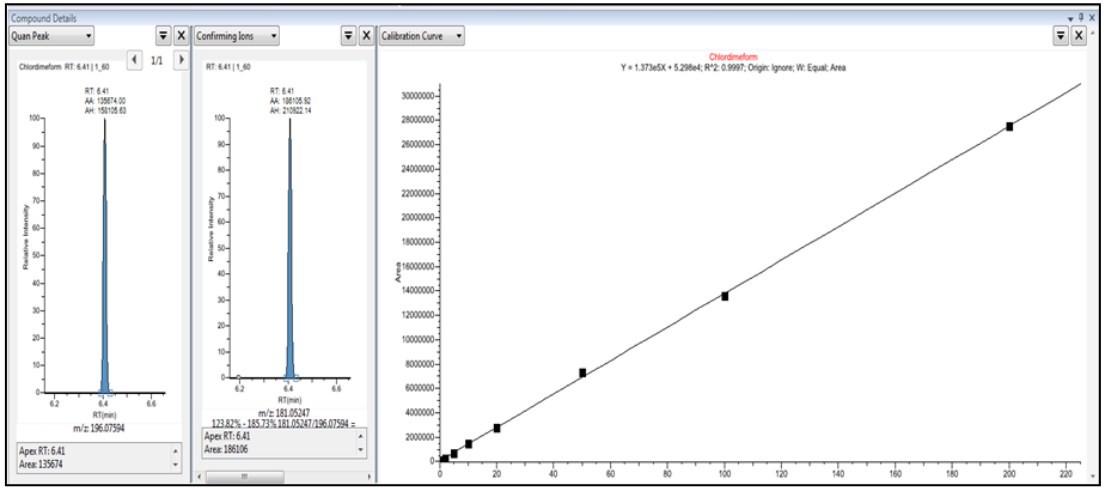
Requirements for High Resolution Targeted Screening or Quantitation

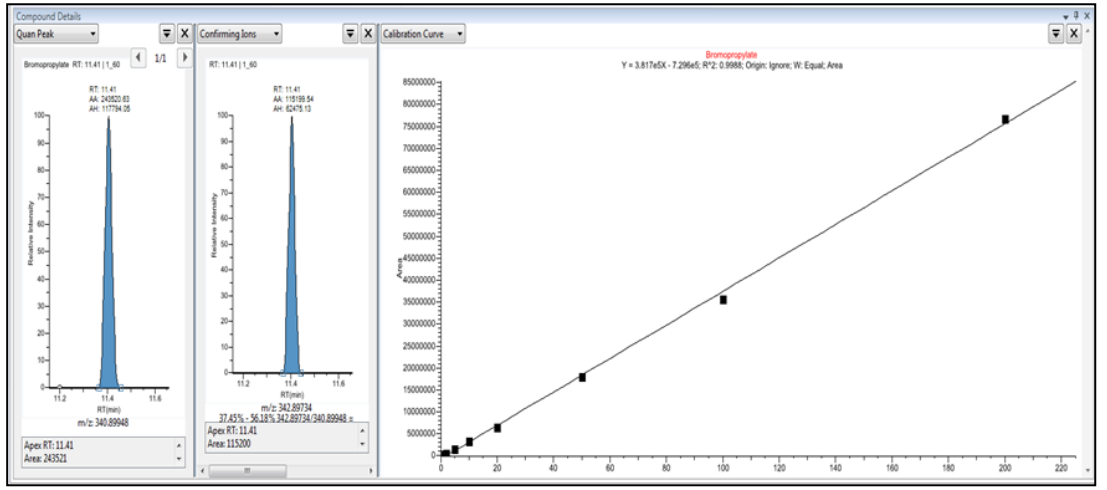
Requirement	Required for…
High Enough Resolution (Selectivity)	Good Mass Accuracy Low Level Detection
High Mass Accuracy	Confident Confirmation of Identity
High Dynamic Range	Accurate Quantitation Accurate Ion Ratio

Full-scan Evaluation with Pesticides

- 102 pesticides spiked into QuEChERS extracted apple
- 60K Resolution
- Average RSD at 10 ppb (N=5) = 2.9%
- Average R^2 from 1-200 ppb = 9.9984



Chlordimeform



Bromopropylate

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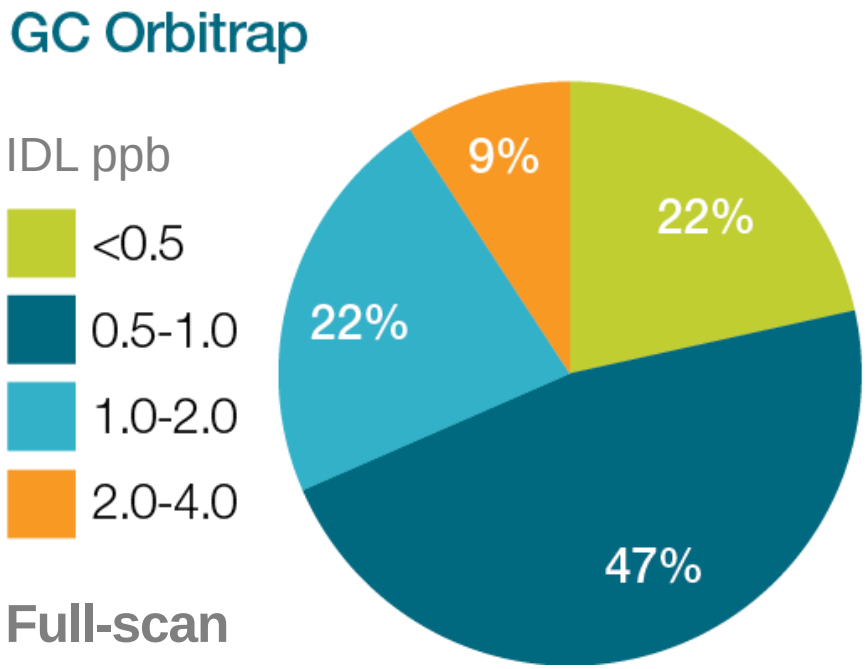
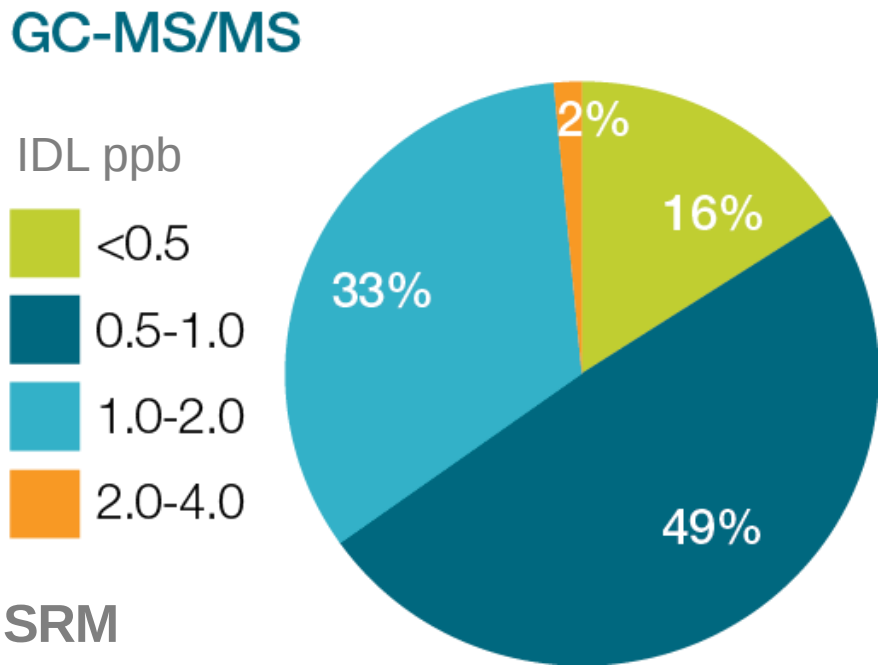
Requirements for High Resolution Targeted Screening or Quantitation

Requirement	Required for…
High Enough Resolution (Selectivity)	Good Mass Accuracy Low Level Detection
High Mass Accuracy	Confident Confirmation of Identity
High Dynamic Range	Accurate Quantitation Accurate Ion Ratio
High Sensitivity	Low Level Detection

High Sensitivity Full-scan

150 compounds in mixed vegetable matrix

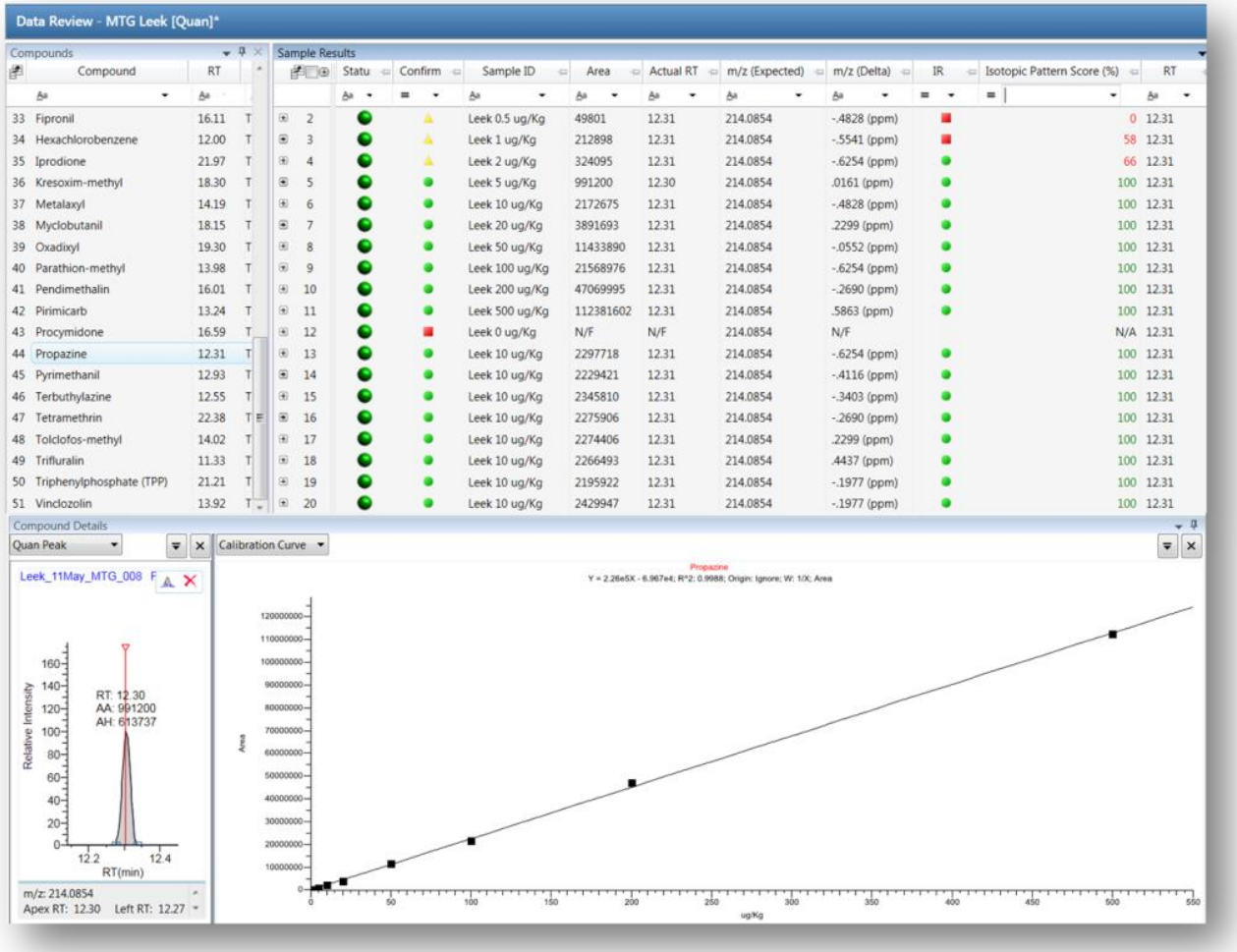




Triple-quadrupole-level sensitivity possible with a non-target acquisition

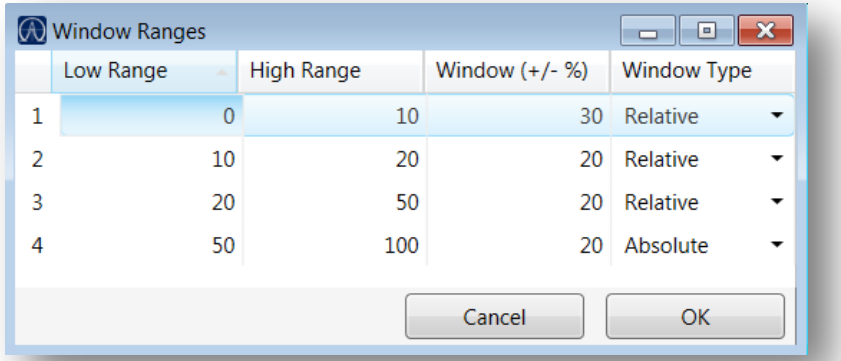
*Acquired on the Q Exactive GC system – the Exactive GC system provides equivalent performance.

Full-featured Screening and Quantitation with Thermo Scientific TraceFinder Software

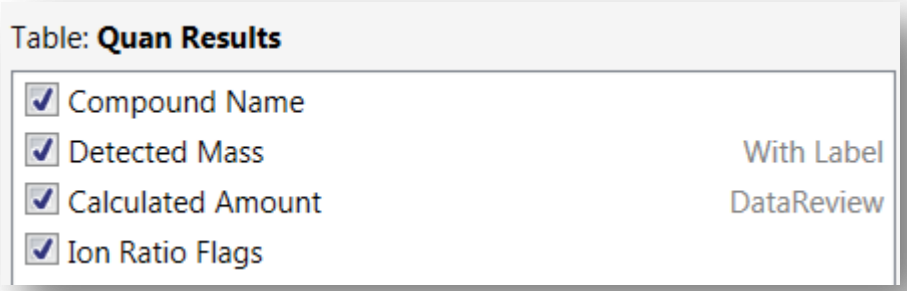


High Throughput Target Quantitation

High Resolution Enabled



Flexible Ion Ratio Confirmation



Custom Reporting

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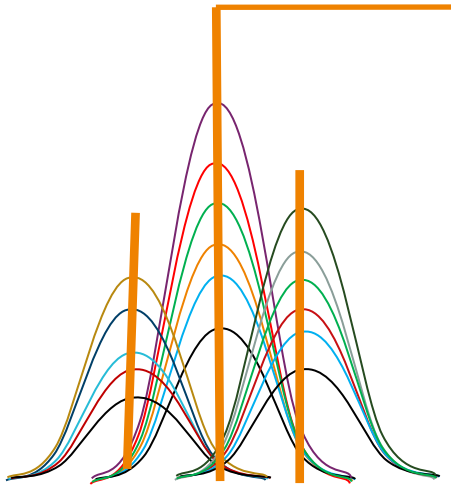
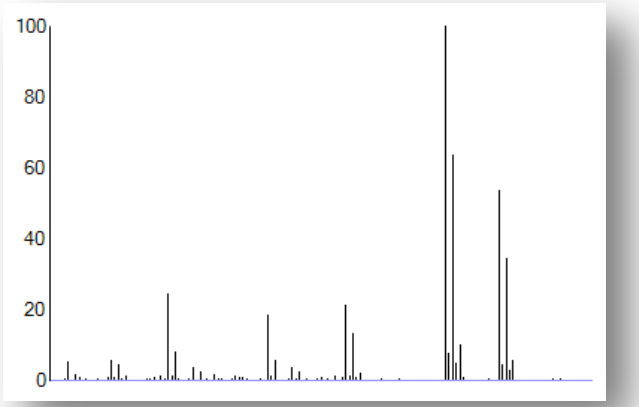
Peak Detection and Candidate Matching

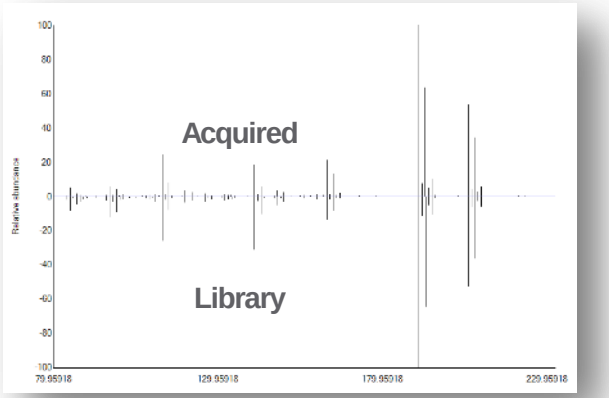


Deconvolve TIC

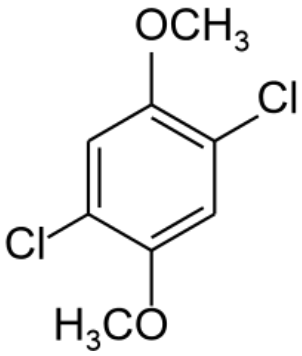


Create “clean” spectrum

Library search



Candidate Compounds



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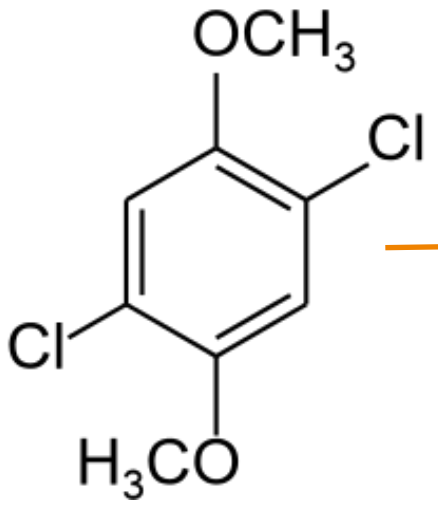
High Resolution Filtering

Candidate Compounds



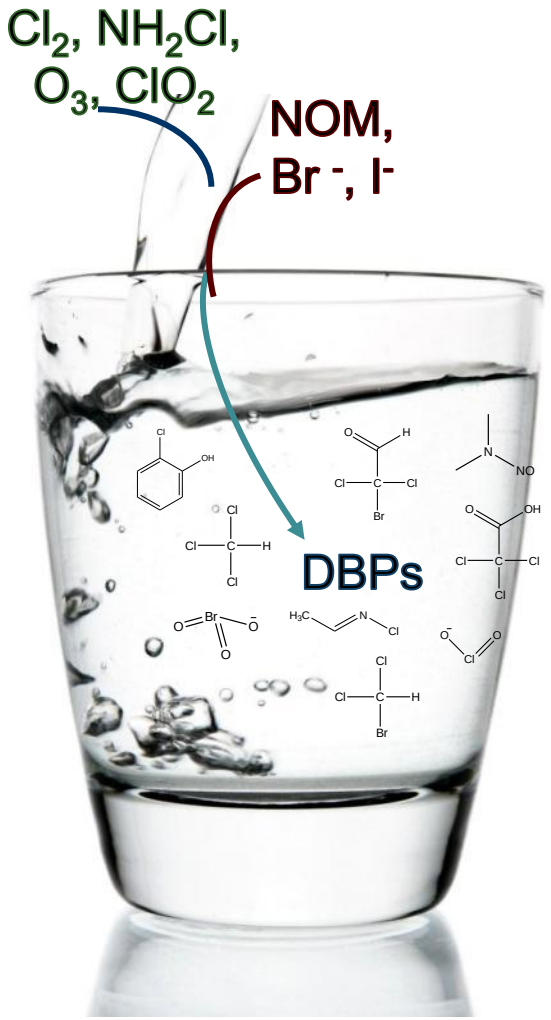
$C_8H_8Cl_2O_2$

Subset formulae

Acq m/z	Fragment ID	Theo m/z	Mass Error (ppm)
147.9477	$C_5Cl_2H_2O$	147.9477	0.20277
148.9369	$C_5Cl[37]ClHO$	148.9369	0.2679
149.9448	$C_5Cl[37]ClH_2O$	149.9448	0.06602
151.9419	$C_5[37]Cl_2\ H_2O$	151.9418	0.72528
154.9895	$C_7ClH_4O_2$	154.9894	0.38712
155.9974	$C_7ClH_5O_2$	155.9973	0.89745
157.9943	$C_7[37]ClH_5O_2$	157.9943	0.25381
159.9479	$C_6Cl_2H_2O$	159.9477	0.87529
161.9446	$C_6\ Cl[37]ClH_2O$	161.9448	0.80213
162.9711	$C6Cl_2H_5O$	162.9712	0.36816
163.9745	$C_5[13]CCl_2H_5O$	163.9745	0.3342
164.9682	$C_6Cl[37]ClH_5O$	164.9682	0.24186
165.9716	$C_5CCl[37]ClH_5O$	165.9716	0.02832

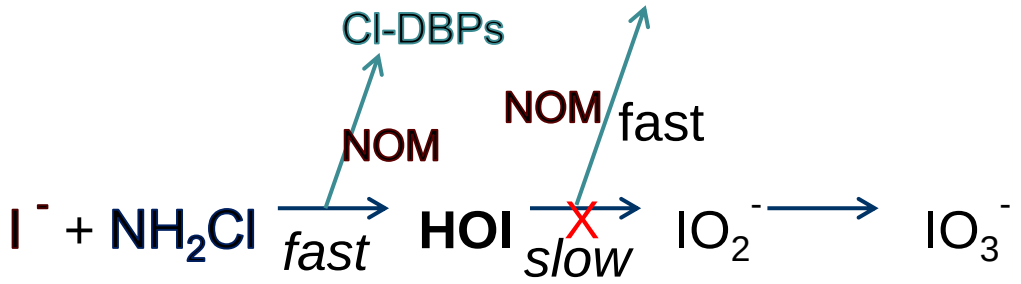
$$\text{HRF Score} = \frac{\sum (m/z * \text{Intensity})_{\text{explained}}}{\sum (m/z * \text{Intensity})_{\text{observed}}} \times 100\%$$

Introduction: Disinfection By-Products (DBP)



- > 600 DBPs identified *(Richardson, 2002)*
- Risk of health effects: bladder/colon cancer, reproductive and developmental effects
- 50% of the total halogenated material formed in chlorinated water is still unknown

- **Emerging DBPs** → **Iodo-DBPs**

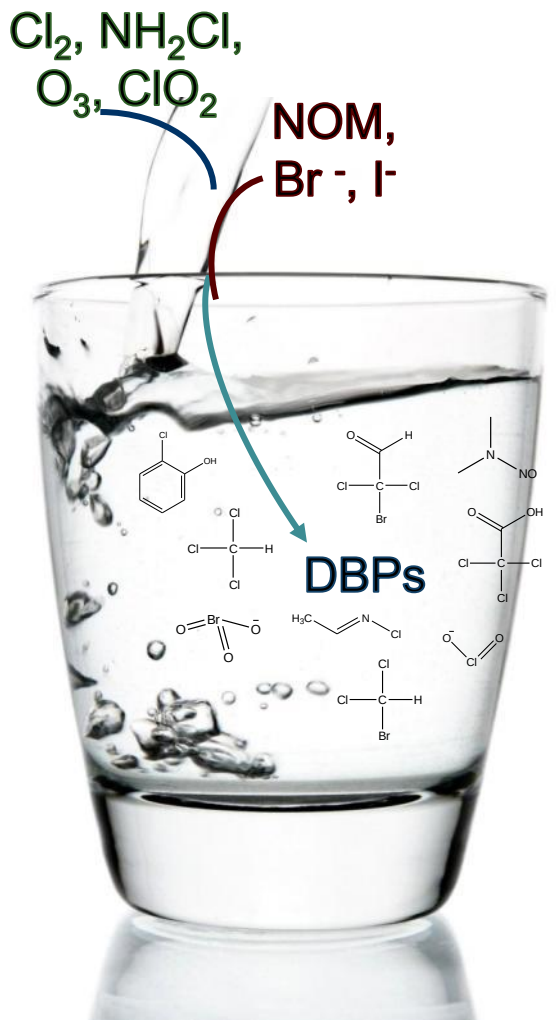


- Toxicity: iodo- > bromo- > chloro- DBPs

Sample Preparation

- Lab-scale experiment using two sample types:
  - Certified reference material
  - Llobregat River (LLOB) water

- Both sample types were subjected to **chlorination** and **chloramination** (NH_2Cl) reactions



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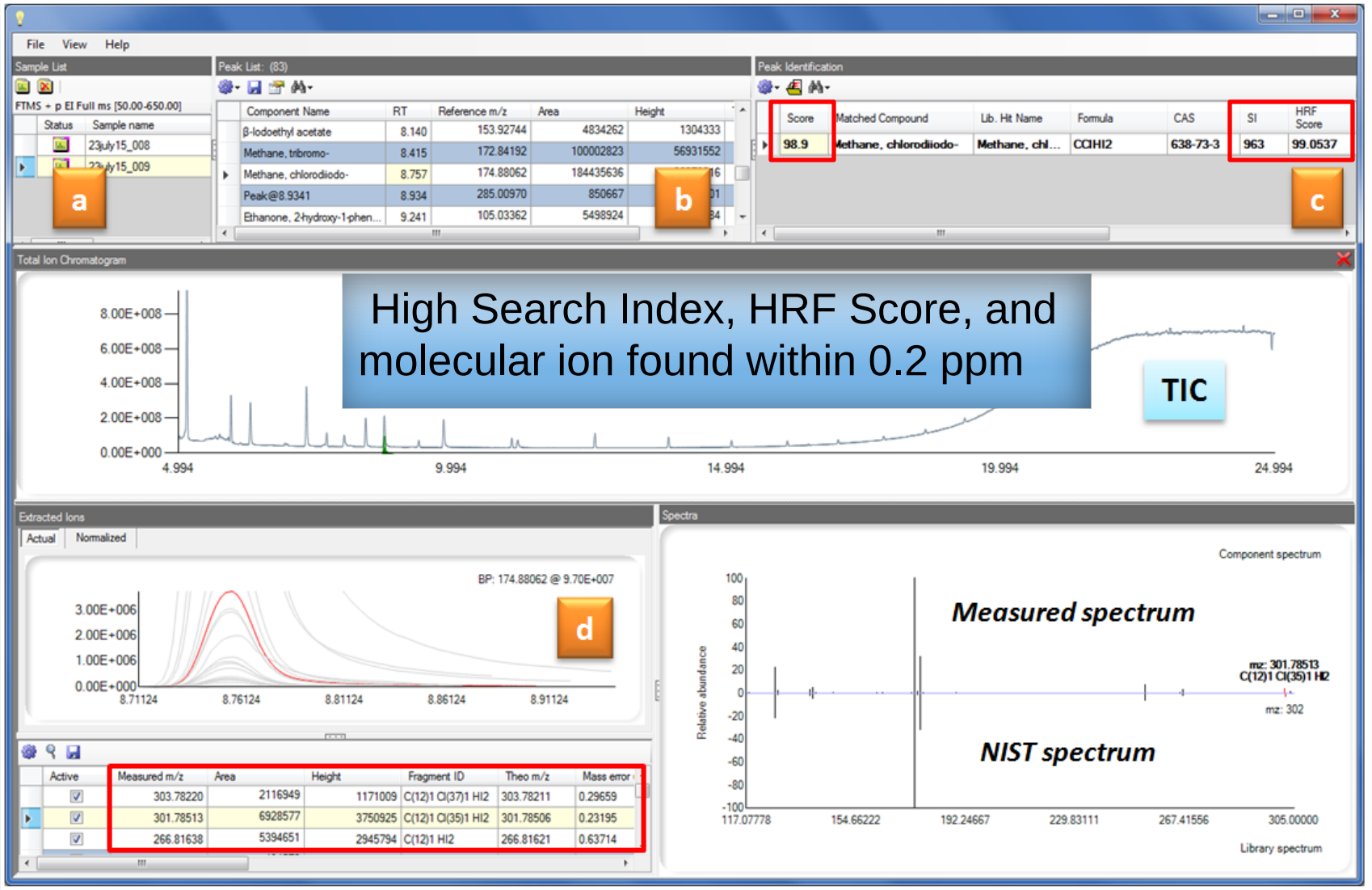
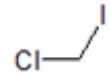
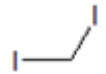
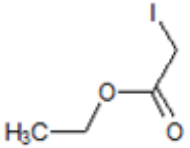
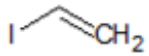
Thermo Scientific TraceFinder Software: Automatic Peak Detection and Identification



RT (min)	Identity	Elemental Composition	Chemical Structure
3.71	Iodomethane	CH_3I	
5.36	Chloroiodomethane	CH_2ClI	
5.76	Unknown		
7.36	Diiodomethane	CH_2I_2	
8.03	Ethyl iodoacetate	$C_4H_7IO_2$	
8.14	Iodoethene	C_2H_3I	
8.77	Chlorodiiodomethane	$CHClI_2$	
9.85	Bromodiiodomethane	$CHBrI_2$	

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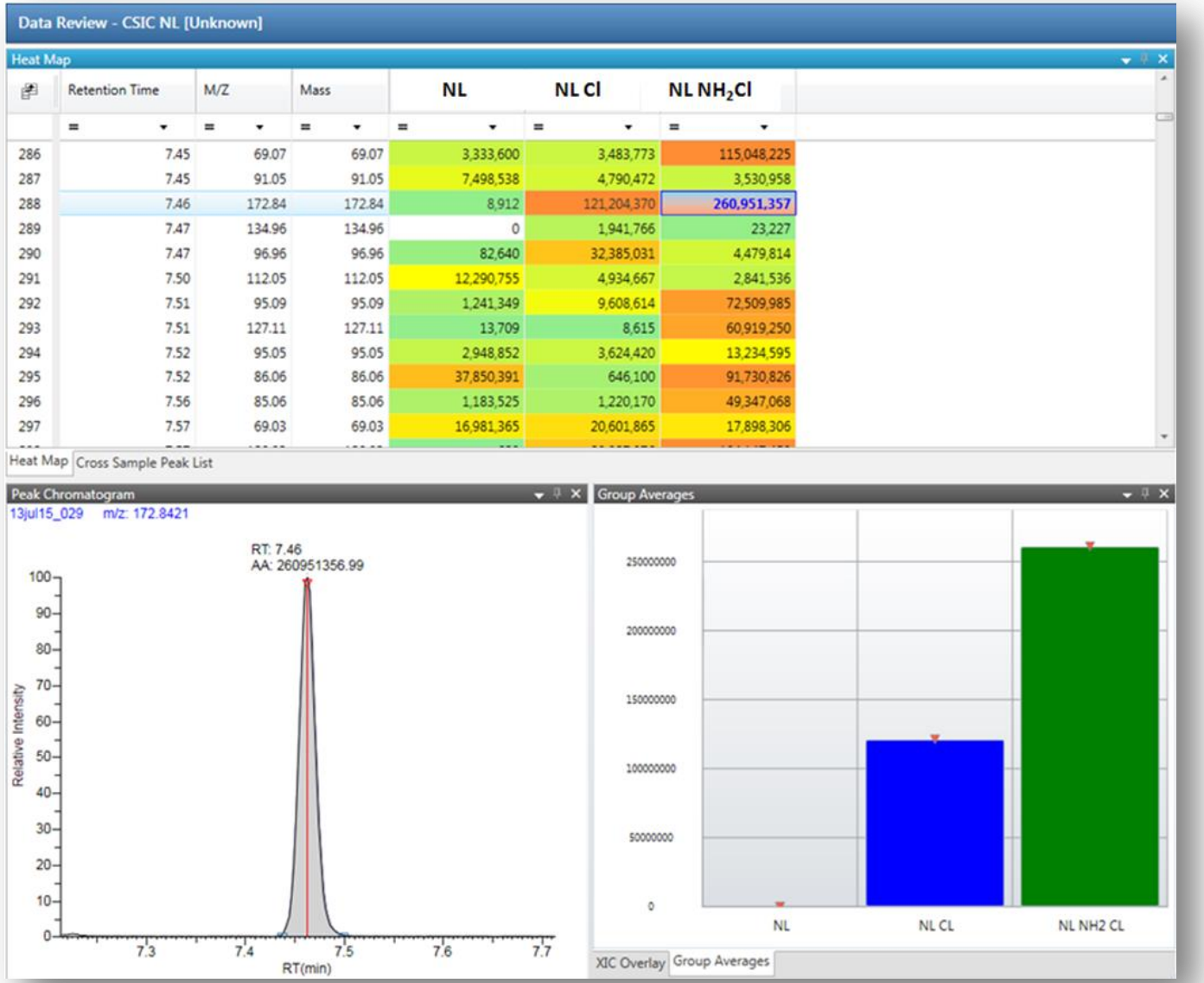
Thermo Scientific TraceFinder Software Cross Sample Peak List



Cross Sample Peak Table with Heat Map

Cross Sample Compound Chart

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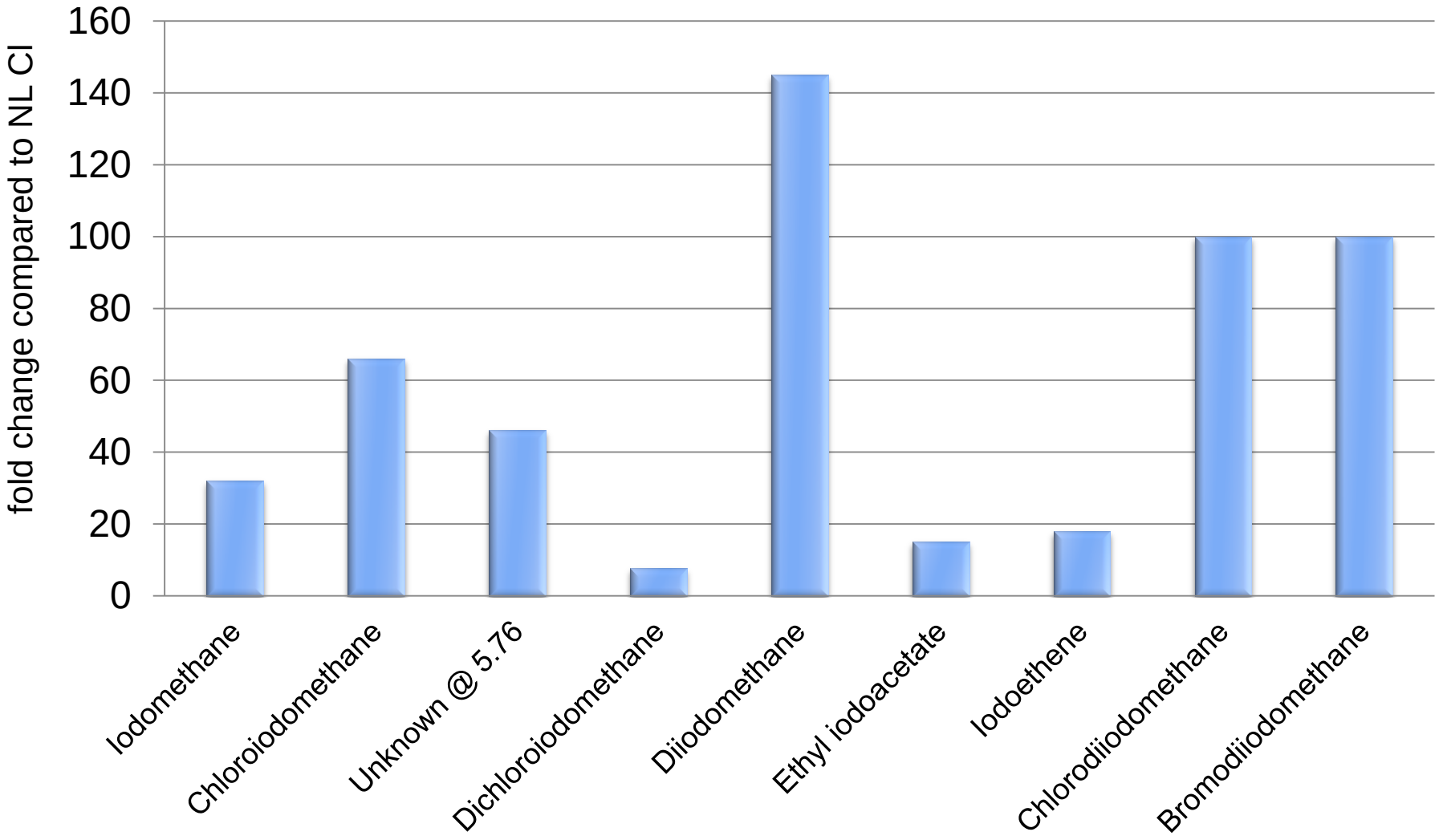
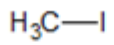
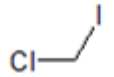
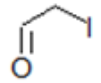
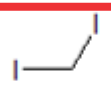
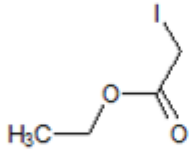
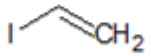
Fold Change NL NH_2Cl vs. NL Cl

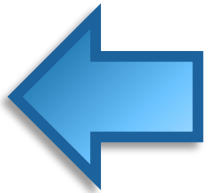


DBP Detected and Confirmed in the Samples Analyzed

RT (min)	Identity	Elemental Composition	Chemical Structure	Theoretical m/z (EI)	Measured m/z (EI)	Δ(ppm)	Theoretical m/z $[M+H]^+$	Measured m/z $[M+H]^+$	Δ(ppm)
3.71	Iodomethane	CH_3I		141.92739	141.92745	0.4	142.93522	142.93522	0.0
5.36	Chloroiodomethane	CH_2ClI		175.88842	175.88839	0.2	176.89625	176.89620	0.3
5.76	Iodoacetaldehyde	C_2H_3IO		169.92231	169.92234	0.2	170.93013	170.93014	0.06
7.36	Diiodomethane	CH_2I_2		267.82404	267.82424	0.8	268.83186	268.83192	0.2
8.03	Ethyl iodoacetate	$C_4H_7IO_2$		213.94852	213.94840	0.6	214.95635	214.95627	0.4
8.14	Iodoethene	C_2H_3I		153.92739	153.92742	0.2	154.93522	154.93519	0.2
8.77	Chlorodiiodomethane	$CHClI_2$		301.78507	301.78509	0.1	301.78507	301.78511	0.1
9.85	Bromodiiodomethane	$CHBrI_2$		345.73455	345.73459	0.1	345.73455	345.73446	0.3

Presentation Overview

- Orbitrap GC/MS Systems Overview
- Orbitrap GC/MS System for Targeted Screening and Confirmation
- Orbitrap GC/MS System for Known Unknowns Identification
- Orbitrap GC/MS System for True Unknowns Identification



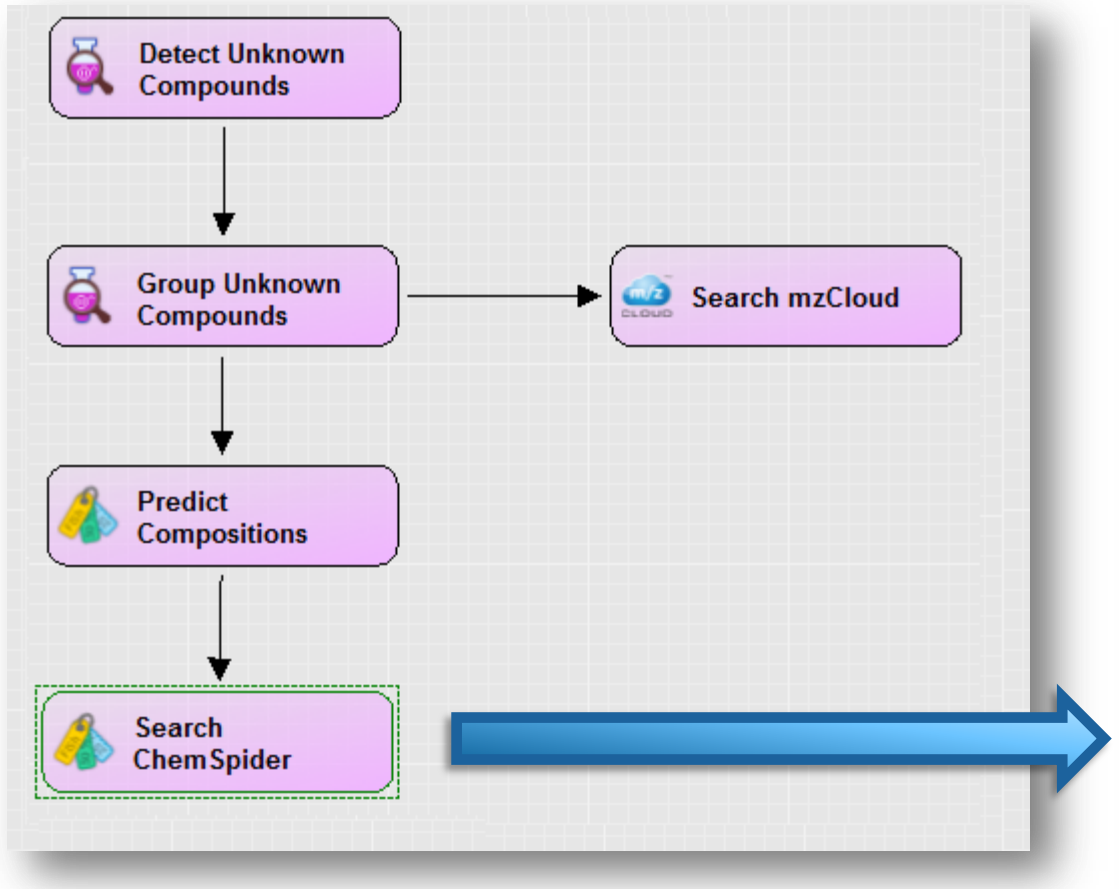
Unknown Unknown's Toolkit

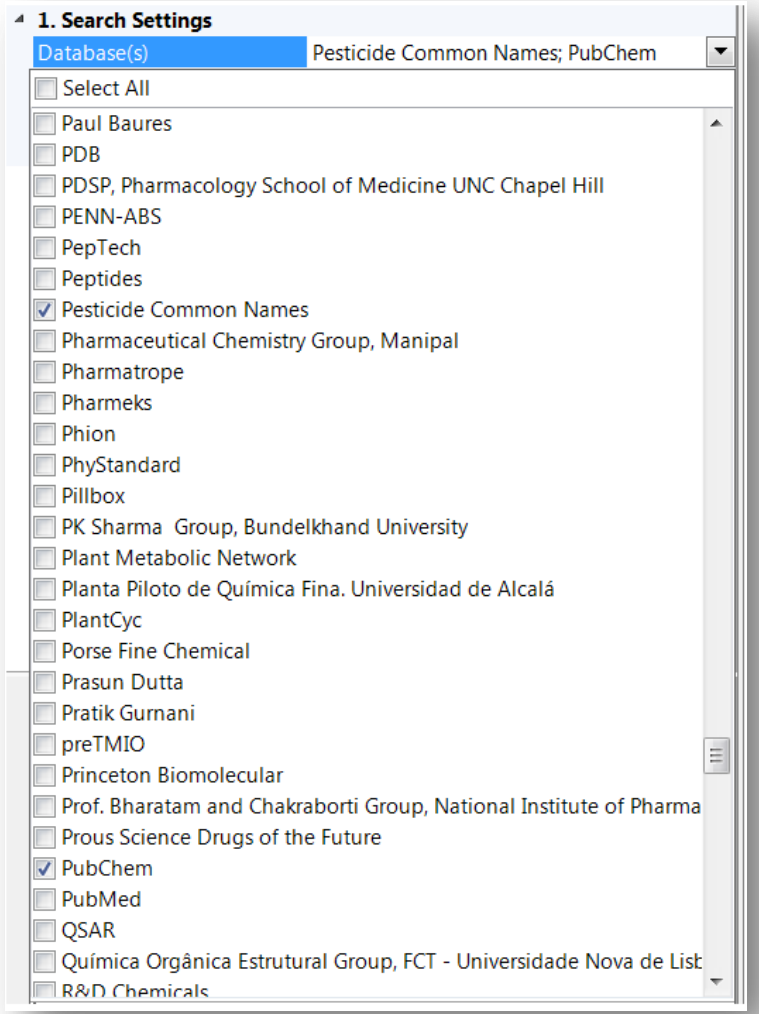
Analytical Tool	Analytical Utility
Chemical Ionization	Determination of Molecular Ion
High Mass Accuracy	Narrow Down Possible Chemical Formula
Isotope Pattern	Confirm Chemical Formula
MS/MS Data	Suggest Structural Identification

Unknown Unknowns Software tools

Compound Discoverer

Mass Frontier





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Chemical ionization for Molecular Ion

Remove entire ion source or change to CI source in under 2 minutes without venting…

Using CI to Confirm Molecular Ion

Proton transfer

$$M + CH_5^+ \rightarrow [M + H]^+ + CH_4$$

$$M + C_2H_5^+ \rightarrow [M + H]^+ + C_2H_4$$

[M+1.00728]⁺

Adduct formation

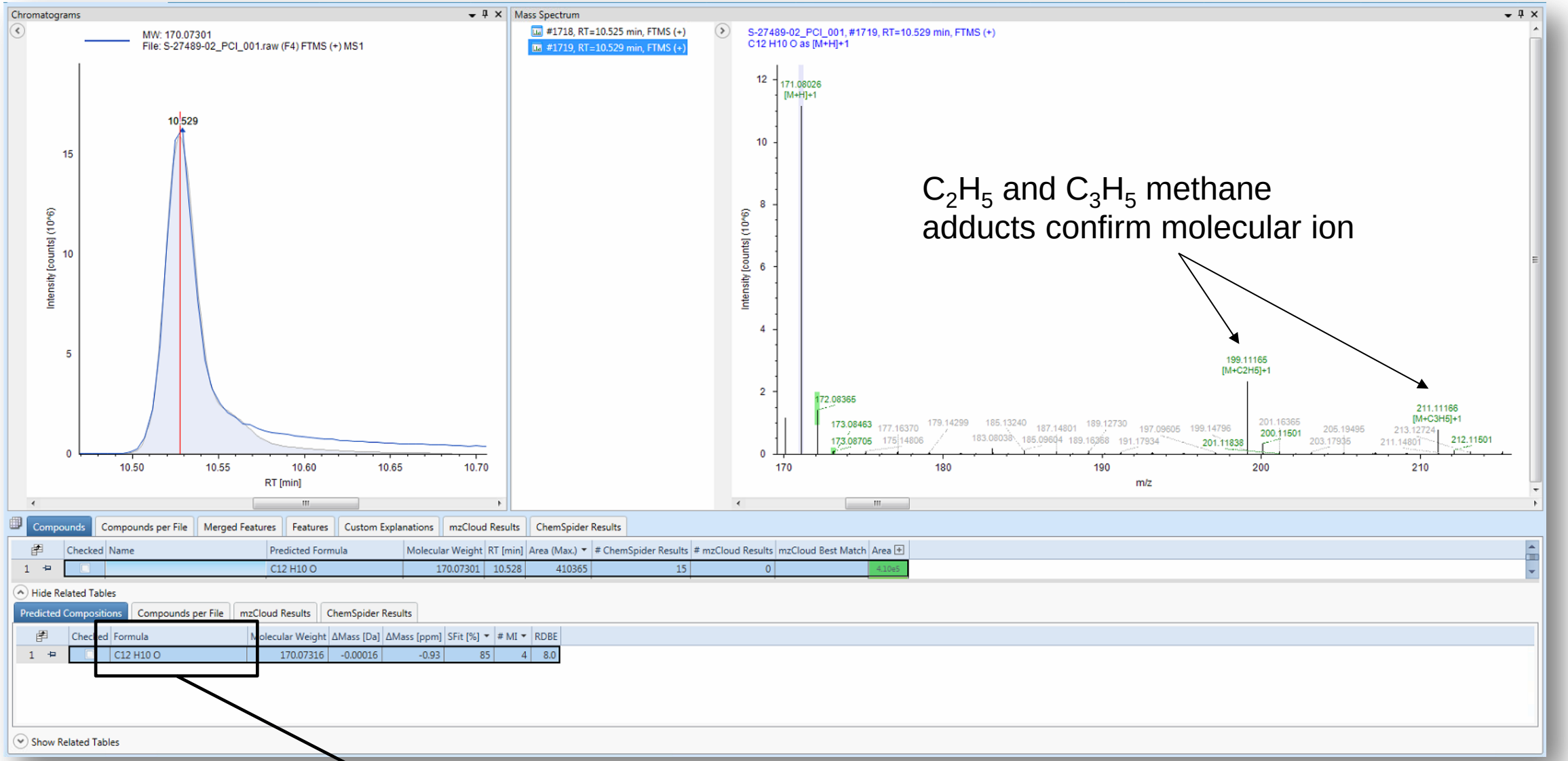
$$M + C_2H_5^+ \rightarrow [M + C_2H_5]^+$$

[M+29.03858]⁺

$$M + C_3H_5^+ \rightarrow [M + C_3H_5]^+$$

[M+41.03858]⁺

Confirmation of Molecular Formula with CI



$C_{12}H_{10}O$ formula unambiguously chosen

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Confirmation of Molecular Formula with CI

0.9 ppm mass error on monoisotope, with high isotopic fit

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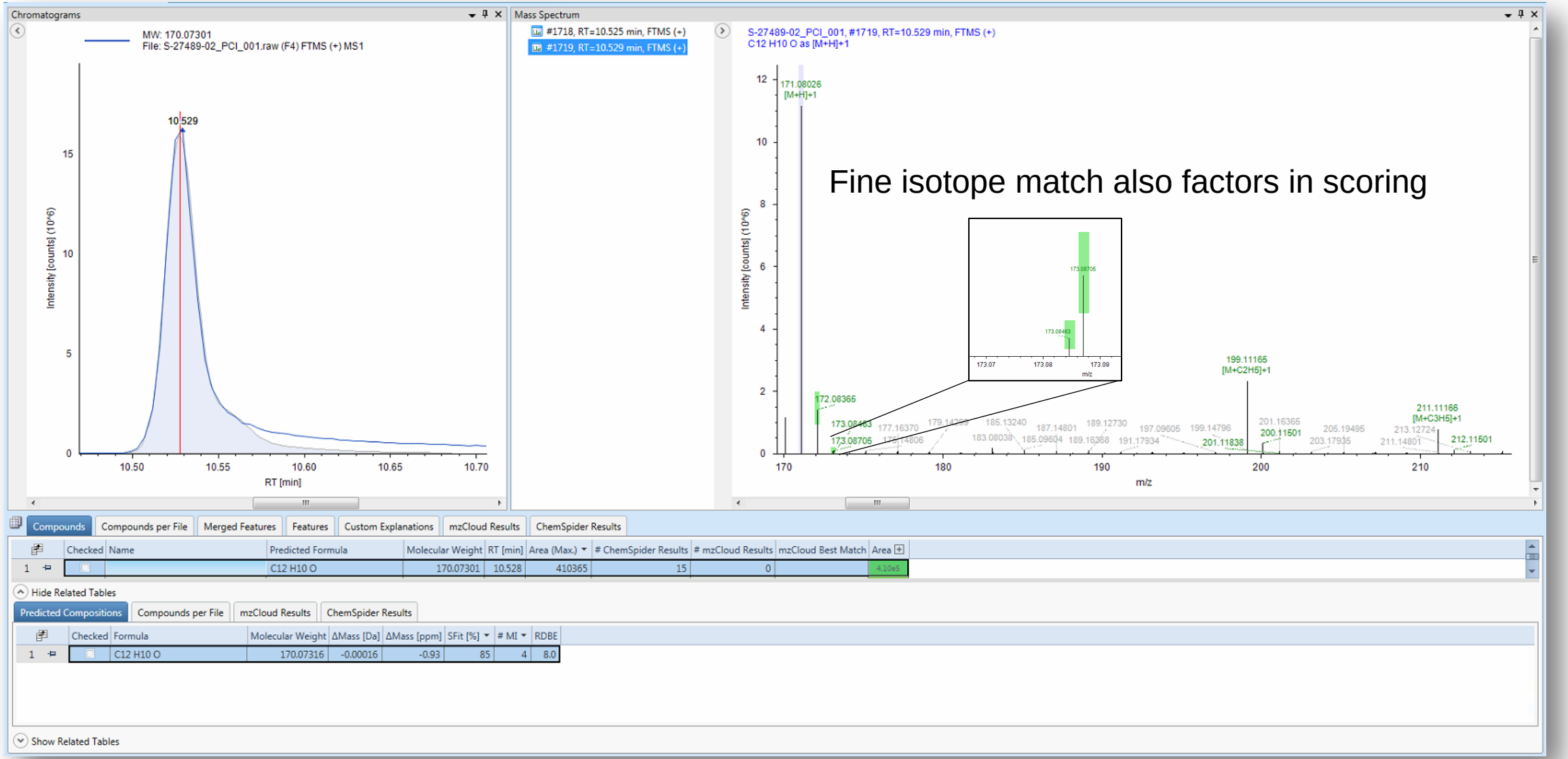
Fine Isotope Match at M+2



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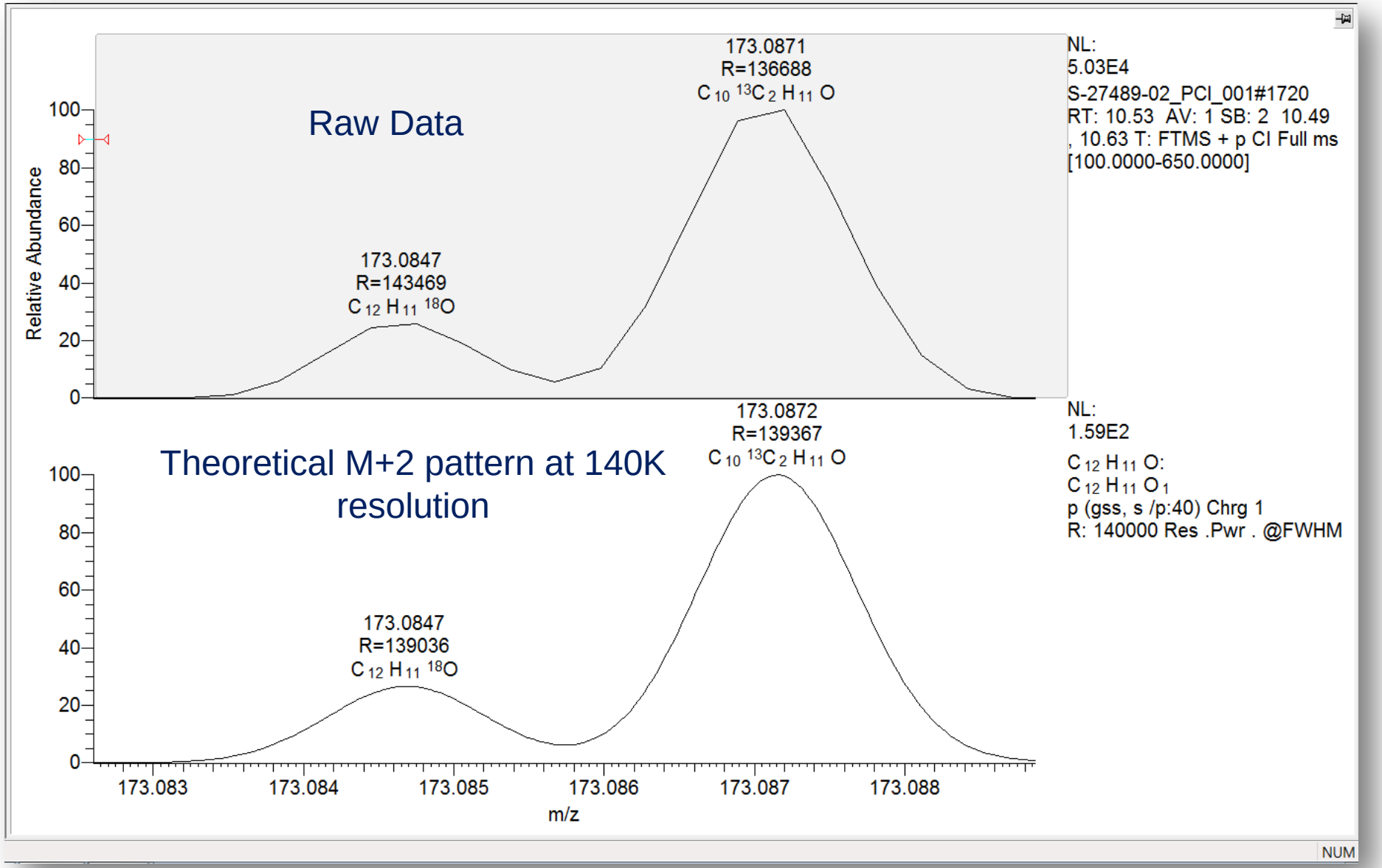
M+2 Isotope Confirms One Oxygen Present



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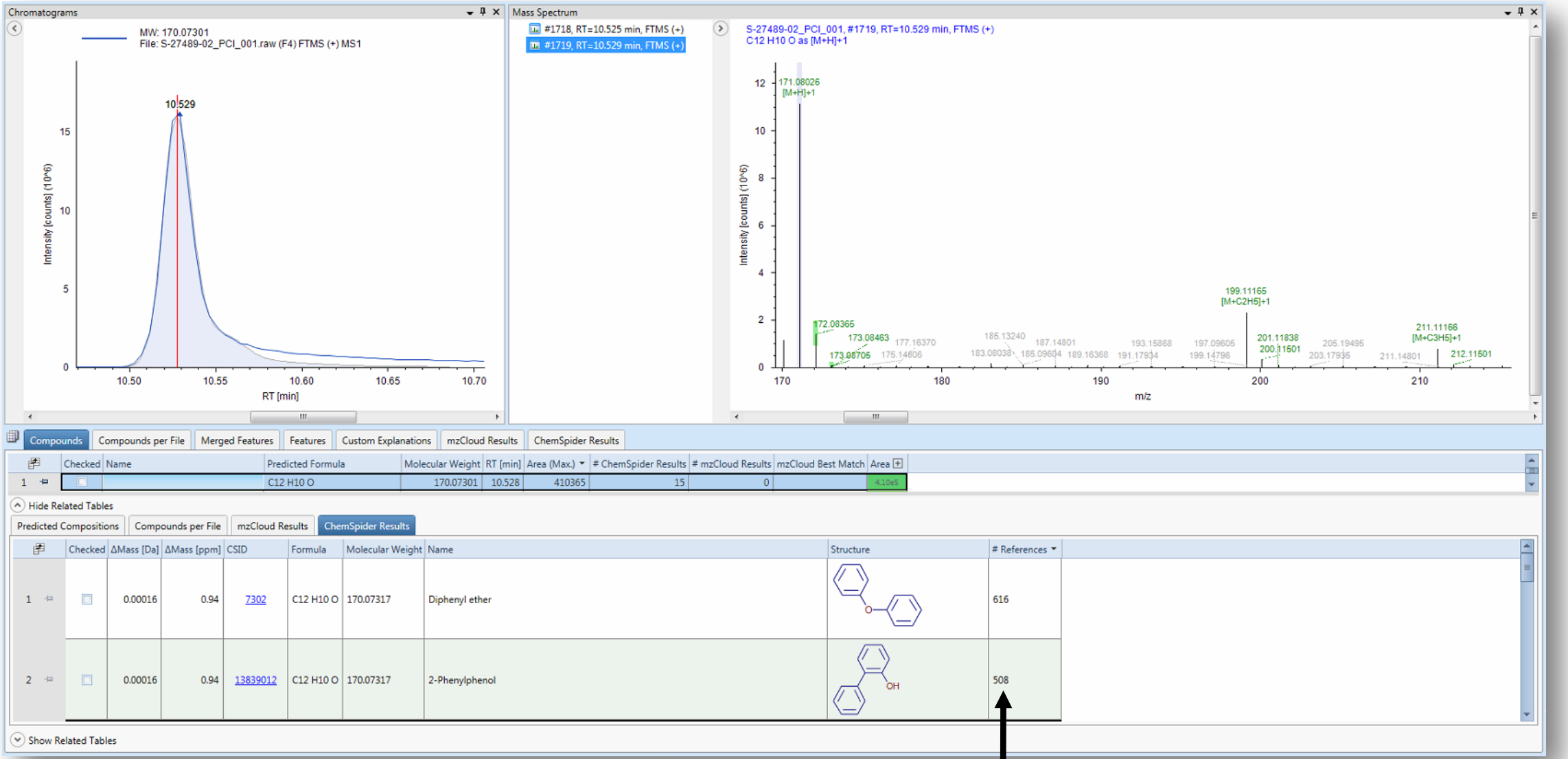
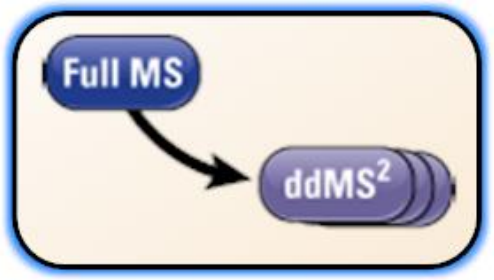
Structure Proposals with Automated Chemspider Searching



O-phenylphenol #2 listed compound based on Chemspider with 508 references

Untargeted CI MS/MS on Molecular Ion



Monitor for $\Delta([M+C_2H_5]^+ - [M+H]^+)$= m/z 28.03130 in fullscan

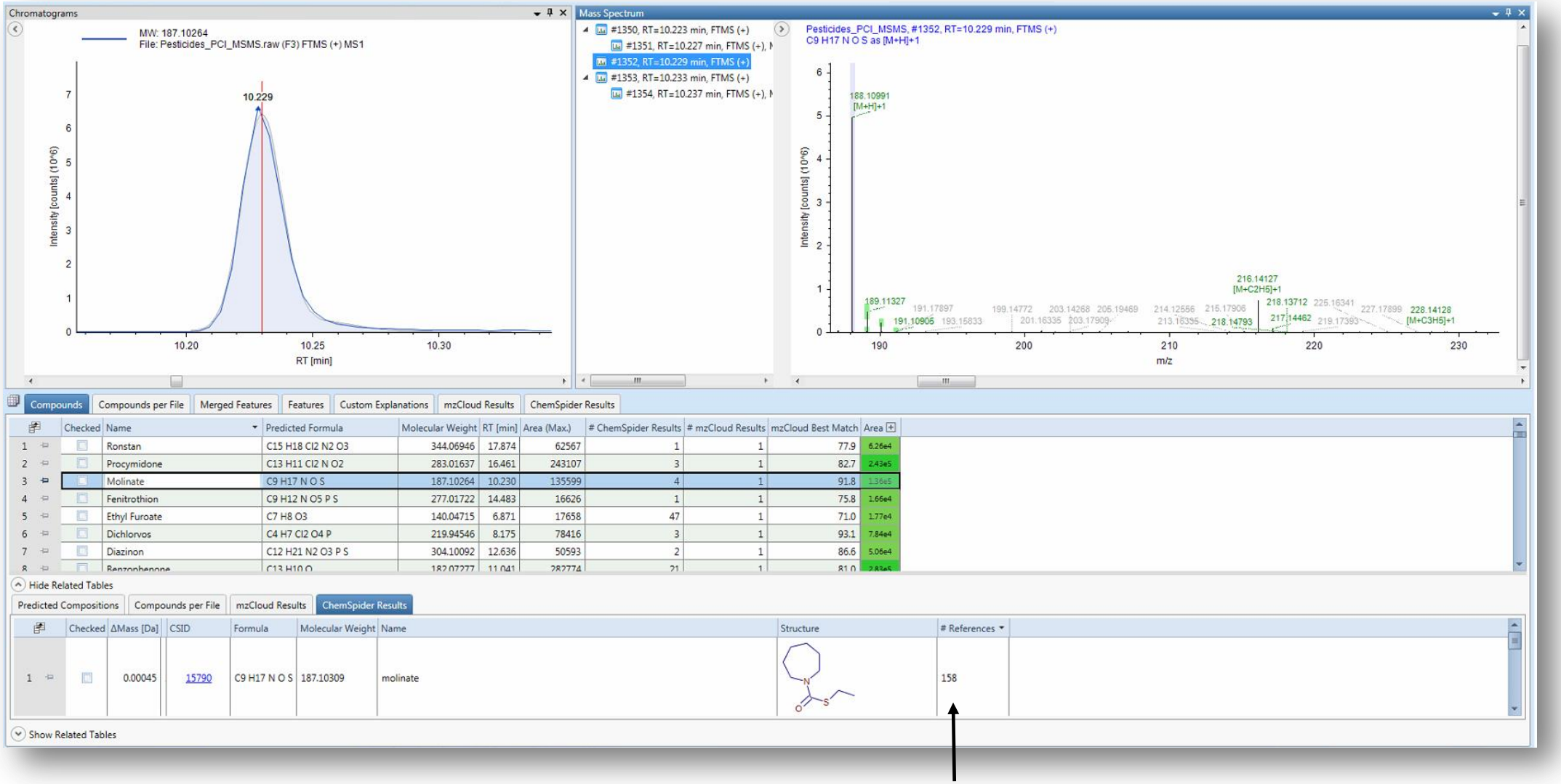
This Δ *m/z* triggers MS/MS event on $[M+H]^+$ ions

Method editor — Mass Tags

File Edit Help Done

	Δ Mass [m/z]	Comment
1	28.03130	C2H5+ - H+
2		

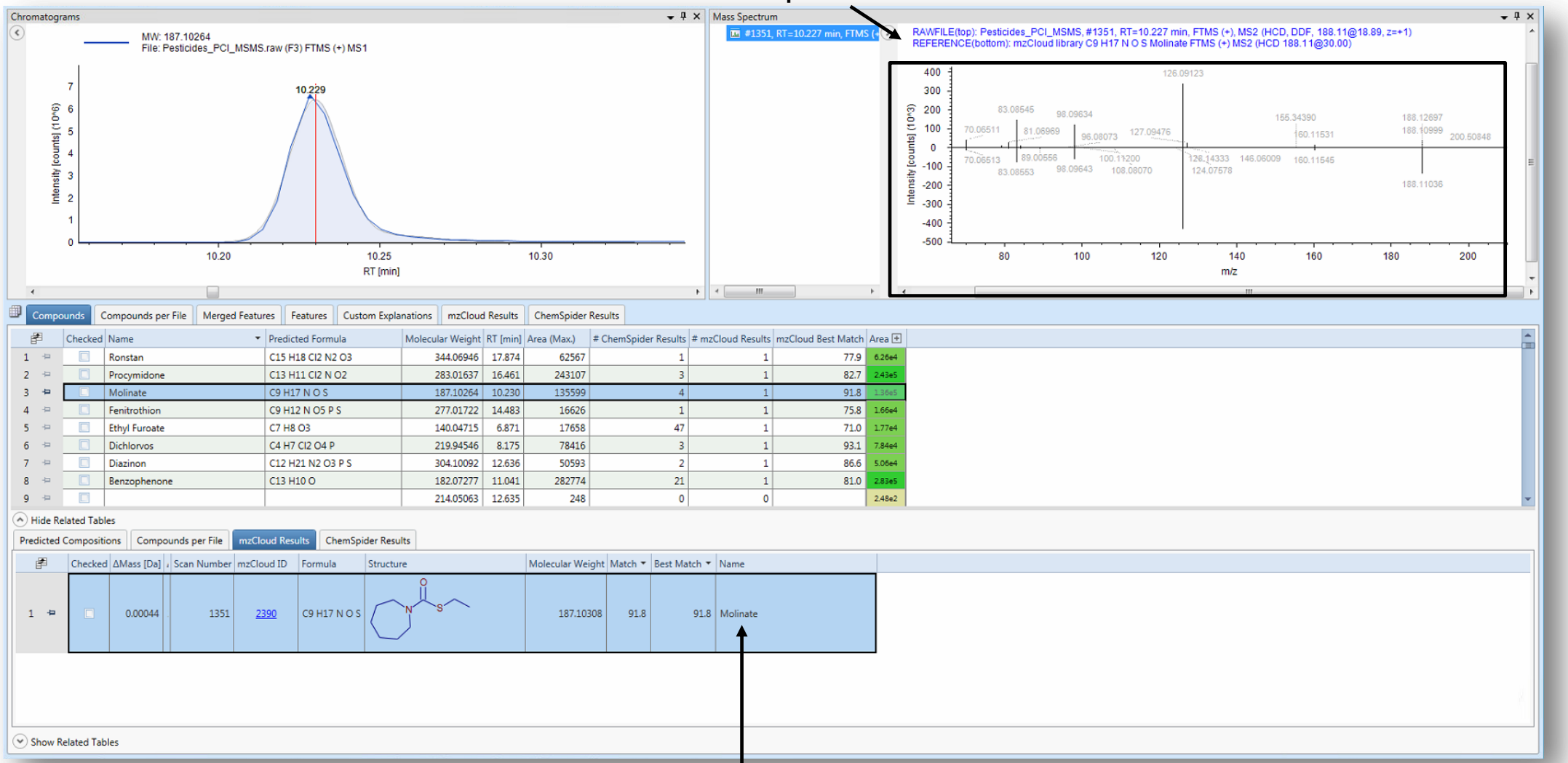
Using MS/MS for Structural Confirmation



Molinate #1 listed compound based on Chemspider with 158 references

Automated mzCloud Search in Compound Discoverer

Molinate MS/MS spectral match



#1 hit with MS/MS mzCloud Search

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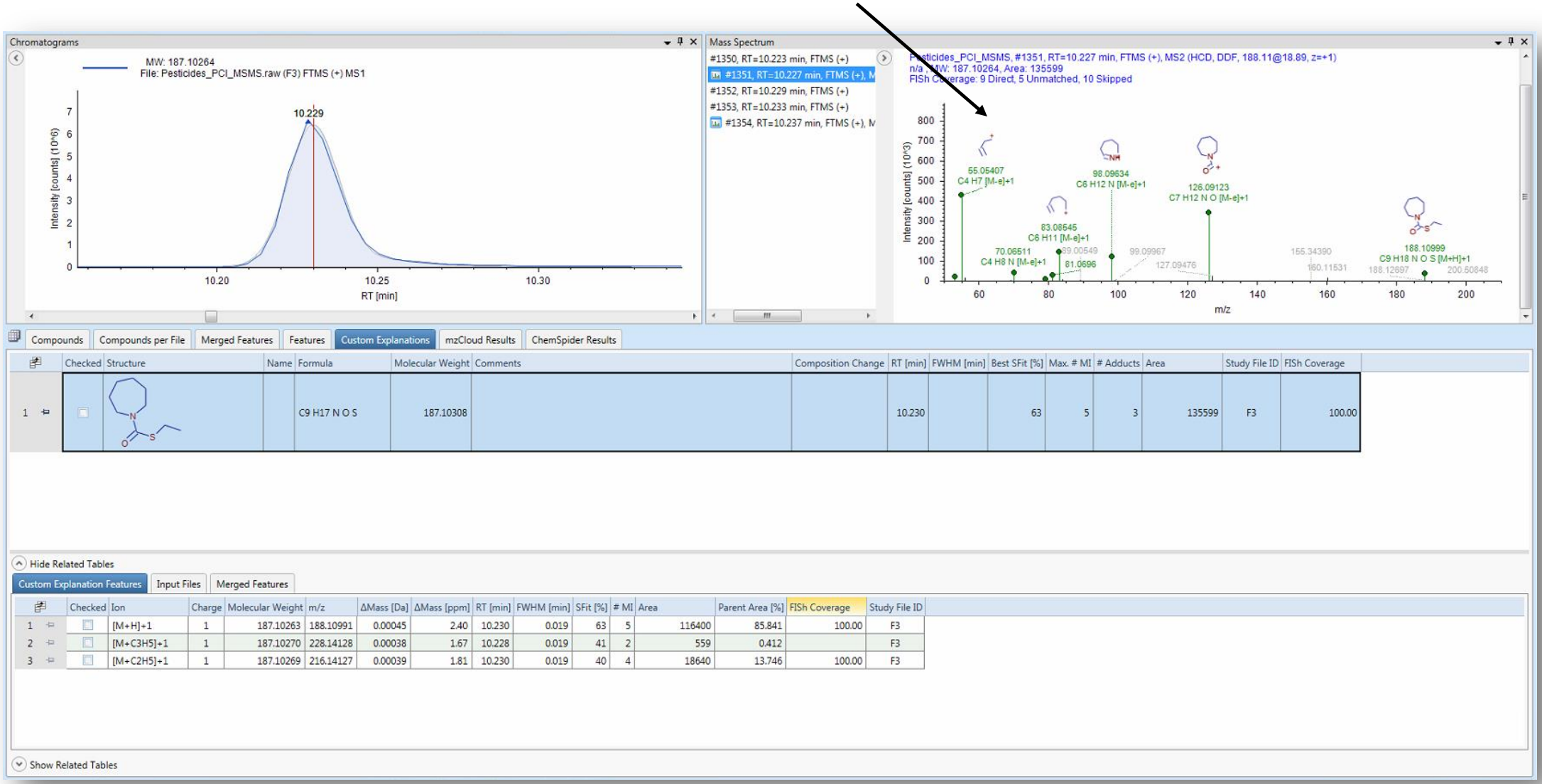
Thermo Scientific Mass Frontier Can Increase Confidence in Structure Proposal

MS/MS fragments rationalized based on fragment library and known reaction mechanisms



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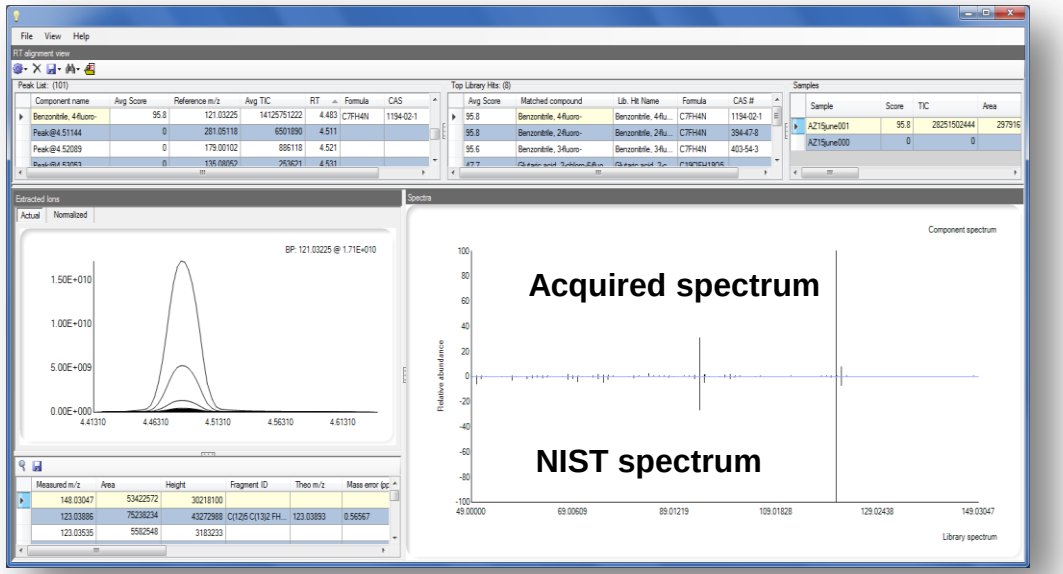
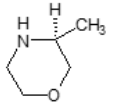
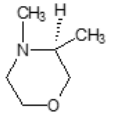
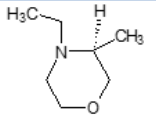
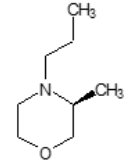
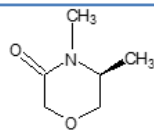
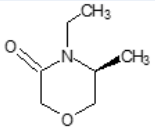
Pharmaceutical Example

API	Phase	Solvent	working concentration
(3S)-3-methylmorpholine	liquid	Methanol	1% v/v
N,N,N'-trimethylethylenediamine	liquid	DMSO	1% v/v
1,2-A imidazo pyridine	liquid	Methanol	1% v/v
4-fluorobenzonitrile	solid	Methanol	100 µg/mL (w/v)
3,5-difluorophenol	solid	Methanol	100 µg/mL (w/v)
2,6 difluorobenzyl bromide	solid	Methanol	100 µg/mL (w/v)

Drug precursors tested

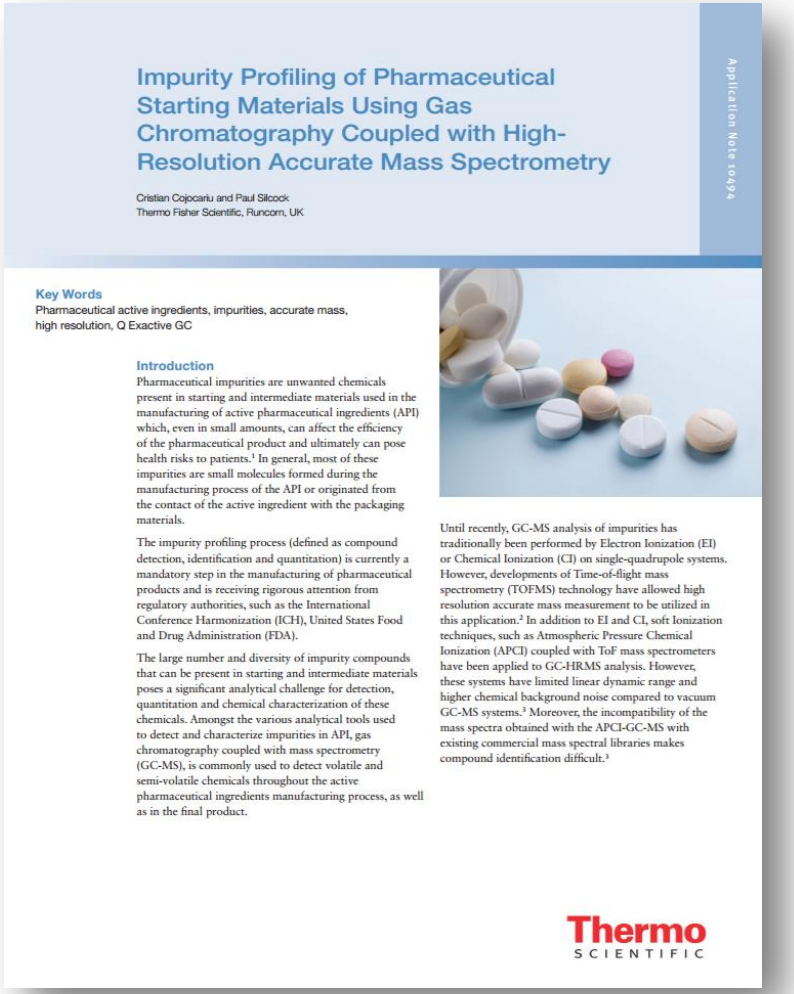


Impurities in (3S)-3-methylmorpholine ID'ed by deconvolution/library search

Retention Time (min)	Compound ID	Exact mass (EI)	Measured mass (EI)	Δppm	Exact mass (PCI)	Measured mass (PCI)	Δppm
3.55	 (3S)-3-methylmorpholine Molecular Formula = $C_5H_{11}NO$	101.08352	101.08358	0.6	102.09134	102.09136	0.2
3.75	 Molecular Formula = $C_6H_{13}NO$	115.09917	115.09925	0.7	116.10699	116.10703	0.4
4.32	 Molecular Formula = $C_7H_{15}NO$	129.11482	129.11486	0.4	130.12264	130.12268	0.3
5.06	 Molecular Formula = $C_8H_{17}NO$	155.13047	155.13048	0.1	156.13829	156.13825	0.3
5.87	 Molecular Formula = $C_6H_{11}NO_2$	129.07843	129.07843	0.0	130.08626	130.08634	0.6
6.23	 Molecular Formula = $C_7H_{13}NO_2$	143.09408	143.09414	0.4	144.10193	144.10193	0.2

Impurities confirmed by accurate mass CI molecular Ions

Pharmaceutical Application Notes



Application Note 10494

Impurity Profiling of Pharmaceutical Starting Materials Using Gas Chromatography Coupled with High-Resolution Accurate Mass Spectrometry

Cristian Cojocariu and Paul Silcock
Thermo Fisher Scientific, Runcorn, UK

Key Words
Pharmaceutical active ingredients, impurities, accurate mass, high resolution, Q Exactive GC

Introduction

Pharmaceutical impurities are unwanted chemicals present in starting and intermediate materials used in the manufacturing of active pharmaceutical ingredients (API) which, even in small amounts, can affect the efficiency of the pharmaceutical product and ultimately can pose health risks to patients.[1] In general, most of these impurities are small molecules formed during the manufacturing process of the API or originated from the contact of the active ingredient with the packaging materials.

The impurity profiling process (defined as compound detection, identification and quantitation) is currently a mandatory step in the manufacturing of pharmaceutical products and is receiving rigorous attention from regulatory authorities, such as the International Conference Harmonization (ICH), United States Food and Drug Administration (FDA).

The large number and diversity of impurity compounds that can be present in starting and intermediate materials poses a significant analytical challenge for detection, quantitation and chemical characterization of these chemicals. Amongst the various analytical tools used to detect and characterize impurities in API, gas chromatography coupled with mass spectrometry (GC-MS), is commonly used to detect volatile and semi-volatile chemicals throughout the active pharmaceutical ingredients manufacturing process, as well as in the final product.

Until recently, GC-MS analysis of impurities has traditionally been performed by Electron Ionization (EI) or Chemical Ionization (CI) on single-quadrupole systems. However, developments of Time-of-flight mass spectrometry (TOFMS) technology have allowed high resolution accurate mass measurement to be utilized in this application.[2] In addition to EI and CI, soft Ionization techniques, such as Atmospheric Pressure Chemical Ionization (APCI) coupled with ToF mass spectrometers have been applied to GC-HRMS analysis. However, these systems have limited linear dynamic range and higher chemical background noise compared to vacuum GC-MS systems.[3] Moreover, the incompatibility of the mass spectra obtained with the APCI-GC-MS with existing commercial mass spectral libraries makes compound identification difficult.[3]

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Application Note 10888

Confident Identification of Leachable Impurities from Pharmaceutical Container Closure Materials using Orbitrap-Mass-Spectrometer-Based GC-MS

Dominic Roberts,[1] Andrew Fellden,[2] Richard Barlow,[2] Kyle D'Silva,[1] and Paul Silcock[1]
[1]Thermo Fisher Scientific, Runcorn, UK
[2]Smithers Rapra, Shawbury, UK

Key Words
Extractables and Leachables, Q Exactive GC, Orbitrap mass spectrometry, differential analysis, unknown identification, container closure system, pharmaceutical.

Introduction

The investigation of potentially toxic chemical impurities leaching from a wide variety of plastics, polymers, and packaging products destined for pharmaceutical products has received a great deal of attention and remains a challenging analysis for chemists. Often termed extractables and leachables (E/L) studies, their aim is to identify, quantify, and ultimately minimize any impurities that can migrate from packaging into a final product or drug. "Extractables" are those chemicals that can extract from components of a container closure system into solvents under accelerated laboratory conditions, such as elevated temperature and aggressive solvent, with the aim to extract the maximum amount without deforming or degrading the material. "Leachables" are defined as chemicals that can migrate from the packaging into a drug product over the course of its shelf life.

The potential, versus the actual, impact of the product on its user:

- Extractable = possible impact.
- Leachable = actual impact

The object on which the testing is performed:

- Extractable = the container material
- Leachable = the final product

Extractable testing is primarily used to mitigate risk by identifying potentially toxic leachables very quickly and allowing the selection of a different packaging material. In general, for most dosage forms, any material that is in direct contact with an API (Active Pharmaceutical ingredient) should be considered for extractable and leachable analysis and in some cases, secondary or tertiary packaging, e.g., labels should also be considered. Leachables can come from the container closure system and any components used in the manufacturing process. They may also be the product of reactions between the drug and packaging material and may continue to form during storage.[1] A controlled extractables experiment is accomplished by exposing the material to extremes of solvents, pH, and temperatures to test the product under worst case scenarios. The confident detection and identification of compounds present is a very demanding task and it is essential that analysts use the available technology to accurately and comprehensively characterize products.

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www.thermofisher.com/OrbitrapGCMS

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Toxicology Application Note

High Confidence, Non-Targeted Screening for Drugs of Abuse in Urine

Dominic Roberts,[1] Andrea Steuer,[2] Michael Poetzsch,[2] Thomas Kraemer[2] and Paul Silcock[1]
[1]Thermo Fisher Scientific, Runcorn, UK
[2]Department of Forensic Pharmacology and Toxicology, Zurich Institute of Forensic Medicine, University of Zurich, Zurich, Switzerland

Application Note 10495

Key Words
Drugs of abuse, GC-MS, urine, screening, high resolution, Q Exactive GC, Orbitrap mass spectrometry, accurate mass

Introduction

Drug abuse is a condition that is characterized by a destructive pattern of using a substance, usually through self-administration, which leads to significant problems or distress. Almost any substance, that on consumption can cause a euphoric feeling, can be abused. Examples of drugs of abuse (DoA) include depressants (opioids, barbiturates, benzodiazepines, alcohol), stimulants (amphetamines, cocaine), hallucinogens (LSD, mescaline, phencyclidine), and cannabinoids (marijuana). The reasons for DoA testing are diverse. For example, DoA screening can be performed for criminal and other forensic investigations, high-risk employment functions, clinical toxicology, or rehabilitation programs. For such tests, urine is generally accepted as the sample of choice as it is non-invasive, reliable, economical, widely utilized, and strictly regulated.[1] One limitation of testing in urine is that it will usually only provide information about current or recent substance use as a specimen is likely to be negative after a period of 2-3 days after drug administration. There are some compounds and their metabolites that remain detectable for longer periods, e.g., THC-COOH and some benzo diazepines.[1] To prolong the detection period as long as possible, sensitive analytical techniques are important.

Laboratory testing of urine for DoA is a challenging application. This is primarily due to the high number of compounds and metabolites that need to be screened for in a sample that has a variable chemical background. Furthermore, depending on exposure, the levels of such compounds can be present at both trace and very high concentrations. Gas chromatography coupled with mass spectrometry (GC-MS) is well-suited for DoA screening and confirmation as it provides excellent chromatographic resolution, peak capacity and extensive spectral libraries to aid in identification.[2,3] However, higher sensitivity and specificity would increase the confidence in positive results and improve the robustness of the system, especially in a high throughput routine laboratory environment. One further challenge is that the evaluation of informa-

tion rich electron impact spectra generated using GC-MS is difficult if performed manually, especially when analyte peaks are often overlapped by matrix and background ions.

In this application note, the performance of the Thermo Scientific™ Q Exactive™ GC Orbitrap™ GC-MS/MS system was evaluated for the screening of DoA in urine. This work aims to demonstrate the application of a non-targeted workflow using the Q Exactive GC Orbitrap GC-MS/MS system to detect and identify DoA. This work focuses on analyzing real case urine samples using a full-scan, non-targeted acquisition and high-mass resolving power to obtain accurate mass measurements in support of spectral library matching. The evaluation of scan speed in combination with high in-scan dynamic range and high sensitivity will be made for the detection of low and high intensity components. In addition, unique software algorithms for automated deconvolution and identification were also assessed for routine screening.

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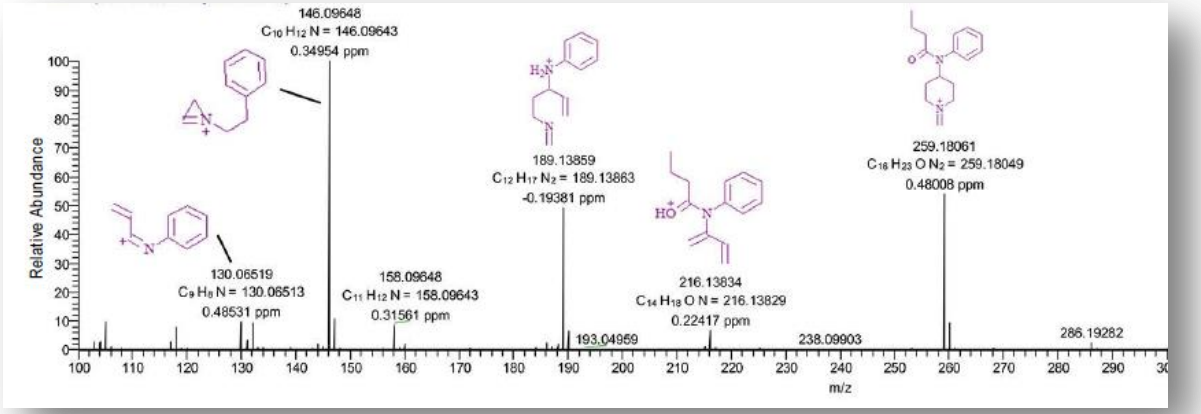

Sample	Compound	Base Peak (*m/z*)	HRF (%)	Base Peak Mass Accuracy (ppm)	Molecular Ion Mass Accuracy (ppm)
Urine A	Cocaine	82.06512	100.0	1.5	—
	Methadone	72.08077	99.7	0.5	—
	Morphine	268.1332	99.9	0.8	0.2
	Paracetamol	109.05221	99.0	0.6	0
Urine B	Tramadol	114.09134	99.7	0.8	—
Urine C	Mirtazapine	195.09167	98.2	0.2	—
	Lamotrigine	184.97935	100.0	0.4	0.3
Urine D	Morphine	268.1332	96.7	0.8	0.2
	Paracetamol	109.05221	98.9	0.9	0.5
Urine E	Myristicin	180.07809	98.9	0.6	—
Urine F	Butyrfentanyl	146.09646	—	0.4	0.0

www.thermofisher.com/OrbitrapGCMS

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Presentation Summary

- Industry-best resolution, mass accuracy, dynamic range, and sensitivity
- Triple-quadrupole-level quantitation
- Deconvolution/library search for known unknown identification
- Unique capabilities for true unknown identification
  - Industry-best mass accuracy
  - Highest resolution for fine isotope detection
  - Automated compound identification without spectral library reference

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Thank You

Please join me in the
Gas Chromatography and Mass Spectrometry
section of our booth where I'll
address comments and questions.