Toxicants Screening

in the Workplace by Orbitrap™ HRAMS

PRESENTED BY

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โครงการ “สถานประกอบกิจการสีขาว”

โรงงานสีขาว พนักงานสดใส
เพราะทุกคนร่วมใจ ห่างไกลยาเสพติด

บริษัทในเครือ [redacted] เป็นสถานประกอบกิจการซึ่งอยู่ภายใต้ข้อบังคับ
กฎหมายว่าด้วยการป้องกันและปราบปรามยาเสพติด
กรมสวัสดิการและคุ้มครองแรงงาน

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ขอมอบเกียรติบัตรให้ไว้เพื่อแสดงว่า

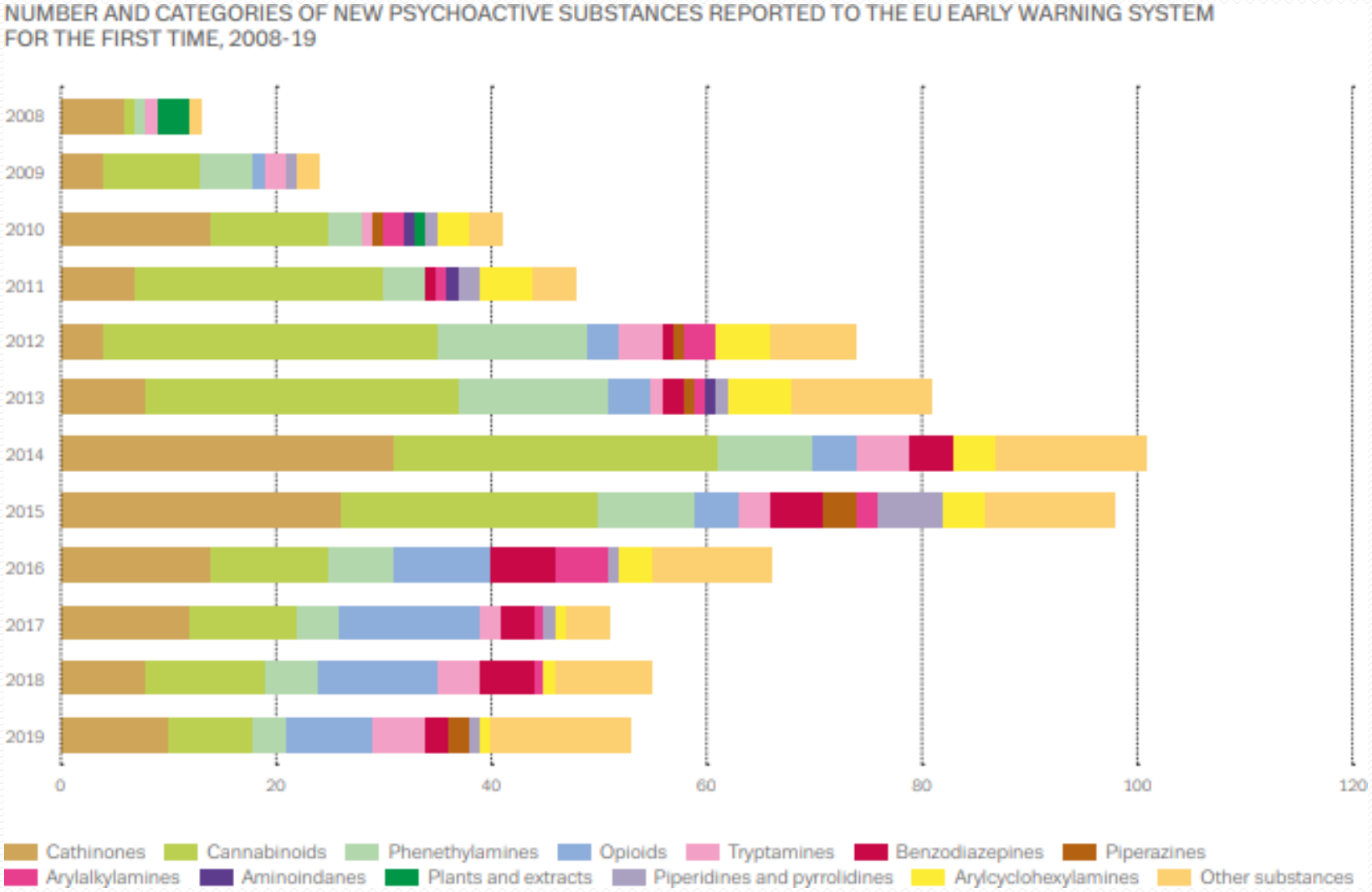
บริษัท [redacted] จำกัด

มีระบบการจัดการด้านยาเสพติดในสถานประกอบกิจการ
ตามโครงการโรงงานสีขาว ระดับที่ ๓

ให้ไว้ ณ วันที่ ๑๙ มีนาคม พ.ศ. ๒๕๕๘

(นายพินิจ หาญพาณิชย์)
ผู้ว่าราชการจังหวัดสมุทรปราการ

New Psychoactive Substances (NPS)



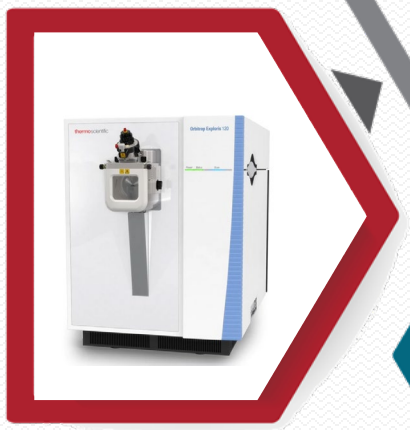
Thermo Scientific™ Tox Explorer™ Collection

Sample Preparation Guidelines

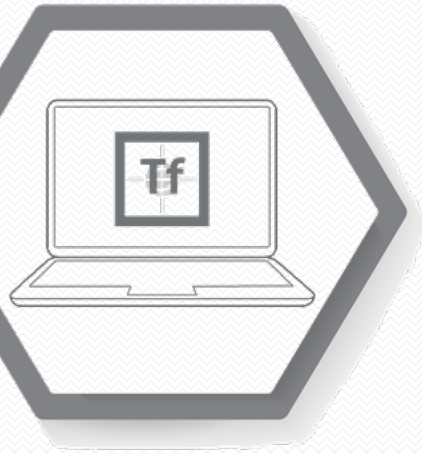
LIBRARY AND SOFTWARE
DATA ANALYSIS

Chromatography

Mass Spectrometry



Reporting



TraceFinder™
Optimized for Quantitation

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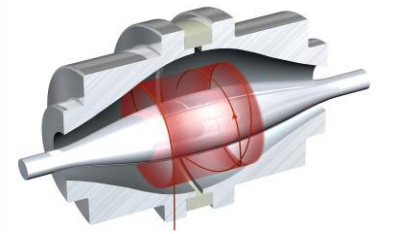
Orbitrap™ HRAMS



Training

Support

Fast confident results

Mass Analyzer : Orbitrap™ Technology

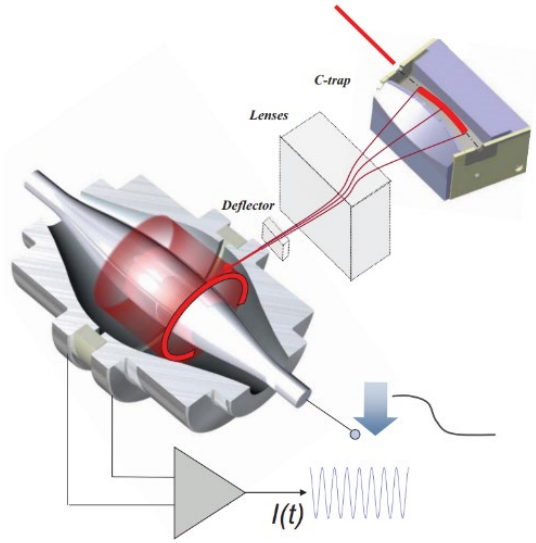
Anal. Chem. **2000,** *72,* 1156−1162

Electrostatic Axially Harmonic Orbital Trapping: A High-Performance Technique of Mass Analysis

Alexander Makarov*

HD Technologies Ltd., Atlas House, Simonsway, Manchester, M22 5PP, U.K.

This work describes a new type of mass analyzer which employs trapping in an electrostatic field. The potential distribution of the field can be represented as a combination of quadrupole and logarithmic potentials. In the absence of any magnetic or rf fields, ion stability is achieved only due to ions orbiting around an axial electrode. Orbiting ions also perform harmonic oscillations along the electrode with frequency proportional to $(m/z)^{-1/2}$. These oscillations are detected using image current detection and are transformed into mass spectra using fast FT, similarly to FT ICR. Practical aspects of the trap design are presented. High-mass resolution up to 150 000 for ions produced by laser ablation has been demonstrated, along with high-energy acceptance and wide mass range.



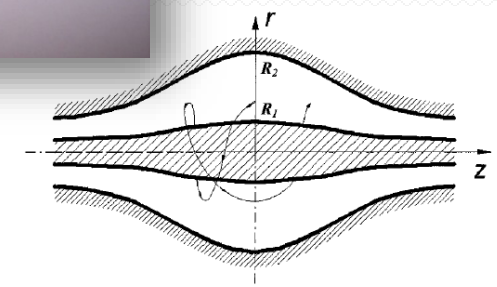


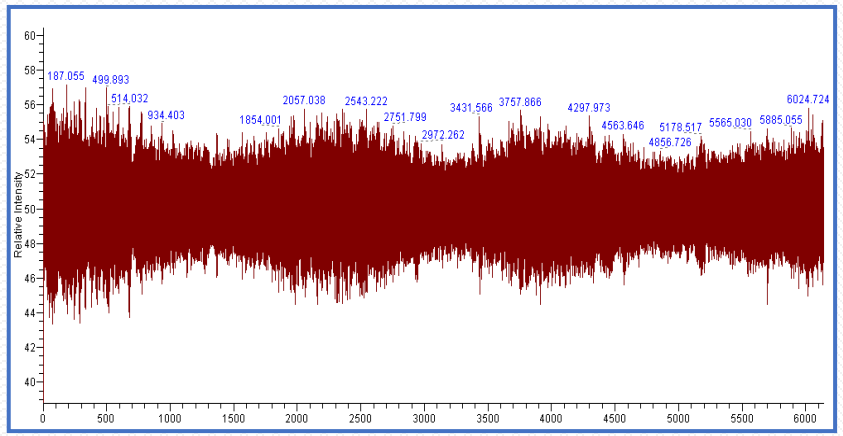
Figure 1. Equipotentials of the quadro-logarithmic field and an example of a stable ion trajectory

Mass Analyzer : Orbitrap™ Technology

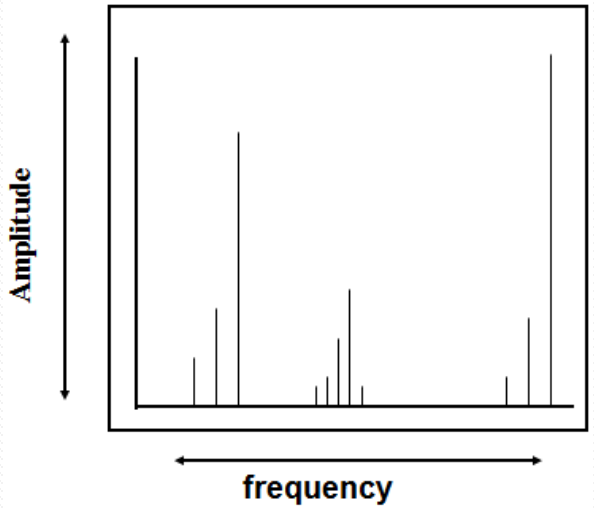
Image Current

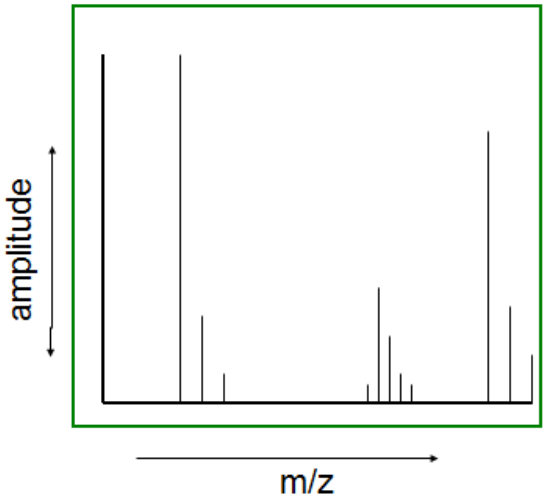
Frequency Domain

Mass Spectrum



Fourier Transform



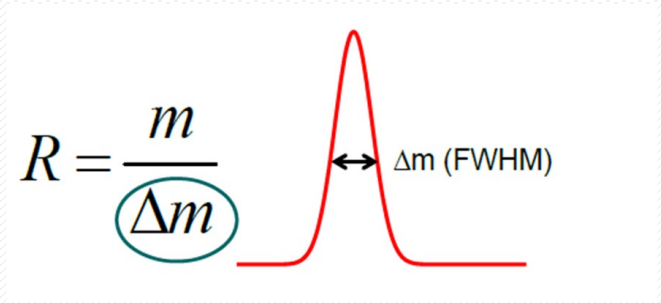


$$\omega_z = \sqrt{\frac{k}{m/q}}$$

Mass Resolution

- Ability of a mass spectrometer to distinguish between ions of nearly equal m/z ratios.

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



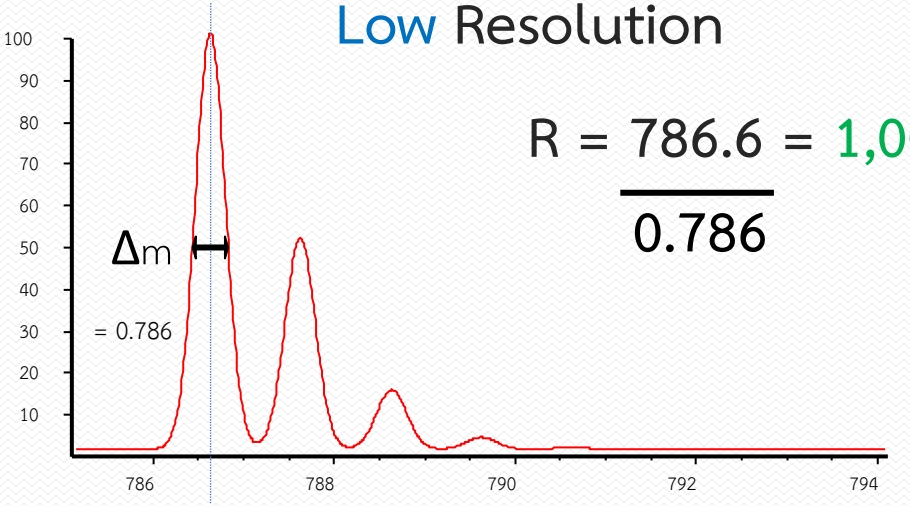
m - measured mass

Δm - peak width measured at 50% peak intensity (Full Width Half Maximum)

C = 12.0000	
H = 1.0078	
N = 14.0031	
O = 15.9949	
S = 31.9721	

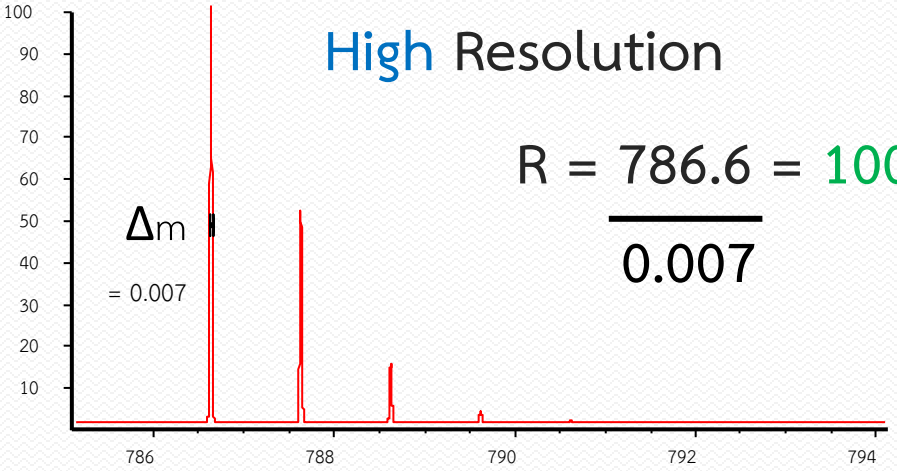
CO	=	27.9949
N_2	=	28.0061
C_2H_4	=	28.0313

Low Resolution



$$R = \frac{786.6}{0.786} = 1{,}000$$

High Resolution



$$R = \frac{786.6}{0.007} = 100{,}000$$

- It is possible to have combinations of atoms which have the same nominal mass but different accurate mass
- Nominal mass measurements cannot distinguish these compounds
- These elemental combinations have the same nominal mass but different accurate mass
- If such compounds can be mass measured with sufficient accuracy it is possible to determine elemental composition

Mass Accuracy

- **Mass Accuracy** is the precision of which the mass is measured by MS.
- Typical way of reporting mass error in **ppm** (relative measure).
- Increases confidence in identification.

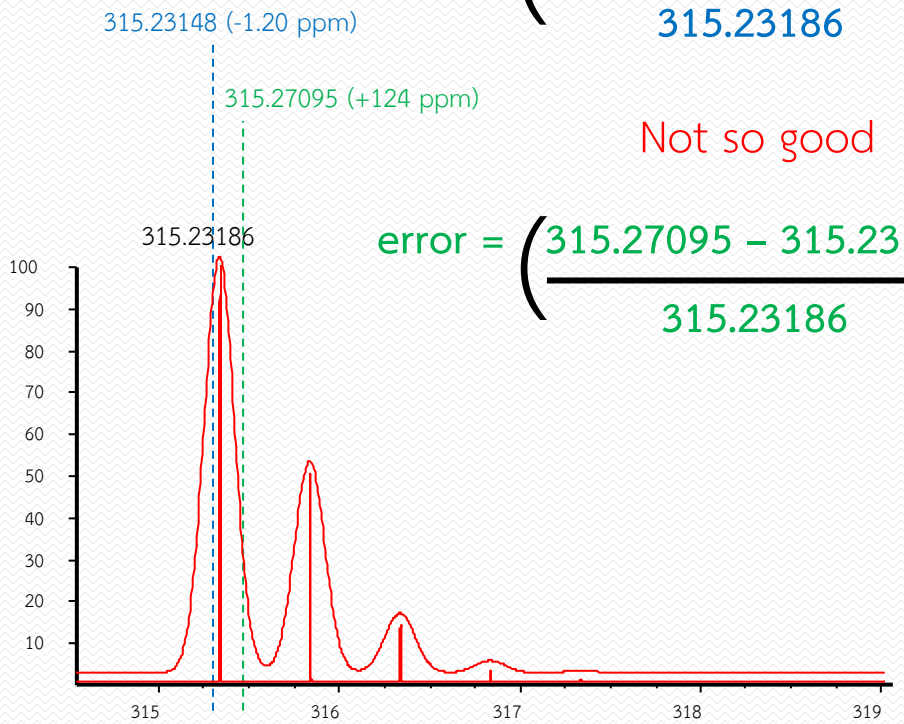
$$\text{Mass error} = \left(\frac{\text{Measured} - \text{Theoretical}}{\text{Theoretical}}\right) \times 10^6 = \text{ppm}$$

$[M+H]^+ = 315.23148$

Mass Error	Number of Hits
± 200 ppm	265
± 100 ppm	133
± 30 ppm	39
± 10 ppm	14
± 5 ppm	5
± 3 ppm	4
± 1 ppm	1

Good

$$\text{error} = \left(\frac{315.23148 - 315.23186}{315.23186}\right) \times 10^6$$



Not so good

$$\text{error} = \left(\frac{315.27095 - 315.23186}{315.23186}\right) \times 10^6$$

Mass Resolution & Accuracy

Measured Mass	Mass Error (Da)	Possible Formula	Exact Mass
32.0	± 0.2	O_2	31.9898
		CH_3OH	32.0261
		N_2H_4	32.0374
		S	31.9721
32.02	± 0.02	CH_3OH	32.0261
		N_2H_4	32.0374
32.0257	± 0.002	CH_3OH	32.0261

C = 12.0000

O = 15.9949

S = 31.9721

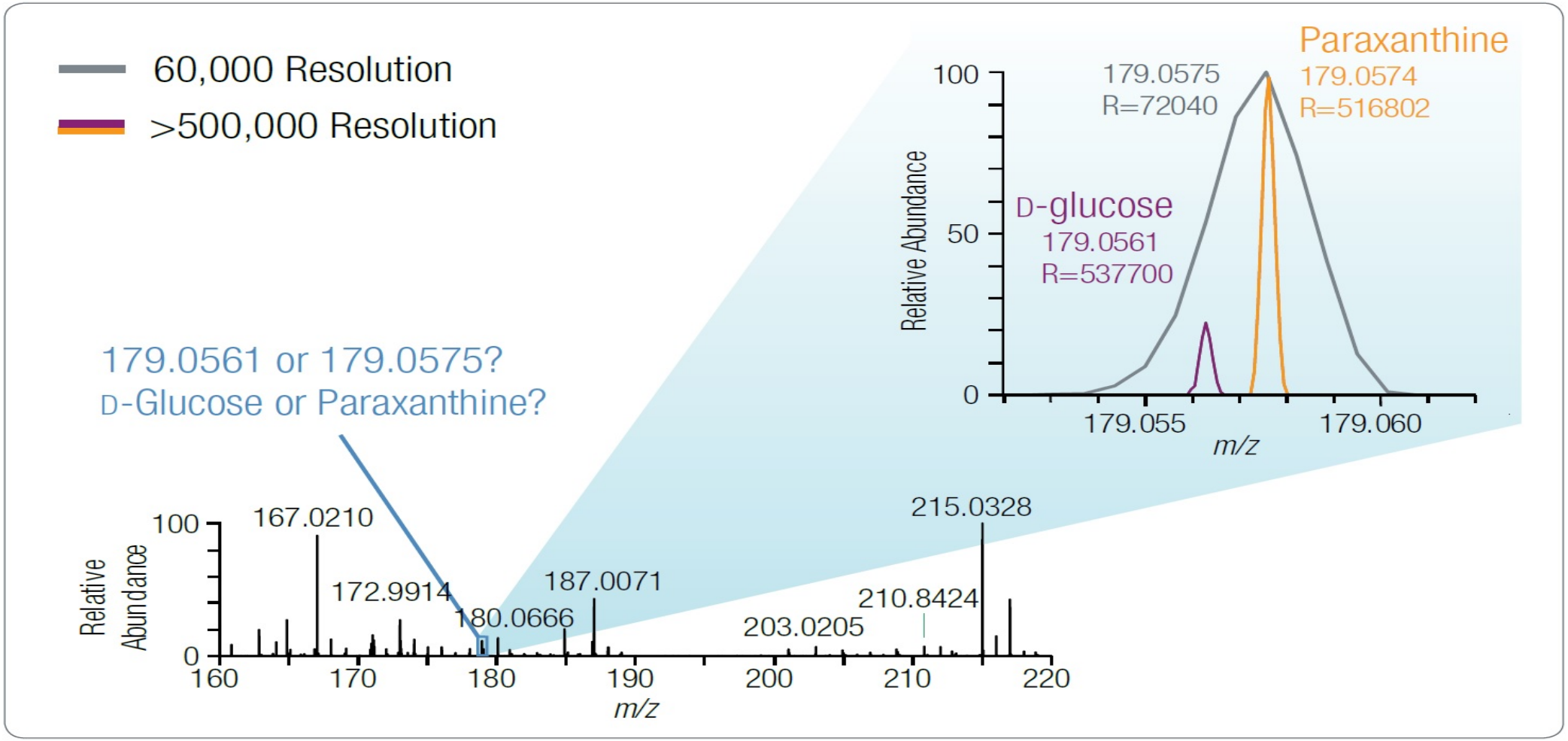
H = 1.0078

N = 14.0031

- **Main advantage:** the possibility to determine the elemental composition of individual molecular or fragment ions, a powerful tool for the structural elucidation or confirmation.

Mass Resolution & Accuracy

- Isobaric compounds separation

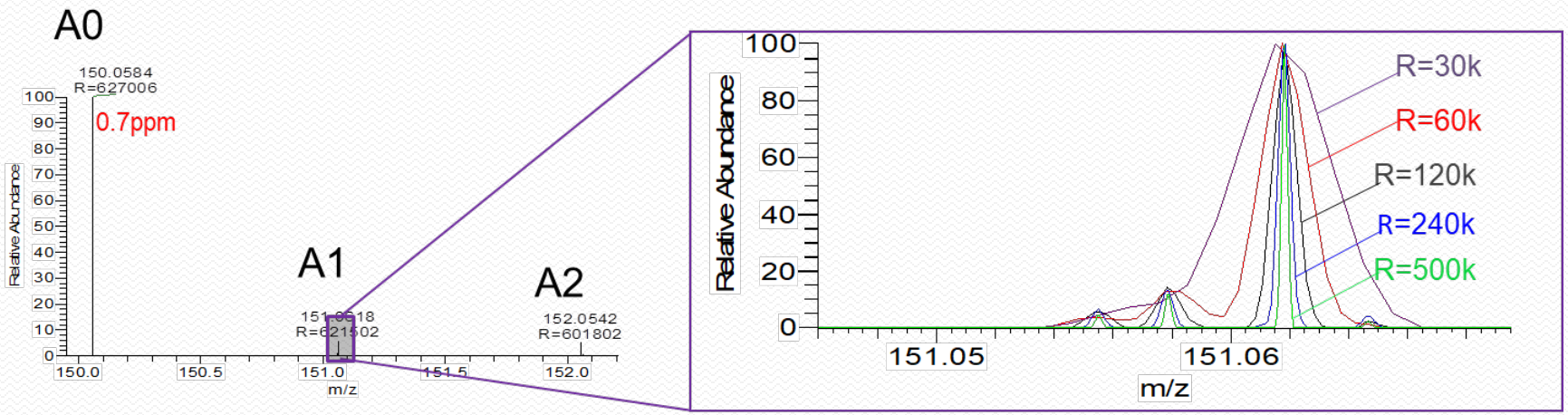


Mass Resolution & Accuracy

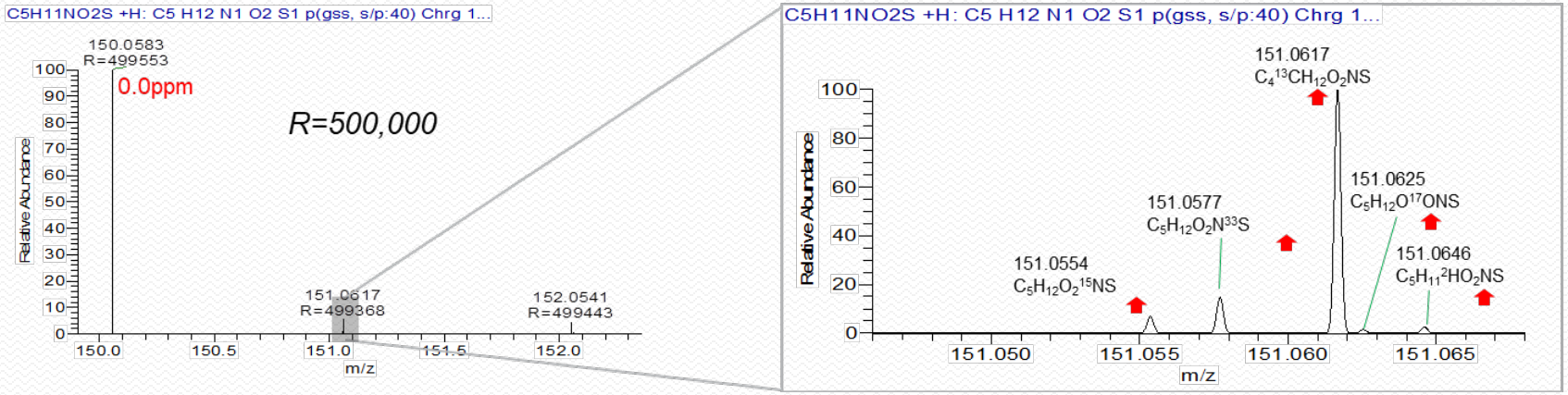
- Fine Isotopic Pattern

L-Methionine ($C_5H_{11}NO_2S$) $[M+H]^+$

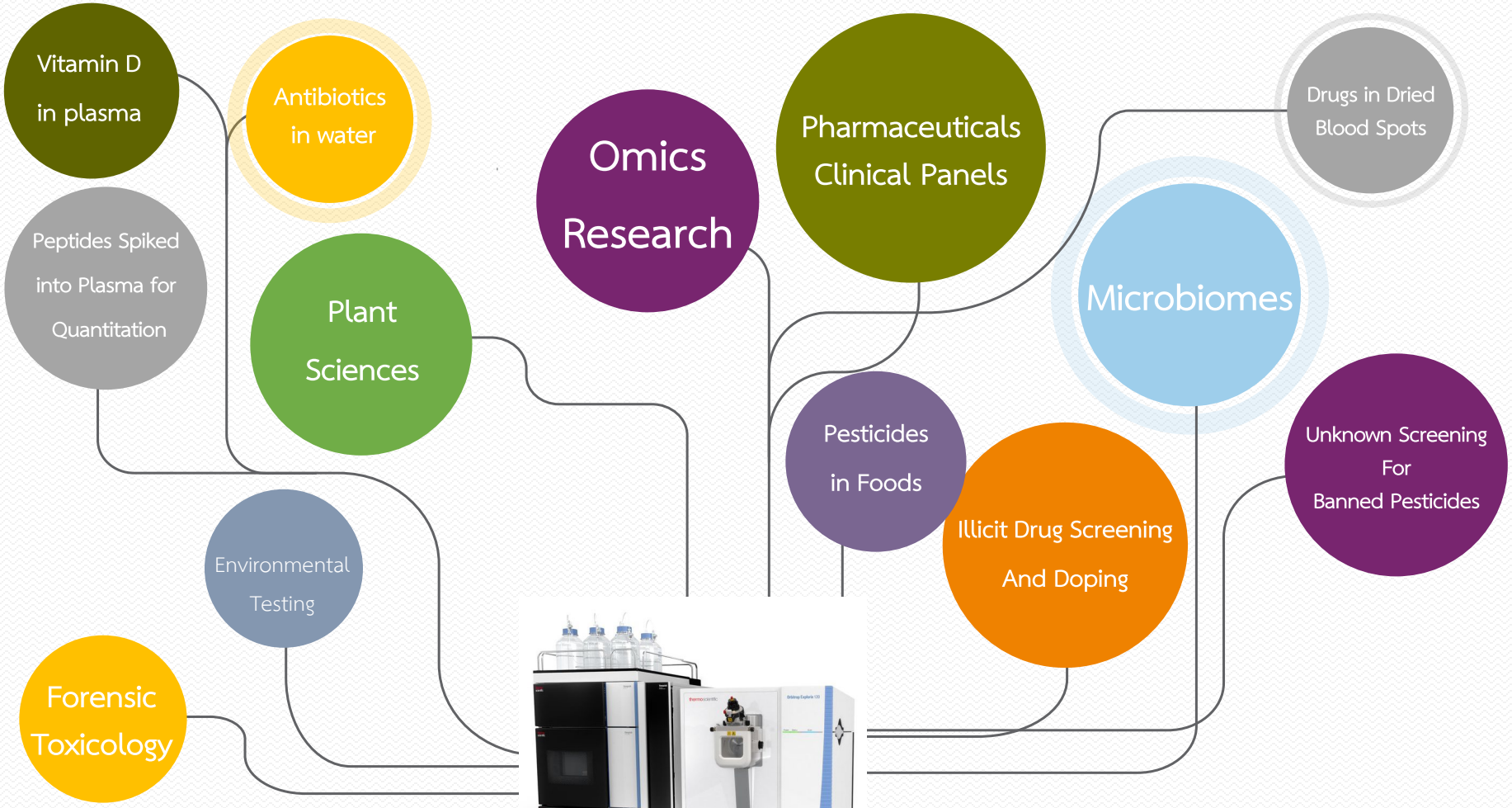
Observed



Simulated



Orbitrap Applications Universe



Clinical Sample Preparation

1. 100 µL urine sample was mixed with 500 µL acetonitrile in the 1.5 ml tube

2. Centrifuged for 5 min

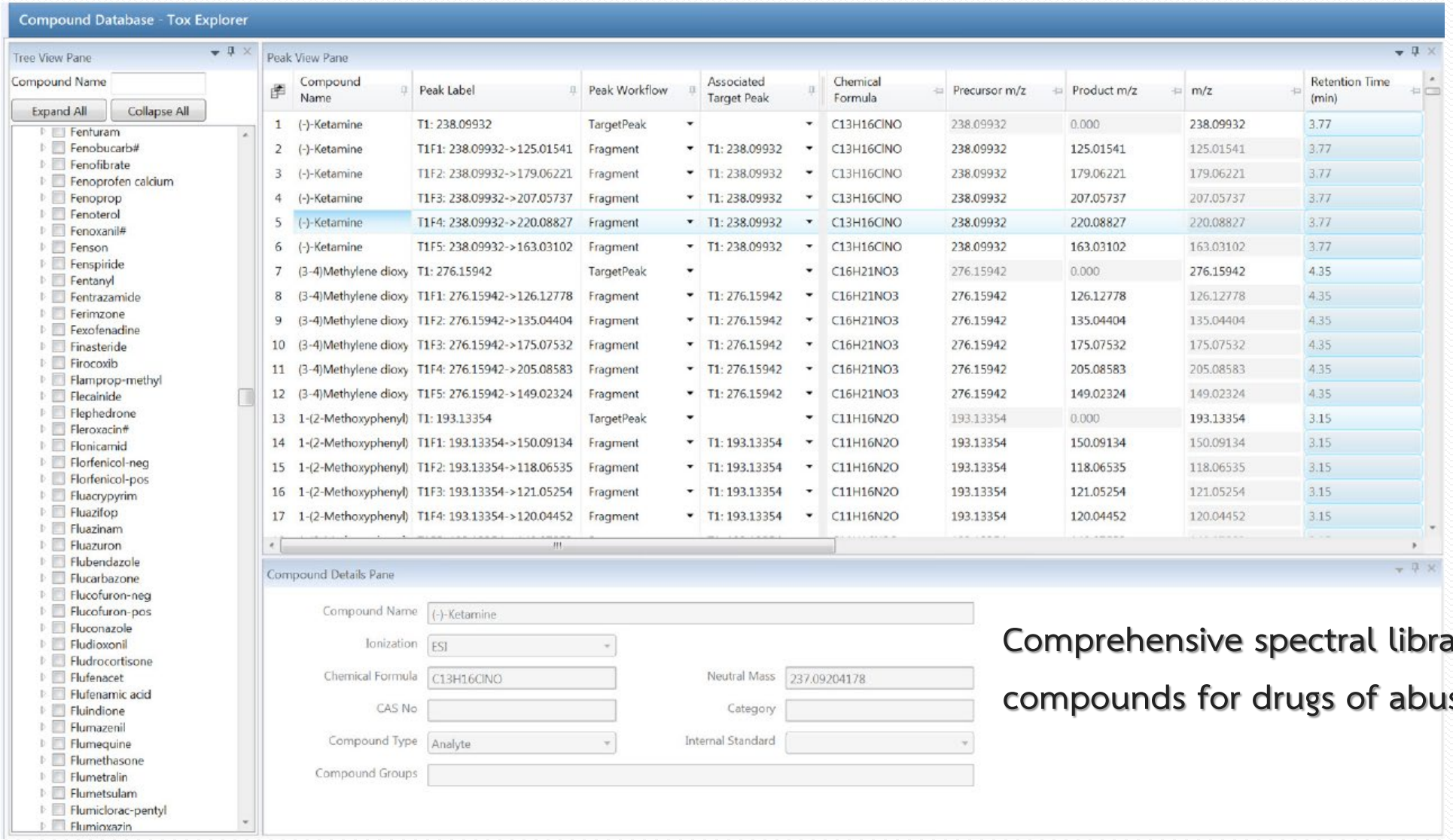
3. The supernatant was gently evaporated to dryness

4. Reconstituted in 50 µL of a mixture consisting of 2 mM aqueous ammonium formate plus 0.1% formic acid (pH 3)

5. Finally, 10 µL was injected onto the UHPLC – Orbitrap MS

Tox Explorer™ Collection HRAM MS/MS Database

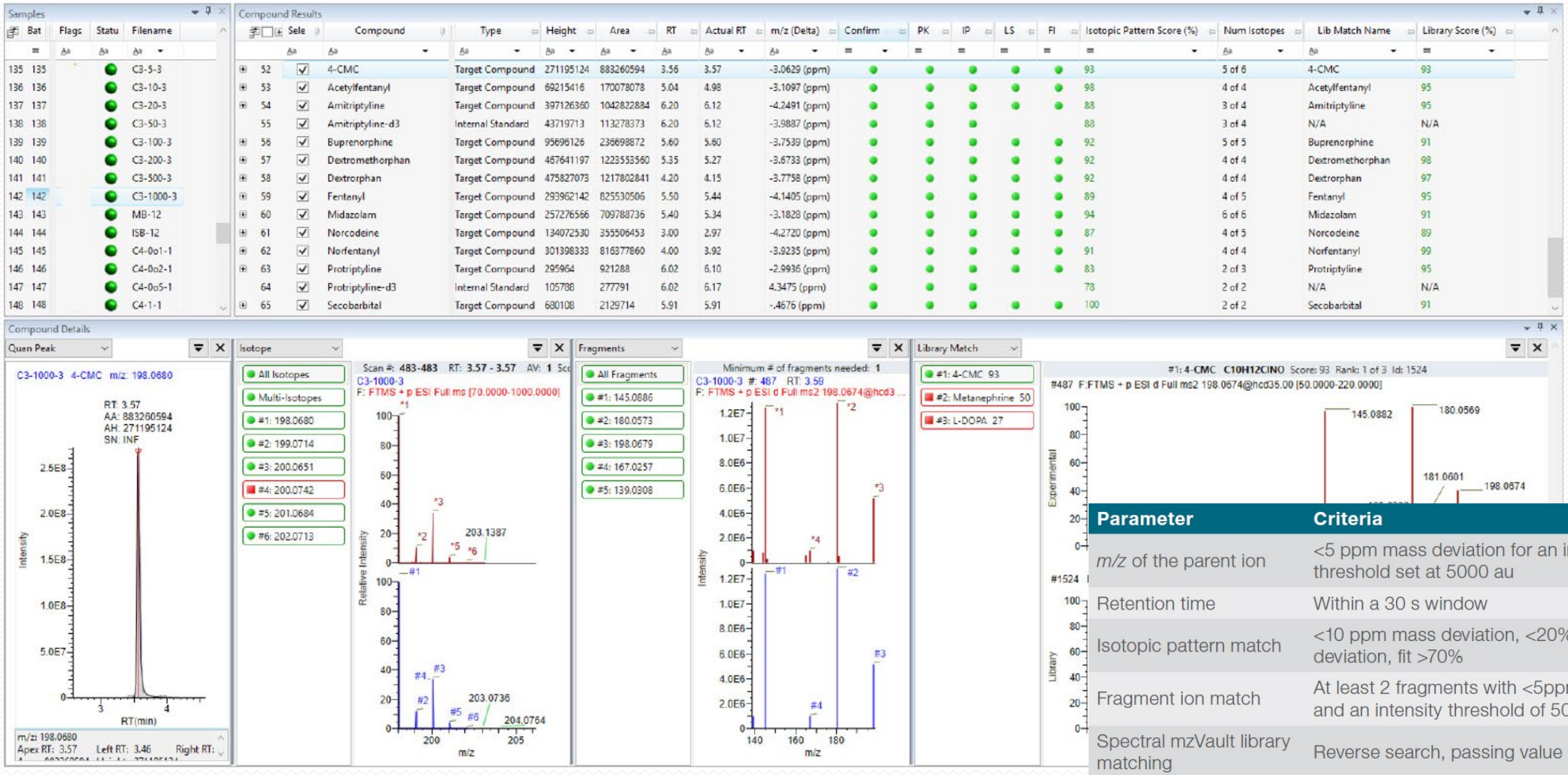
Tox Explorer™ Collection compound database in TraceFinder software containing all analyte information



Comprehensive spectral library of 1500+ compounds for drugs of abuse and NPS

Targeted Screening – Compound Library Matching

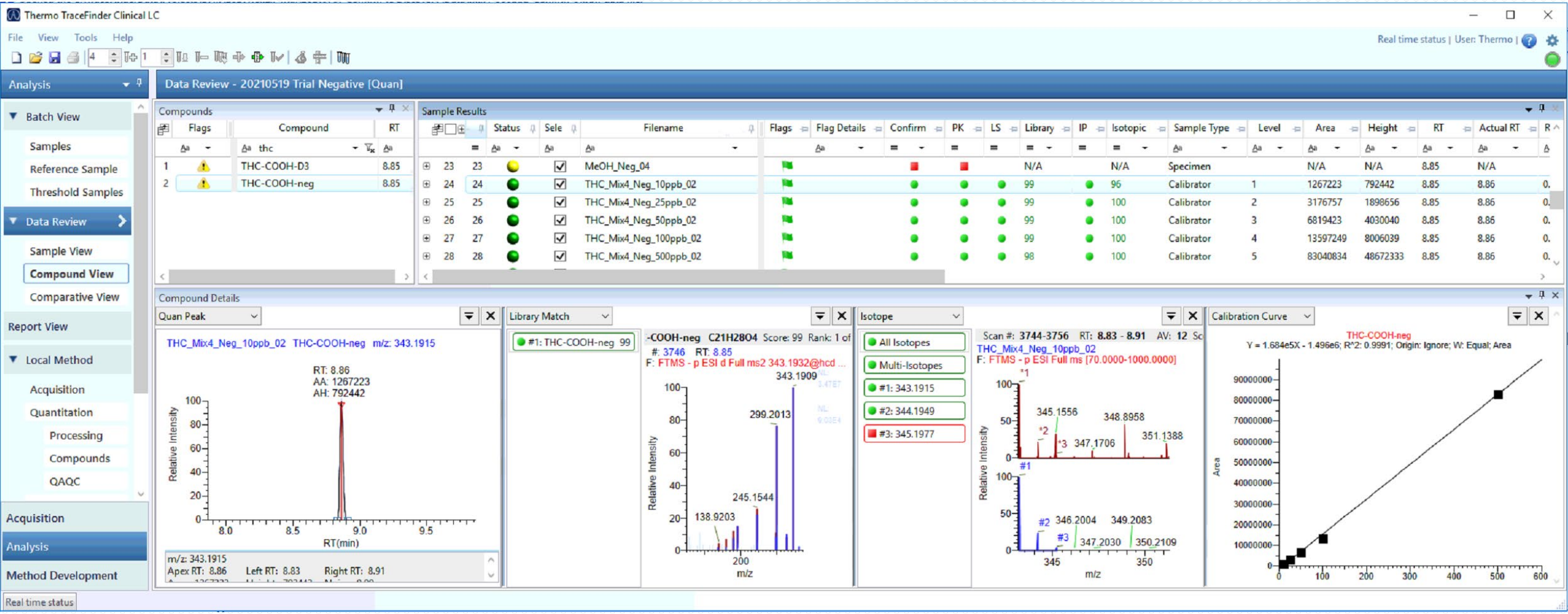
Data review from TraceFinder 5.1 software of targeted screening



Parameter	Criteria
m/z of the parent ion	<5 ppm mass deviation for an intensity threshold set at 5000 au
Retention time	Within a 30 s window
Isotopic pattern match	<10 ppm mass deviation, <20% intensity deviation, fit >70%
Fragment ion match	At least 2 fragments with <5ppm deviation and an intensity threshold of 5000 au
Spectral mzVault library matching	Reverse search, passing value >70%

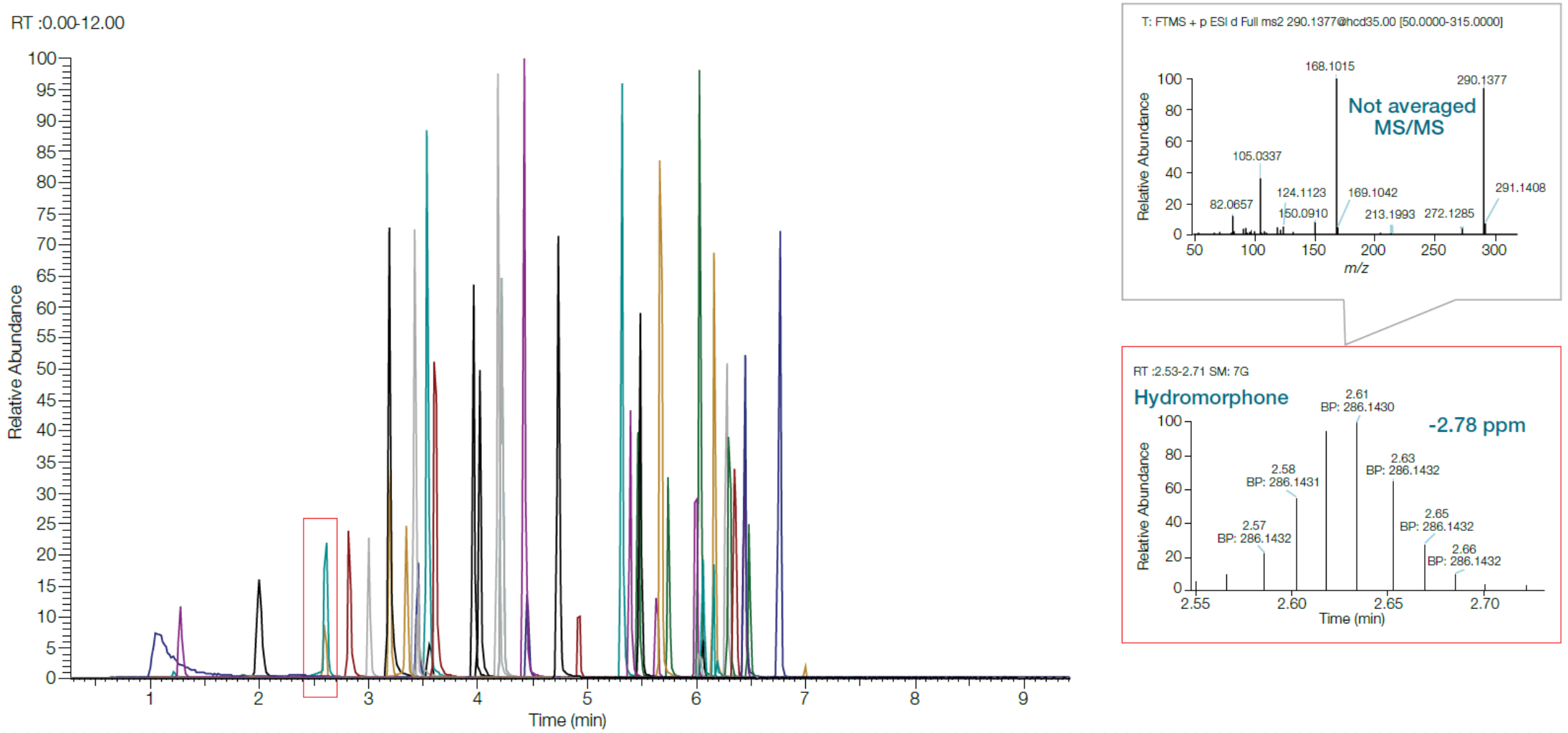
Targeted Quantitation – Residue Level Detection

Data review from TraceFinder 5.1 software of quantitation of THC-COOH



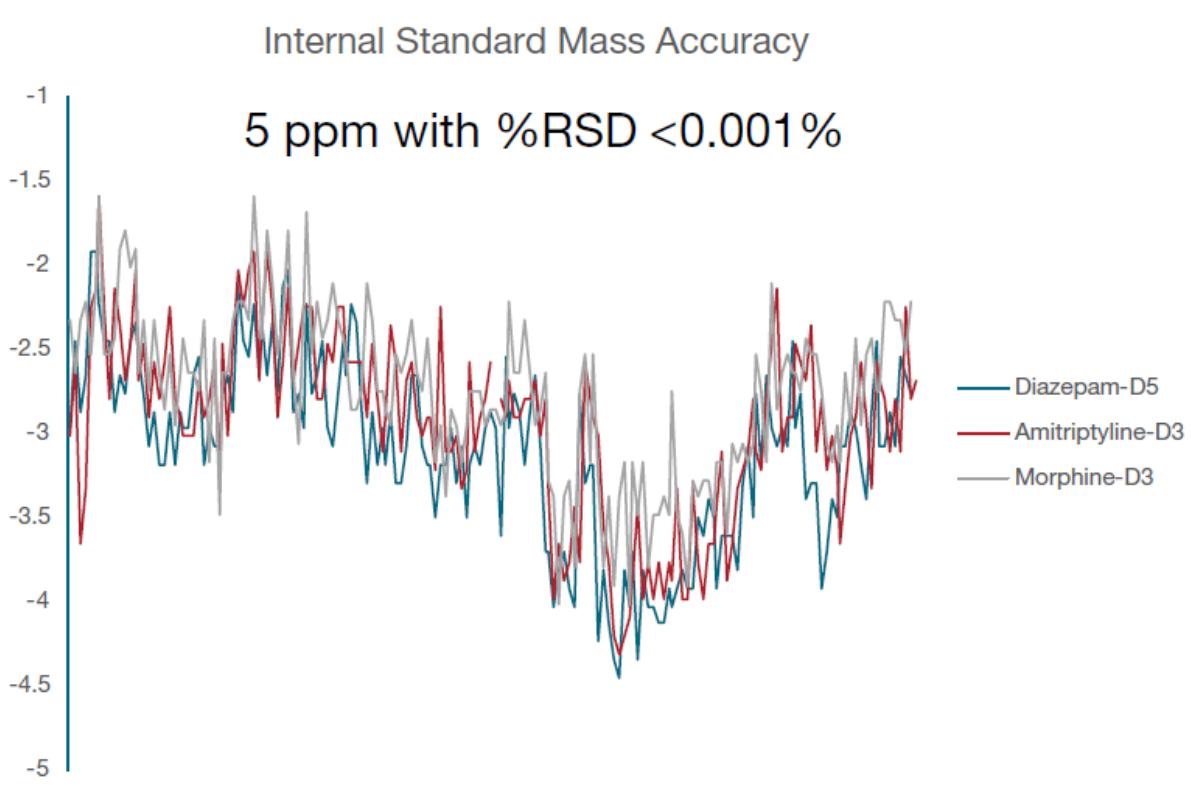
Reproducible Chromatograms

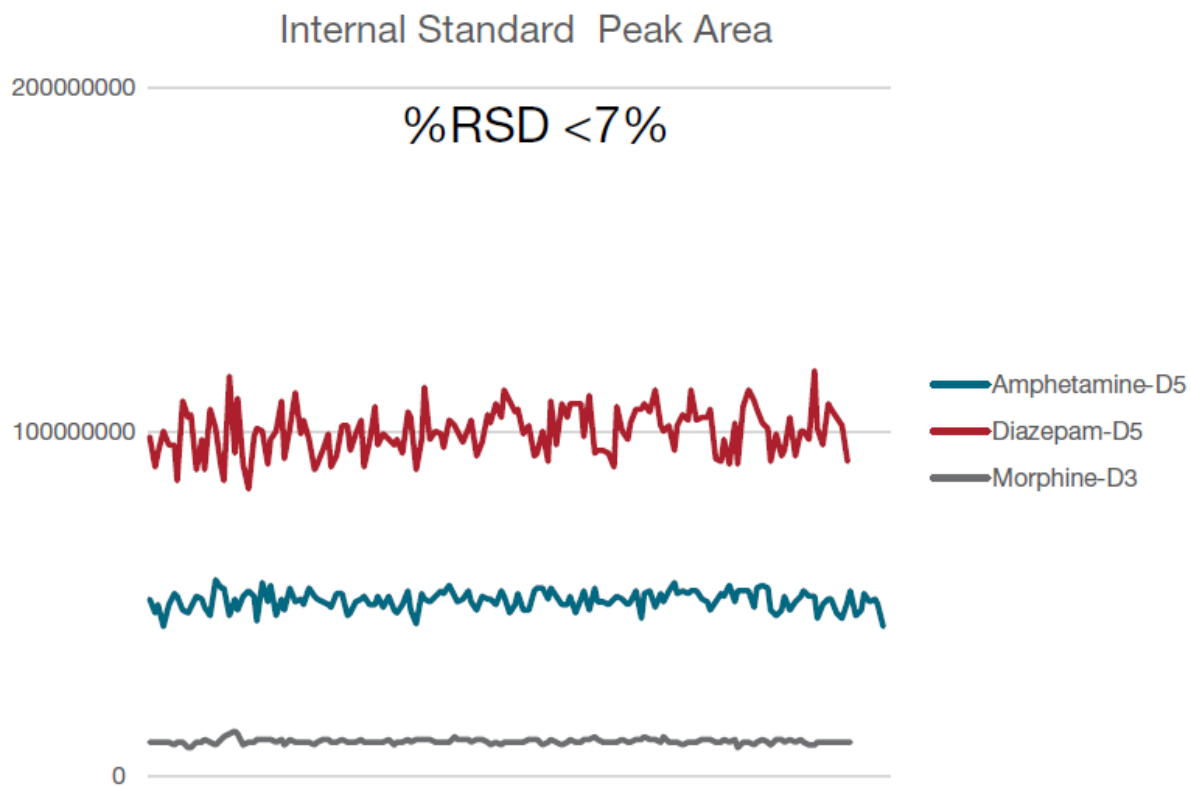
XIC chromatograms of four mixes of 54 drugs of abuse compounds (mass accuracy 5 ppm)



Robustness of Method

Robustness of mass accuracy and peak area for over 400 injections for the internal standard, amphetamine-D5, diazepam-D5 and morphine-D3





Key Summary – Tox Explorer™ Collection

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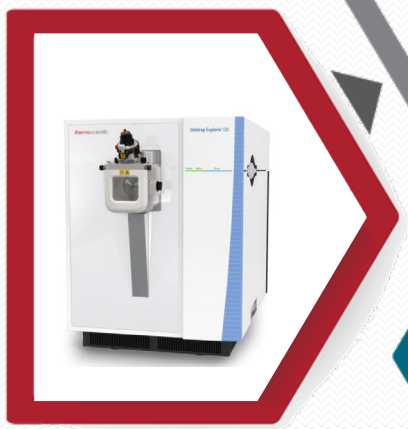

Reporting

TraceFinder™
Optimized for Quantitation

Tf

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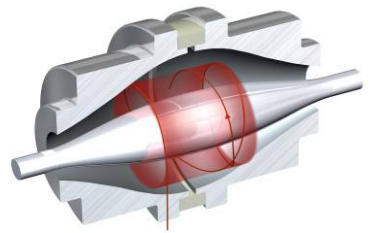
Targeted Screening and Quantitation for Drugs of Abuse and NPS

Training

Support

Fast confident results

Orbitrap™ HRAMS



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กรมสวัสดิการและคุ้มครองแรงงาน

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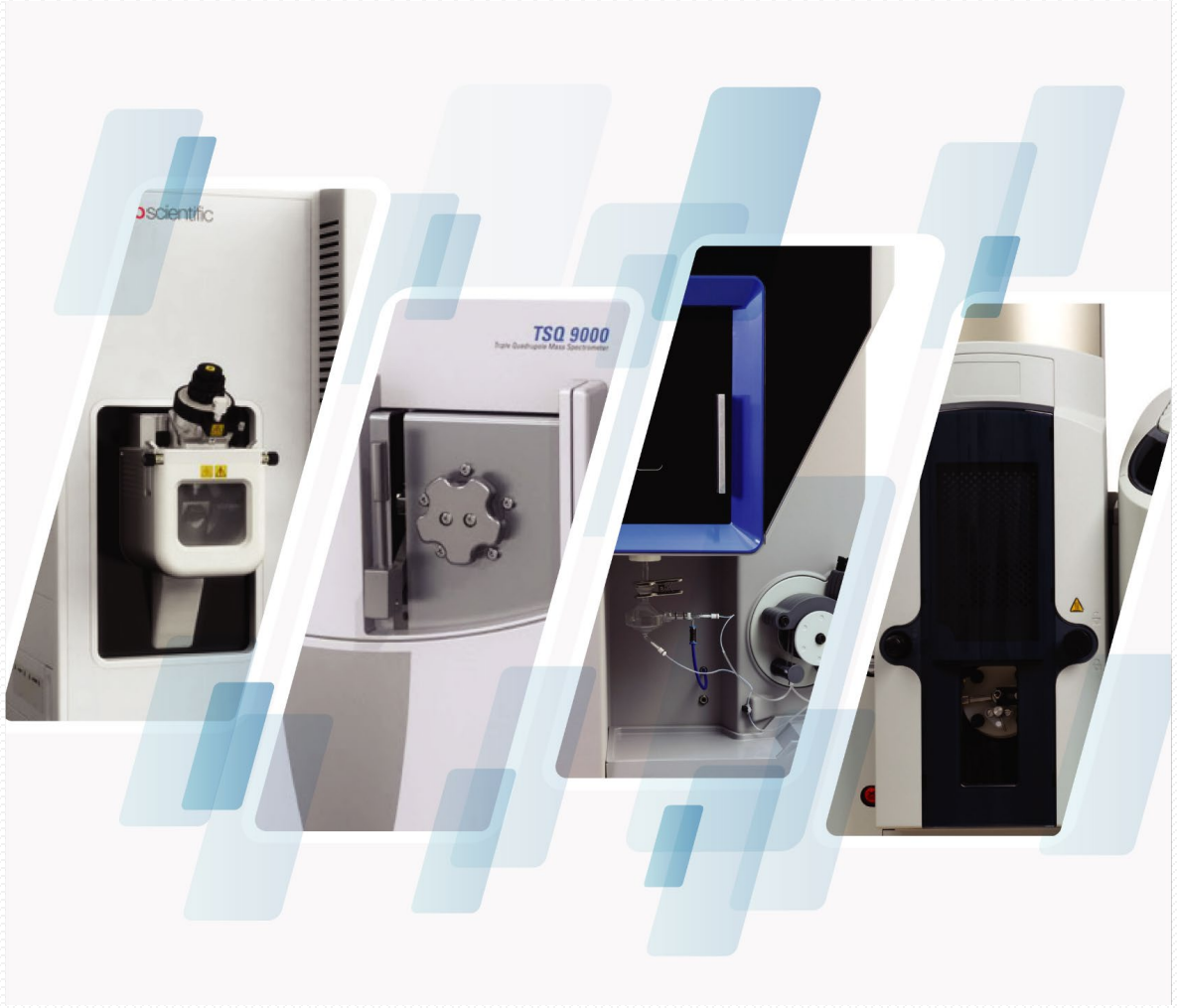

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