



**ThermoFisher**  
S C I E N T I F I C

# Accelerate Unknown Detection in Emerging Drug Testing Using Thermo Scientific™ Compound Discoverer™ and mzCloud™

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ClinTox Marketing Manager  
Thermo Fisher Scientific

The world leader in serving science

# Emerging/Designer Drugs – “Fixing Bad”



Roughly 15-45 new ‘designer drugs’ hit the streets (globally) each year<sup>1</sup>

A trillion dollar business globally

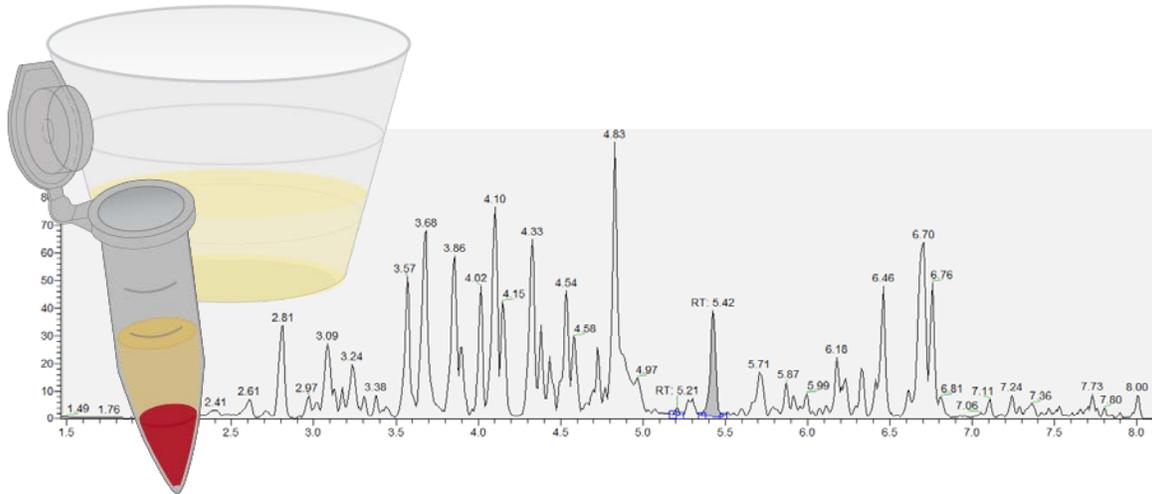
**New designer drugs are NOT on current target analysis lists/ databases!**

# How do you find something you don't know to look for?

- Sometimes we get lucky
  - “Bag of white powder”
  - Single (or small number) or analytes
  - Relatively pure



1



- Usually, we don't.
  - Complex sample matrices
  - Blood/Plasma – Urine – Hair
  - Classic ‘needle in a haystack’ problem

For forensic use only.

# What “Identifies” a Compound?

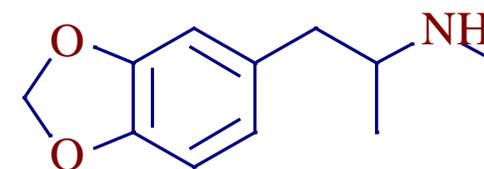
- Molecular weight (Accurate mass)
- Elemental Composition
- Isotope Ratio
- Fragmentation pattern (MS<sup>2</sup> or MS<sup>n</sup>)
- Retention Time



Our Database of Drugs



MW	<input checked="" type="checkbox"/>
Elemental Comp	<input checked="" type="checkbox"/>
Isotope Ratio	<input checked="" type="checkbox"/>
Spectral Match	<input checked="" type="checkbox"/>
RT	<input checked="" type="checkbox"/>



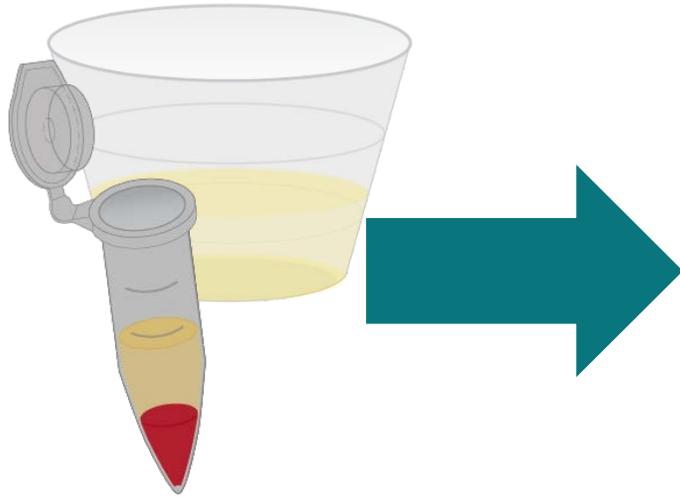
For forensic use only.

# Typical Approaches – Playing ‘Catch-up’

- Rely heavily on targeted screening approaches using as complete a database as possible
  - Only can find what you already know.
- Rely on seizures of drugs during arrests which are transferred to reference libraries for identification
  - Only can find what others have identified
- Leaves most labs lagging far behind the real situation at street level.

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# How to Find What you Don't Know Is There



	Formula	Molecular Weight	RT [min]	Area (Max.)
10	C9 H18 F3 N2 O6 P S	370.05820	2.735	717604
11	C9 H9 N O2	163.06344	2.729	306788
12	C9 H12 N2 O2	180.09000	2.721	295418
13	C25 H47 F2 N O5 P2 S	573.26112	3.561	232104
14	C39 H50 F2 N6 O7 S	784.34272	4.117	213147
15	C17 H31 F2 N O2 P2	381.17982	4.113	203454
16	C40 H54 N2 O14	786.35790	4.093	2189681
17	C8 H9 N O	135.06855	1.406	10921051
18	C8 H14 N6 O2	226.11777	0.983	195996268
19	C8 H6	102.04721	2.401	1481012
20	C8 H9 N	119.07377	2.402	1449914
21	C28 H46 F N7 O14 P2	785.25624	6.668	1106722
22	C10 H22 N2 O3	218.16312	1.000	1434028
23	C18 H35 F2 N O6 P2	461.18987	5.044	875361
24	C2 H5 N O7	155.00691	0.870	112925

Need to take a complex biological sample and determine what (if any) compounds are suspect

Step 1 – Find out what is there

Create a list of unknown peaks (unique molecular weights)

Proceed to find and identify suspect compounds

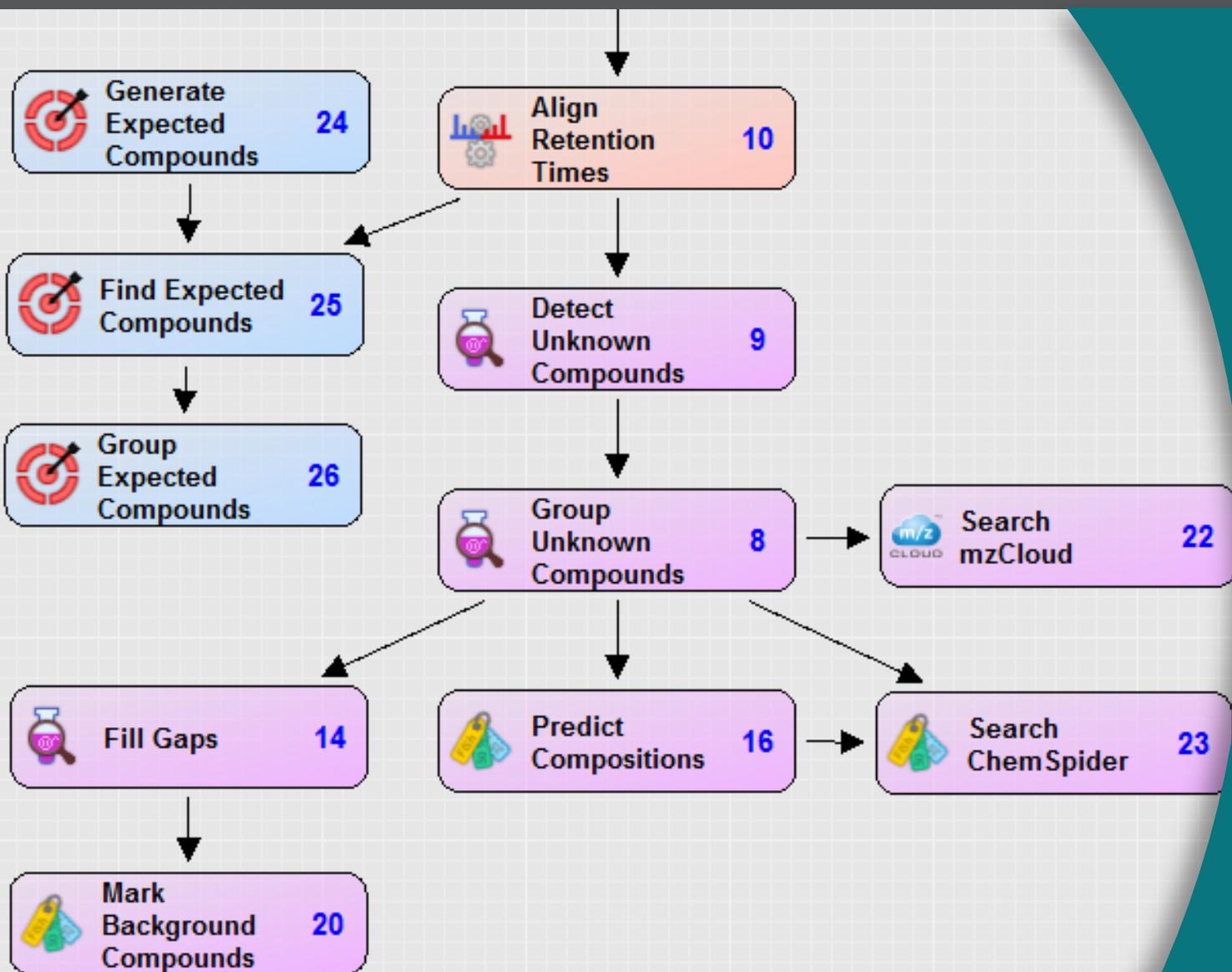
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# Thermo Scientific Compound Discoverer: Destination Unknowns

Unknown Analysis

Identification

Metabolism



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# Challenges: Terminology

- Too many terms:
  - A peak, a “feature”, a compound, a component....

## Our (Thermo) Terminology

- A “peak”
  - Spectral peak – a single observed  $m/z$  in a spectra
  - Chromatographic peak – one or more  $m/z$  that create a time dependent elution
- A “feature”
  - A single  $m/z$  chromatographic peak
- A component
  - Collection of all observed features from isotopes and adducts
  - Assignable a single molecular weight
  - Analogous to a “compound”

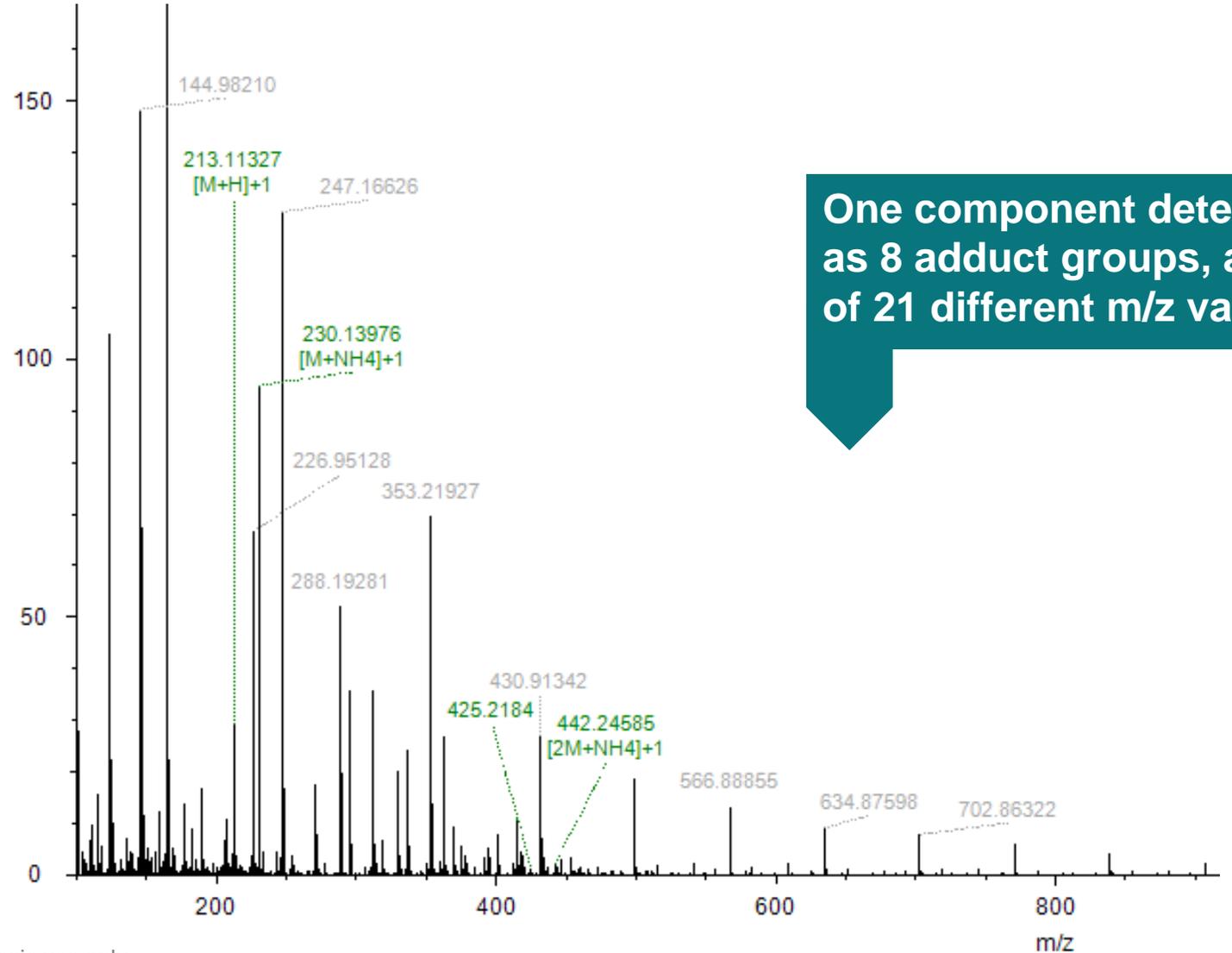
For forensic use only.

# One Compound isn't just One Feature

Full MS at 70,000 resolution

Human plasma sample

Untargeted peak detection  
with Compound Discoverer



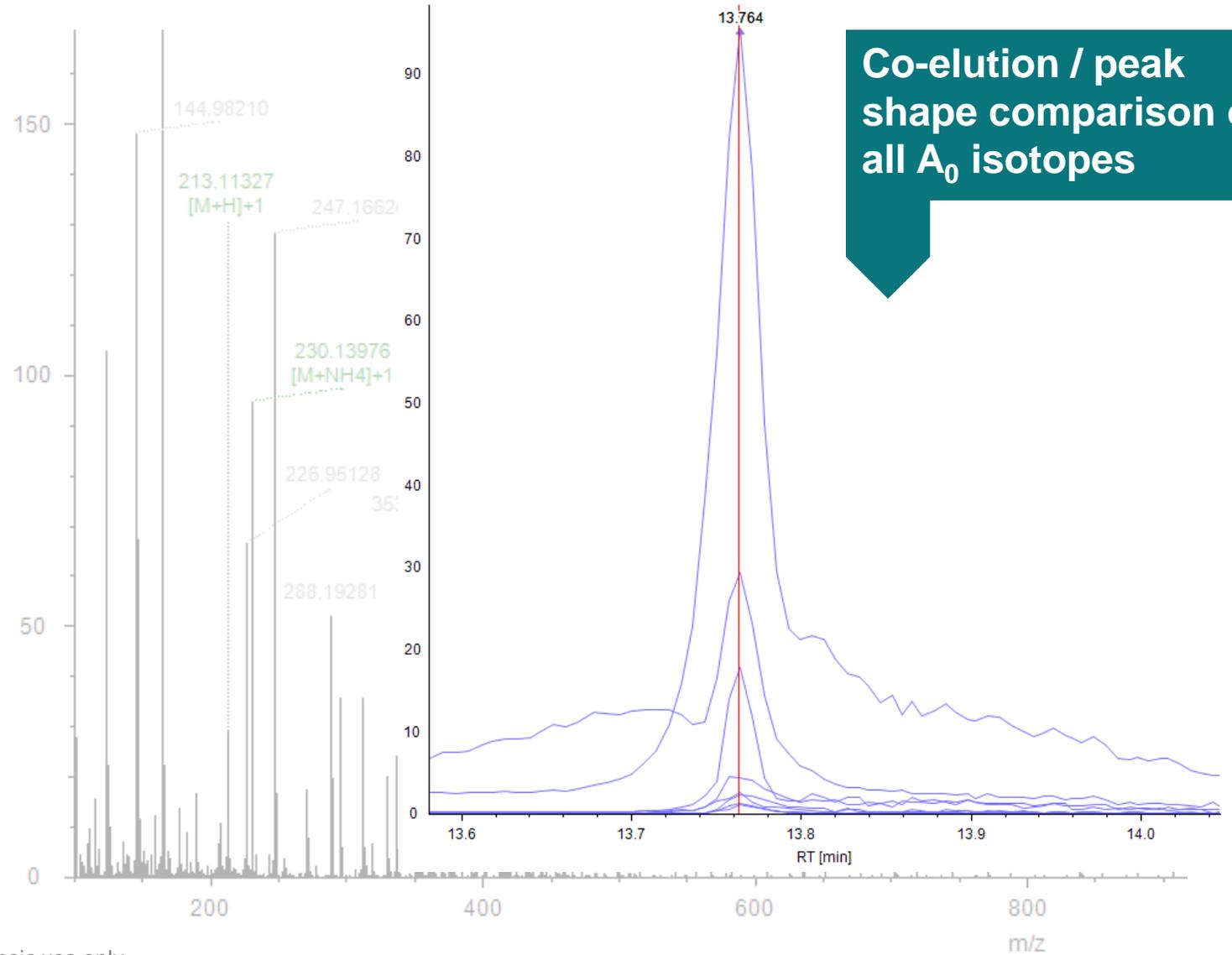
For forensic use only.

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Untargeted peak detection with Compound Discoverer



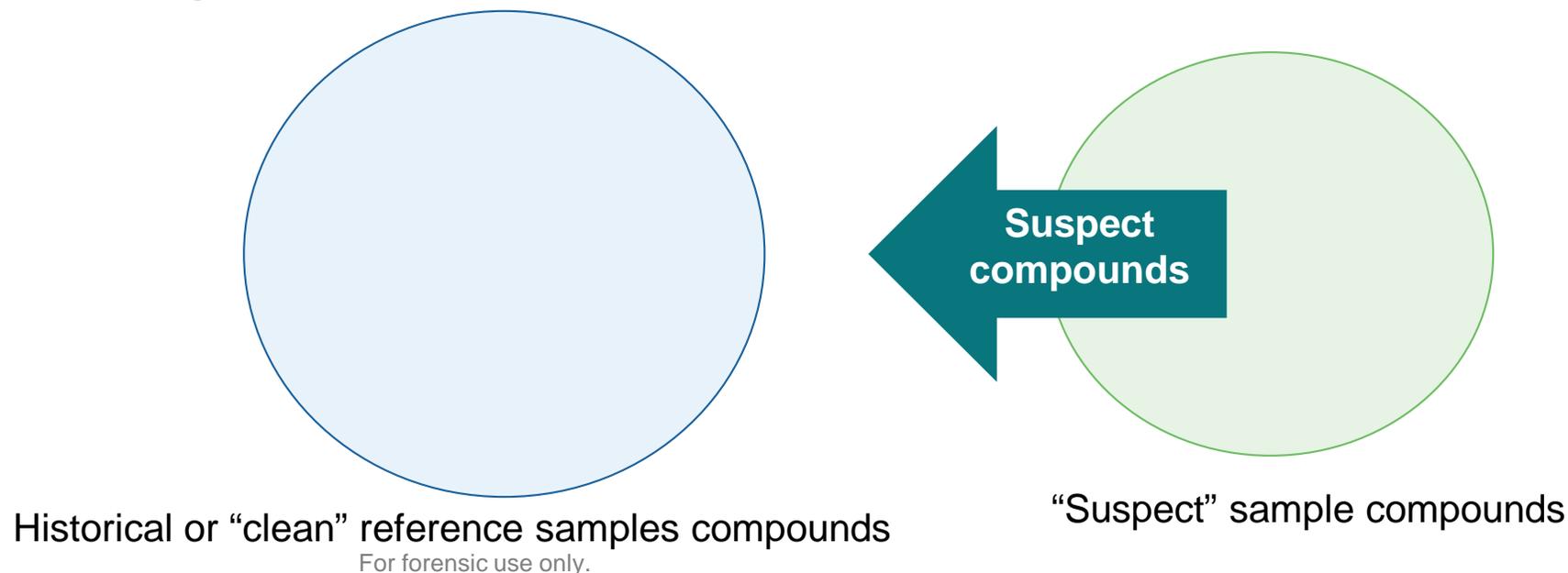
For forensic use only.

# What's in a Peak...

- An 'average' sample will contain:
  - Between hundreds to tens of thousands of features
  - Dozens to several thousand unique compounds
- An 'average' compound is detected as:
  - Between 2 to 20+ individual isotopes
  - Multiple different adducts
- Source fragmentation adds to this complexity.

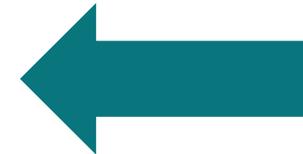
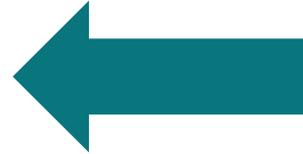
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- With our list of components in our samples we can ask...
- Is there something in this sample (group) that isn't in my control?
- Is there something that I haven't seen before?
- Is there anything suspect?



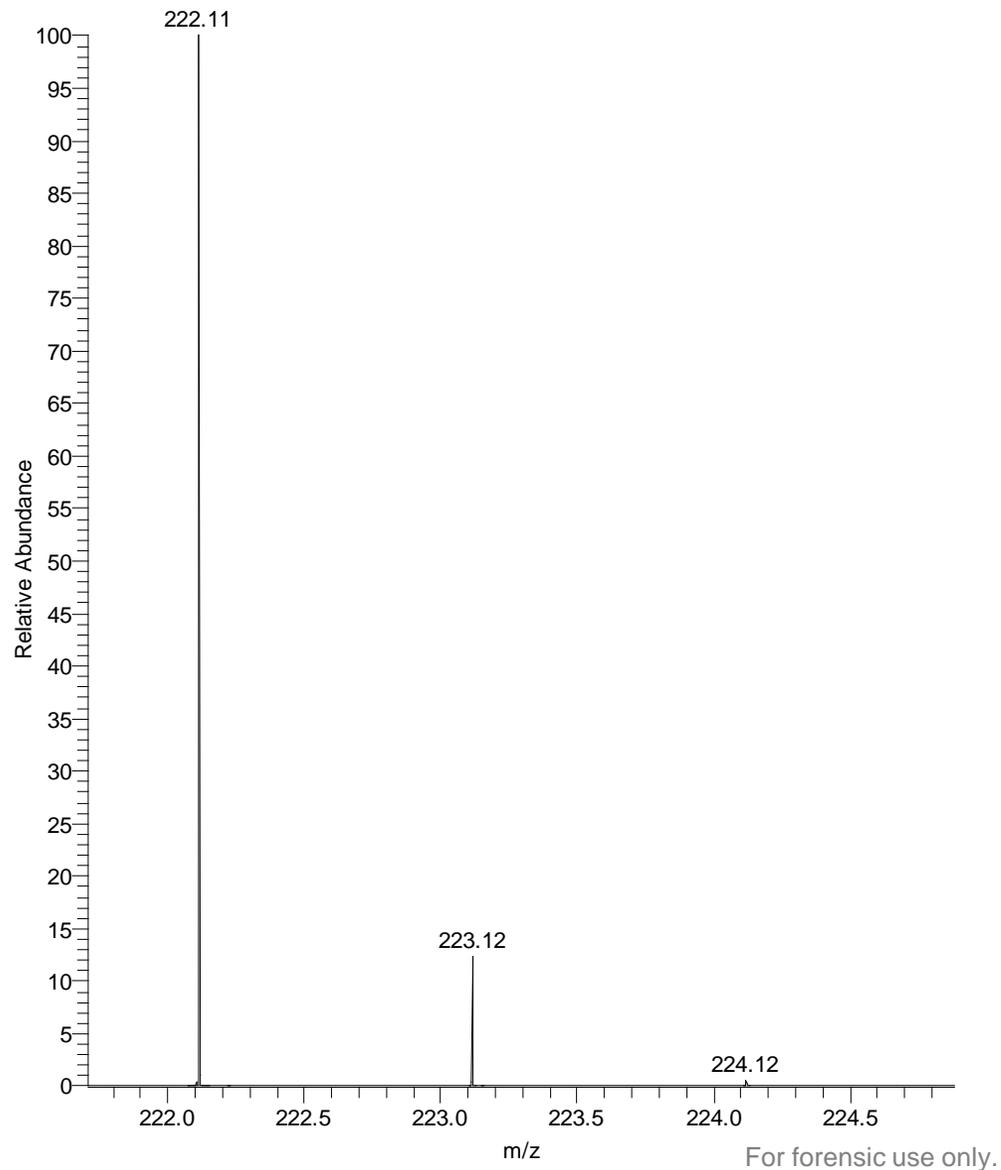
# What “Identifies” a Compound?

- Molecular weight (Accurate mass)
- Elemental Composition
- Isotope Ratio
- Fragmentation pattern ( $MS^2$  or  $MS^n$ )
- Retention Time



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# Molecular Weight – What Does it Tell us?



Single  $m/z$  value

Assume [M+H]

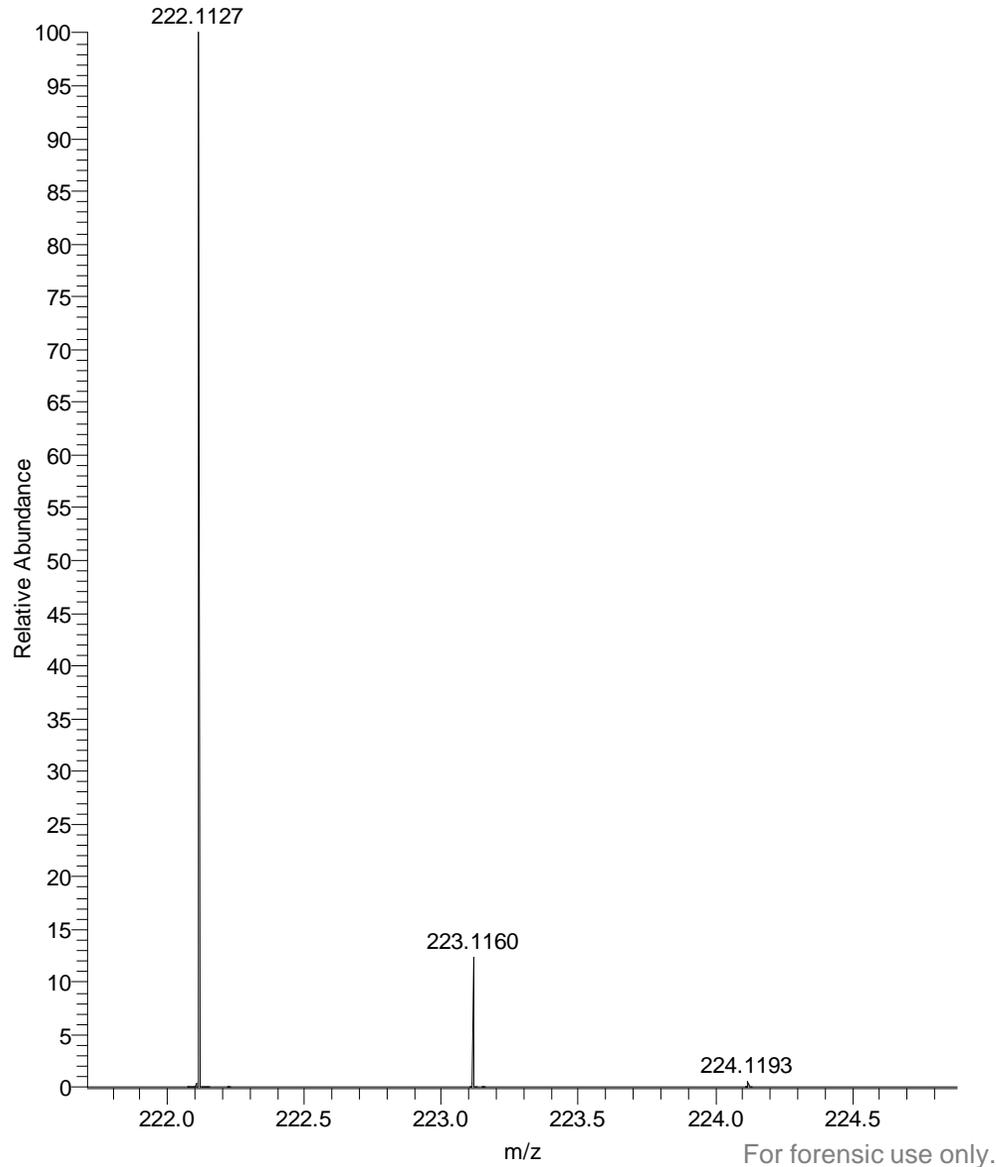
Calculated MW – 221.11

Search ChemSpider +/- 0.25

115,383 possibilities

...we have no clue what this is...

# Molecular Weight – How about Accurate Mass!



Single  $m/z$  value

Assume [M+H]

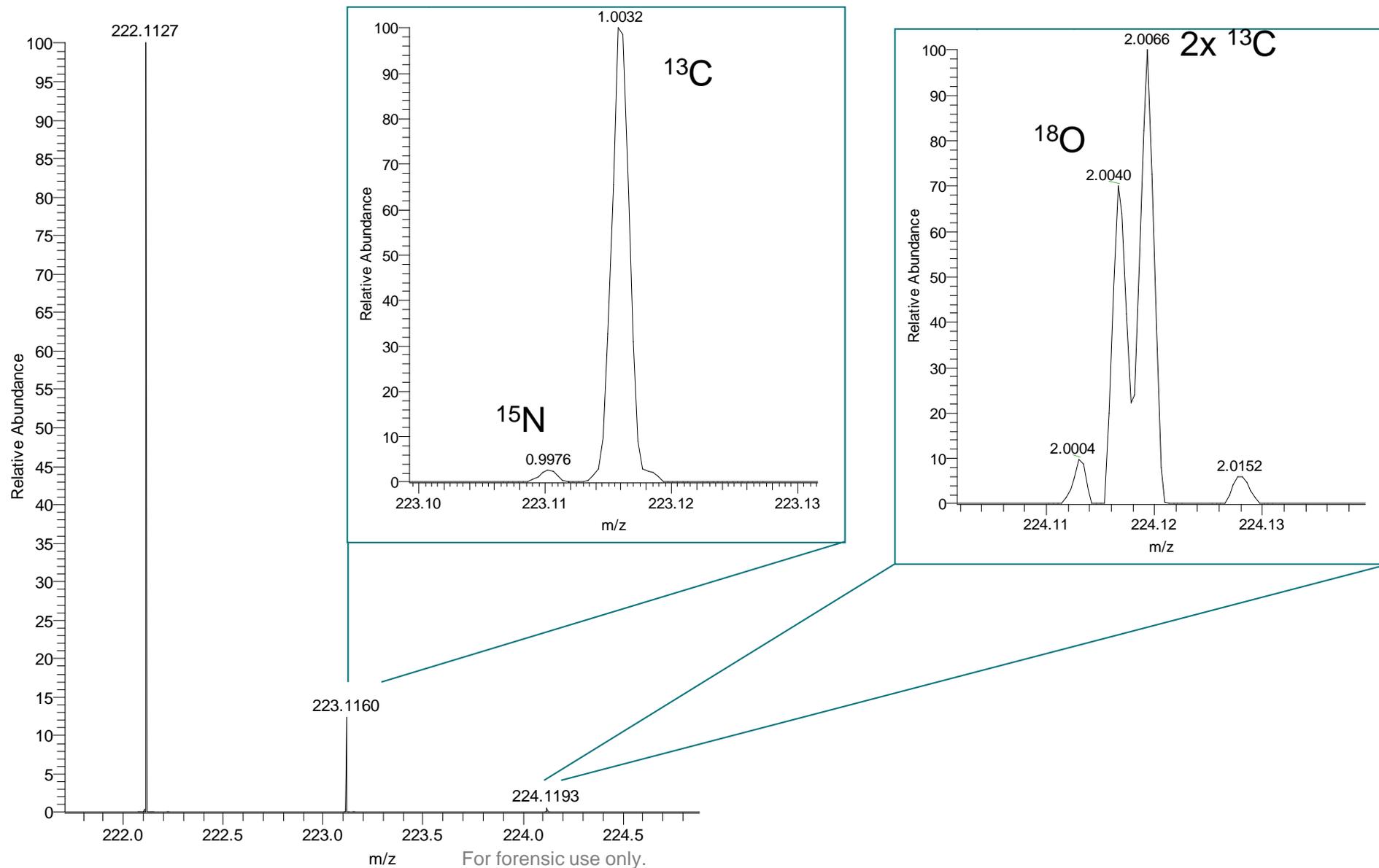
Calculated MW – 221.1054

Search ChemSpider +/- 5ppm

6,435 possibilities

...we still have no clue what this is...

# Going Even Further – Elemental Composition with Very High Resolution



# Elemental Composition – Surely that will help...

Elements in Use

Isotope	Mass	Min	Max
▶ 14 N	14.0031	0	10
▶ 16 O	15.9949	0	15
▶ 12 C	12.0000	0	30
▶ 1 H	1.0078	0	60
▶ 32 S	31.9721	0	10
▶ 35 Cl	34.9689	0	4
▶ 31 P	30.9738	0	10
▶ 19 F	18.9984	0	6

These are real unknown compounds

Must use an 'open' elemental composition set

Can't 'cheat' and artificially limit elements and ranges

Must include fluorine (common synthetic trick to 'hide' designer drugs)

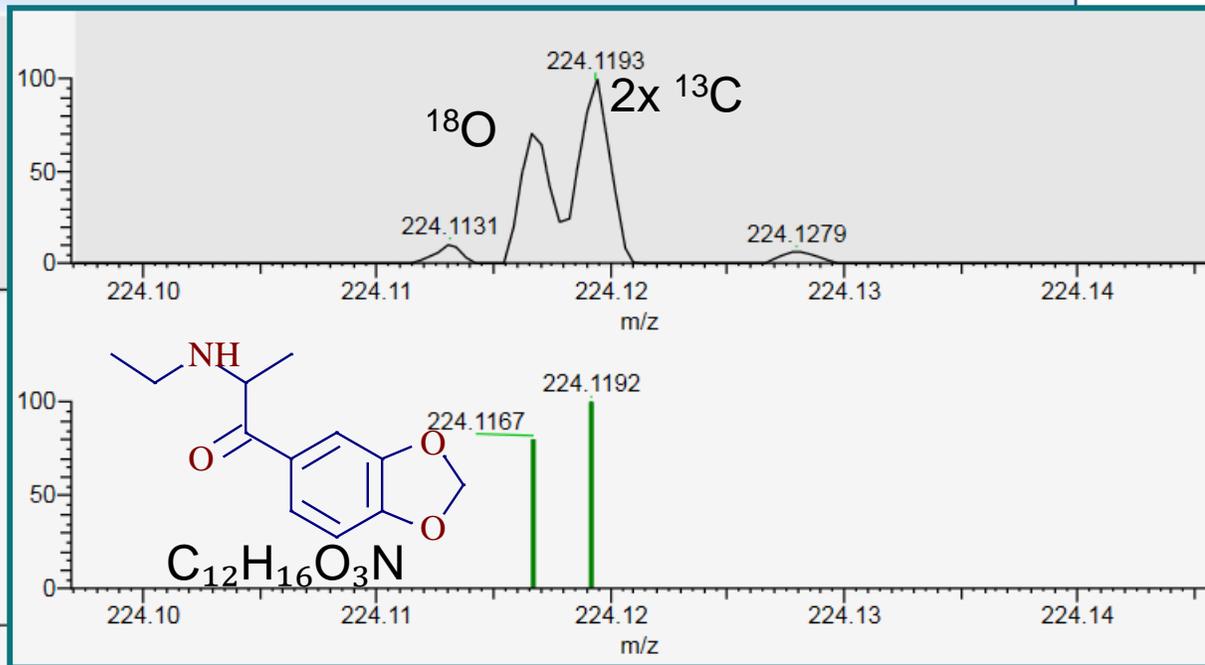
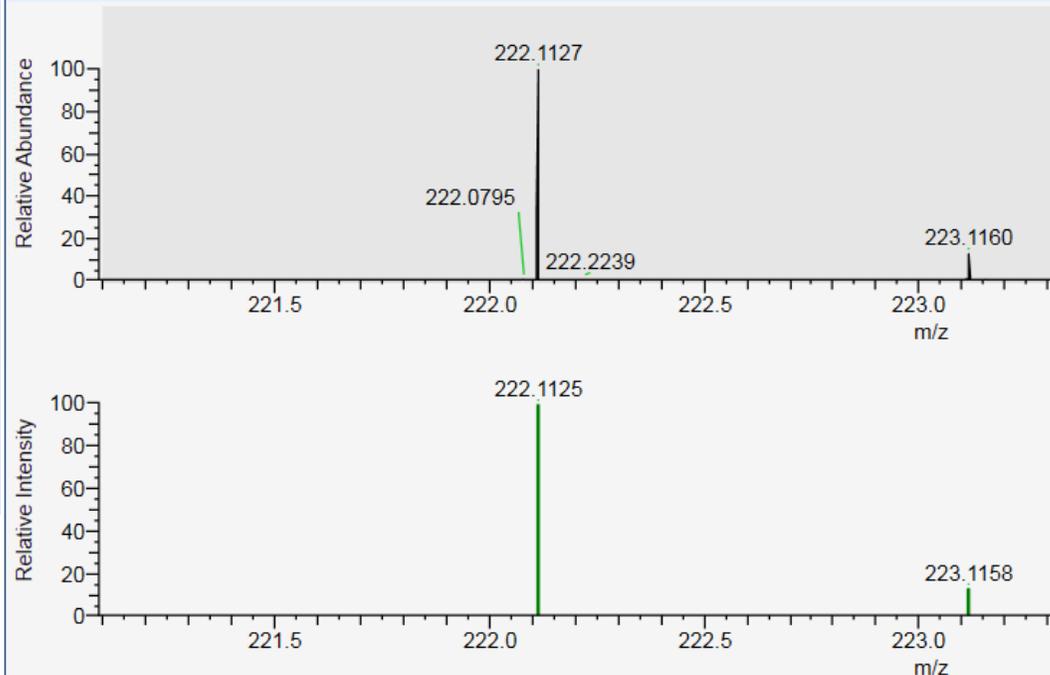
For forensic use only.

# Elemental Composition – Surely that will help...

Workspace 1: 161121\_113342\_C9002749\_H\_ESI\_Pos

Chromatogram 161121\_113342\_C9002749\_H\_ESI\_Pos

Spectrum 1 1 - 161121\_113342\_C9002749\_H\_ESI\_Pos

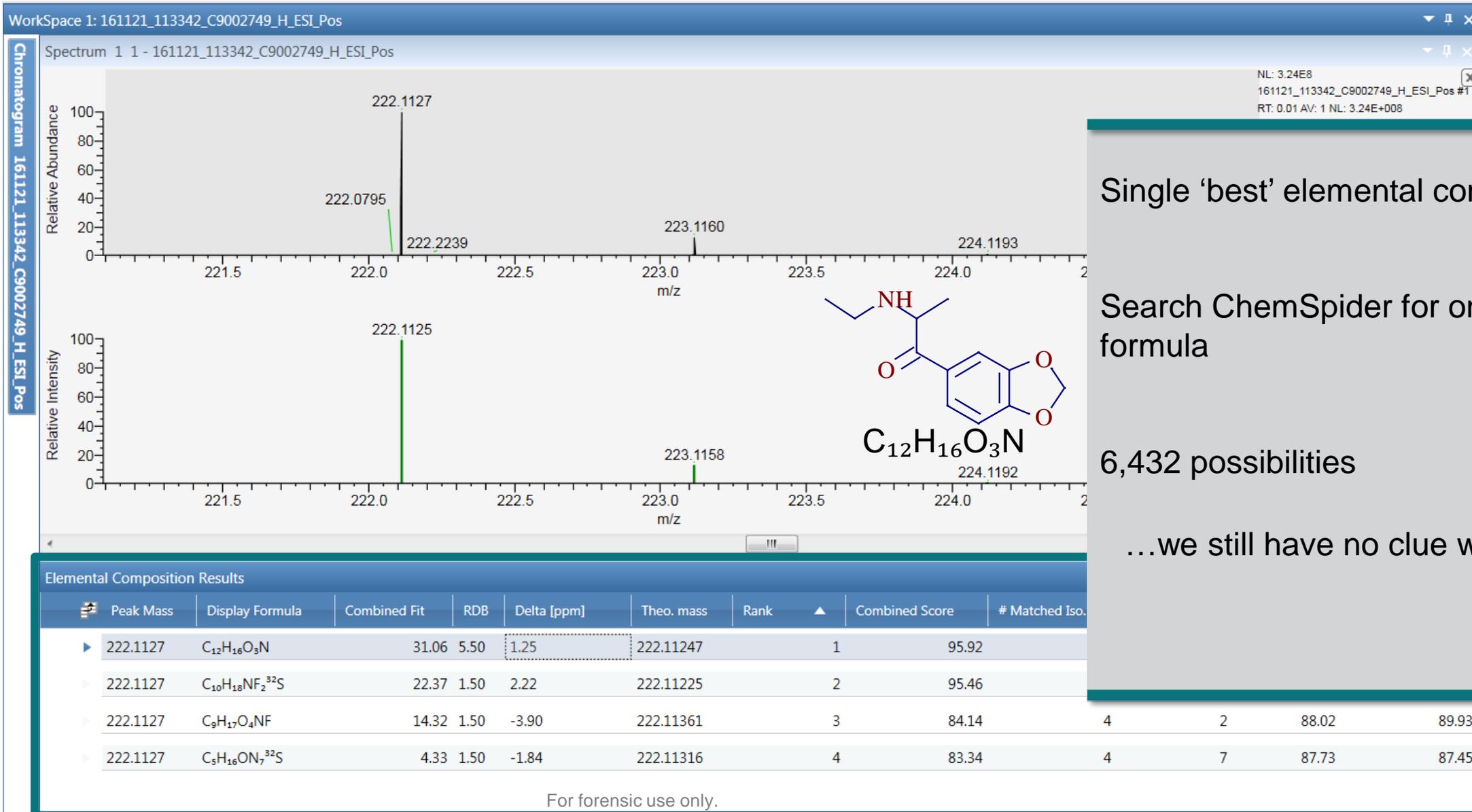


Elemental Composition Results

Peak Mass	Display Formula	Combined Fit	RDB	Delta [ppm]	Theo. mass	Rank	Combined Score	# Matched Iso.	# Missed Iso.	MS Cov. [%]	Pattern Cov. [%]
222.1127	$\text{C}_{12}\text{H}_{16}\text{O}_3\text{N}$	31.06	5.50	1.25	222.11247	1	95.92	5	1	99.52	99.30
222.1127	$\text{C}_{10}\text{H}_{18}\text{NF}_2^{32}\text{S}$	22.37	1.50	2.22	222.11225	2	95.46	4	4	99.52	94.89
222.1127	$\text{C}_9\text{H}_{17}\text{O}_4\text{NF}$	14.32	1.50	-3.90	222.11361	3	84.14	4	2	88.02	89.93
222.1127	$\text{C}_5\text{H}_{16}\text{ON}_7^{32}\text{S}$	4.33	1.50	-1.84	222.11316	4	83.34	4	7	87.73	87.45

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# Elemental Composition – Surely that will help...



Single 'best' elemental composition

Search ChemSpider for only that formula

6,432 possibilities

...we still have no clue what this is...

# What “Identifies” a Compound?

- Molecular weight (Accurate mass)
- Elemental Composition 
- Isotope Ratio
- Fragmentation pattern ( $MS^2$  or  $MS^n$ ) 
- Retention Time

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## Fragmentation Libraries

Integrated solutions for small molecule research applications in LC- HRAM MS



High Quality – Extensive Curation

HRAM MS/MS and MS<sub>n</sub> data

Integrated search with Compound Discoverer



**mzCloud** is a state of the art mass spectral database that assists analysts in identifying compounds in areas such as life sciences, metabolomics, pharmaceutical research, toxicology, forensic investigations, environmental analysis, food control and various industrial applications. mzCloud™ features a freely searchable collection of high resolution/accurate mass spectra using a new third generation spectra correlation algorithm.

Online access to the database is free of charge and no registration is required.

[read more...](#)



Enter  
Database



New mzCloud App!

Search for Compounds by Name or ID

Search

6,845 (+52)  
compounds

10,711 (+77)  
trees

2,398,307 (+29,645)  
spectra

707,074 (+1,194)  
QM models

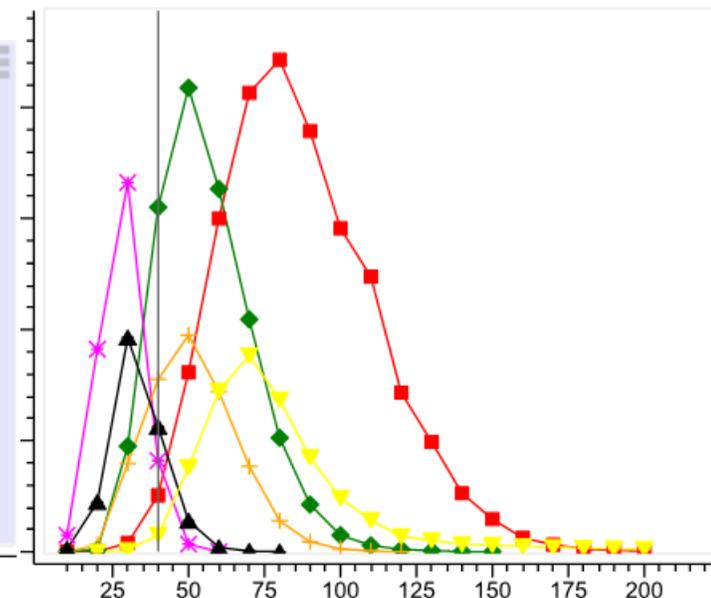
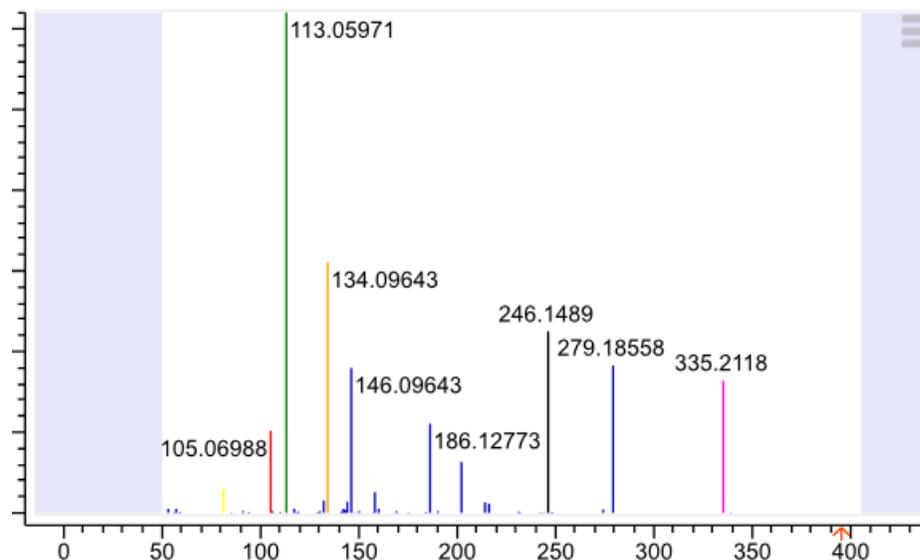
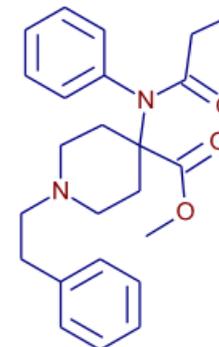
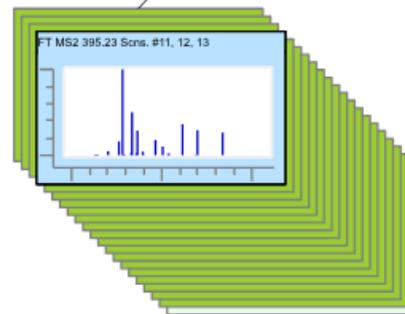
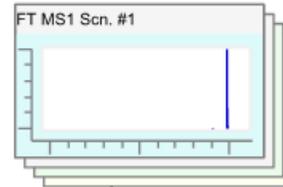
[view more  
statistics](#)

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## Extensive MS/MS and MS<sup>n</sup>

- Dozens to thousands of spectra per compound
- 10-20 Different HCD Energies
- Dynamically optimized trap CID energy
- No limits on how you run your instrument

Filtered Recalibrated



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# Diversity is Critical – Don't Blind your Unknown Analysis

mzCloud contains a wide structure diversity

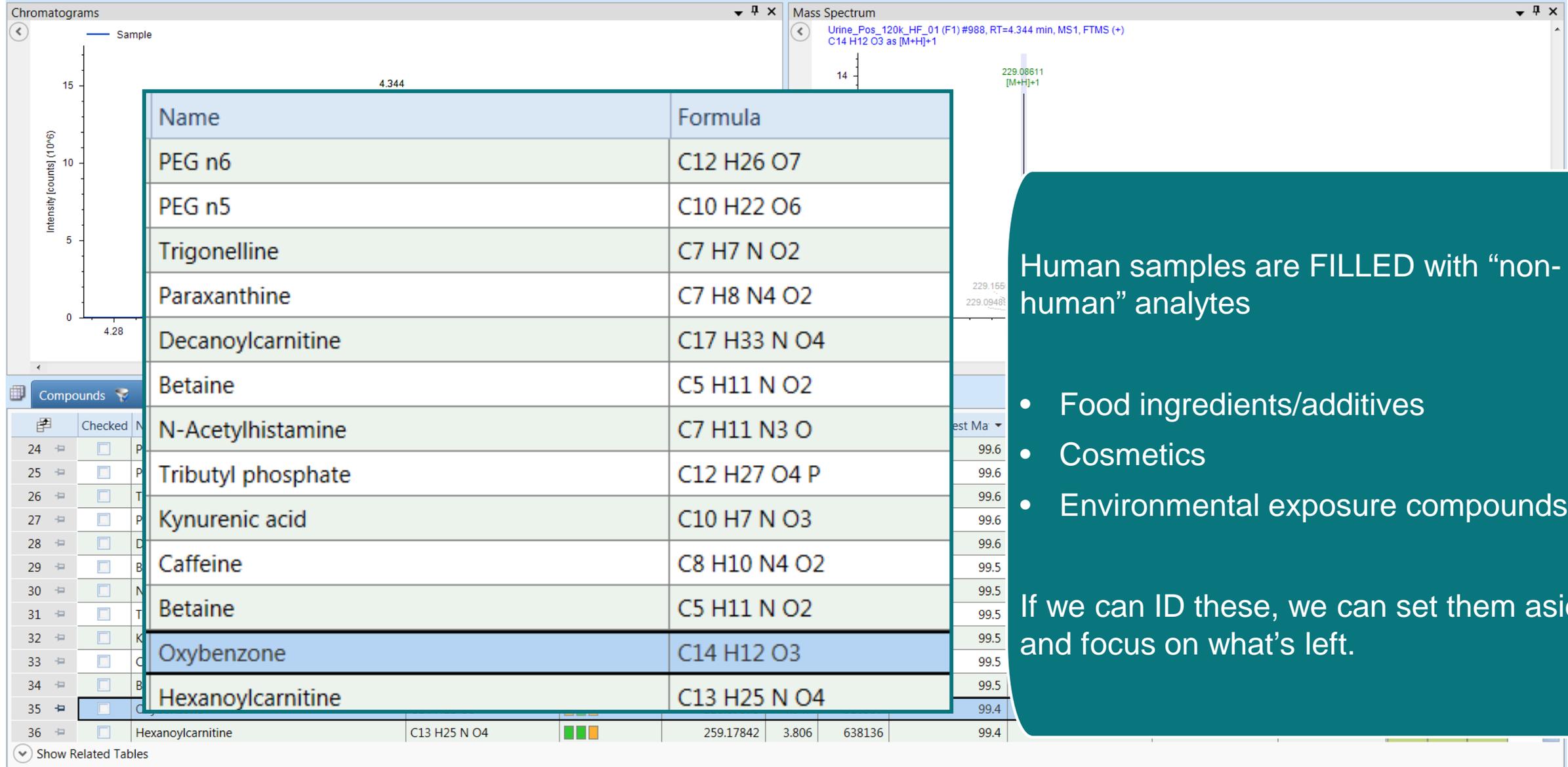
Compounds grouped into sixteen broad categories

“If it ionizes, we put it into mzCloud”

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Therapeutics/Prescription Drugs
Drugs of Abuse/Illegal Drugs
Sports Doping Drugs
Steroids/Vitamins/Hormones
Endogenous Metabolites
Natural Products/Medicines
Natural Toxins
Counterfeit Drug (Therapeutic)
Extractables/Leachables
Pesticides/Herbicides
Excipients/Additives/Colorants
Illegal Additives
Personal Care Products/Cosmetics
Textile Chemicals/Auxiliary/Dyes
Industrial Chemicals
Perflourinated Hydrocarbons

# “The Lineup” - Finding a Suspect by Process of Elimination

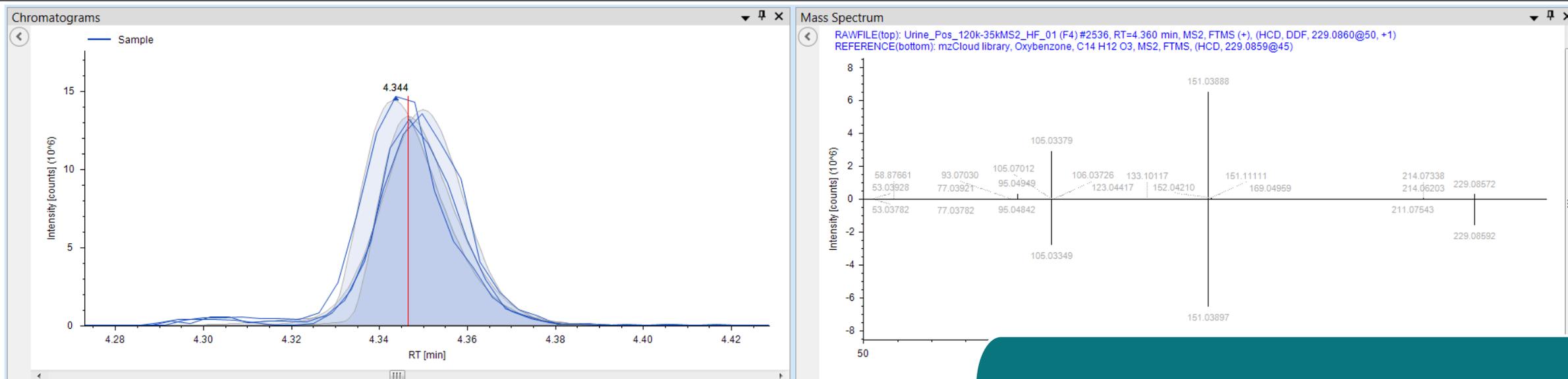


Human samples are FILLED with “non-human” analytes

- Food ingredients/additives
- Cosmetics
- Environmental exposure compounds

If we can ID these, we can set them aside and focus on what’s left.

# “The Lineup” - Finding a Suspect by Process of Elimination



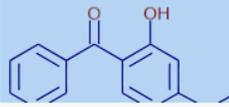
Checked	Name	Formula	Annotation Sc	Molecular Weight	RT [min]	Area (Max.)	mzCloud Bes
<input type="checkbox"/>	Decanoylcarnitine	C17 H33 N O4	■■■	315.24105	5.957	9157928	
<input type="checkbox"/>	Kynurenic acid	C10 H7 N O3	■■■	189.04268	2.926	8911403	
<input type="checkbox"/>	Caffeine	C8 H10 N4 O2	■■■	194.08052	3.117	20415729	
<input type="checkbox"/>	Betaine	C5 H11 N O2	■■■	117.07925	9.221	4173255	
<input checked="" type="checkbox"/>	Oxybenzone	C14 H12 O3	■■■	228.07875	4.347	320937	
<input type="checkbox"/>	Hexanoylcarnitine	C13 H25 N O4	■■■	259.17842	3.806	638136	

Oxybenzone, a sunscreen ingredient

Obviously we don't need to worry about this suspect.

Hide Related Tables

Structure Proposals | Compounds per File | Predicted Compositions | **mzCloud Results** | ChemSpider Results

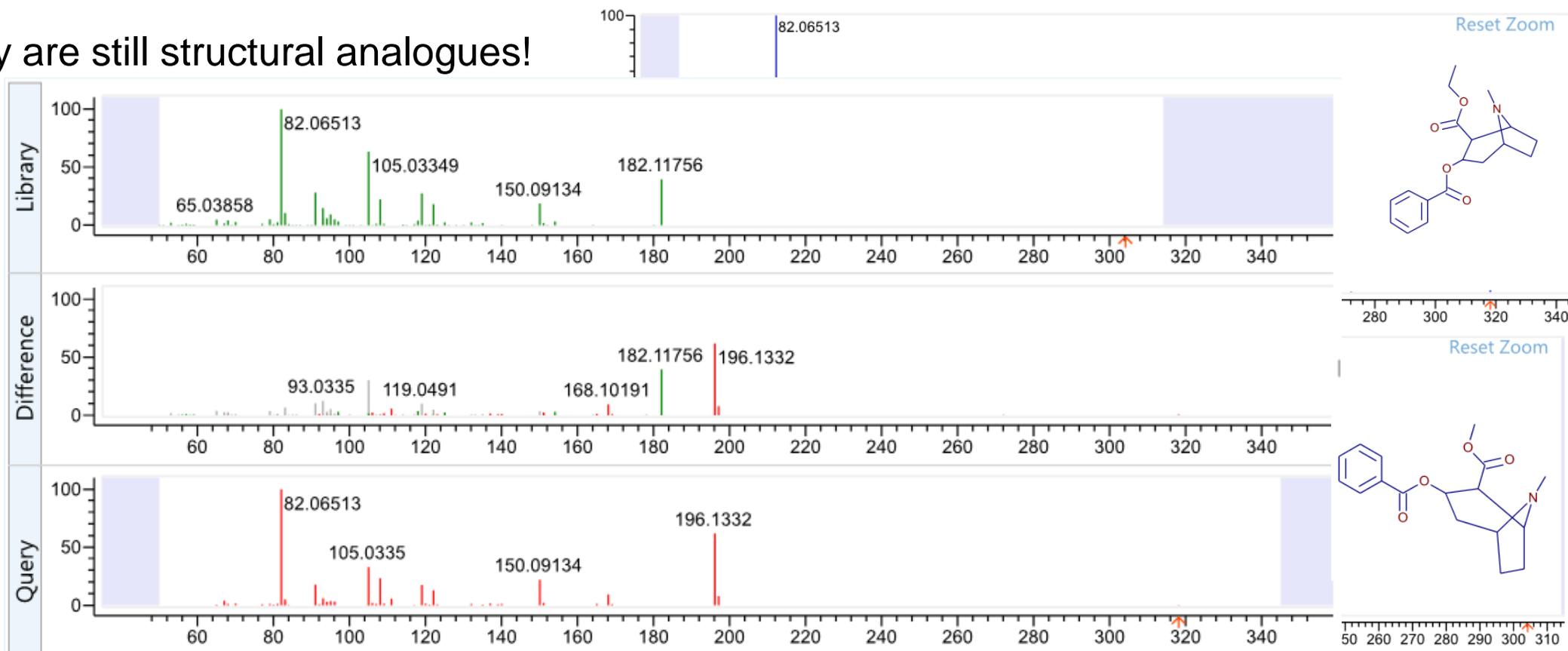
Checked	Compound	Structure	Name	Type	Formula	Best S	Molecular Weight	ΔMass [Da]	ΔMass [ppm]	Scan #	Match	Best Match	mzCloud ID	KEGG ID
<input checked="" type="checkbox"/>	■		Oxybenzone	Identity	C14 H12 O	97.1	228.07864	-0.00011	-0.47	2536	99.4	99.4	<a href="#">863</a>	<a href="#">C14285</a>

Show Related Tables

# Using Libraries more Intelligently – Similarity Searching

- Designer drugs are often synthetic analogues of current compounds.
- Small change in structure = change in MW, formula, RT, and fragments = Totally missed!!

...but, they are still structural analogues!



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# Libraries are for Learning – Not Just ID

**Spectrum search result 1** << Edit search options x

Hit: 1 Best Match: 91.6  
Reference No: 6329  
MDA 2-amido analog  
Monoiso. Mass: 207.08954  
+ Cayman

Hit: 2 Best Match: 90.7  
Reference No: 3061  
3,4-Methylenedioxyamphetamine (MDA)  
Monoiso. Mass: 179.09463  
+ Eawag  
+ Cayman  
+ Cayman

Hit: 3 Best Match: 90.1  
Reference No: 1840  
1-Methylamino-1-(3,4-methylenedioxyphenyl)propane  
Monoiso. Mass: 193.11028  
+ Thermo

Hit: 4 Best Match: 90.0  
Reference No: 5784  
N-Hydroxy MDA  
Monoiso. Mass: 195.08954  
+ Cayman

Hit: 5 Best Match: 89.7  
Reference No: 5364  
2,3-Methylenedioxyamphetamine  
Monoiso. Mass: 179.09463

**Query** FT MS1 Scn. **Library record** Discard Filtered Recalibrated

6/21 FT HCD 60 NCE MS2 208.10 Combined Scans #18, 19, 20 6/21

**Spectra compare** Library Difference Query

**Precursors and Fragment**

MS<sup>1</sup> m/z 208.09683 HCD 60: IW 1  
MS<sup>2</sup>

Blue Structure: Heuristic  
Brown Structure: Quant

Algorithm match  
HighChem HighRes 91.6  
Opt. Dot Product 63.8  
NIST (Modified) 69.2  
-1 M : 0.916197010447319

Library Metadata

Library	Reference No	Best Match	Score
MDA 2-amido analog	6329	91.6	91.6
3,4-Methylenedioxyamphetamine (MDA)	3061	90.7	90.7
1-Methylamino-1-(3,4-methylenedioxyphenyl)propane	1840	90.1	90.1
N-Hydroxy MDA	5784	90.0	90.0
2,3-Methylenedioxyamphetamine	5364	89.7	89.7

m/z	Library	Difference	Query
79.05408			79.05410
95.04898		95.04898	95.04898
105.0697	105.0697	105.0697	105.0697
133.0646		133.0646	133.0646
135.0438	135.0440		135.0438
151.0750		151.0750	151.0750
163.07530	163.0750		163.0750

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# Libraries are for Learning – Not Just ID

**Hit: 1 Best Match: 91.6**  
Reference No: 6329  
**MDA 2-amido analog**  
Monoiso. Mass: 207.08954  
+ Cayman

**Hit: 2 Best Match: 90.7**  
Reference No: 3061  
**3,4-Methylenedioxyamphetamine (MDA)**  
Monoiso. Mass: 179.09463  
+ Eawag  
+ Cayman  
+ Cayman

**Hit: 3 Best Match: 90.1**  
Reference No: 1840  
**1-Methylamino-1-(3,4-methylenedioxyphenyl)propane**  
Monoiso. Mass: 193.11028  
+ Thermo

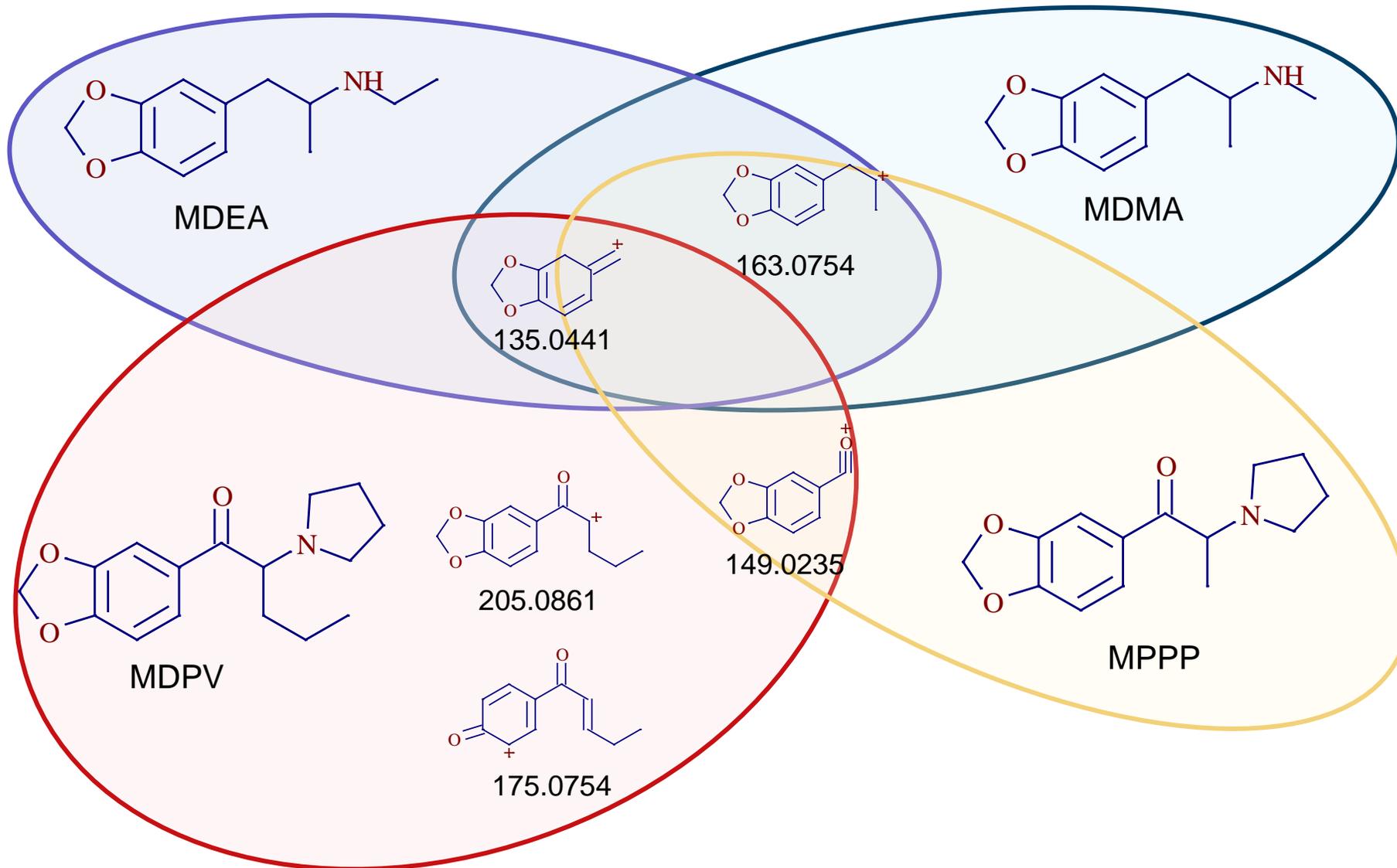
**Hit: 4 Best Match: 90.0**  
Reference No: 5784  
**N-Hydroxy MDA**  
Monoiso. Mass: 195.08954

**All MDA/MDMA analogues with different MW's... suspicious!**

Algorithm	match
HighChem HighRes	91.6
Opt. Dot Product	63.8
NIST (Modified)	69.2

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# Getting Creative – Using What we Know in New Ways

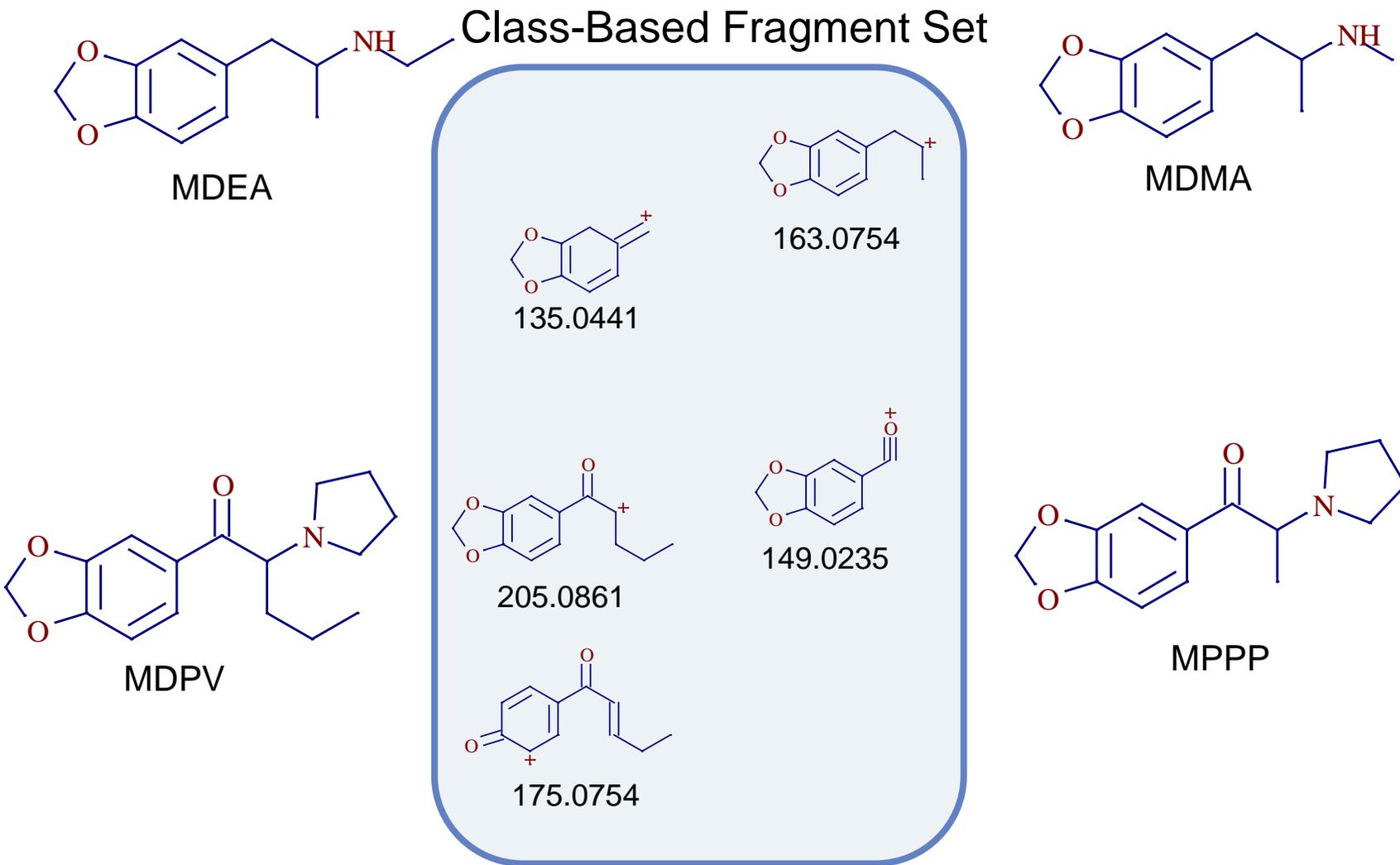


Many new designer drugs are synthetic analogues of existing drugs designed to escape targeted detection

Except for “entirely new” classes of drugs, we know at least a few analogues already.

We can USE that knowledge!

# Compound Class Fragment Ion Searching



Build a representative 'set' of fragment ions from known compounds

Recruit high frequency fragment ions to the fragment set

Use this set of associated fragments to find structurally related analogues

# Using What We Know

Example scenario:

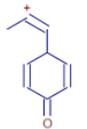
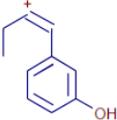
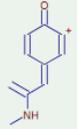
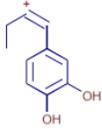
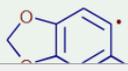
Eight total samples – 4 each for urine and plasma

2 “suspect” samples and 2 “clean” samples for each matrix.

Search for ‘ecstasy-like’ compounds using fragments from known analogues (11 total fragments in the set).

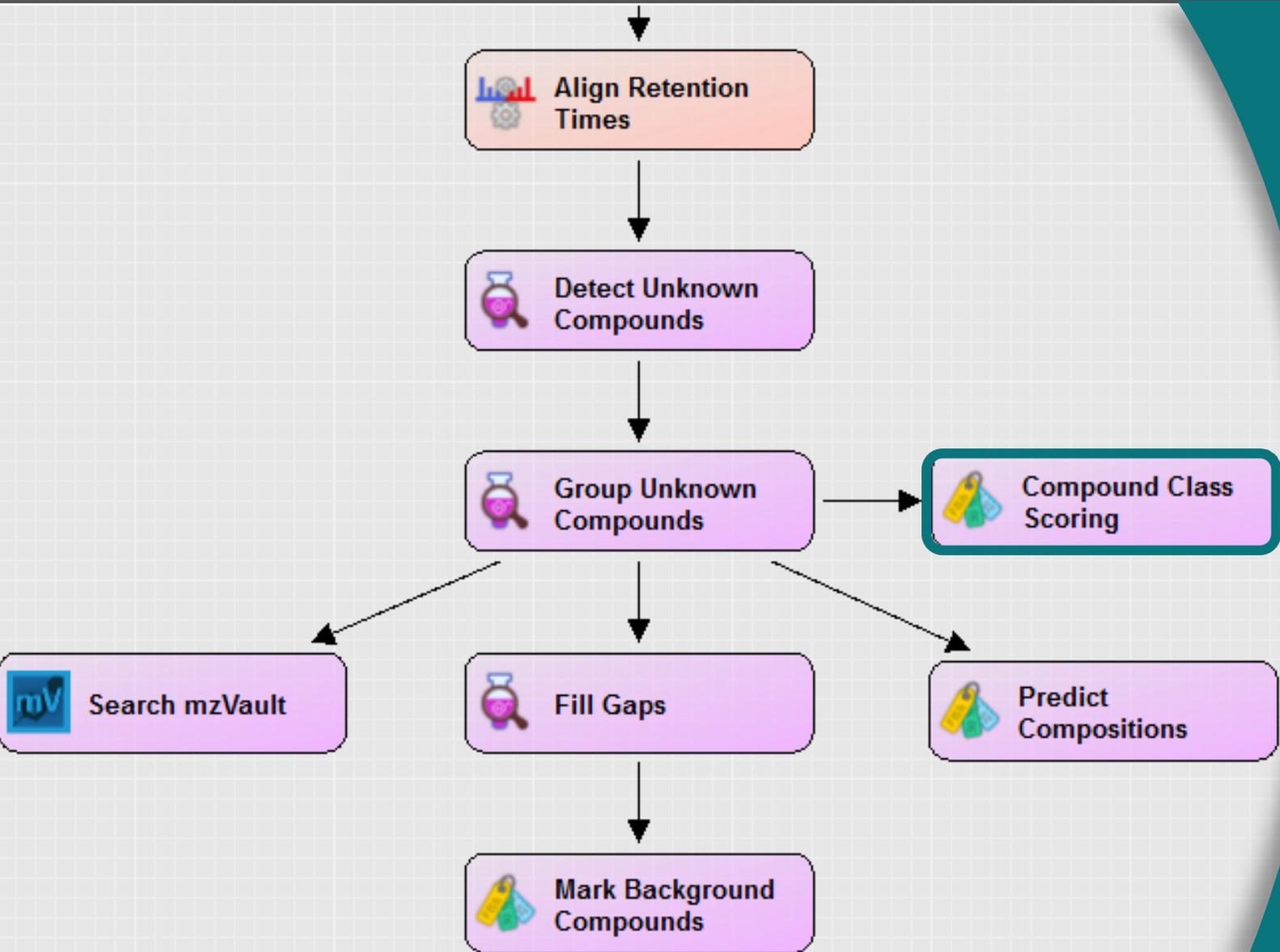
Edit 'Ecstasy Analogues' (11 fragments)

New... Edit... Delete Import

	m/z	Structure	Formula	Charge	Comment
6	133.06479		C9 H9 O	1	
7	135.04406		C8 H7 O2	1	
8	147.08044		C10 H11 O	1	
9	160.07569		C10 H10 N O	1	
10	163.07536		C10 H11 O2	1	
11	175.06370		C10 H9 N O2	1	

OK Cancel

# Our Workflow – Not “unknown” for long...



Combined approach

Unknown detection

Multiple tools

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# Use All the Tools Together – Seeing Everything at Once

Compound Discoverer 2.1.0.398

File Reporting Libraries View Window Help

Start Page x Forensic\_Plasma-Urine\_01cdResult x Urine\_MaxID\_01 x Forensic x

Chromatograms

Matrix: Urine Status: Clean

Matrix: Urine Status: Suspect

2.627

2.776

Mass Spectrum

Urine\_Suspect\_C (F11) #1624, RT=2.614 min, MS2, FTMS (+), (HCD, DDF, 163.0751@(30:60:90), +1)

Ecstasy Analogues, Class Coverage: 54.55

FISH Coverage: 6 Direct, 1 Unmatched, 61 Skipped

Urine (suspect)

Urine (clean)

Formula	Annotation Sc	Molecular Weight	RT [min]	Area (Max.)	Class Coverage	Group Areas	Ratio	Log2 Fold Change
C10 H10 O2		162.06786	2.623	507846	5.45e1	3.33e1	0.792	2.73
C10 H13 N O2		179.09438	2.623	1042395	3.64e1	0.00e0	0.963	2.51
C15 H33 N2 O6 P		368.20900	3.737	73886	9.09e0	0.00e0	1.159	3.38
C8 H24 N5 O2 P S		285.13918	6.397	60296	9.09e0	0.00e0	1.013	2.69
		479.27302	6.126	51365	0.00e0	0.00e0	1.141	2.58
C7 H19 N10 O2 P		306.14372	5.995	213929	0.00e0	0.00e0	0.985	4.09
C35 H78 N5 O8 P		727.55823	8.884	219342	0.00e0	0.00e0	0.761	4.83

8		C19 H42 N9 O5 P	507.30542	5.985	171610	0.00e0	0.00e0	2.93e4	2.60e4	2.94e4	1.48e5	0.886	5.047	-0.18	2.34
9		C29 H61 N10 O4 P	644.46156	9.110	315458	0.00e0	0.00e0	9.02e3	7.48e3	9.58e3	2.98e5	0.829	31.141	-0.27	4.96
10			370.09288	0.248	10136097	0.00e0	0.00e0	1.23e5	3.65e4	6.87e4	2.53e6	0.297	36.858	-1.75	5.20
11		C39 H73 N O8	683.53146	8.985	522785	0.00e0	0.00e0	1.40e4	6.46e3	9.80e3	4.93e5	0.460	50.350	-1.12	5.65
12		C36 H61 N5 O2	595.48082	8.565	734812	0.00e0	0.00e0	4.09e4	1.01e4	1.96e4	2.87e5	0.246	14.651	-2.02	3.87
13		C38 H65 N5 O3	639.50613	9.101	777062	0.00e0	0.00e0	9.15e3	8.22e3	9.56e3	7.17e5	0.899	74.956	-0.15	6.23
14		C8 H11 N O	137.08389	0.652	5545592	0.00e0	0.00e0	1.18e4	7.86e3	8.41e5	4.95e6	0.664	5.881	-0.59	2.56
15		C5 H7 N O3	129.04239	2.546	9062178	0.00e0	0.00e0	1.04e4	5.84e3	1.55e6	8.66e6	0.559	5.585	-0.84	2.48
16			349.28157	8.360	457217			4.91e3	4.42e3	5.12e4	4.18e5	0.899	8.179	-0.15	3.03

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# The New Tool in the Kit – Class Based Searching

Compound Discoverer 2.1.0.398

File Reporting Libraries View Window Help

Start Page x Forensic\_Plasma-Urine\_01cdResult x Urine\_MaxID\_01 x Forensic x

Chromatograms

Mass Spectrum

Urine\_Suspect\_C (F11)#1624, RT=2.614 min, MS2, FTMS (+), (HCD, DDF, 163.0751@(30;60;90), +1)  
Ecstasy Analogues, Class Coverage: 54.55  
FISH Coverage: 6 Direct, 1 Unmatched, 61 Skipped

Checked	Name	Formula	Annotation Sc	Molecular Weight	RT [min]	Area (Max.)	Class Coverage	Group Areas	Ratio	Log2 Fold Change		
<input type="checkbox"/>		C10 H10 O2		162.06786	2.623	507846	5.45e1	7.34e3, 5.81e3, 9.64e3, 6.39e4	0.792	6.617	-0.34	2.73
<input type="checkbox"/>		C10 H13 N O2		179.09438	2.623	1042395	3.64e1	8.12e3, 7.82e3, 4.01e4, 2.28e5	0.963	5.696	-0.05	2.51
<input type="checkbox"/>		C15 H33 N2 O6 P		368.20900	3.737	73886	9.09e0	1.90e3, 2.20e3, 6.06e3, 6.30e4	1.159	10.407	0.21	3.38

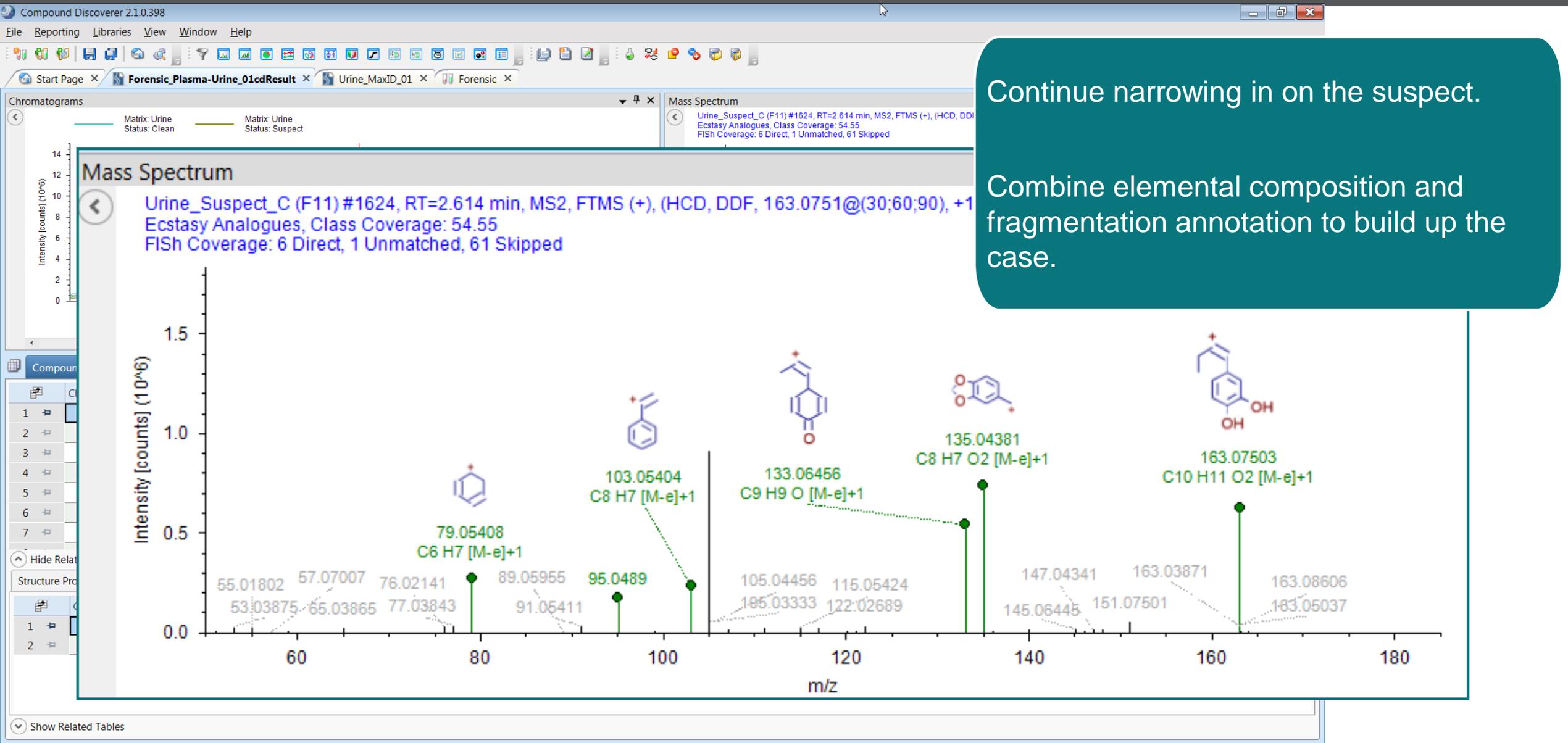
Structure Proposals	Compounds per File	Predicted Compositions	Merged Features	Compound Class Matches	mzVault Results	
Checked	Name	Description	FISH Coverage	Class Coverage	# Matched Frag.	# Missed Frag.
<input type="checkbox"/>	Ecstasy Analogues	Ecstasy Analogues	85.71	54.55	6	5
<input type="checkbox"/>	Cathinone (simple)	Simple cathinones, alkylated and ha	14.29	33.33	1	2

Show Related Tables

Bring in more tools – Class Based score

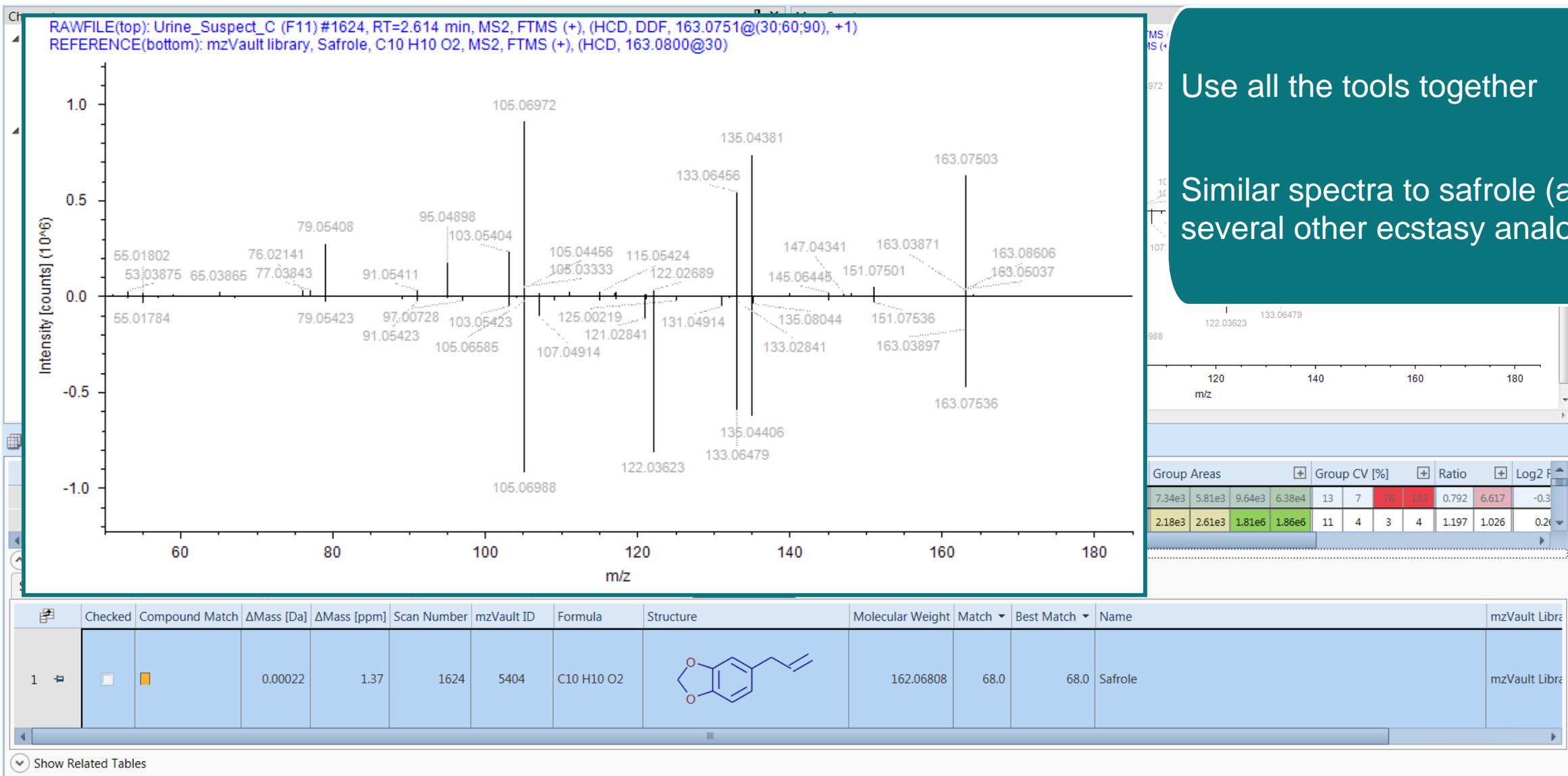
Suspect compound has a 55% class score.

# The New Tool in the Kit – Class Based Searching



For forensic use only.

# Use All the Tools Together – Seeing Everything at Once



Use all the tools together

Similar spectra to safrole (and several other ecstasy analogues)

For forensic use only.



## Combine Multiple Tools

- Untargeted Detection and Differential Analysis
- Similarity Searching
- Class-Based Peak Annotation



## Compound Discoverer

Integrated solutions for small  
molecule structure identification

thermo  
scientific

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### Compound Discoverer 2.1 Released! Get your Demo here.

JUL 31 Posted by [Tim Stratton](#)

#### For current Compound Discoverer 2.0 users:

The electronic upgrade to Compound Discoverer 2.1 is free! Follow the download instructions below and use the instructions for the CD 2.0 to CD 2.1 upgrade.

#### For new users:

To download the Compound Discoverer 2.1 Demo (CD 2.1 demo), go to the Thermo Scientific Software Portal (Flexera) and download it from the "Compound Discoverer 2.1 Demo" folder.

[CLICK HERE FOR FULL INSTRUCTIONS.](#)

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### Compound Discoverer at ASMS 2017

APR 14 Posted by [Tim Stratton](#)

Thanks to everyone who was able to join us at this years Compound Discoverer Users Meeting and parallel Node Developer Workshop at ASMS this year!

Thank you.